

FIG. 1A

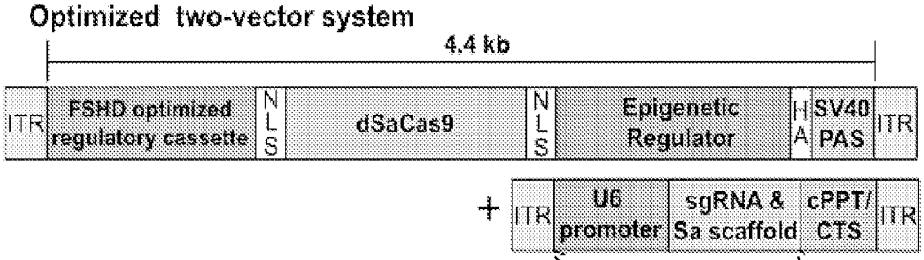


FIG. 1B

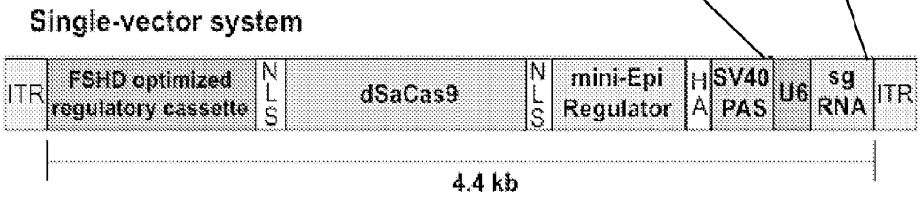


FIG. 1C

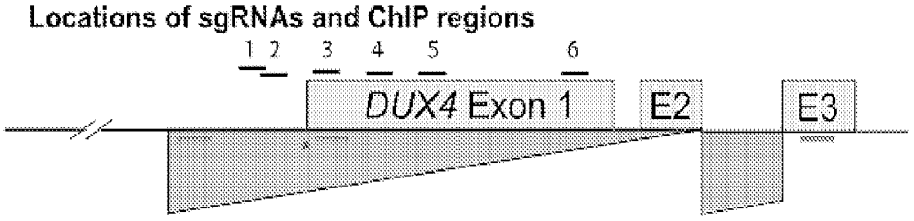


FIG. 1D

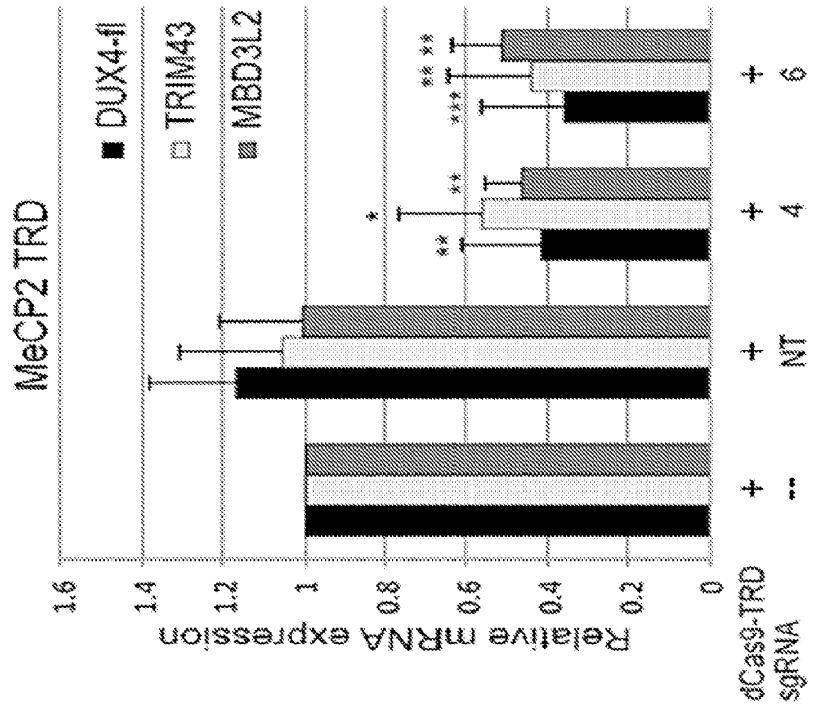

MeCP2 TRD
DUX4-fl
TRIM43
MBD3L2
Relative mRNA expression
1.6
1.4
1.2
1
0.8
0.6
0.4
0.2
0
dCas9-TRD
sgRNA
+ -- + NT + 4 + 6

FIG. 2B

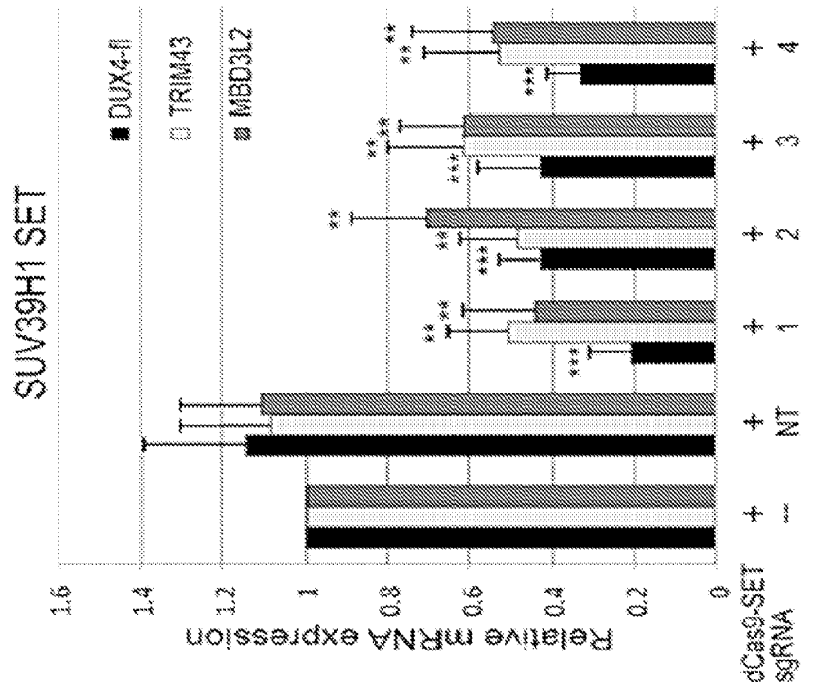

SUV39H1 SET
DUX4-fl
TRIM43
MBD3L2
Relative mRNA expression
1.6
1.4
1.2
1
0.8
0.6
0.4
0.2
0
dCas9-SET
sgRNA
+ -- + NT + 1 + 2 + 3 + 4

FIG. 2A

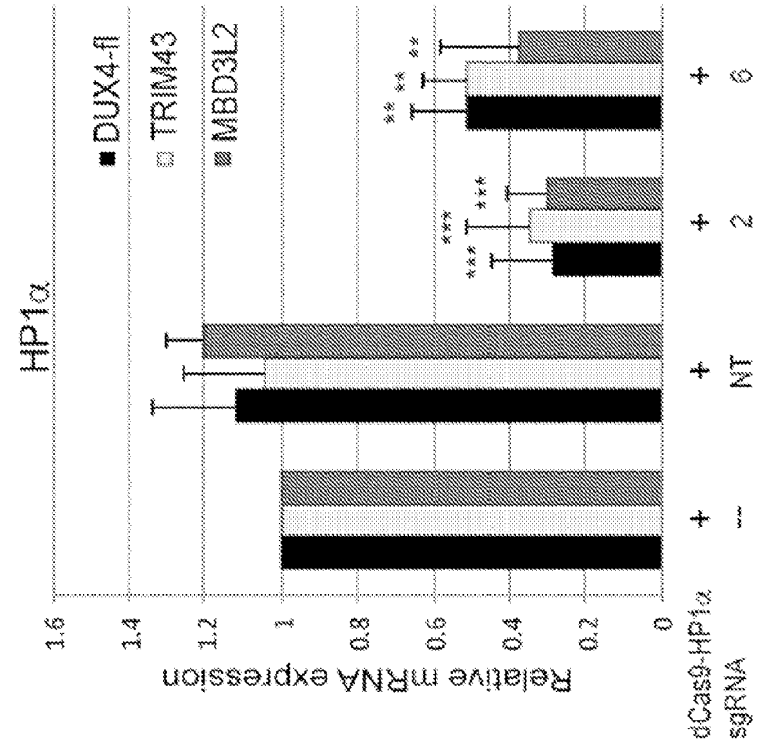

HP1α
DUX4-fl
TRIM43
MBD3L2
Relative mRNA expression
1.6
1.4
1.2
1
0.8
0.6
0.4
0.2
0
dCas9-HP1α
sgRNA
+
–
+
NT
+
2
+
6
**
***
**

FIG. 2D

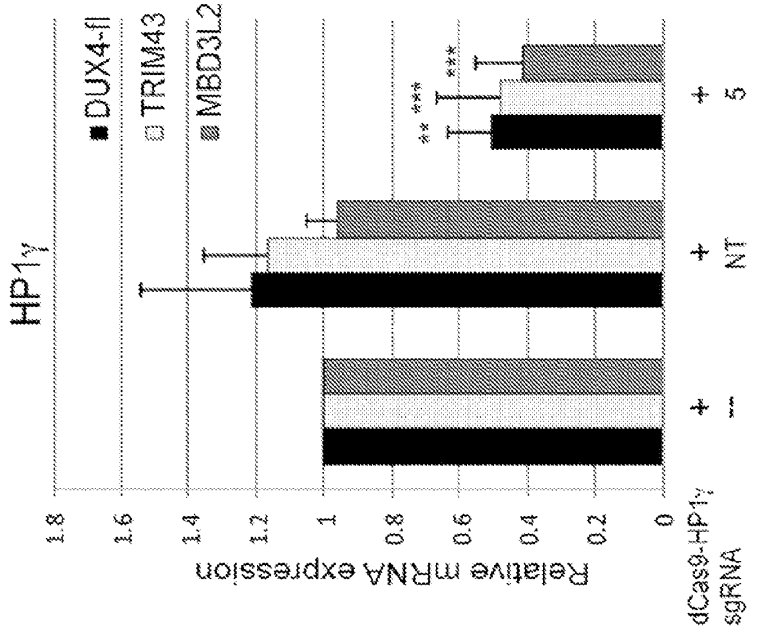

HP1γ
DUX4-fl
TRIM43
MBD3L2
Relative mRNA expression
1.8
1.6
1.4
1.2
1
0.8
0.6
0.4
0.2
0
dCas9-HP1γ
sgRNA
+
–
+
NT
+
5
**
***
***

FIG. 2C

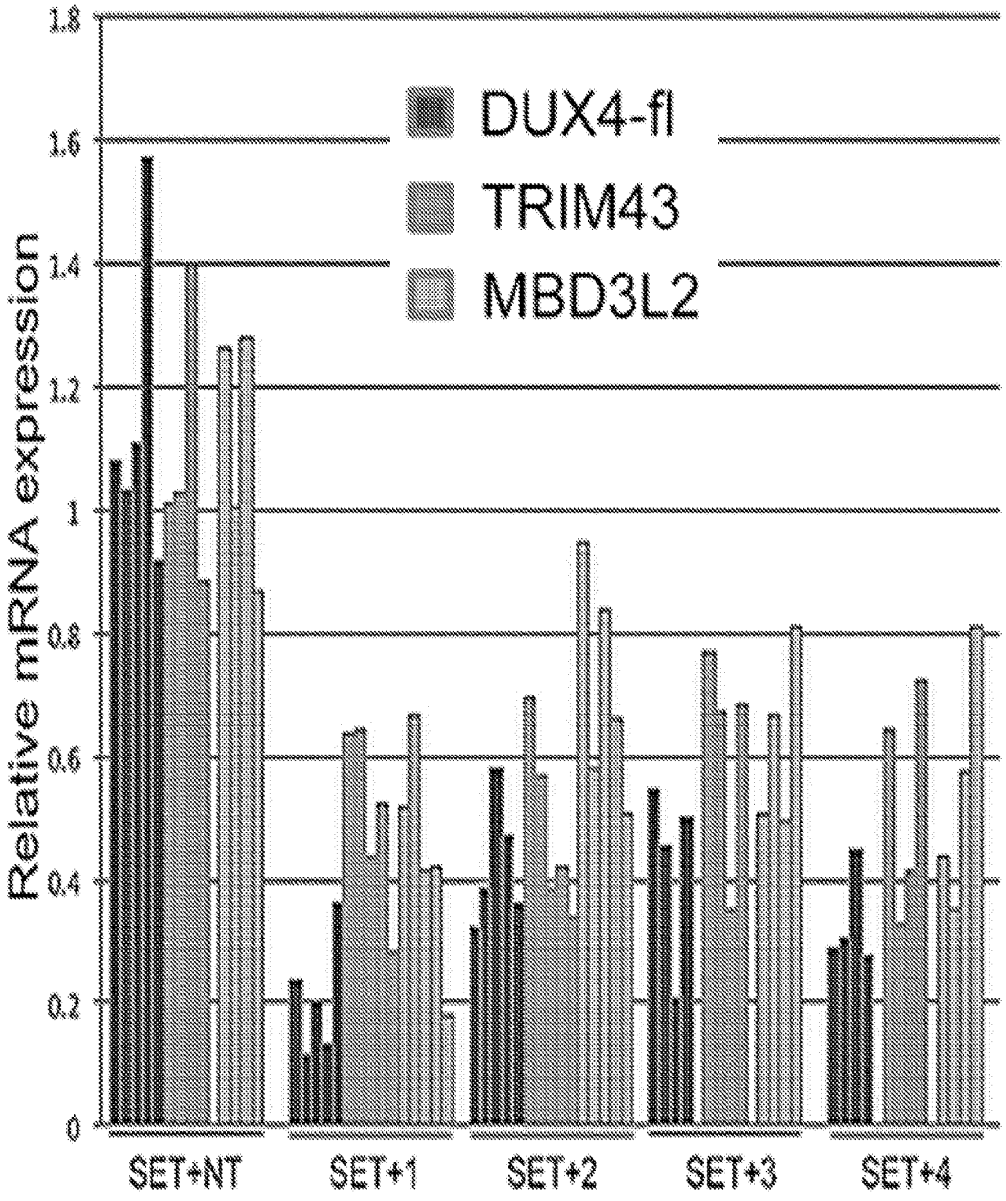

1.8
1.6
1.4
1.2
1
0.8
0.6
0.4
0.2
0
Relative mRNA expression
DUX4-fl
TRIM43
MBD3L2
SET+NT
SET+1
SET+2
SET+3
SET+4

FIG. 3A

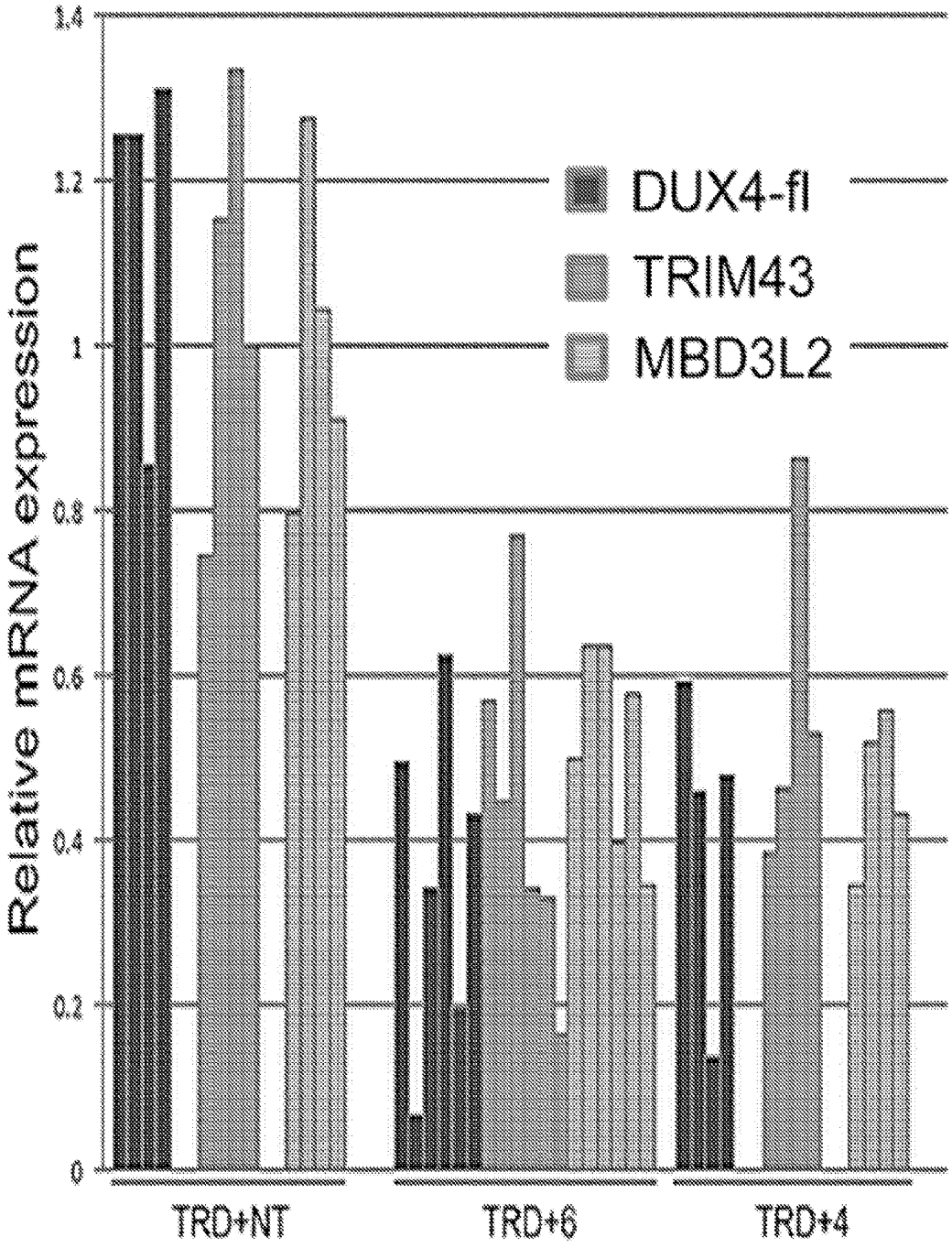

1.4
1.2
1
0.8
0.6
0.4
0.2
0
Relative mRNA expression
DUX4-fl
TRIM43
MBD3L2
TRD+NT
TRD+6
TRD+4

FIG. 3B

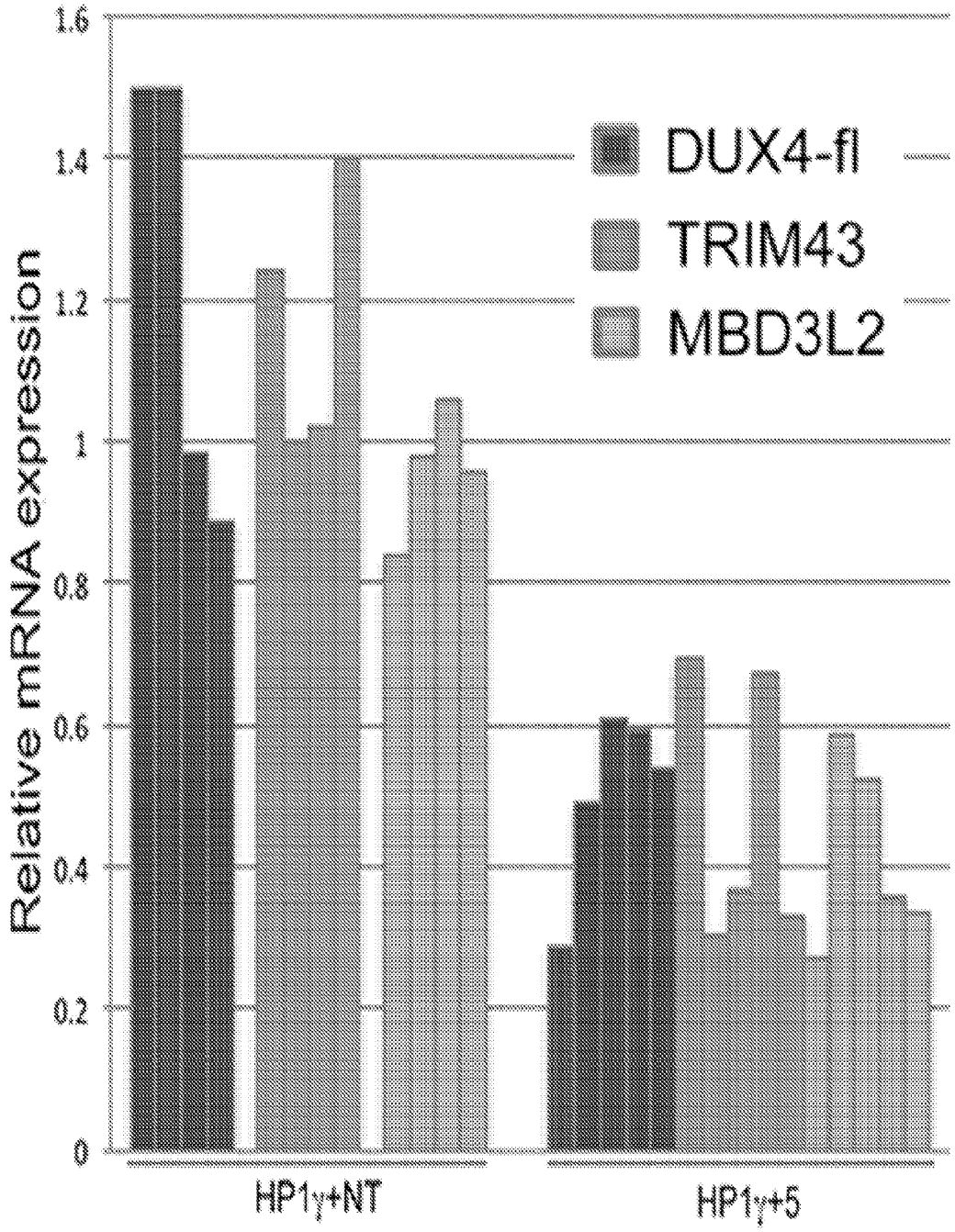

Relative mRNA expression
1.6
1.4
1.2
1
0.8
0.6
0.4
0.2
0
DUX4-fl
TRIM43
MBD3L2
HP1γ+NT
HP1γ+5

FIG. 3C

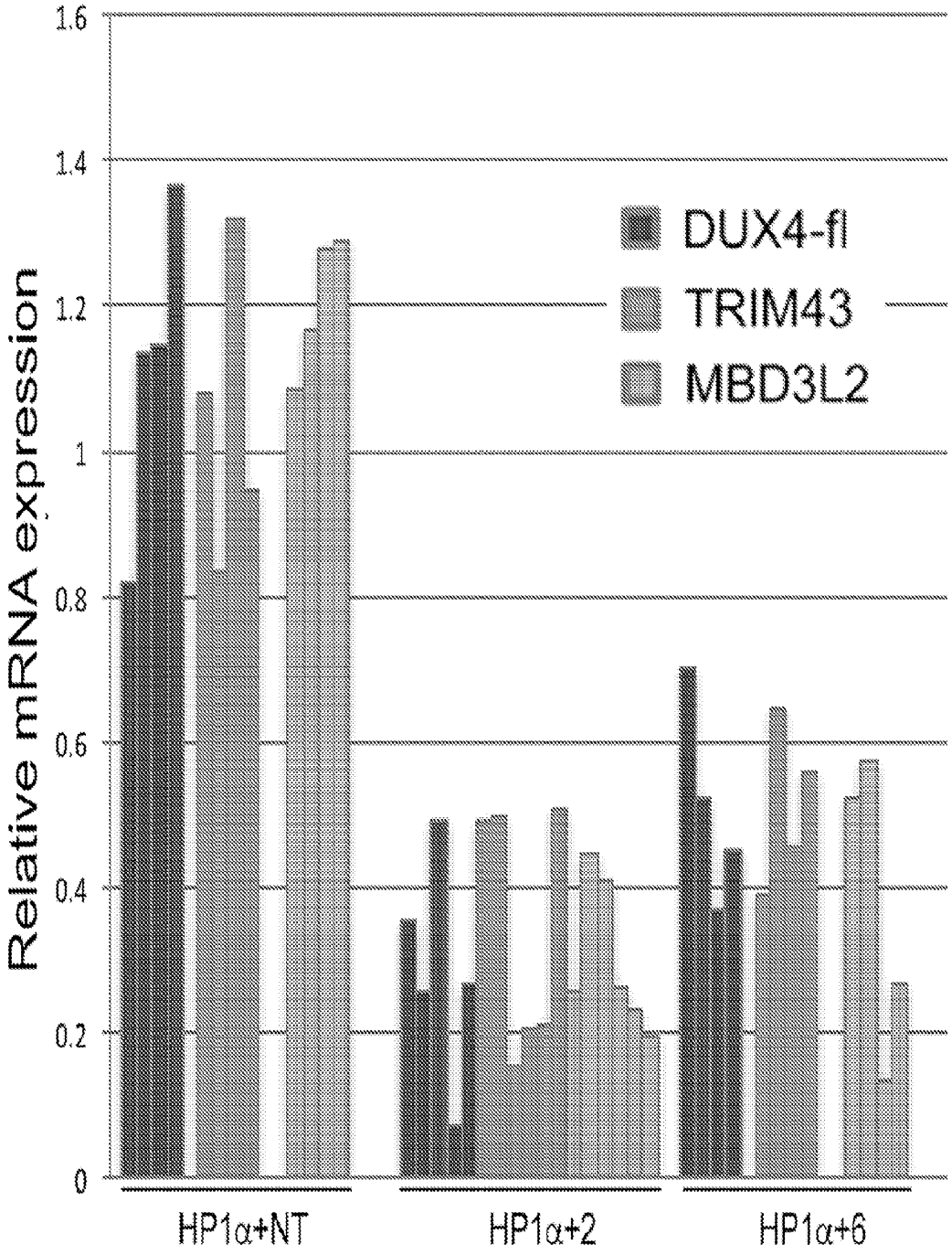

1.6
1.4
1.2
1
0.8
0.6
0.4
0.2
0
Relative mRNA expression
DUX4-fl
TRIM43
MBD3L2
HP1α+NT
HP1α+2
HP1α+6

FIG. 3D

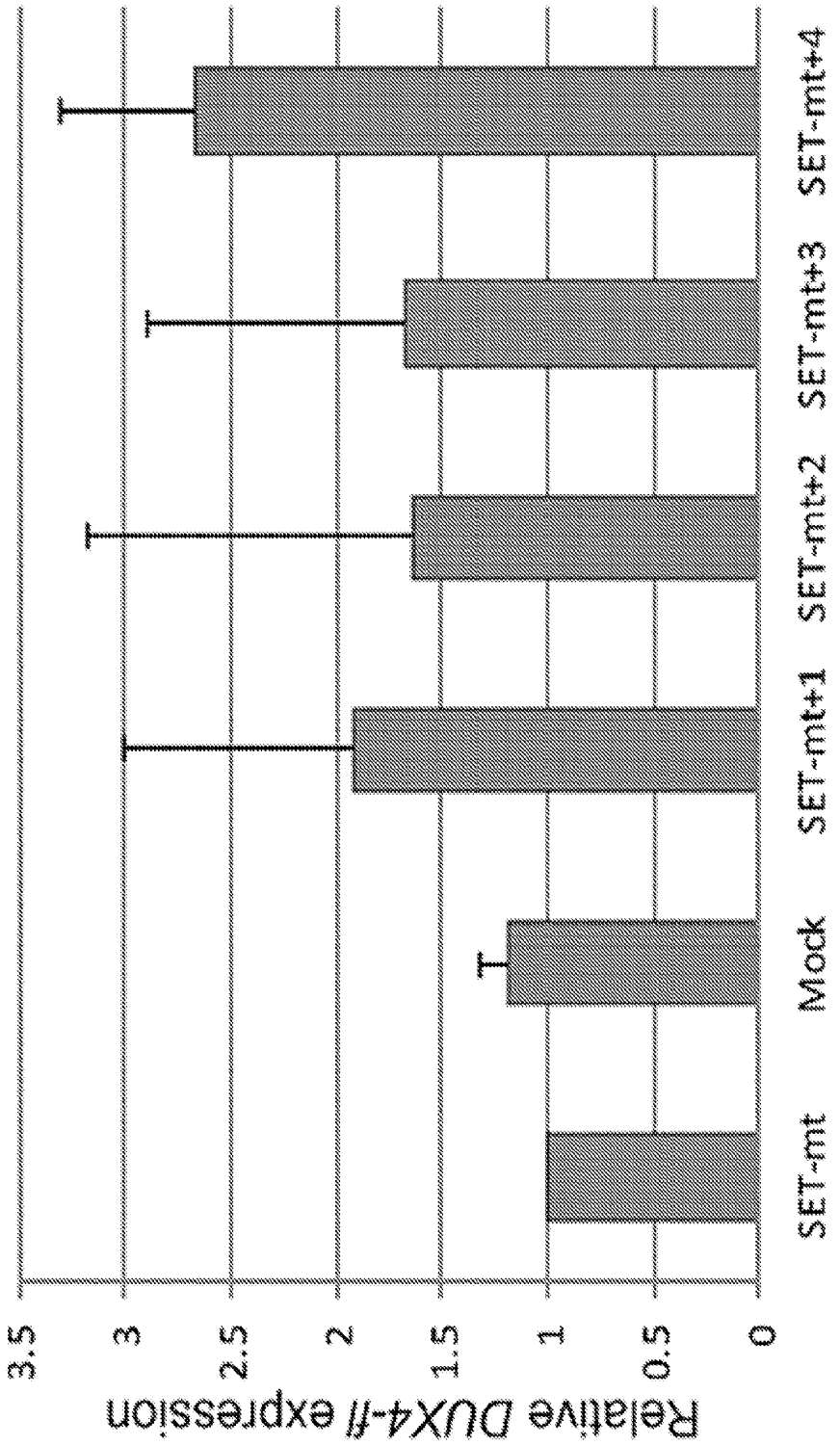

Relative DUX4-fl expression
3.5
3
2.5
2
1.5
1
0.5
0
SET-mt
Mock
SET-mt+1
SET-mt+2
SET-mt+3
SET-mt+4

FIG. 4A

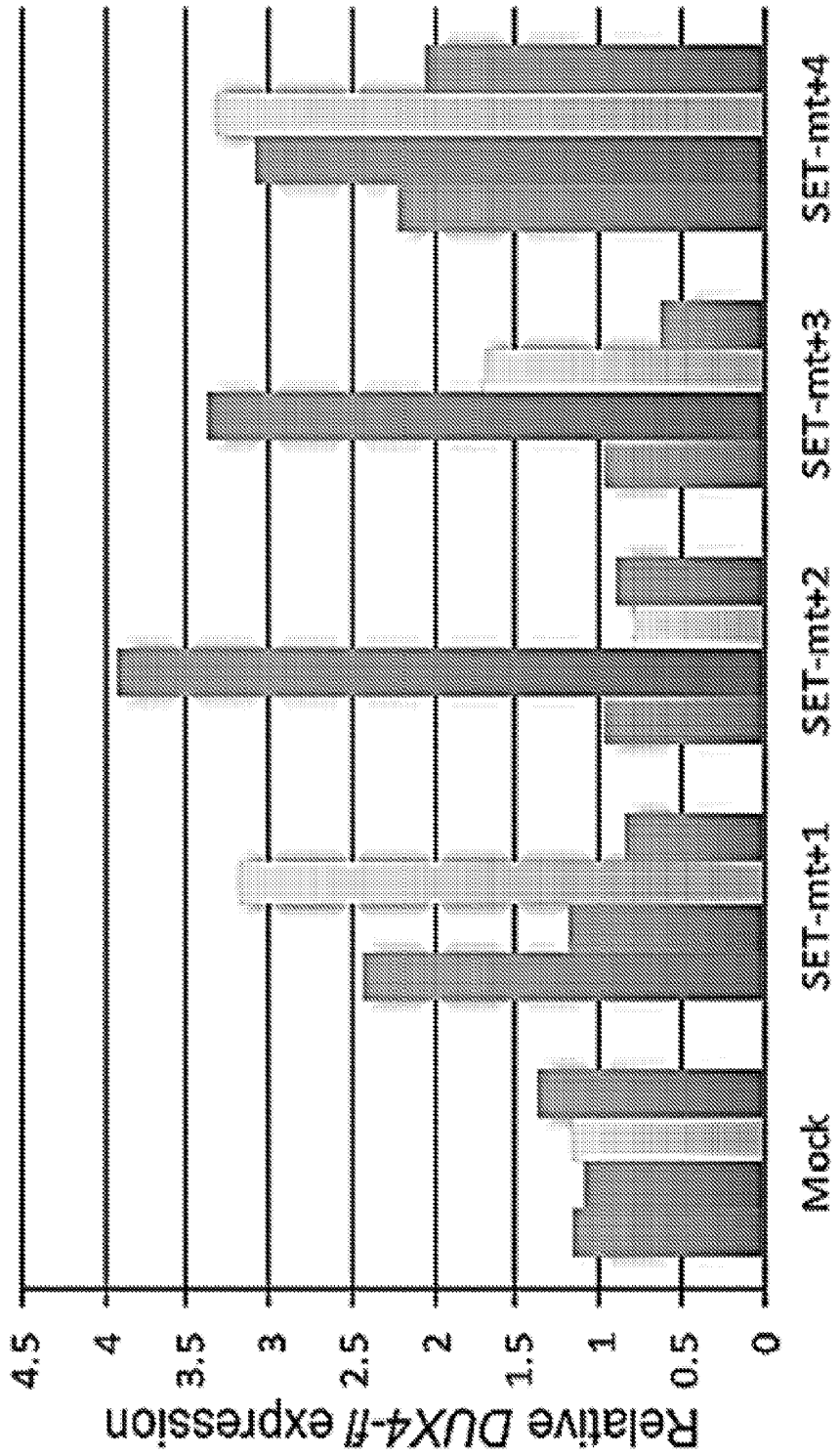

Relative DUX4-fl expression
4.5
4
3.5
3
2.5
2
1.5
1
0.5
0
Mock
SET-mt+1
SET-mt+2
SET-mt+3
SET-mt+4

FIG. 4B

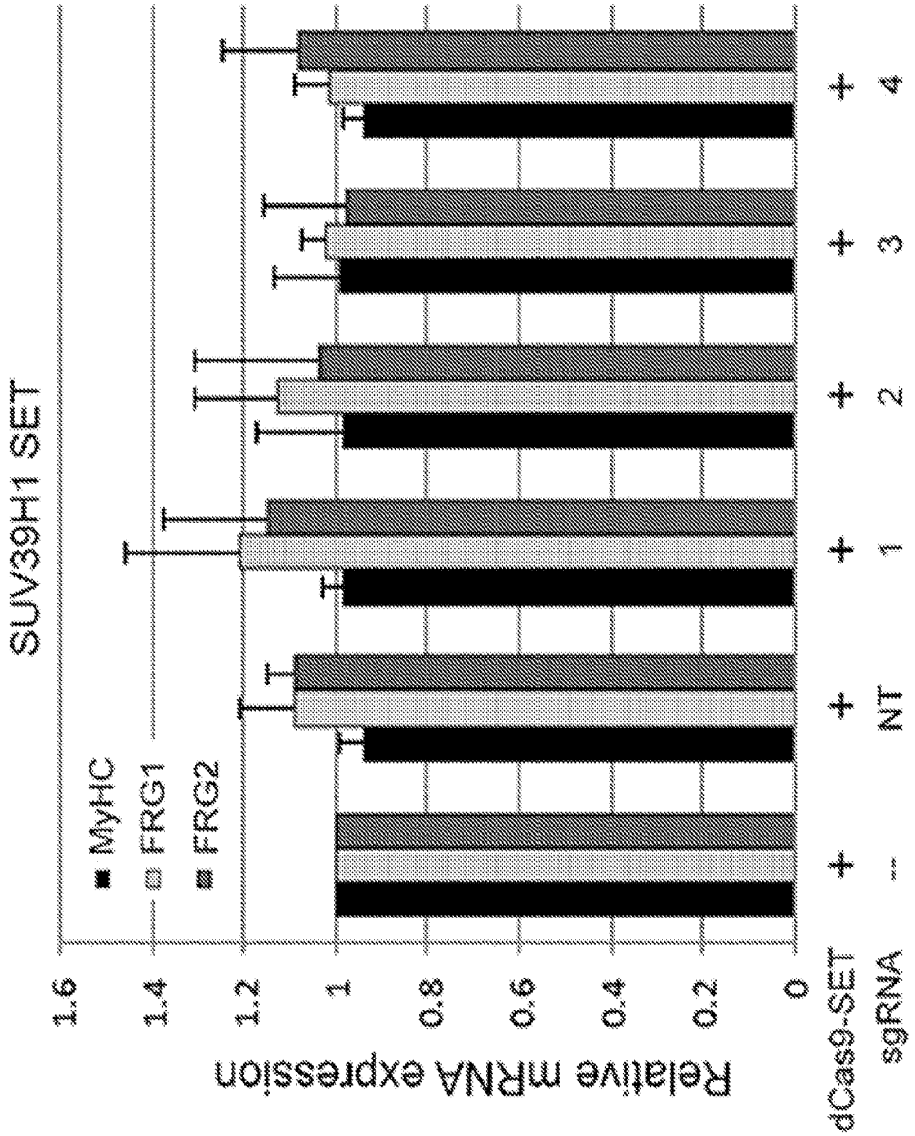

SUV39H1 SET
MyHC
FRG1
FRG2
Relative mRNA expression
1.6
1.4
1.2
1
0.8
0.6
0.4
0.2
0
dCas9-SET
sgRNA
-
+
NT
1
2
3
4

FIG. 5A

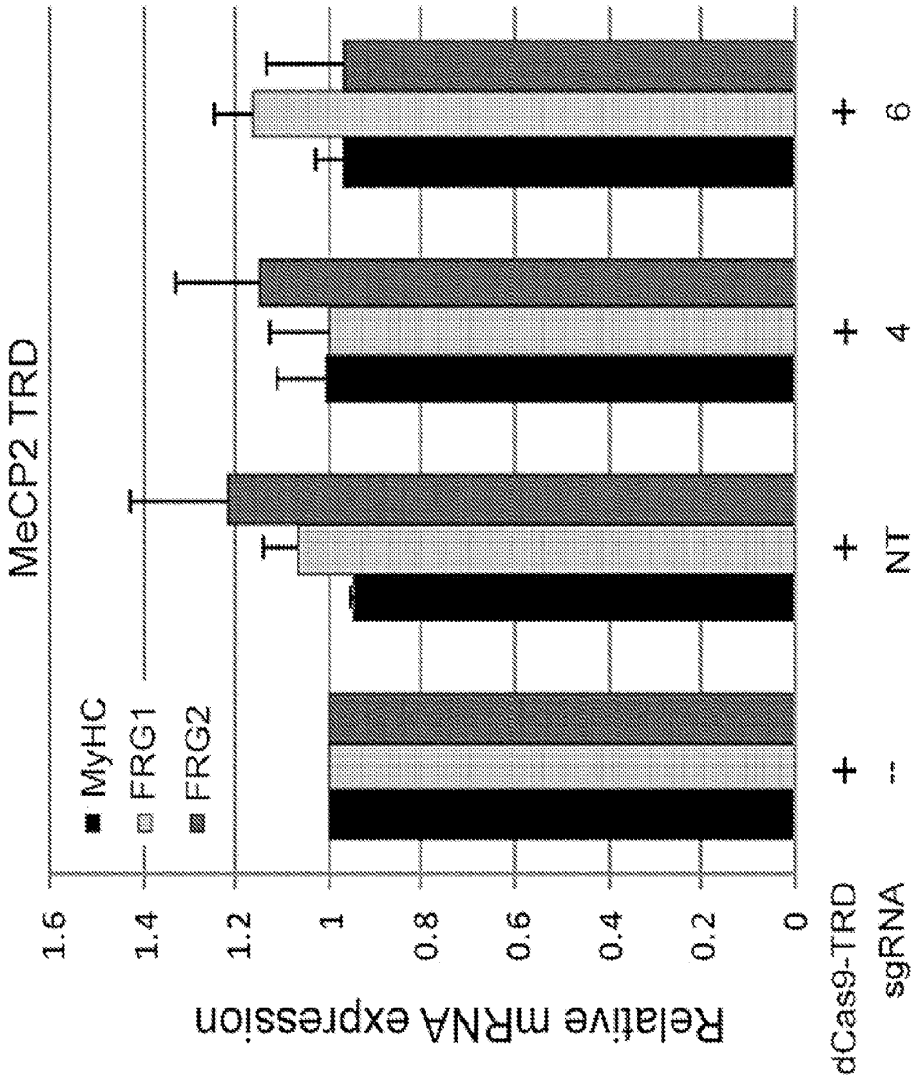

MeCP2 TRD
MyHC
FRG1
FRG2
Relative mRNA expression
1.6
1.4
1.2
1
0.8
0.6
0.4
0.2
0
dCas9-TRD
sgRNA
+
-
+
NT
+
4
+
6

FIG. 5B

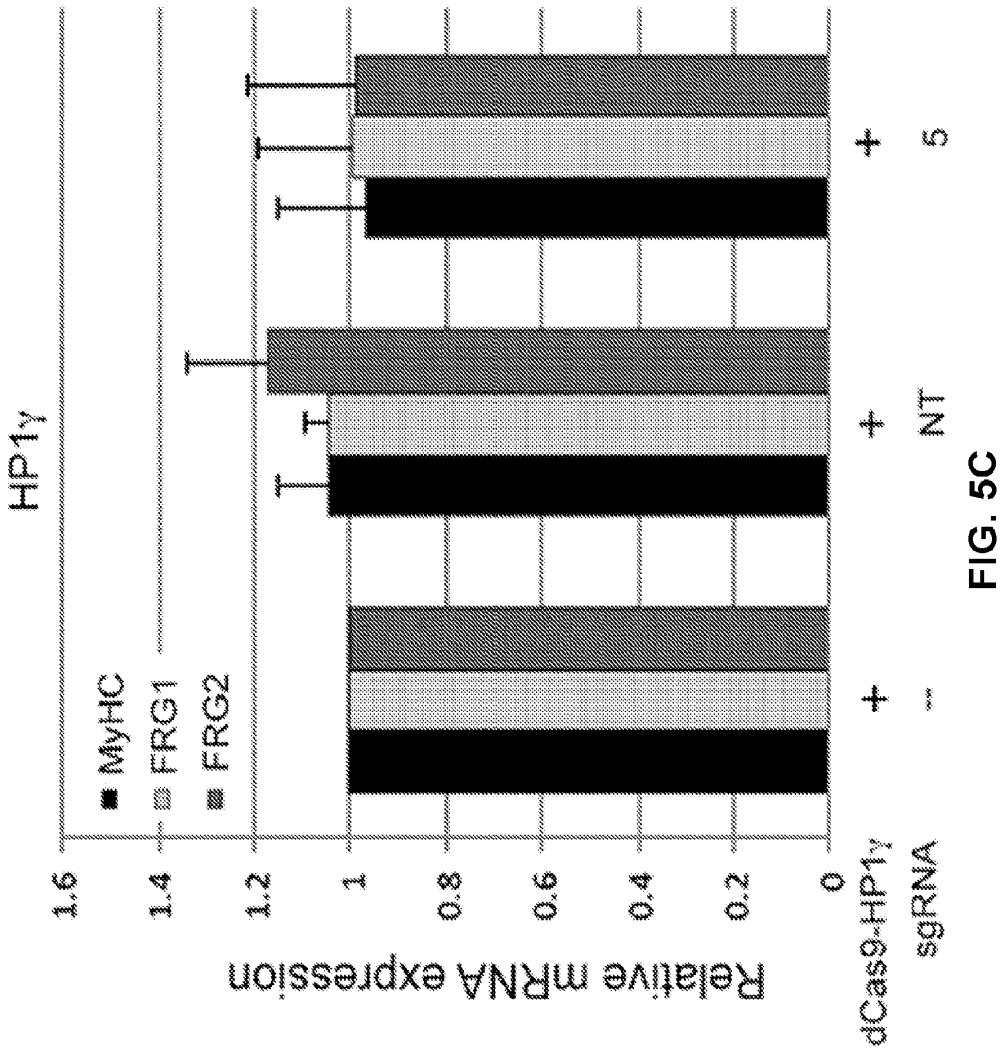

HP1γ
MyHC
FRG1
FRG2
Relative mRNA expression
1.6
1.4
1.2
1
0.8
0.6
0.4
0.2
0
dCas9-HP1γ
sgRNA
+
-
+
NT
+
5

FIG. 5C

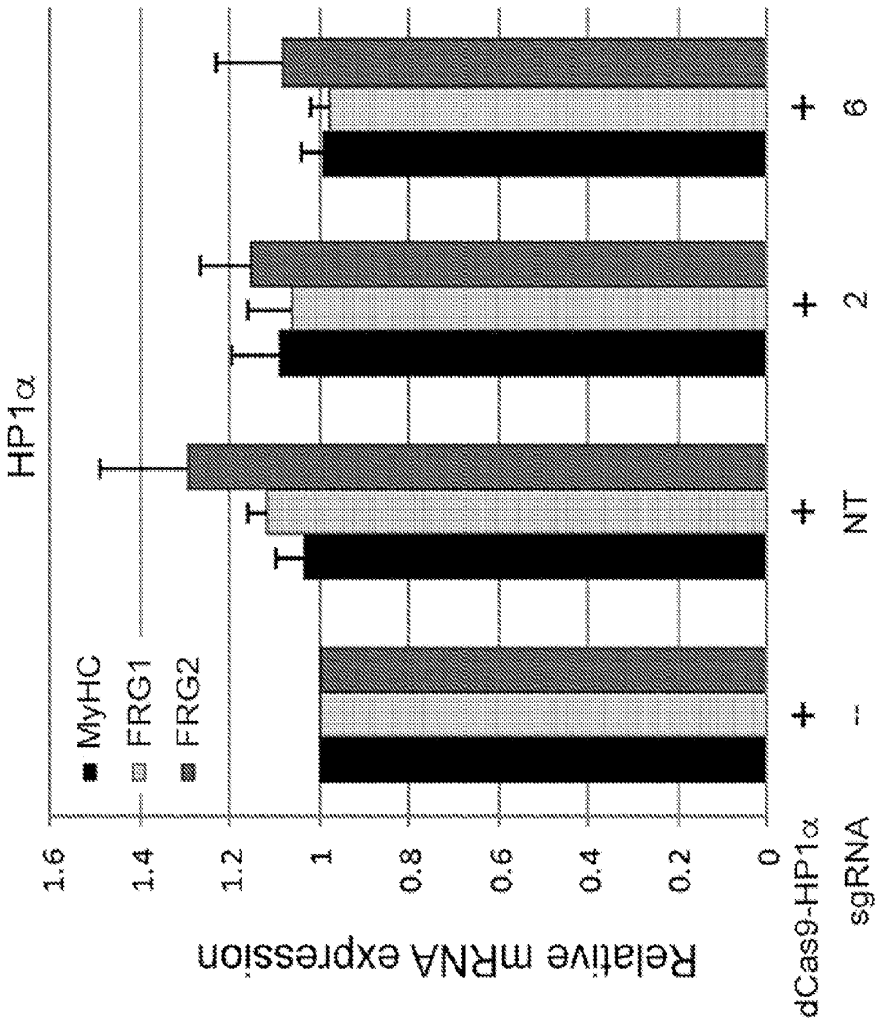

HP1α
MyHC
FRG1
FRG2
Relative mRNA expression
1.6
1.4
1.2
1
0.8
0.6
0.4
0.2
0
dCas9-HP1α
sgRNA
+
–
+
+
+
NT
2
6

FIG. 5D

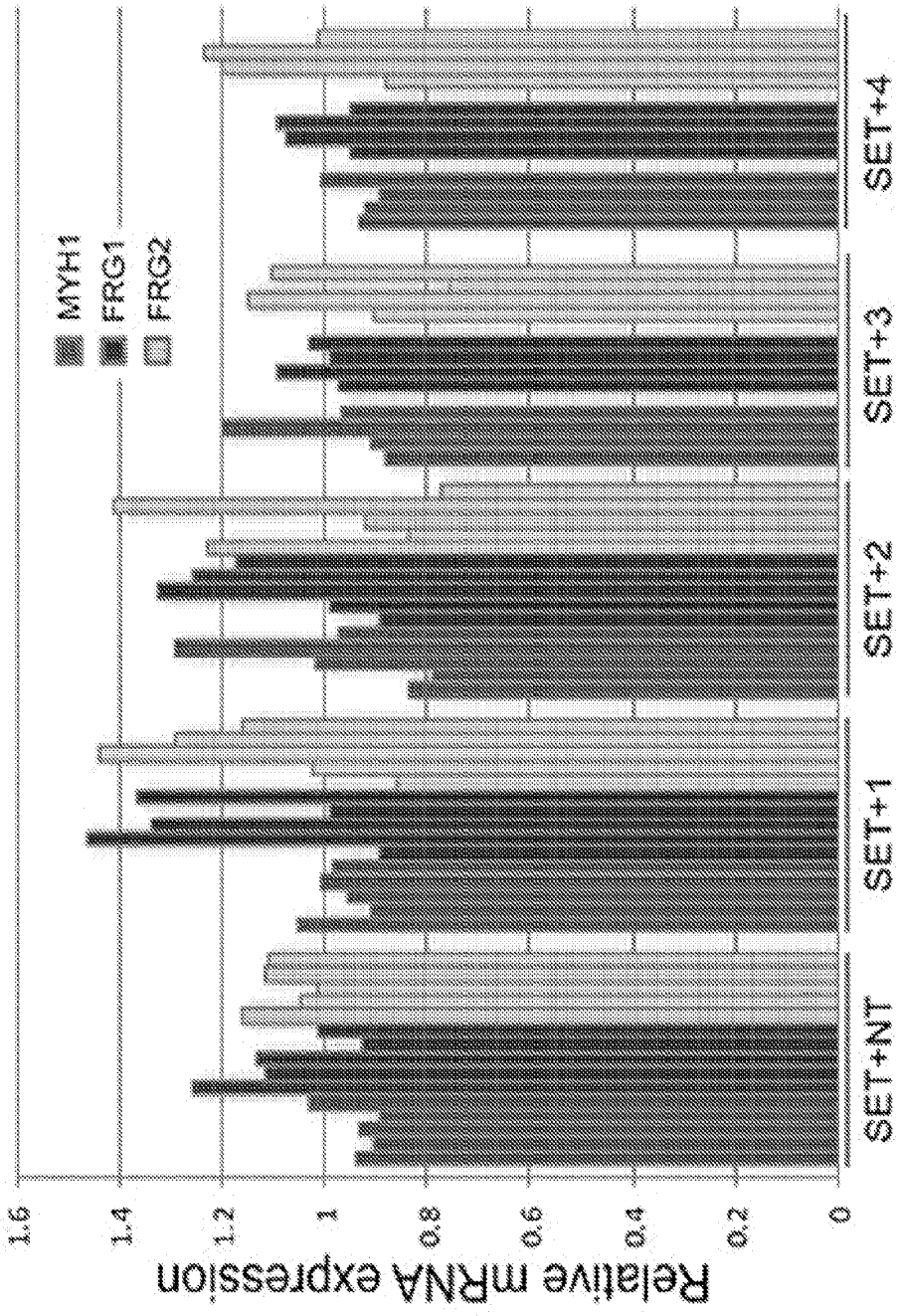

Relative mRNA expression
1.6
1.4
1.2
1
0.8
0.6
0.4
0.2
0
MYH1
FRG1
FRG2
SET+NT
SET+1
SET+2
SET+3
SET+4

FIG. 6A

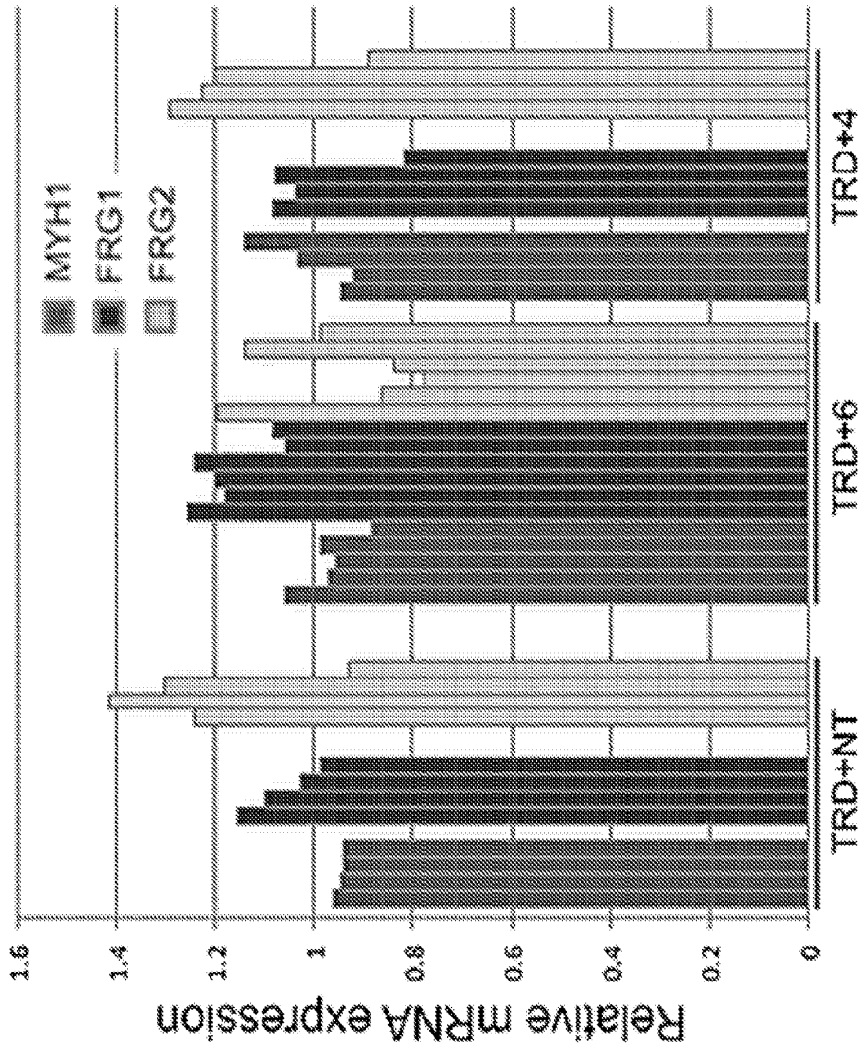

MYH1
FRG1
FRG2
Relative mRNA expression
1.6
1.4
1.2
1
0.8
0.6
0.4
0.2
0
TRD+NT
TRD+6
TRD+4

FIG. 6B

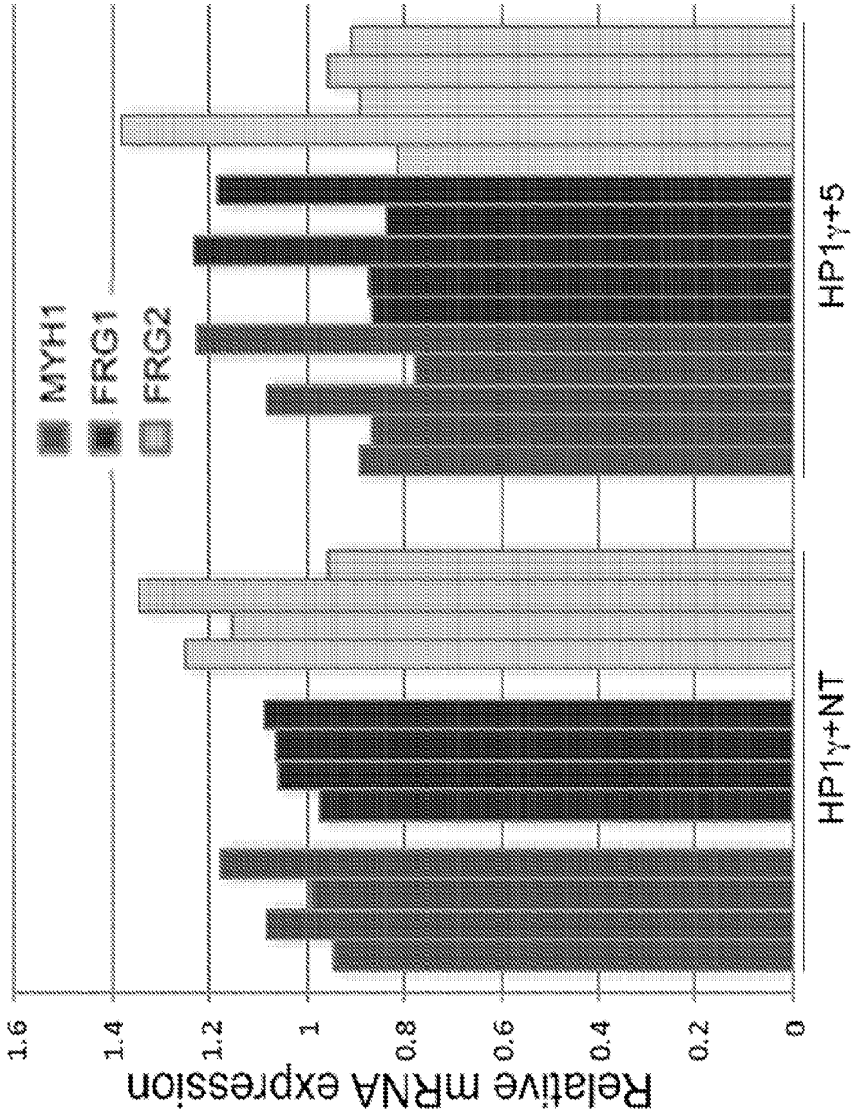

MYH1
FRG1
FRG2
Relative mRNA expression
1.6
1.4
1.2
1
0.8
0.6
0.4
0.2
0
HP1γ+NT
HP1γ+5

FIG. 6C

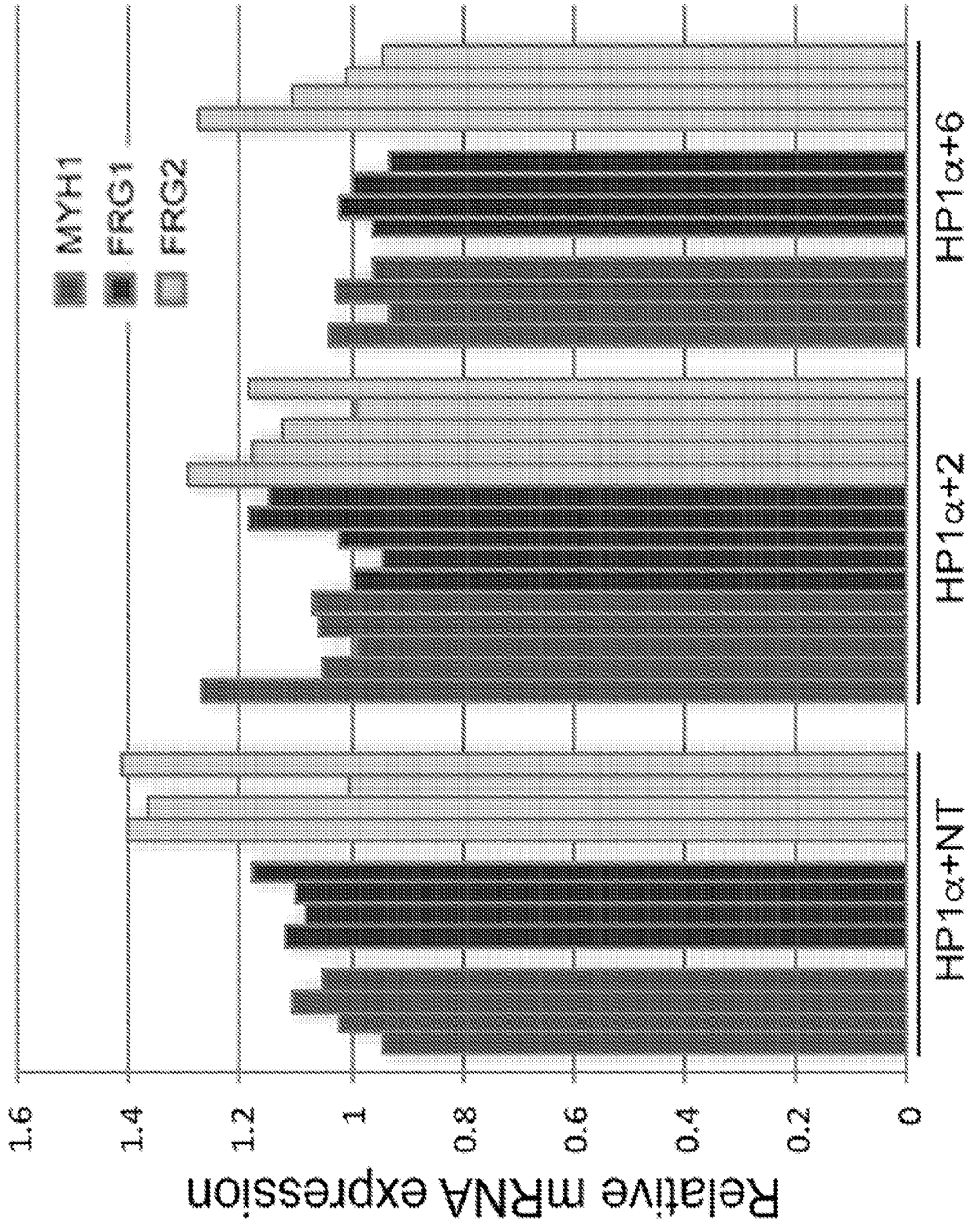

MYH1
FRG1
FRG2
Relative mRNA expression
0
0.2
0.4
0.6
0.8
1
1.2
1.4
1.6
HP1α+NT
HP1α+2
HP1α+6

FIG. 6D

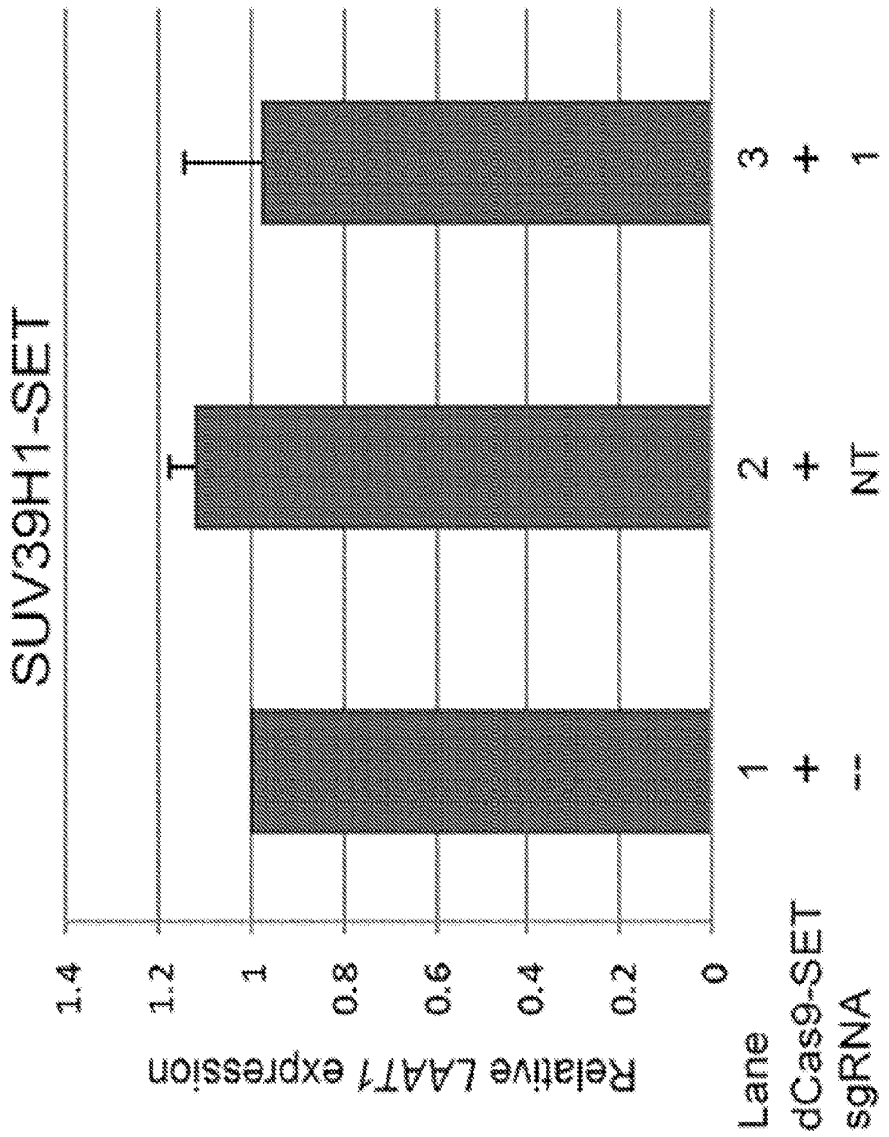

SUV39H1-SET
Relative LAAT1 expression
1.4
1.2
1
0.8
0.6
0.4
0.2
0
Lane
dCas9-SET
sgRNA
1
+
-
2
+
NT
3
+
1

FIG. 7A

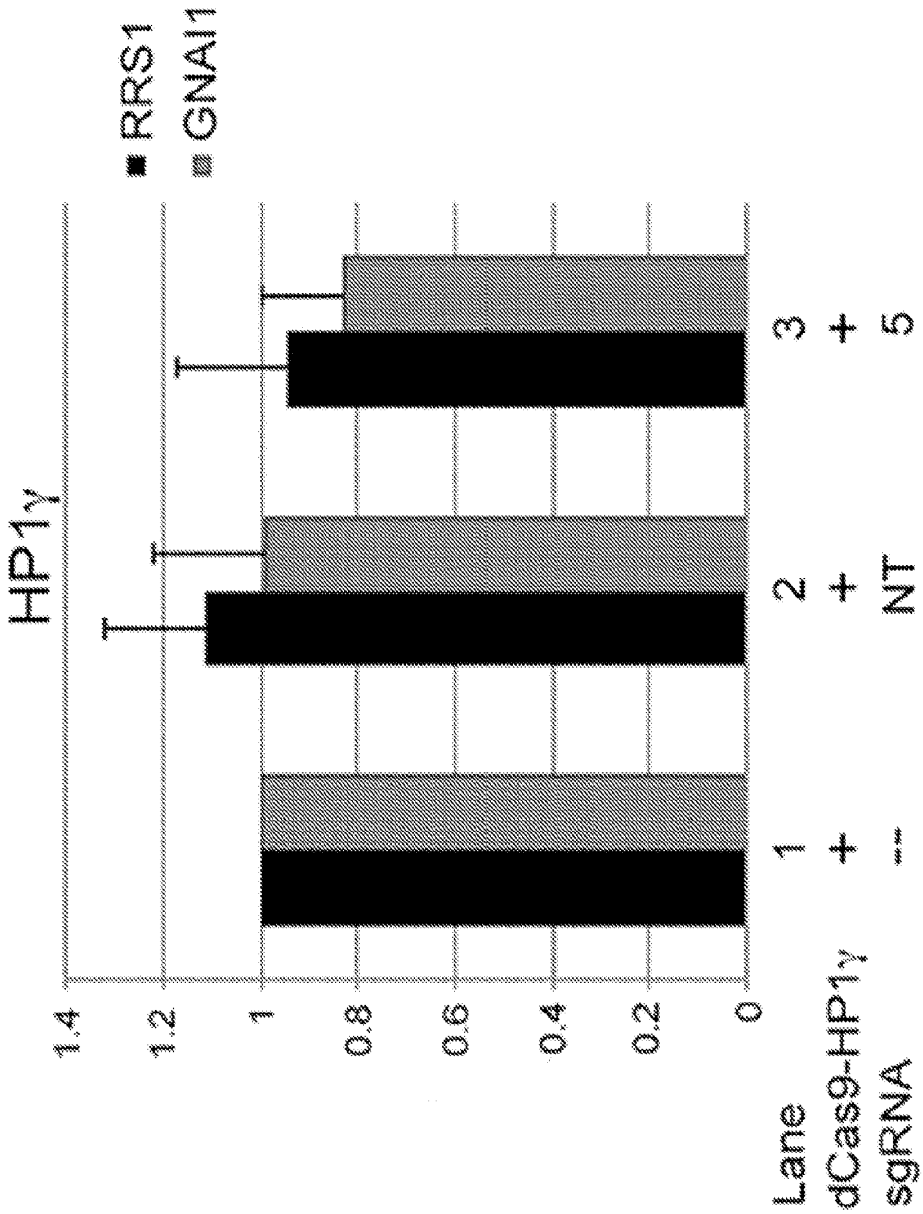

RRS1
GNAI1
HP1γ
1.4
1.2
1
0.8
0.6
0.4
0.2
0
Lane
dCas9-HP1γ
sgRNA
1
+
--
2
+
NT
3
+
5

FIG. 7B

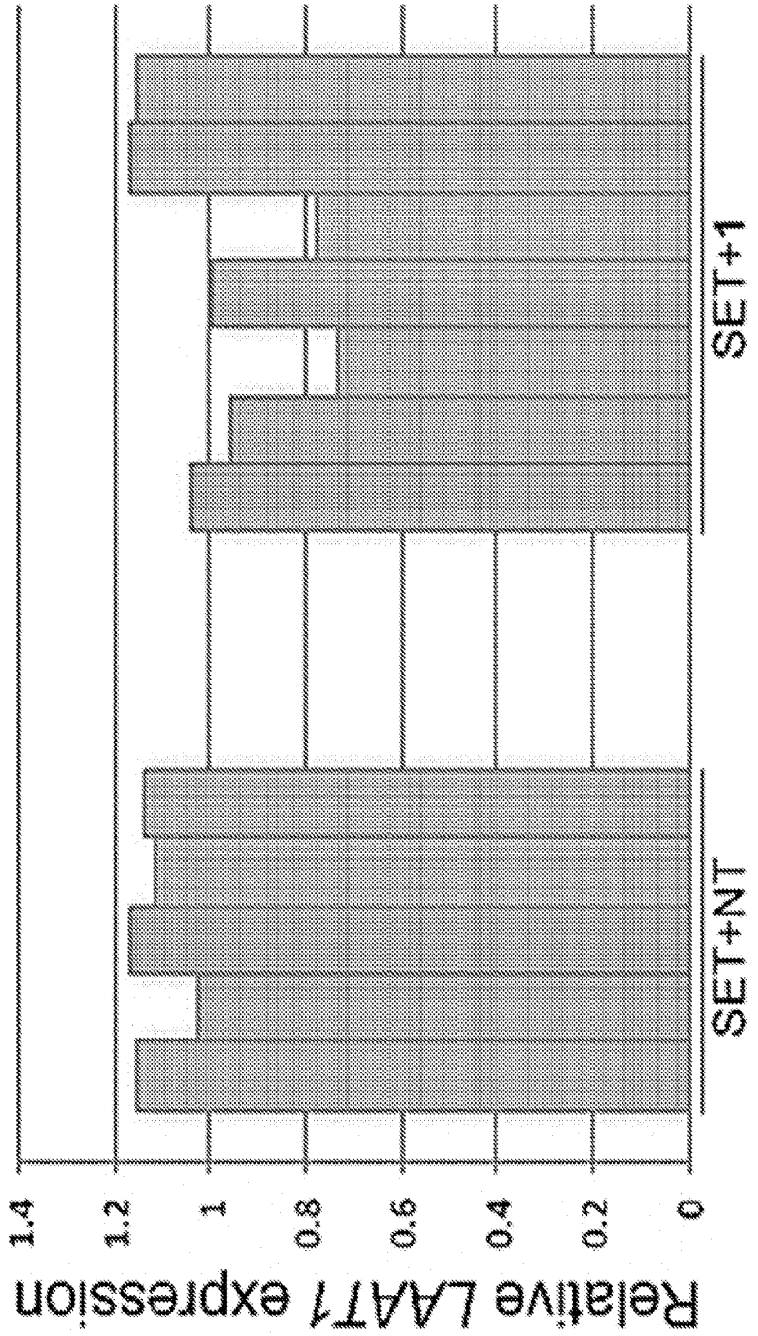


FIG. 8A

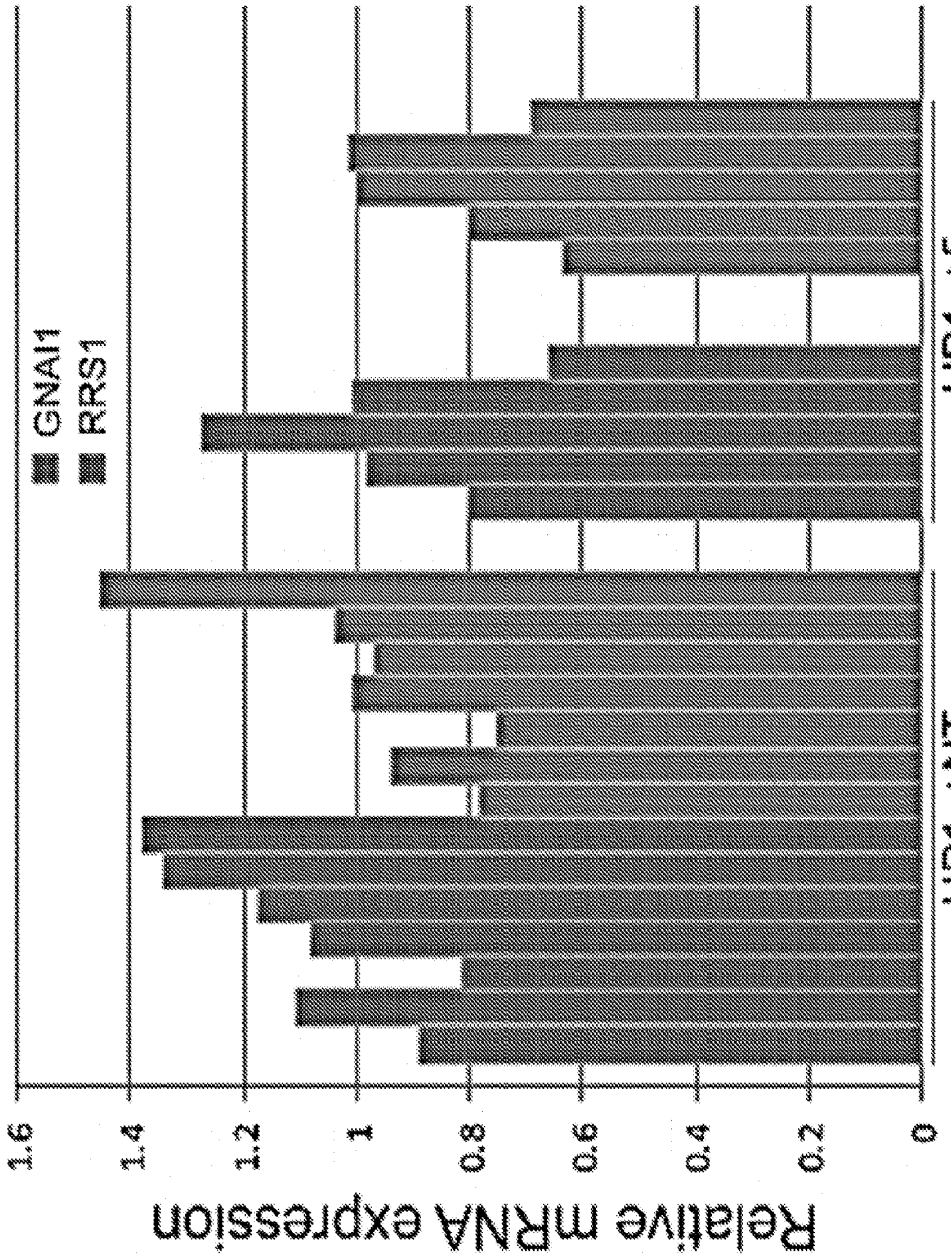

GNAI1
RRS1
Relative mRNA expression
1.6
1.4
1.2
1
0.8
0.6
0.4
0.2
0
HP1γ+NT
HP1γ+5

FIG. 8B

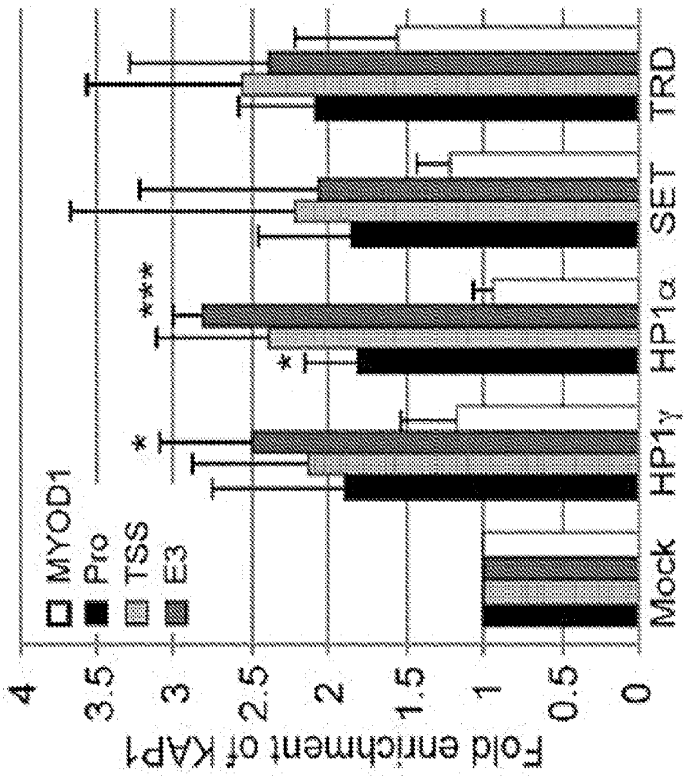

Fold enrichment of KAP1
4
3.5
3
2.5
2
1.5
1
0.5
0
MYOD1
Pro
TSS
E3
Mock
HP1γ
HP1α
SET
TRD
*
*
***
*

FIG. 9B

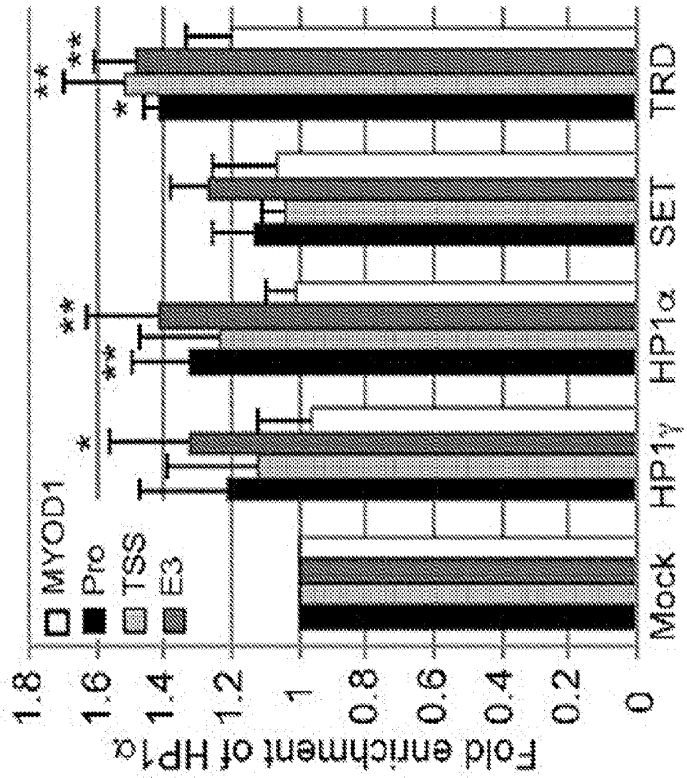

Fold enrichment of HP1α
1.8
1.6
1.4
1.2
1
0.8
0.6
0.4
0.2
0
MYOD1
Pro
TSS
E3
Mock
HP1γ
HP1α
SET
TRD
*
**
**
**
**
*

FIG. 9A

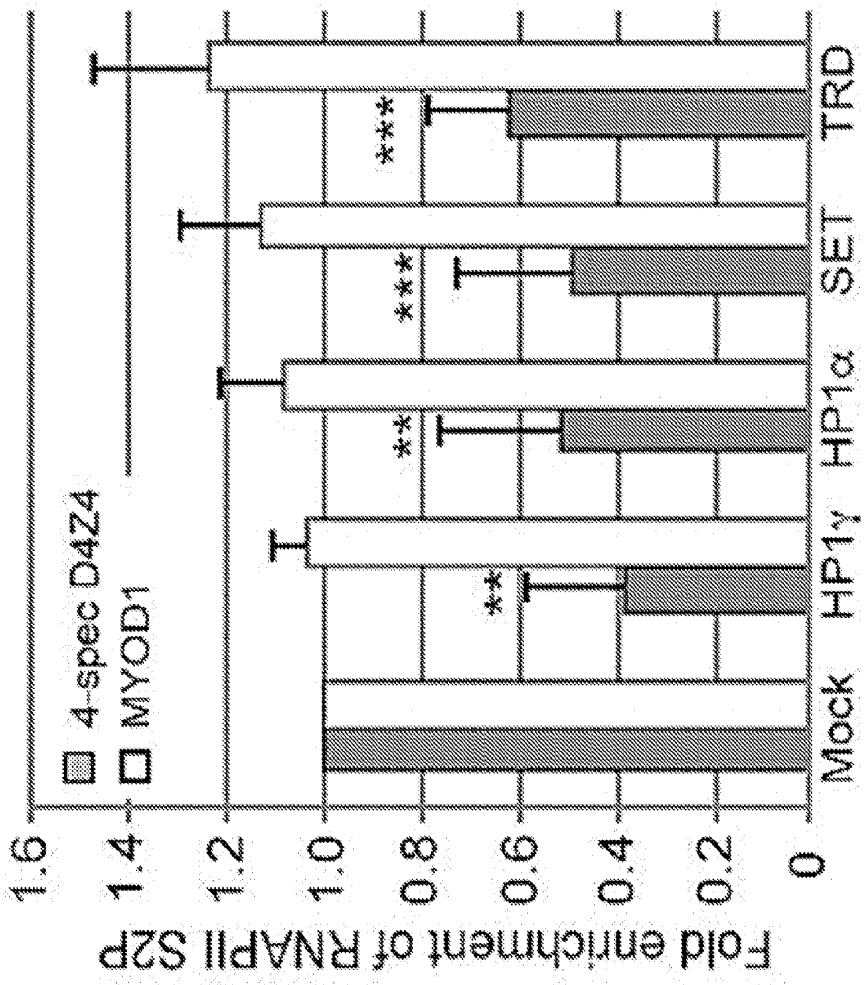

Fold enrichment of RNAPII S2P
1.6
1.4
1.2
1.0
0.8
0.6
0.4
0.2
0
4-spec D4Z4
MYOD1
Mock
HP1γ
HP1α
SET
TRD
**
**
***
***

FIG. 9C

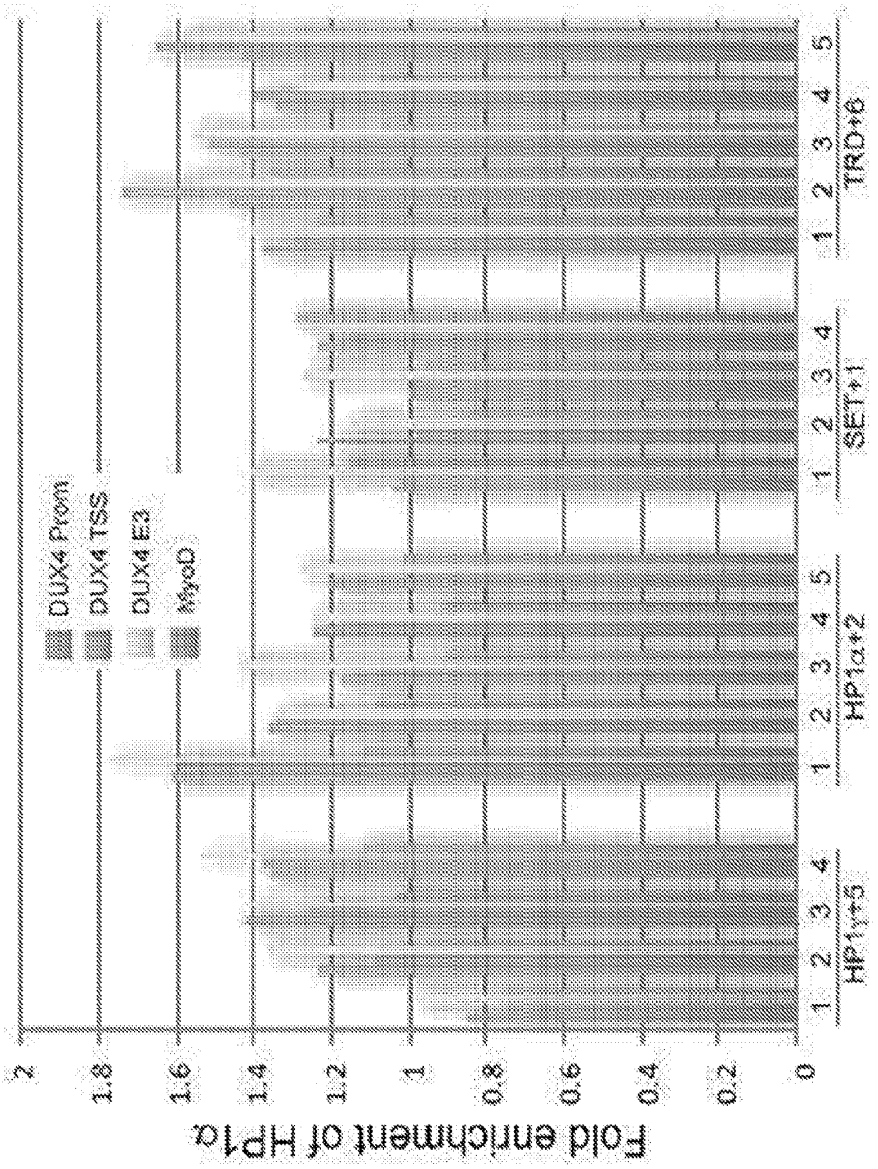

Fold enrichment of HP1α
2
1.8
1.6
1.4
1.2
1
0.8
0.6
0.4
0.2
0
DUX4 Prom
DUX4 TSS
DUX4 E3
MyoD
1 2 3 4
HP1γ+5
1 2 3 4 5
HP1α+2
1 2 3 4
SET+1
1 2 3 4 5
TRD+6

FIG. 10A

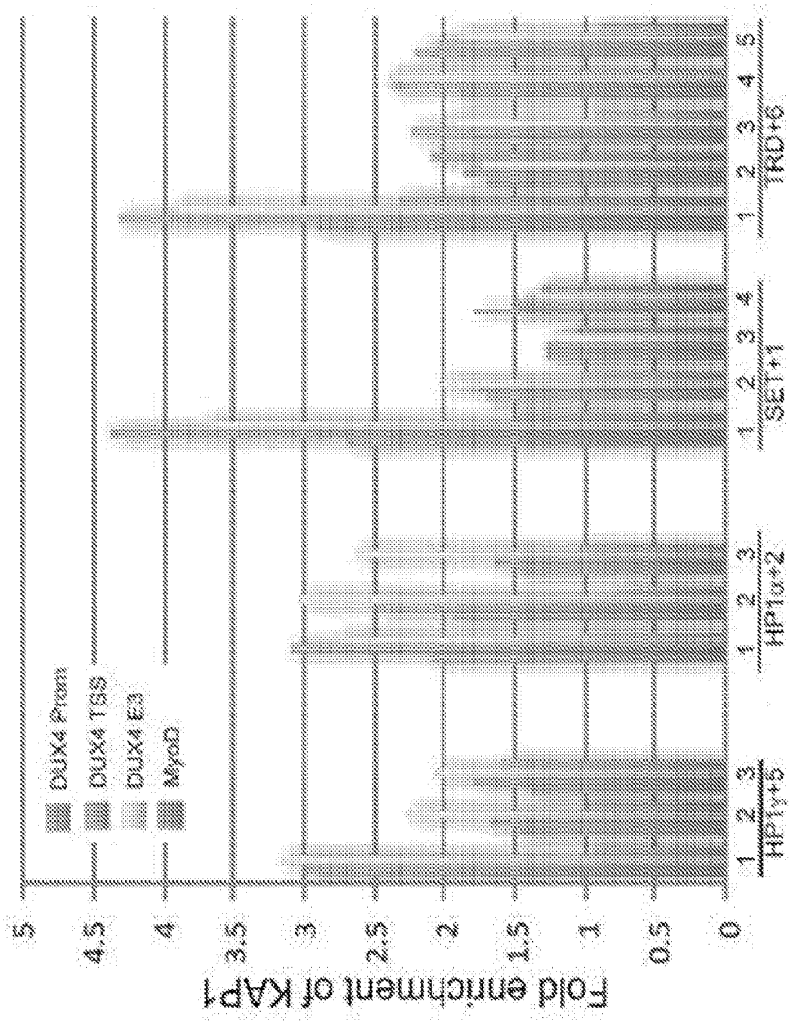

Fold enrichment of KAP1
5
4.5
4
3.5
3
2.5
2
1.5
1
0.5
0
DUX4 Prom
DUX4 TSS
DUX4 E3
MyoD
1 2 3
HP1γ+5
1 2 3
HP1α+2
1 2 3 4
SET+1
1 2 3 4 5
TRD+6

FIG. 10B

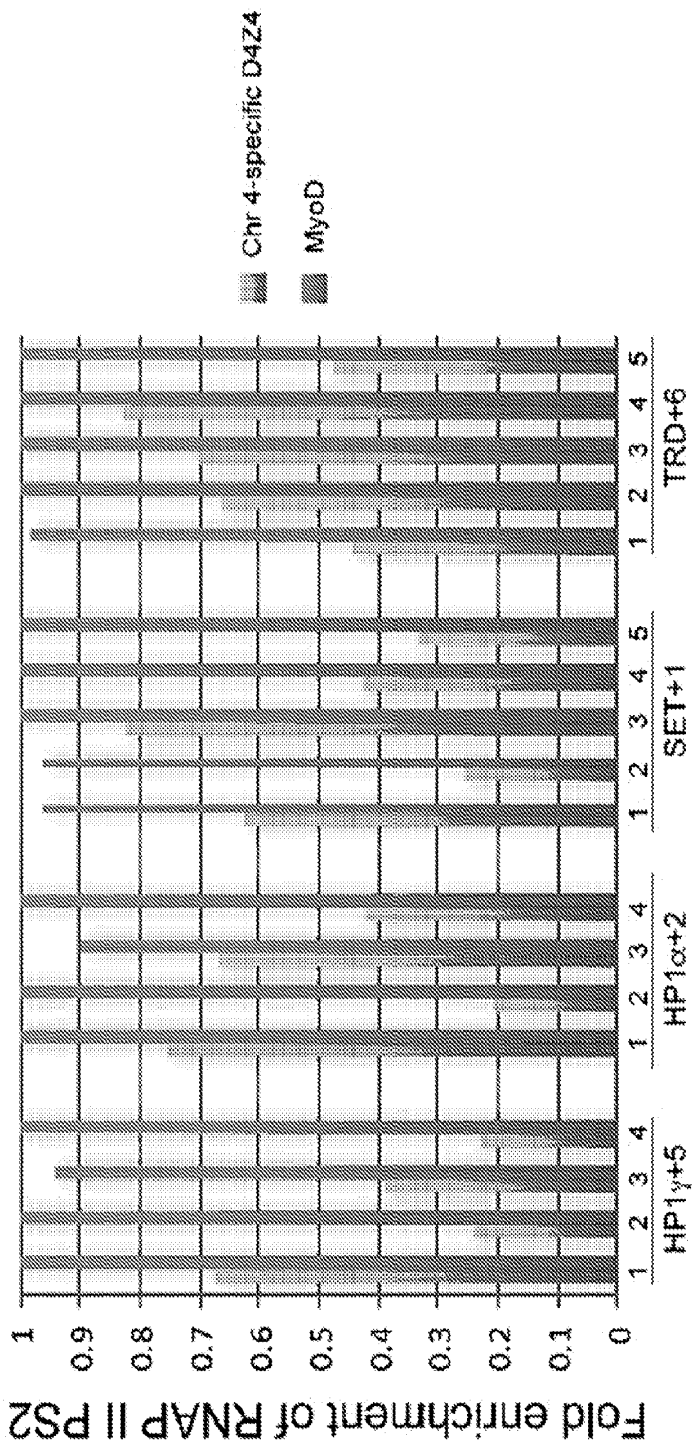

Chr 4-specific D4Z4
MyoD
Fold enrichment of RNAP II PS2
0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1
1 2 3 4
HP1γ+5
1 2 3 4
HP1α+2
1 2 3 4 5
SET+1
1 2 3 4 5
TRD+6

FIG. 10C

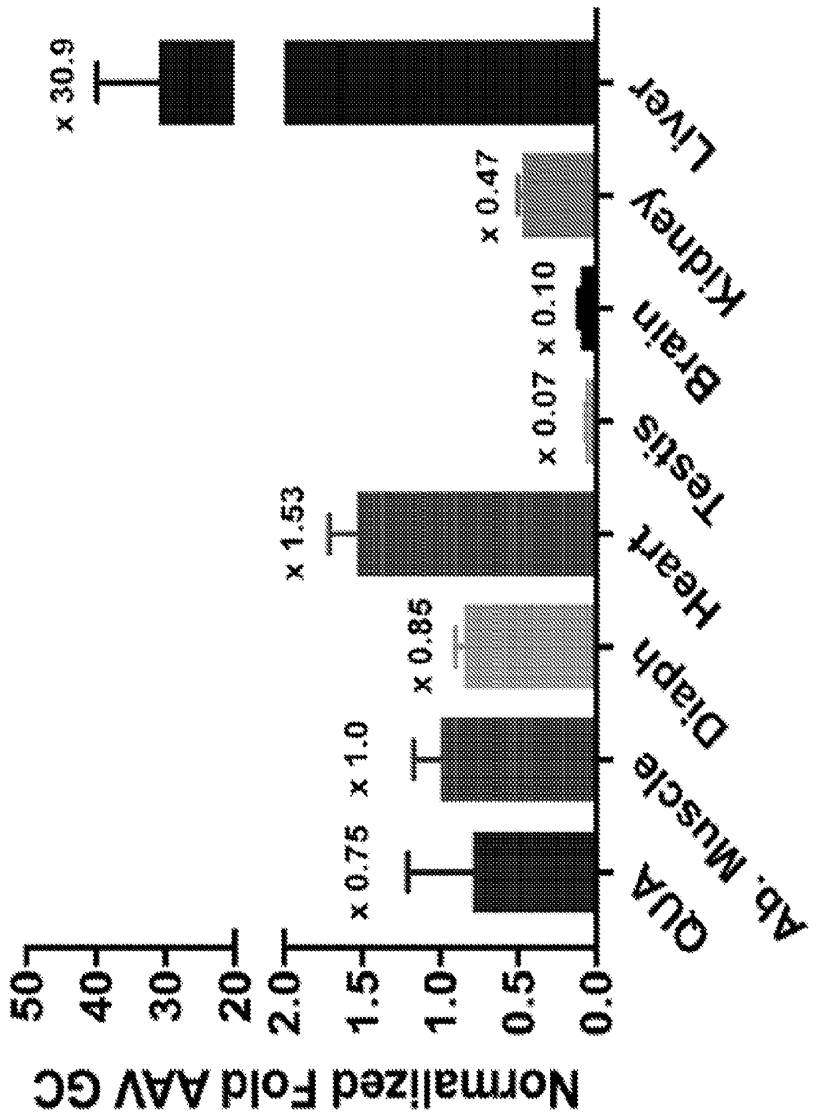
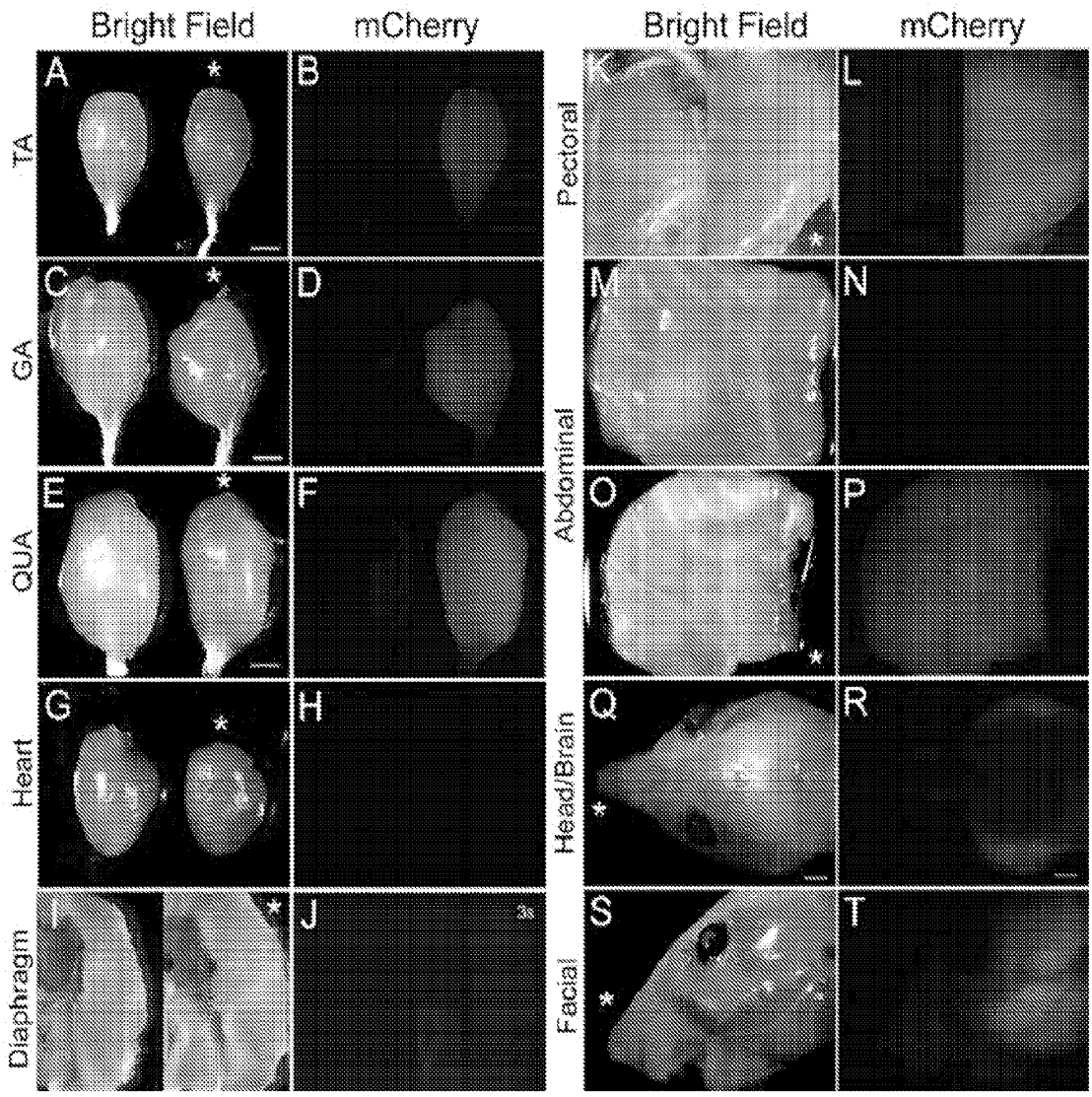

Normalized Fold AAV GC
50
40
30
20
2.0
1.5
1.0
0.5
0.0
GUA
Ab. Muscle
Diaph
Heart
Testis
Brain
Kidney
Liver
x 0.75
x 1.0
x 0.85
x 1.53
x 0.07
x 0.10
x 0.47
x 30.9

FIG. 11



FIGs. 12A-12T

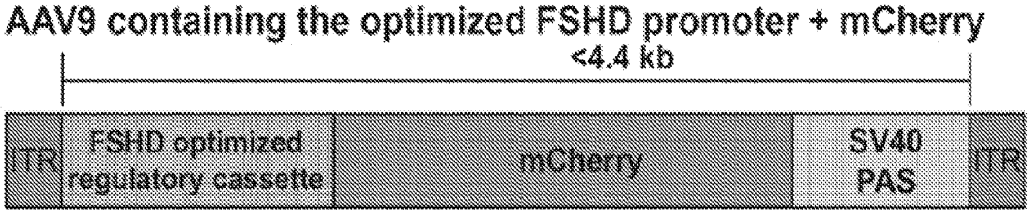
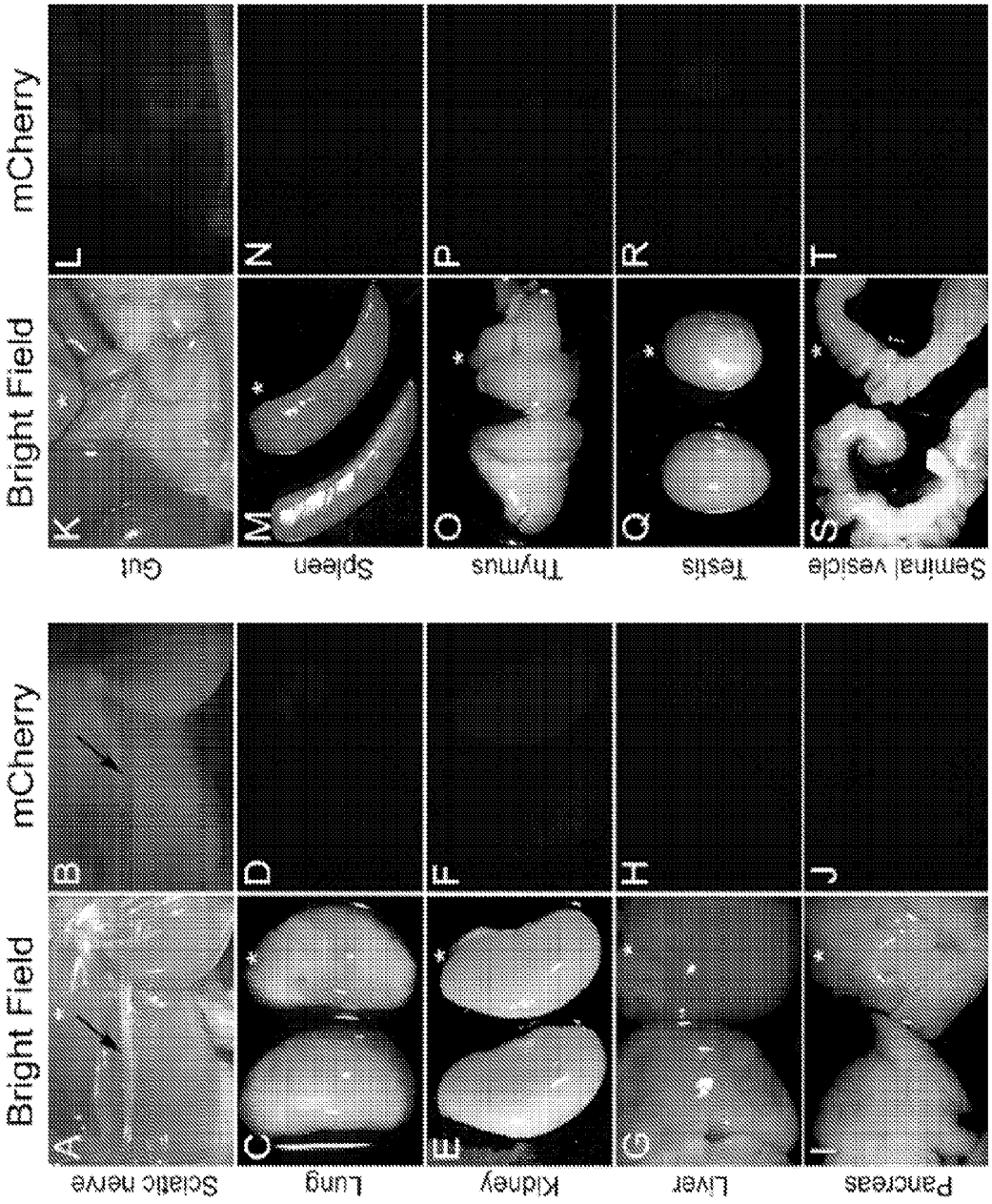


FIG. 12U


Bright Field
mCherry
A
B
C
D
E
F
G
H
I
J
Sciatic nerve
Lung
Kidney
Liver
Pancreas
K
L
M
N
O
P
Q
R
S
T
Gut
Spleen
Thymus
Testis
Semina| vesicle

FIGs. 13A-13T

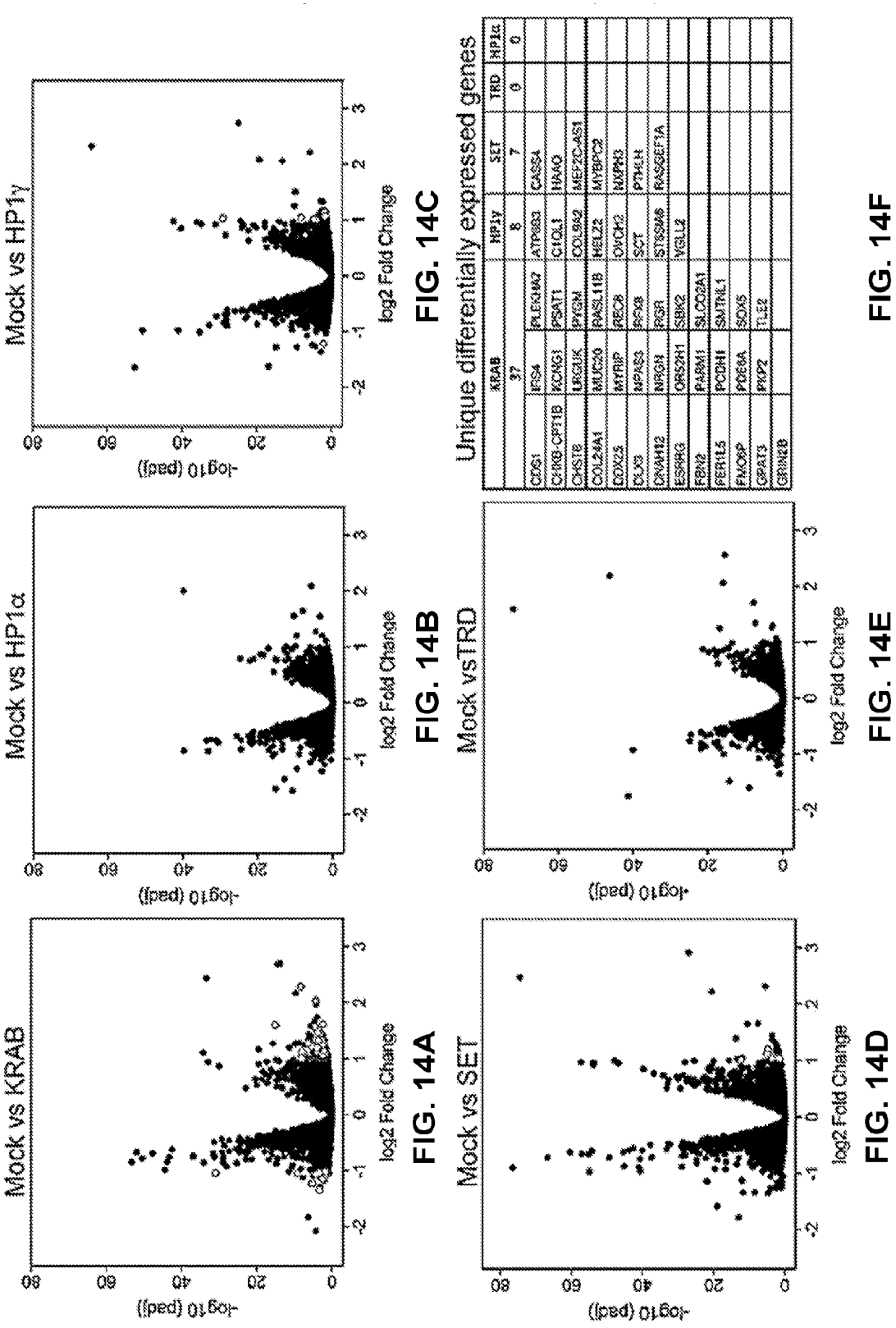


FIG. 14A FIG. 14B FIG. 14C FIG. 14D FIG. 14E FIG. 14F

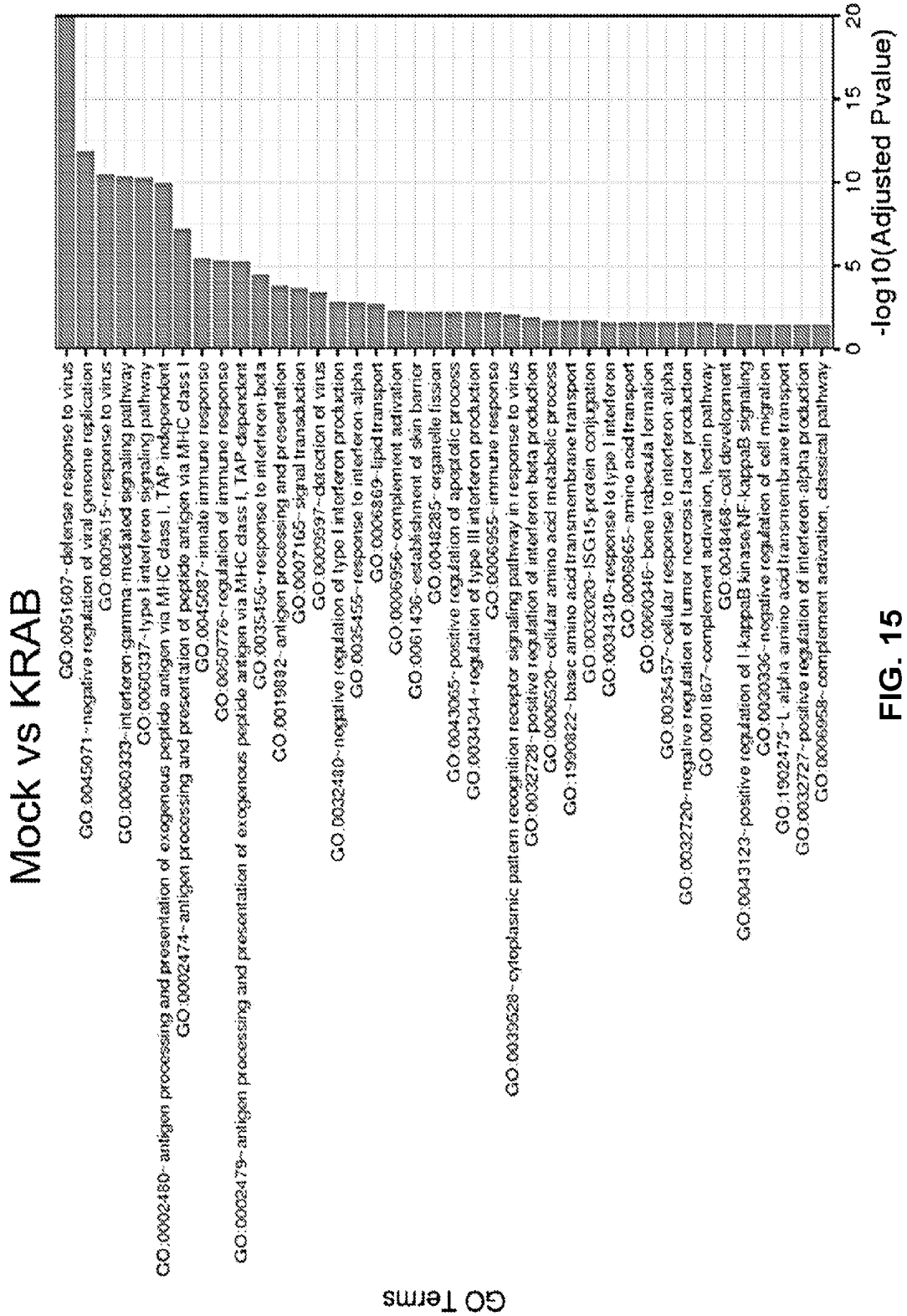

Mock vs KRAB
GO:0051607~defense response to virus
GO:0045071~negative regulation of viral genome replication
GO:0009615~response to virus
GO:0060333~interferon-gamma mediated signaling pathway
GO:0060337~type I interferon signaling pathway
GO:0002480~antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP independent
GO:0002474~antigen processing and presentation of peptide antigen via MHC class I
GO:0045087~innate immune response
GO:0050776~regulation of immune response
GO:0002479~antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP dependent
GO:0035456~response to interferon-beta
GO:0019882~antigen processing and presentation
GO:0007165~signal transduction
GO:0009597~detection of virus
GO:0032480~negative regulation of type I interferon production
GO:0035455~response to interferon-alpha
GO:0006869~lipid transport
GO:0006956~complement activation
GO:0061436~establishment of skin barrier
GO:0048285~organelle fission
GO:0043065~positive regulation of apoptotic process
GO:0034344~regulation of type III interferon production
GO:0006955~immune response
GO:0039528~cytoplasmic pattern recognition receptor signaling pathway in response to virus
GO:0032728~positive regulation of interferon-beta production
GO:0006520~cellular amino acid metabolic process
GO:1990622~basic amino acid transmembrane transport
GO:0032020~ISG15 protein conjugation
GO:0034340~response to type I interferon
GO:0006865~amino acid transport
GO:0060346~bone trabecula formation
GO:0035457~cellular response to interferon-alpha
GO:0032720~negative regulation of tumor necrosis factor production
GO:0001867~complement activation, lectin pathway
GO:0048468~cell development
GO:0043123~positive regulation of I-kappaB kinase/NF-kappaB signaling
GO:0030336~negative regulation of cell migration
GO:1902475~L-alpha-amino acid transmembrane transport
GO:0032727~positive regulation of interferon-alpha production
GO:0006958~complement activation, classical pathway
GO Terms
0
5
10
15
20
-log10(Adjusted Pvalue)

FIG. 15

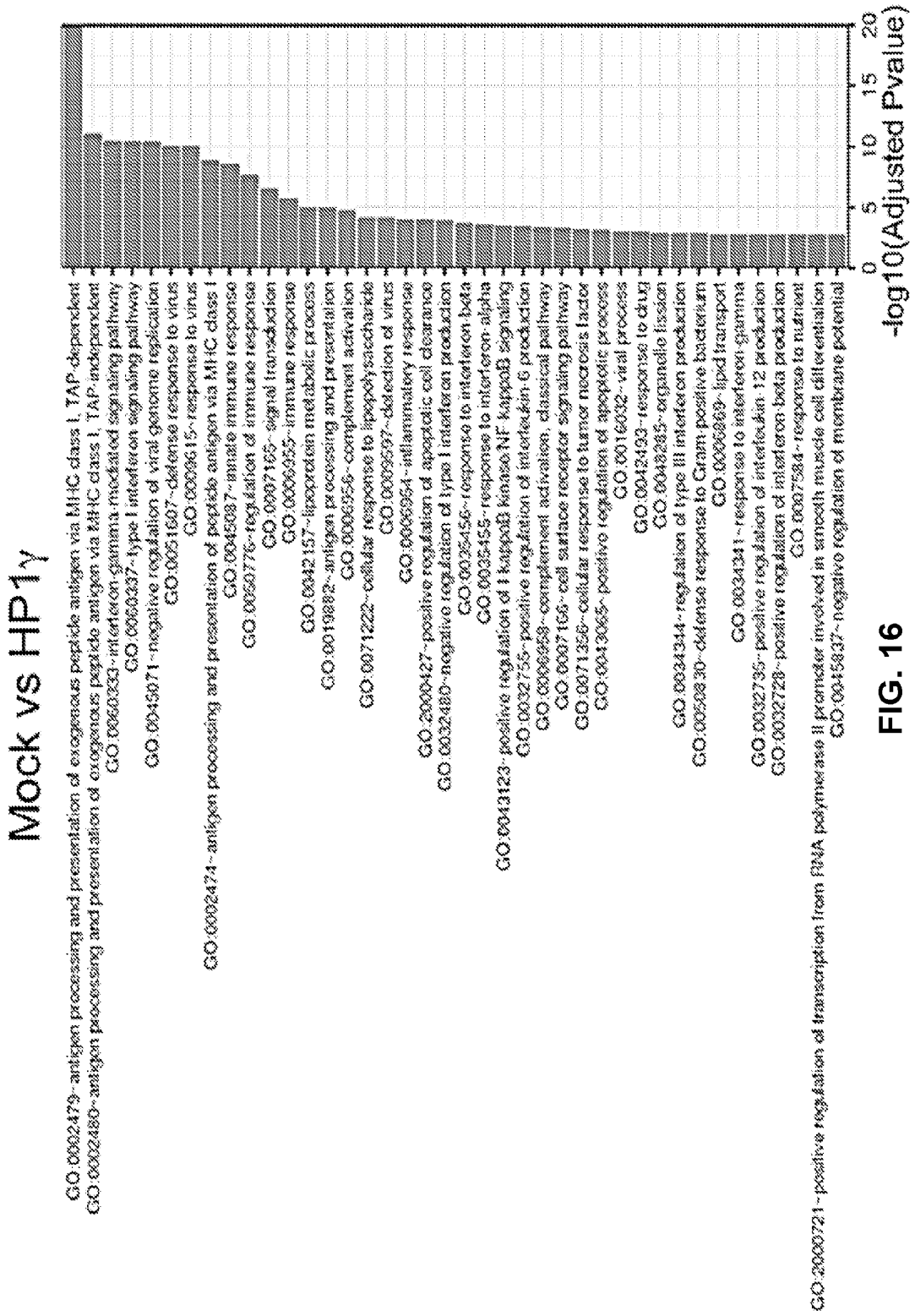

Mock vs HP1γ
GO:0002479~antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent
GO:0002480~antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-independent
GO:0060333~interferon-gamma-mediated signaling pathway
GO:0060337~type I interferon signaling pathway
GO:0043071~negative regulation of viral genome replication
GO:0051607~defense response to virus
GO:0009615~response to virus
GO:0002474~antigen processing and presentation of peptide antigen via MHC class I
GO:0045087~innate immune response
GO:0050776~regulation of immune response
GO:0007165~signal transduction
GO:0006955~immune response
GO:0042157~lipoprotein metabolic process
GO:0019882~antigen processing and presentation
GO:0006956~complement activation
GO:0071222~cellular response to lipopolysaccharide
GO:0009597~detection of virus
GO:0006954~inflammatory response
GO:2000427~positive regulation of apoptotic cell clearance
GO:0032480~negative regulation of type I interferon production
GO:0035456~response to interferon-beta
GO:0035455~response to interferon-alpha
GO:0043123~positive regulation of I-kappaB kinase/NF-kappaB signaling
GO:0032755~positive regulation of interleukin-6 production
GO:0006958~complement activation, classical pathway
GO:0007166~cell surface receptor signaling pathway
GO:0071356~cellular response to tumor necrosis factor
GO:0043065~positive regulation of apoptotic process
GO:0016032~viral process
GO:0042493~response to drug
GO:0048285~organelle fission
GO:0034344~regulation of type III interferon production
GO:0050830~defense response to Gram-positive bacterium
GO:0006869~lipid transport
GO:0034341~response to interferon-gamma
GO:0032735~positive regulation of interleukin-12 production
GO:0032728~positive regulation of interferon-beta production
GO:0007584~response to nutrient
GO:0045838~negative regulation of membrane potential
GO:2000721~positive regulation of transcription from RNA polymerase II promoter involved in smooth muscle cell differentiation
0
5
10
15
20
-log10(Adjusted Pvalue)
GO Terms

FIG. 16

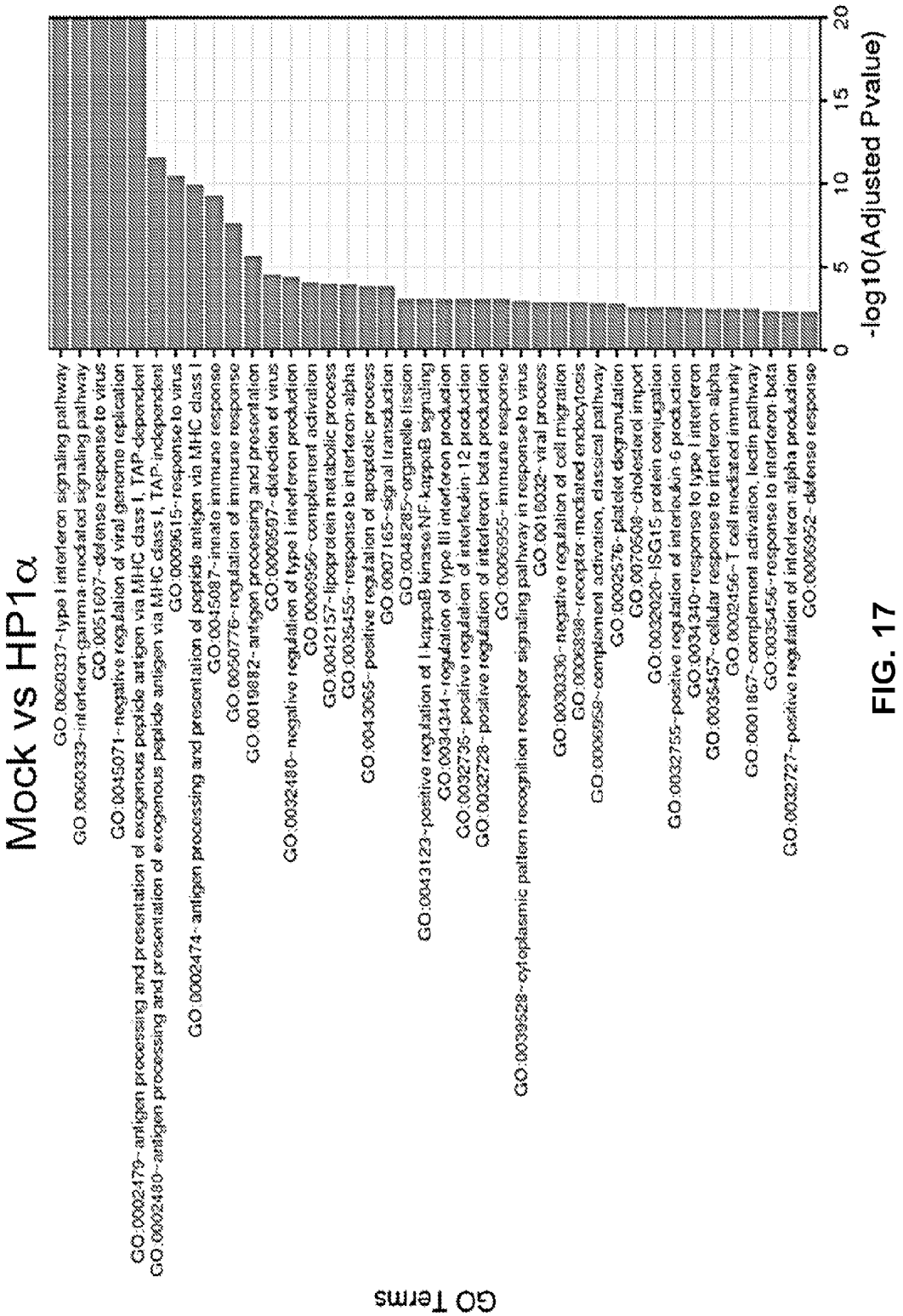

Mock vs HP1α
GO 0060337~type I interferon signaling pathway
GO 0060333~interferon-gamma-mediated signaling pathway
GO 0051607~defense response to virus
GO 0045071~negative regulation of viral genome replication
GO 0002479~antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent
GO 0002480~antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-independent
GO 0009615~response to virus
GO 0002474~antigen processing and presentation of peptide antigen via MHC class I
GO 0045087~innate immune response
GO 0050776~regulation of immune response
GO 0019882~antigen processing and presentation
GO 0009597~detection of virus
GO 0032480~negative regulation of type I interferon production
GO 0006956~complement activation
GO 0042157~lipoprotein metabolic process
GO 0035455~response to interferon-alpha
GO 0043065~positive regulation of apoptotic process
GO 0007165~signal transduction
GO 0048285~organelle fission
GO 0043123~positive regulation of I-kappaB kinase/NF-kappaB signaling
GO 0034344~regulation of type III interferon production
GO 0032735~positive regulation of interleukin-12 production
GO 0032728~positive regulation of interferon-beta production
GO 0006955~immune response
GO 0039528~cytoplasmic pattern recognition receptor signaling pathway in response to virus
GO 0019032~viral process
GO 0030336~negative regulation of cell migration
GO 0006898~receptor-mediated endocytosis
GO 0006958~complement activation, classical pathway
GO 0002576~platelet degranulation
GO 0070628~cholesterol import
GO 0032020~ISG15 protein conjugation
GO 0032755~positive regulation of interleukin-6 production
GO 0034340~response to type I interferon
GO 0035457~cellular response to interferon-alpha
GO 0002456~T cell mediated immunity
GO 0001867~complement activation, lectin pathway
GO 0035456~response to interferon-beta
GO 0032727~positive regulation of interferon-alpha production
GO 0006952~defense response
GO Terms
0
5
10
15
20
-log10(Adjusted Pvalue)

FIG. 17

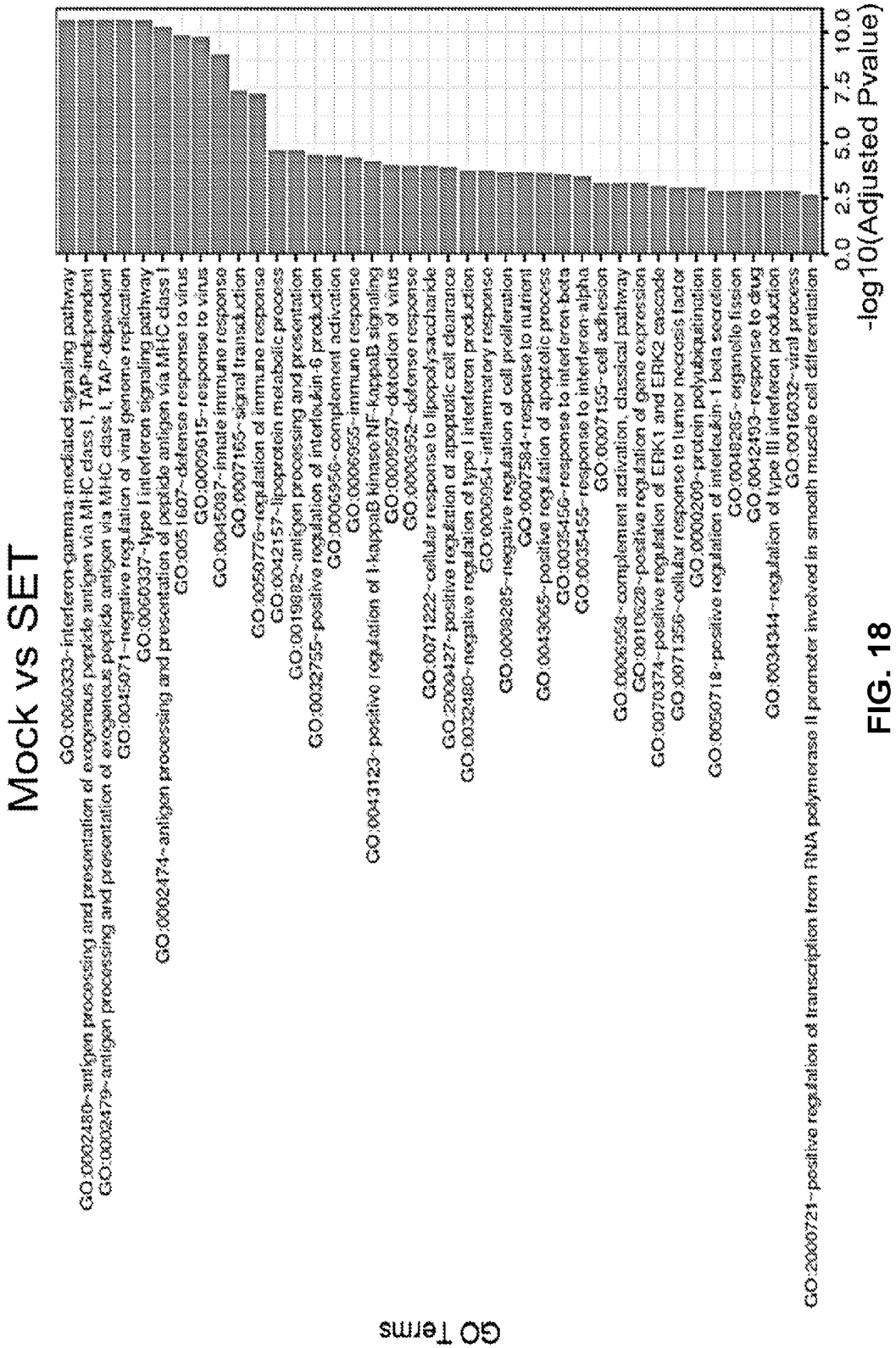

Mock vs SET
GO:0060333~interferon-gamma-mediated signaling pathway
GO:0002480~antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-independent
GO:0002479~antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent
GO:0045071~negative regulation of viral genome replication
GO:0060337~type I interferon signaling pathway
GO:0002474~antigen processing and presentation of peptide antigen via MHC class I
GO:0051607~defense response to virus
GO:0009615~response to virus
GO:0045087~innate immune response
GO:0007165~signal transduction
GO:0050776~regulation of immune response
GO:0042157~lipoprotein metabolic process
GO:0019882~antigen processing and presentation
GO:0032755~positive regulation of interleukin-6 production
GO:0006956~complement activation
GO:0006955~immune response
GO:0043123~positive regulation of I-kappaB kinase/NF-kappaB signaling
GO:0009597~detection of virus
GO:0006952~defense response
GO:0071222~cellular response to lipopolysaccharide
GO:2000427~positive regulation of apoptotic cell clearance
GO:0032480~negative regulation of type I interferon production
GO:0006954~inflammatory response
GO:0008285~negative regulation of cell proliferation
GO:0007584~response to nutrient
GO:0043065~positive regulation of apoptotic process
GO:0035456~response to interferon-beta
GO:0035455~response to interferon-alpha
GO:0007155~cell adhesion
GO:0006958~complement activation, classical pathway
GO:0010628~positive regulation of gene expression
GO:0070374~positive regulation of ERK1 and ERK2 cascade
GO:0071356~cellular response to tumor necrosis factor
GO:0000209~protein polyubiquitination
GO:0050718~positive regulation of interleukin-1 beta secretion
GO:0048285~organelle fission
GO:0042493~response to drug
GO:0034344~regulation of type III interferon production
GO:0016032~viral process
GO:2000721~positive regulation of transcription from RNA polymerase II promoter involved in smooth muscle cell differentiation
GO Terms
0.0 2.5 5.0 7.5 10.0
-log10(Adjusted Pvalue)

FIG. 18

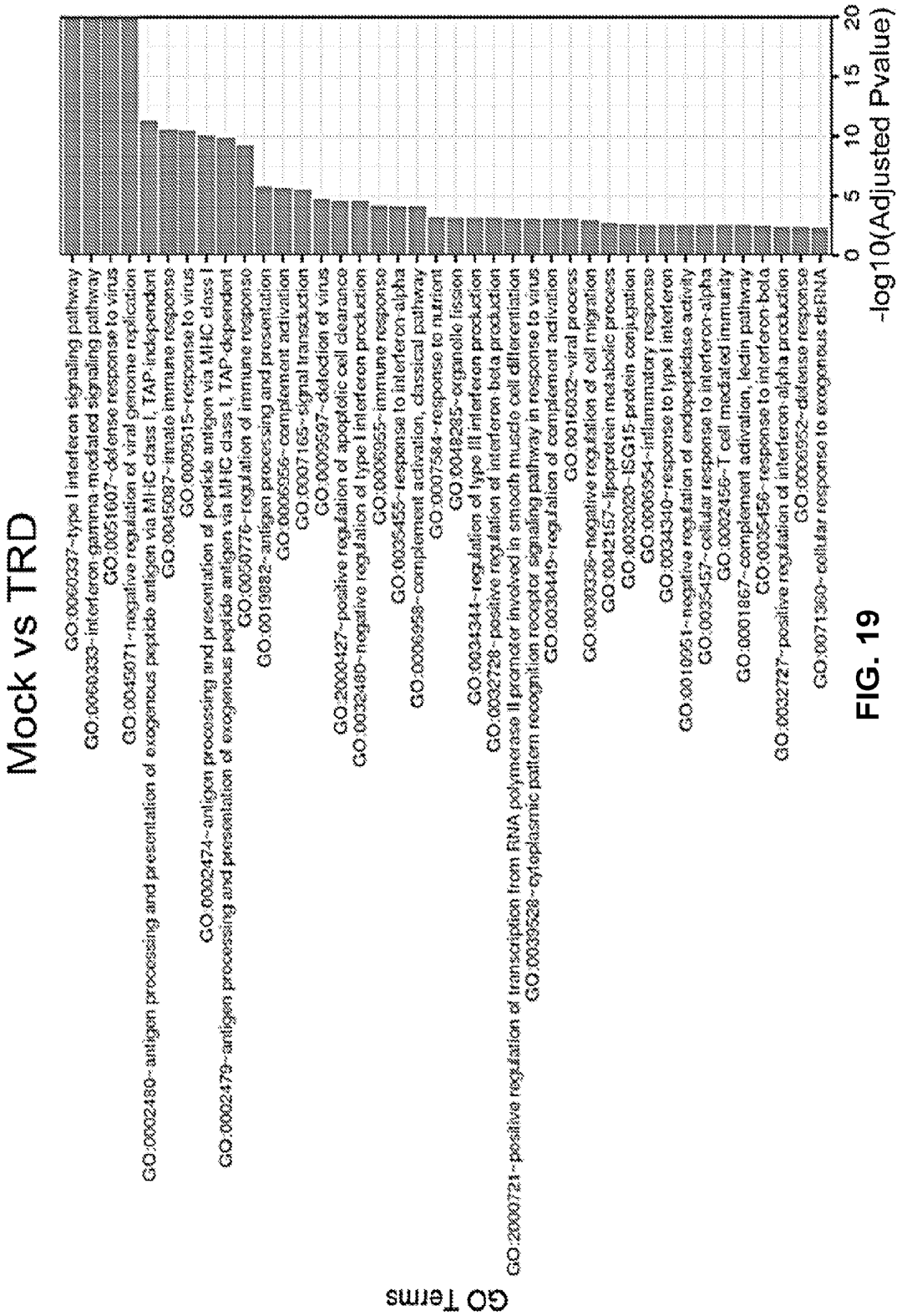

Mock vs TRD
GO Terms
GO:0060337~type I interferon signaling pathway
GO:0060333~interferon-gamma-mediated signaling pathway
GO:0051607~defense response to virus
GO:0045071~negative regulation of viral genome replication
GO:0002480~antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-independent
GO:0045087~innate immune response
GO:0009615~response to virus
GO:0002474~antigen processing and presentation of peptide antigen via MHC class I
GO:0002479~antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent
GO:0050776~regulation of immune response
GO:0019882~antigen processing and presentation
GO:0006956~complement activation
GO:0007165~signal transduction
GO:0009597~detection of virus
GO:2000427~positive regulation of apoptotic cell clearance
GO:0032480~negative regulation of type I interferon production
GO:0060965~immune response
GO:0035455~response to interferon-alpha
GO:0006958~complement activation, classical pathway
GO:0007584~response to nutrient
GO:0048235~organelle fission
GO:0034344~regulation of type III interferon production
GO:0032728~positive regulation of interferon-beta production
GO:2000721~positive regulation of transcription from RNA polymerase II promoter involved in smooth muscle cell differentiation
GO:0039528~cytoplasmic pattern recognition receptor signaling pathway in response to virus
GO:0030449~regulation of complement activation
GO:0016032~viral process
GO:0030336~negative regulation of cell migration
GO:0042157~lipoprotein metabolic process
GO:0032020~ISG15 protein conjugation
GO:0006954~inflammatory response
GO:0034340~response to type I interferon
GO:0010951~negative regulation of endopeptidase activity
GO:0035457~cellular response to interferon-alpha
GO:0002456~T cell mediated immunity
GO:0001867~complement activation, lectin pathway
GO:0035456~response to interferon-beta
GO:0032727~positive regulation of interferon-alpha production
GO:0060962~defense response
GO:0071360~cellular response to exogenous dsRNA
0
5
10
15
20
-log10(Adjusted Pvalue)

FIG. 19

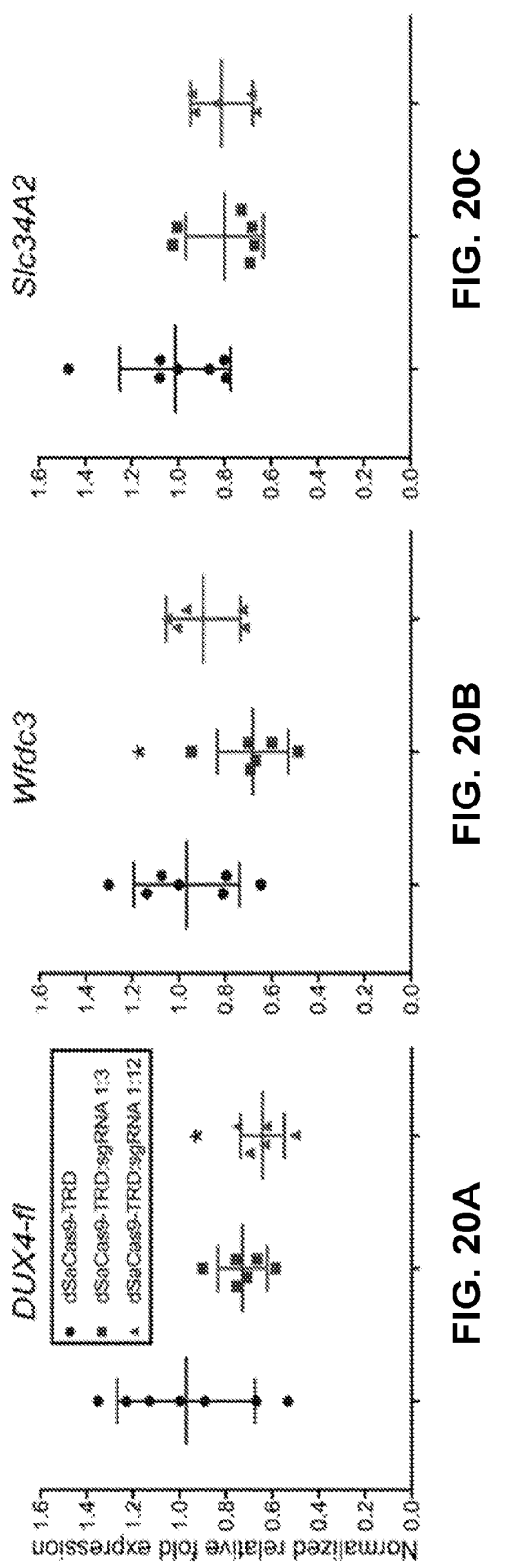


FIG. 20A

FIG. 20B

FIG. 20C

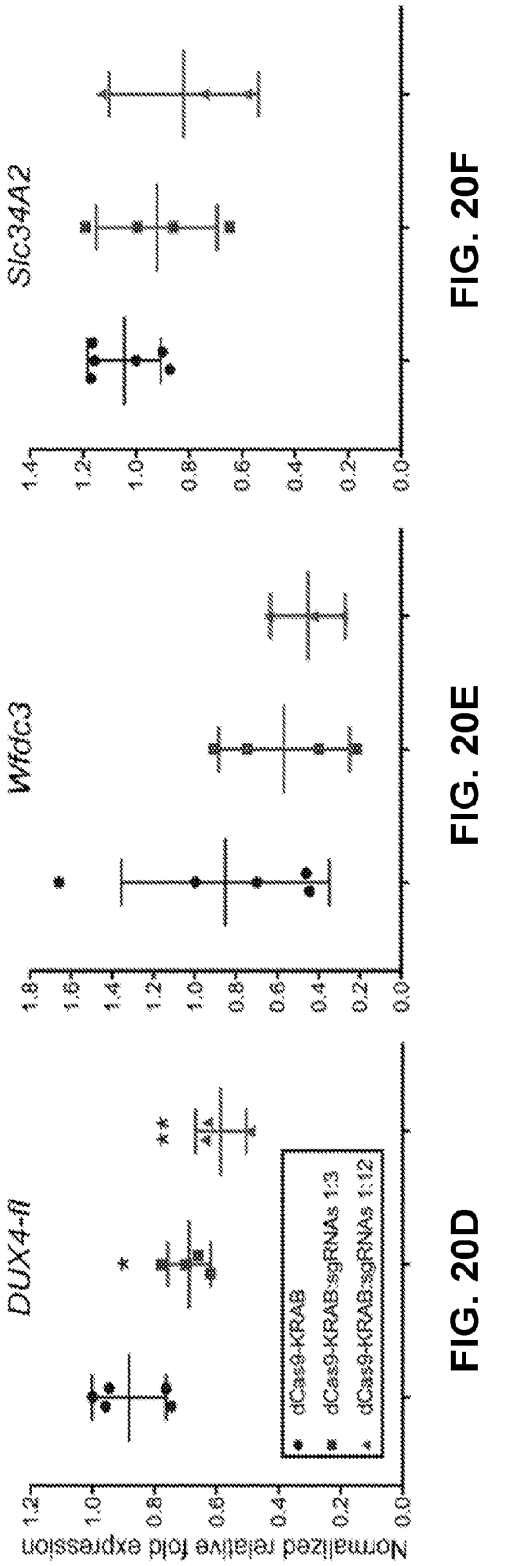


FIG. 20D

FIG. 20E

FIG. 20F

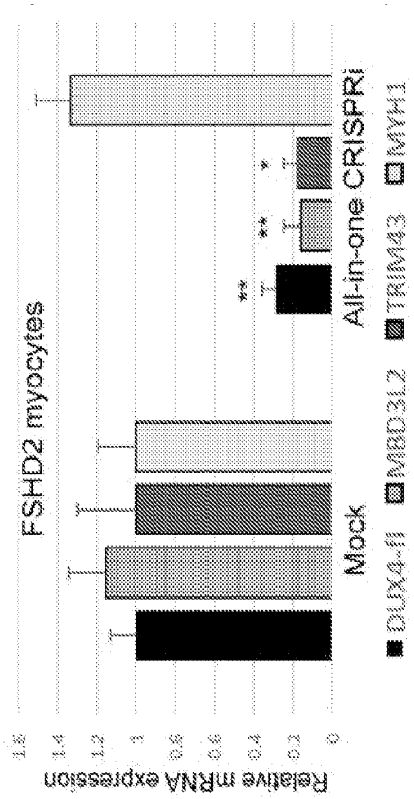


FIG. 21B

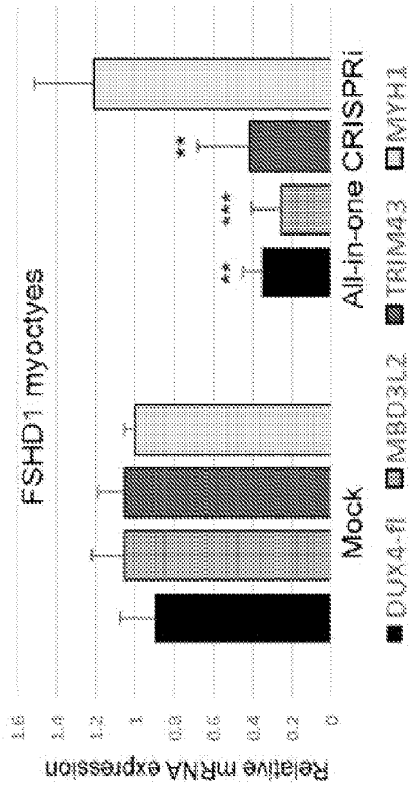


FIG. 21A

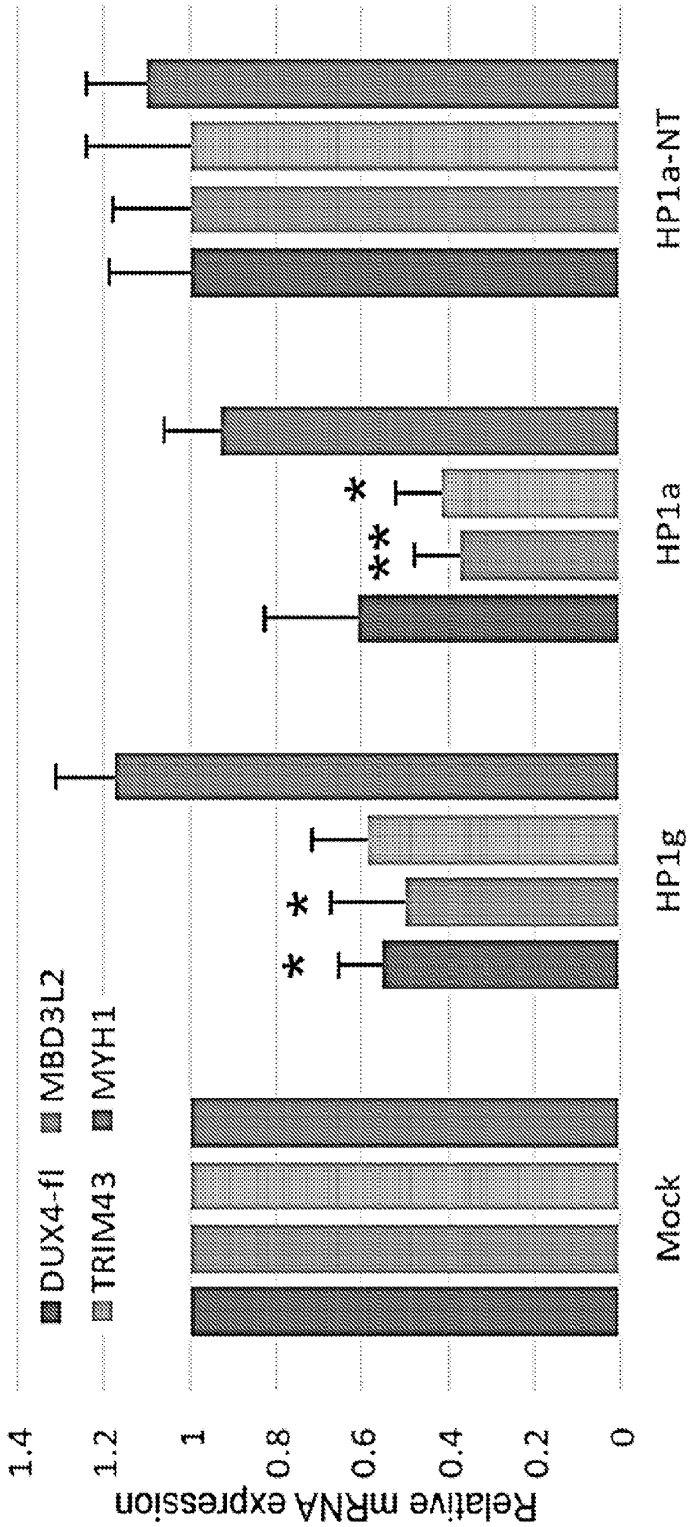
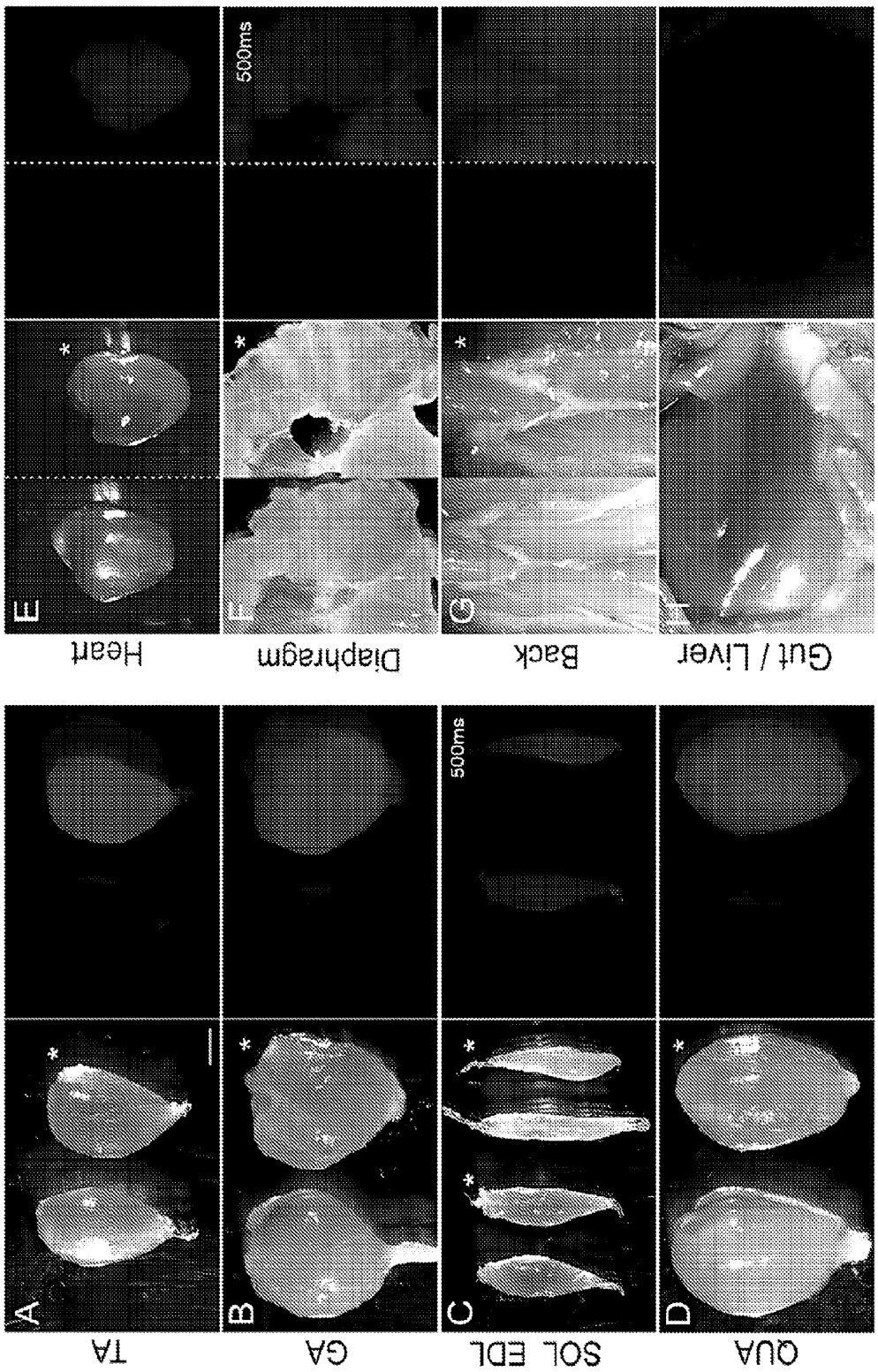

Relative mRNA expression
1.4
1.2
1
0.8
0.6
0.4
0.2
0
DUX4-fl
MBD3L2
TRIM43
MYH1
Mock
HP1g
HP1a
HP1a-NT
*
*
*
**

FIG. 22


TA
GA
SOL EDL
QUA
Heart
Diaphragm
Back
Gut / Liver
500ms
500ms
A
B
C
D
E
F
G
H

FIGs. 23A-23H

Significant DEGs following targeting of dSaCas9-repressors to *DUX4*

ID	log2FoldChange	pvalue	padj	Mock-Expt 1	Mock-Expt 2	Mock-Expt 3	Mock-Expt 4	Mock-Expt 5	TRD-Expt 1	TRD-Expt 4	TRD-Expt 5	TRD-Expt 2	TRD-Expt 3	GeneName
ENSG00000165949	5.1434	3.23E-50	9.92E-47	214.0296	121.0269	108.3395	398.9009	129.6874	5014.6440	6797.4487	8124.3894	5163.0733	5640.4684	IFI27
ENSG00000130303	4.9226	2.65E-27	1.85E-24	35.5072	15.1284	32.3773	63.2404	17.1487	527.3759	1299.9628	1673.8692	673.8204	730.5159	BST2
ENSG00000126709	4.6597	1.08E-34	1.19E-31	2281.3382	1274.0242	936.4514	3874.4154	1098.5913	32365.0309	50648.6526	54117.0072	39222.5765	38630.5875	IFI6
ENSG00000134326	4.4732	3.93E-21	1.40E-18	1.9726	2.1612	3.7338	5.8376	2.1436	37.5971	80.5364	124.5195	72.6584	46.9301	CMPK2
ENSG00000137959	3.9509	5.35E-19	1.31E-16	63.1239	30.7881	39.8490	301.6080	67.5232	635.0865	1648.3704	2175.0095	1128.8006	883.7023	IFI44L
ENSG00000111335	3.7181	1.01E-25	6.23E-23	45.3703	29.1761	27.3962	107.0222	39.6565	339.7131	757.2174	974.7226	583.8624	434.4018	OAS2
ENSG00000157601	3.3082	2.81E-15	4.32E-13	86.7954	81.0448	62.2641	360.9567	92.1745	615.7803	1329.7263	1985.1680	1085.5515	777.4460	MX1
ENSG00000111331	3.2077	3.70E-68	1.90E-64	49.3156	33.4985	32.3773	77.8343	38.5847	335.3257	468.3568	611.3705	382.3217	331.1673	OAS3
ENSG00000089127	3.1811	3.11E-27	2.08E-24	49.3156	38.9015	37.3584	135.2371	70.7386	305.8577	695.0643	882.8639	560.5079	417.9437	OAS1
ENSG00000026337	2.9459	1.98E-37	2.76E-34	30.5757	30.2567	19.9245	27.2420	25.7231	110.7591	289.7560	319.4641	204.1356	163.8127	HCP5
ENSG00000185885	2.9435	9.18E-16	1.50E-13	152.8783	83.2060	68.4905	327.8771	116.8258	649.3125	1293.8351	1583.0312	922.0701	741.1416	IFITM1
ENSG00000134321	2.8955	3.38E-07	1.18E-05	10.8494	6.4836	9.9622	33.0796	9.6462	37.5971	140.0633	264.3489	103.7978	49.7318	RSAD2
ENSG00000183486	2.8245	1.20E-11	1.07E-09	25.6441	19.4508	16.1887	67.1321	16.0769	103.6461	244.2354	287.8238	198.9457	119.5390	MX2
ENSG00000234745	2.7564	3.04E-36	3.94E-33	5739.4877	4304.7893	4556.4838	5057.2855	4614.0835	21770.7697	30888.3869	44132.9899	31154.8960	31226.2357	HLA-B
ENSG00000138646	2.6628	1.86E-22	7.96E-20	19.7262	19.4508	9.9622	26.2691	19.2923	52.8392	158.4466	196.9858	119.3674	105.3714	HERC5
ENSG00000138642	2.6455	9.89E-15	1.42E-12	76.9323	38.9015	34.8679	143.9935	62.1642	276.3897	499.8510	623.6183	383.1867	284.2371	HERC6
ENSG00000133106	2.5653	1.29E-18	2.91E-16	74.9597	70.2388	43.5848	154.6957	70.7386	279.4381	558.5025	672.6096	456.4993	353.0443	EPSTI1
ENSG00000135114	2.5249	1.96E-15	3.11E-13	8.8768	9.7254	6.2264	42.8089	16.0769	38.6133	116.4276	115.3337	80.4433	83.2345	OASL
ENSG00000204525	2.3335	5.68E-33	5.81E-30	6464.2846	6163.7271	5905.1233	6199.5043	5500.4591	20837.9545	37125.5377	40210.6245	28578.9818	29283.5056	HLA-C
ENSG00000243649	2.2594	7.79E-37	9.97E-34	52.1745	72.4000	78.4527	83.6719	55.7334	159.5335	502.4772	478.6858	280.2539	321.4270	CFB
ENSG00000185745	2.2399	4.34E-08	2.41E-07	201.2075	200.9911	179.3205	585.7033	180.0618	580.2151	1472.4158	2091.3158	1250.7629	831.4599	IFIT1
ENSG00000115267	2.2131	4.42E-13	4.89E-11	71.0144	71.3194	54.8679	157.8145	86.8155	190.0179	474.4645	612.3912	358.9672	273.6114	IFIH1
ENSG00000240652	2.2108	3.86E-52	3.45E-49	37.4798	30.2567	34.8679	44.7547	39.6565	150.3885	216.2228	228.6260	124.5573	156.7289	HLA-G
ENSG00000227766	2.1853	1.18E-50	4.53E-47	84.8228	94.0120	98.3772	126.4808	78.2411	278.4220	514.7328	546.0488	458.4401	424.1420	HCG4P5
ENSG00000137965	2.1084	8.60E-16	1.42E-13	323.5101	260.4240	214.1884	549.7049	284.0260	622.0561	1717.5266	1968.8376	1416.8394	1068.7669	IFI44
ENSG00000206341	2.0682	2.33E-45	5.11E-42	157.8098	127.5105	120.7923	343.0206	116.8258	404.4232	687.9270	754.2618	570.0227	487.8961	HLA-H
ENSG00000204642	2.0648	7.58E-15	1.56E-12	231.7832	150.2030	158.1507	214.0444	152.1951	530.4244	957.6831	987.9911	641.8161	732.1560	HLA-F
ENSG00000271581	2.0615	3.90E-19	9.67E-17	29.5823	25.9343	19.9245	34.0525	26.7849	79.2588	140.0633	146.9739	99.4728	112.4552	AL671883.2
ENSG00000166278	1.9595	3.44E-10	2.42E-08	18.7262	18.3702	11.2075	17.5127	15.0051	39.6294	77.0348	101.0445	49.3089	60.2122	C2
ENSG00000121858	1.9051	1.33E-08	6.40E-07	15.7610	11.8866	9.7358	17.5127	23.5795	28.4519	76.1594	80.6315	45.8440	38.9608	TNFSF10
ENSG00000119917	1.8727	6.52E-10	4.37E-08	182.4676	175.0568	140.7168	343.4440	169.3438	379.0197	996.2005	1294.1867	726.5843	492.3235	IFIT3
ENSG00000110492	1.8587	8.76E-13	9.34E-11	648.9529	676.4539	663.7349	647.9708	557.3341	1554.6921	3102.4029	3604.9427	1973.0223	1941.8441	MDK
ENSG00000204622	1.8579	1.16E-08	5.73E-07	16.7673	32.4179	17.4939	17.5127	9.6462	60.9683	70.0317	93.9000	45.8440	64.6396	HLA-J
ENSG00000115155	1.8279	5.26E-12	4.96E-10	35.5072	21.6119	31.1320	27.2420	23.5795	50.8069	128.8832	97.9826	118.5024	112.4552	OTOF
ENSG00000090030	1.8094	1.88E-05	1.15E-03	9.8631	15.1284	17.4839	17.5127	15.0051	30.4842	68.2809	45.9293	56.2238	64.6396	ETV7
ENSG00000228078	1.7904	4.58E-08	2.01E-06	21.6988	12.9672	14.9434	12.6481	13.9334	31.5003	50.7730	36.1359	71.7984	58.4413	HLA-U
ENSG00000128284	1.7466	2.42E-22	1.01E-19	40.4388	49.7075	52.3018	57.4028	55.7334	100.5977	217.9736	234.7499	170.4013	154.0723	APOL3
ENSG00000177989	1.7110	2.08E-10	1.53E-08	14.7947	19.4508	21.1698	20.4315	21.4359	52.8392	68.2809	77.5695	55.3588	64.6396	CDF3B
ENSG00000160932	1.6950	1.23E-27	9.03E-25	1669.8251	1610.0900	1475.6582	2063.5826	1459.7867	4359.2345	6340.4921	7164.9766	4631.9748	4659.3634	LY6E
ENSG00000105894	1.6162	1.11E-07	1.79E-05	179.5087	156.6866	168.1130	179.0190	146.8361	271.3093	625.0326	659.3412	615.0017	478.1559	PTX
ENSG00000108679	1.5891	1.03E-76	7.93E-73	1277.2732	1656.5557	1757.0917	1511.9318	1355.8224	4814.1061	4692.9971	4857.2826	4136.3405	4532.1149	LGALS3BP
ENSG00000166710	1.5631	1.41E-18	3.12E-16	40812.5176	30490.1339	29498.2201	39087.4270	32474.3591	72666.1043	124055.8464	115650.0713	102892.1192	93799.2172	B2M
ENSG00000274286	1.5477	1.97E-06	5.64E-05	10.8494	20.5313	11.2075	12.6481	19.2923	26.4195	52.5238	70.4250	41.5191	30.9916	ADRA2B
ENSG00000025708	1.5293	1.40E-41	2.38E-38	195.2896	153.4448	149.4337	201.3963	200.4259	450.1454	595.2692	600.1433	449.7903	506.4810	TYMP
ENSG00000100342	1.5235	4.83E-40	7.11E-37	202.1938	199.9105	204.2261	253.9345	220.7901	490.7949	716.0738	872.6574	555.3100	527.7424	APOL1

FIG. 24A

FIG. 24A, continued

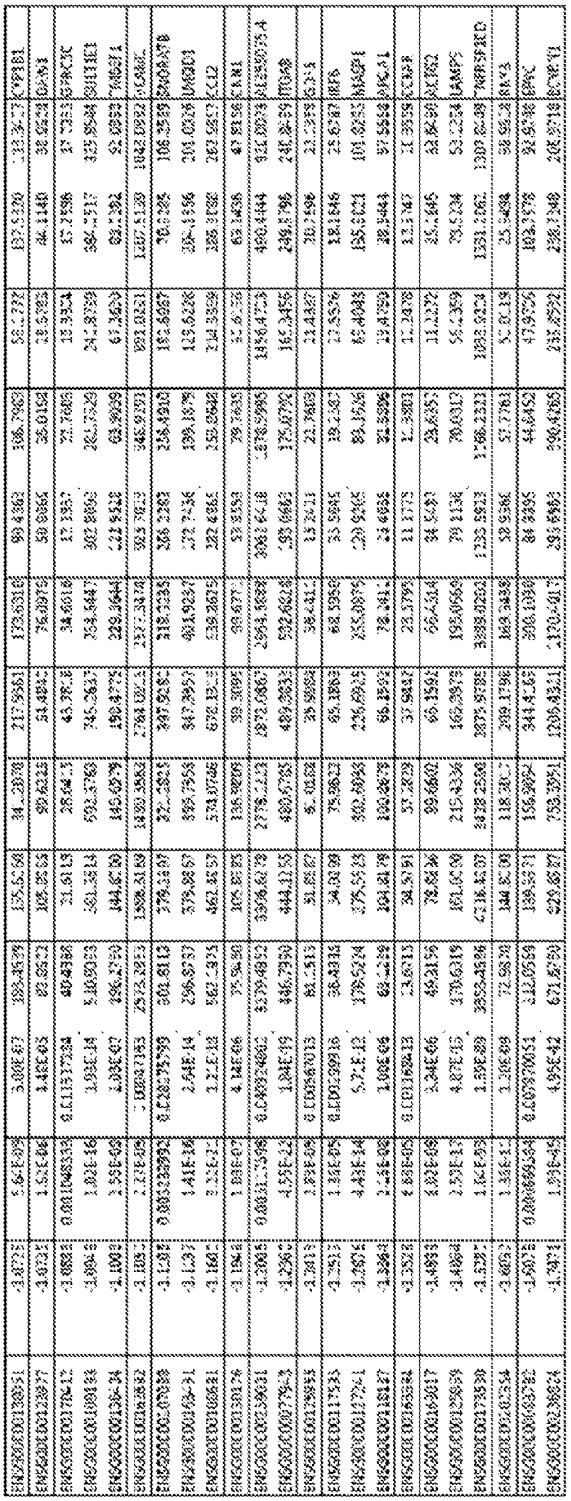


FIG. 24B

Table 52: Significant DEGs following targeting of dSaCas9-repressors to DUX4

ID	log2FoldChange	padj	Mock Expt 1	Mock Expt 2	Mock Expt 3	Mock Expt 4	SET Expt 3	SET Expt 1	SET Expt 4	SET Expt 2	SET Expt 5	Short Gene Name
ENSG00000001	5.3076	2.34E-48	9.91E-46	14.5804	31.1417	60.8351	16.5021	1488.8838	1218.8562	1228.9679	944.5884	1037.6969	BST2
ENSG00000003	5.5018	2.65E-63	1.69E-60	116.6433	104.2048	383.8553	124.7971	7594.2849	7521.8139	8345.4935	6286.5820	7195.8809	IFI27
ENSG00000001	5.0573	9.30E-48	3.09E-45	1227.8790	900.7124	3824.5095	1057.1652	51662.0853	47350.9159	47920.3600	44241.4976	44024.4244	IFI6
ENSG00000002	4.7966	5.61E-35	6.08E-33	2.0619	3.5933	5.6174	3.0628	110.1838	96.69894	103.7203	67.9475	77.2753	CMPK2
ENSG00000001	4.3818	3.66E-24	3.53E-22	46.9485	36.3282	280.2321	64.9770	2017.5838	1425.0687	2083.6099	1344.5809	1096.7242	IFI44L
ENSG00000002	3.9737	3.24E-33	6.89E-31	28.3154	26.3506	102.9856	38.1611	764.6942	557.2838	854.9951	588.3710	529.4834	OAS2
ENSG00000001	3.6443	1.88E-33	1.75E-31	78.3094	58.8878	347.3422	86.6887	1748.8143	1215.7080	1776.4562	930.2112	1086.1873	MX1
ENSG00000001	3.5339	9.84E-21	7.11E-19	6.2487	9.5820	31.8319	9.2824	208.1149	124.4027	259.4688	94.7437	134.1506	RSAD2
ENSG00000003	3.5538	1.15E-41	3.05E-39	32.2853	31.1417	74.8986	37.1297	484.0852	520.8732	509.5739	446.9225	460.1149	OAS3
ENSG00000002	3.4760	4.61E-73	3.87E-70	29.1608	19.1641	26.2145	24.7331	313.0134	287.2388	364.1335	212.4537	238.1561	HCP5
ENSG00000003	3.4558	3.18E-29	4.54E-27	80.1923	65.8766	315.5103	112.4205	1638.8385	1099.3965	1615.3264	998.5027	920.2298	IFITM1
ENSG00000001	3.4476	2.53E-42	7.11E-40	37.4925	35.9327	130.1363	68.0711	813.6648	581.5575	797.5936	489.0368	585.7752	OAS1
ENSG00000001	3.1465	1.98E-18	1.24E-16	38.7462	15.5708	64.8009	15.4707	267.4346	198.2352	234.6453	173.2183	171.2260	MX2
ENSG00000002	3.0728	0	0	4135.6098	4381.5888	4866.5382	4440.0938	42515.2875	36428.7607	41002.5026	32780.3764	34071.3325	HLA-B
ENSG00000003	3.0155	3.08E-34	6.37E-32	38.7462	9.5820	25.2783	18.5649	204.3573	98.3062	120.1934	118.6089	359.8823	HERC5
ENSG00000001	3.0137	5.16E-24	4.81E-22	37.4925	38.5372	138.5624	59.8201	557.5111	424.7898	563.9544	356.0068	367.0382	HERC6
ENSG00000001	2.9894	5.43E-30	8.51E-28	67.6848	41.9215	148.8638	68.0711	678.9958	509.7478	765.3666	466.7282	435.7478	EPSTI1
ENSG00000002	2.8577	5.59E-65	1.04E-06	3.0415	5.9888	1.8725	12.3756	48.9706	24.2737	34.2401	24.6822	35.4644	RTP4
ENSG00000001	2.6987	1.73E-21	1.33E-19	17.7648	10.7795	16.8522	14.4393	132.7856	91.0264	97.6850	93.7867	82.3438	C2
ENSG00000002	2.6336	0	0	5940.4786	5679.7582	5965.8731	5793.0456	40168.1083	36466.1827	36499.9313	31471.2992	33261.7430	HLA-C
ENSG00000001	2.6227	9.57E-20	6.49E-18	193.7112	172.4768	563.6119	172.2720	2067.1230	1266.2282	2042.3204	943.6094	1134.4838	IFIT1
ENSG00000001	2.6122	1.36E-29	2.01E-27	68.7369	38.5372	151.8687	83.5418	636.2582	387.3679	581.0744	367.3937	359.1355	IFIH1
ENSG00000001	2.5928	1.19E-18	7.56E-17	9.3731	5.9888	41.1942	15.4707	136.5825	91.0264	103.7961	58.3775	86.9301	OAS3L
ENSG00000001	2.5735	8.32E-62	5.10E-59	69.7777	75.4586	280.5160	53.6318	571.6372	393.4363	440.0858	318.7806	298.5478	CFB
ENSG00000001	2.4789	8.80E-107	1.16E-103	133.8920	116.1823	137.6362	112.4155	813.3987	698.8804	698.9006	599.0867	555.8559	HLA-H
ENSG00000001	2.4689	2.57E-78	2.73E-75	90.6668	94.6237	121.7102	75.2808	553.7441	495.5881	624.3780	462.2346	468.0176	HSD4P5
ENSG00000002	2.4641	6.47E-145	1.89E-141	144.7627	252.1150	265.9731	146.4551	1014.2358	867.7849	882.1857	783.7891	797.2983	HLA-F
ENSG00000001	2.4185	3.72E-39	9.26E-37	250.9914	206.0149	528.9713	273.3159	1884.4252	1479.5945	1936.5790	1218.2705	1277.6091	IFI44
ENSG00000002	2.3321	1.24E-34	2.59E-32	29.1608	33.5372	43.0967	38.1611	239.2824	165.8703	138.9345	178.9604	171.2260	HLA-G
ENSG00000002	2.3146	1.61E-67	2.79E-06	5.2073	3.5933	11.2348	5.1569	35.7862	35.3992	28.1977	25.8393	27.2205	KCNAP7
ENSG00000001	2.2943	5.55E-31	9.17E-29	168.7162	135.3464	330.4908	162.9581	1198.8372	245.4050	1277.9608	851.7221	951.6381	IFIT3
ENSG00000001	2.2818	4.44E-09	1.06E-07	6.2487	13.1753	7.4859	9.2824	54.6210	31.3535	61.4307	29.6672	31.6109	SCN2A
ENSG00000001	2.2537	1.42E-23	1.28E-21	20.8252	29.9433	26.2145	22.6904	108.3863	118.3343	122.8615	134.9381	96.5890	OTOF
ENSG00000002	2.2166	2.50E-33	2.18E-31	34.9950	19.1641	32.7681	25.7645	137.3351	120.3571	111.7838	126.3850	107.1260	AL671883.2
ENSG00000001	2.1918	1.46E-11	4.57E-10	11.4580	3.5933	16.8522	22.6904	64.9802	47.5350	74.5225	51.6784	50.0507	TNFSF10
ENSG00000002	2.1867	2.41E-176	5.48E-173	651.9527	638.4039	623.5808	536.1179	3157.8599	2765.1794	2952.7039	2533.3987	2488.4840	MX2
ENSG00000001	2.1422	3.85E-11	1.14E-09	12.4975	14.3731	12.1710	13.4879	52.4462	50.5702	99.6991	37.3233	46.5383	HLA-J
ENSG00000001	2.0072	5.57E-12	1.84E-10	14.5804	15.7686	16.8522	14.4393	75.3393	57.6580	64.4519	48.8074	67.6123	ETV7
ENSG00000001	1.9933	3.79E-70	2.88E-67	151.0314	161.6979	172.2668	141.2992	655.4522	565.3750	771.4090	529.2251	582.8505	PTN
ENSG00000001	1.9604	3.62E-328	1.15E-324	1551.7725	1419.3427	1985.2490	1404.7405	6502.7263	6646.9492	5633.5012	5944.9303	6358.8662	IFI6
ENSG00000001	1.8885	2.31E-67	4.16E-65	10.4146	9.5820	9.3623	13.4879	42.3784	44.5038	46.3248	34.4523	26.3425	GBP5
ENSG00000001	1.8736	4.17E-10	1.07E-08	33.2437	16.7686	16.8522	9.2824	102.6438	69.7869	51.3801	61.2485	39.7096	HLA-J
ENSG00000001	1.8661	9.04E-29	1.35E-26	47.0971	50.3057	55.3377	53.6318	236.0189	166.8817	202.4193	173.2581	151.9602	APOL3
ENSG00000001	1.8246	0	0	29385.7756	28372.4413	37613.1381	31149.8227	133859.7736	107705.4572	120353.4774	98865.5032	103358.6784	B2M

FIG. 24C

ENSG0000001	1.7975	1.84E-17	1.03E-15	453.0342	362.5345	1185.2703	485.7803	2439.1110	3858.0638	1964.7767	1556.0941	1687.6733	ISG15
ENSG0000001	1.7810	3.28E-06	4.29E-05	9.3731	5.9888	14.9797	9.2824	42.3784	34.3877	29.1048	33.4953	26.3425	HOXB2
ENSG0000001	1.7559	1.37E-23	1.28E-21	55.1973	41.9215	102.0493	51.5696	245.7946	180.0300	251.7653	164.6053	164.2013	TUB3
ENSG0000001	1.7253	3.99E-67	2.76E-64	192.6697	156.4320	244.1587	212.4644	789.1795	724.1655	768.3878	588.5596	579.5340	APOL1
ENSG0000001	1.7239	1.81E-61	1.07E-58	152.0529	137.7419	196.6088	180.4916	624.5382	563.3522	542.8061	514.8700	494.3601	PSMB9
ENSG0000001	1.7154	8.41E-275	3.35E-271	1596.5552	1630.0335	1454.9052	1304.6965	4797.3321	5221.8805	4412.9428	5556.3853	4995.4077	LOC653879
ENSG0000001	1.7010	2.58E-181	6.86E-178	9088.8042	9087.3738	9040.3604	8783.2377	35238.0903	29828.3361	27668.1446	27033.5466	26605.6805	HLA-A
ENSG0000001	1.6849	4.09E-09	0.000041847	6.2487	13.1753	11.2248	6.1883	26.3648	23.3623	35.2471	32.5383	21.0746	PSTI2
ENSG0000001	1.6634	1.08E-09	2.62E-08	18.7462	20.3618	19.6605	20.6276	66.8637	55.6373	63.4449	71.7756	49.1726	C20F38
ENSG0000001	1.6508	2.42E-36	5.67E-34	86.4410	91.6394	96.4318	84.5732	397.5804	291.3844	277.9488	258.3830	296.7817	SLC15A3
ENSG0000001	1.6483	9.54E-128	1.89E-124	1570.5167	1740.3393	1079.3722	1826.5752	6369.9407	5554.7486	5126.9612	5190.8084	4275.3866	C1R
ENSG0000001	1.6434	7.96E-13	2.91E-11	32.2852	44.3170	30.8957	33.0042	109.2420	119.3457	143.0027	88.6447	81.6616	PSMB8-AS1
ENSG0000001	1.6270	3.11E-59	1.18E-47	147.8870	143.7307	193.8091	192.8582	517.0162	503.6794	509.5730	519.6550	547.0450	TYMP
ENSG0000001	1.6250	1.45E-28	1.98E-26	89.5654	105.4025	95.4557	80.4477	325.1243	255.8853	322.2596	311.0274	196.8903	SERPING1
ENSG0000001	1.6050	7.41E-33	1.42E-30	80.1923	80.3496	158.3333	102.2636	368.3310	275.1020	371.6056	252.6500	277.4739	IFIT2
ENSG0000001	1.5680	2.61E-11	7.97E-10	26.0365	27.5484	34.6406	34.0356	84.7568	75.8553	86.6073	93.7867	111.5364	KREMEN2
ENSG0000001	1.5328	1.27E-29	1.90E-27	80.1923	91.0294	110.4754	100.0439	318.3087	260.9423	255.7936	241.1659	293.2793	ANGPTL7
ENSG0000001	1.5228	4.80E-76	4.50E-73	534.1680	543.7812	558.9328	524.8028	1853.3476	1467.5477	1878.1694	1246.0337	1421.6145	STAT2
ENSG0000001	1.5207	2.94E-05	0.0001119	11.4560	5.9888	17.7884	13.4079	38.6114	27.3079	40.2825	28.6672	31.6409	IL15RA
ENSG0000001	1.4898	4.53E-05	0.00043694	22.5111	8.3843	8.4261	7.2197	22.6018	72.8211	13.0918	37.3233	51.8068	XIST
ENSG0000001	1.4852	9.57E-06	0.00011832	19.7837	30.7798	12.1710	18.5649	50.8541	39.4448	32.2160	53.5934	41.3698	ADAR2B
ENSG0000001	1.4689	3.26E-05	0.00034112	16.6633	7.1865	11.2348	15.4707	34.8444	42.4790	28.1977	35.4093	40.3918	LTA
ENSG0000001	1.4515	5.62E-12	1.82E-10	32.2852	38.3282	37.4493	58.7897	127.1351	123.3913	116.8191	90.9157	97.4671	ACSM5
ENSG0000001	1.4479	2.95E-05	0.00031225	10.4146	11.9776	15.9160	14.4383	39.5532	35.3992	40.2825	30.6242	28.9767	AL442671.1
ENSG0000001	1.4206	1.61E-29	2.35E-27	145.8041	186.8499	189.1180	132.0167	475.5796	439.9609	471.3047	350.2647	431.1382	USP18
ENSG0000001	1.4081	7.28E-06	8.89E-05	19.7877	13.5708	29.0313	11.3452	44.2619	42.4790	36.3954	53.5924	48.2945	LY75
ENSG0000001	1.3970	3.85E-16	2.04E-14	62.4875	56.3945	72.0899	53.6318	161.9796	152.7221	185.8993	158.8632	136.9808	LINC01358
ENSG0000001	1.3900	3.15E-56	1.31E-53	342.6397	362.5345	343.5971	340.3556	998.2462	891.0472	1024.1814	780.9181	822.7627	BTN3A3
ENSG0000001	1.3766	2.71E-05	0.00029157	21.8706	9.5820	15.9160	16.5021	45.2036	36.4106	45.3178	44.0233	36.6014	CIQTNF7
ENSG0000001	1.3730	4.39E-74	3.89E-71	538.4338	477.9046	748.0497	556.9456	1747.8726	1357.3046	1765.3785	1185.7332	1337.1228	SAMHD1
ENSG0000001	1.3510	2.01E-26	2.39E-24	94.7737	105.4025	115.1566	120.6715	281.5808	257.9081	311.1830	267.0051	242.3506	IL20RA
ENSG0000001	1.3436	1.63E-59	8.67E-57	391.5882	396.4572	579.5279	478.4979	1302.4387	1059.9517	1468.2954	904.3720	977.3053	PARP9
ENSG0000001	1.3331	1.18E-87	1.57E-84	1275.7861	1283.9943	2216.9984	1626.8911	4558.0197	3594.5160	4610.3268	3139.4702	3325.2963	PARP14
ENSG0000001	1.3308	1.38E-24	1.39E-22	97.8571	117.3803	121.7102	125.8284	382.2391	305.4441	286.0195	287.1022	247.6191	CHAC1
ENSG0000001	1.3249	0.000119663	0.00168424	11.4560	13.1753	17.7884	13.4079	30.1337	24.3737	38.2683	38.2803	46.3938	TRAIP1
ENSG0000001	1.3151	1.05E-77	1.05E-74	1223.6849	1183.3828	1687.0928	1421.3764	3873.3815	3209.9182	3859.6591	2922.7908	2337.4539	C1S
ENSG0000001	1.2983	0.001109315	0.00737126	13.5380	27.5484	7.4899	6.1883	35.7862	29.3307	28.1977	30.6242	26.3425	PLEKHG6
ENSG0000001	1.2856	0.000388254	0.00319528	11.4560	30.7798	17.7884	13.4079	38.6114	19.2167	35.2471	33.4953	28.9767	APOL6
ENSG0000001	1.2842	2.90E-49	1.65E-46	297.8570	259.3310	303.3393	315.6025	849.4518	703.9374	720.6489	572.2905	720.9052	TPPP3
ENSG0000001	1.2833	2.12E-14	9.18E-13	505.1071	631.2173	1022.3658	1086.0438	2671.8317	2670.8399	1981.8967	1734.6975	1592.8405	NPNT
ENSG0000001	1.2742	5.94E-59	3.05E-56	501.3459	501.8597	873.5049	632.2363	1751.6395	1317.9598	1858.0282	1170.9059	1309.2201	DDX58
ENSG0000001	1.2702	3.80E-06	4.92E-05	17.7048	27.5484	20.5971	33.0042	66.8617	49.5588	80.5649	46.8934	37.7575	CASP1
ENSG0000001	1.2637	4.40E-08	8.44E-07	31.2437	38.3282	34.6406	24.7531	71.5724	77.8781	72.5084	91.8727	69.3685	C3
ENSG0000001	1.2610	8.85E-10	2.19E-08	33.4956	46.7125	61.7913	46.4121	157.2709	64.7299	143.9027	88.0447	89.5644	WISP2
ENSG0000001	1.2553	9.37E-07	1.36E-05	37.4925	29.9439	44.0819	16.5021	78.1646	58.6615	65.4590	80.3685	93.9548	SLC31A2

FIG. 24C, continued

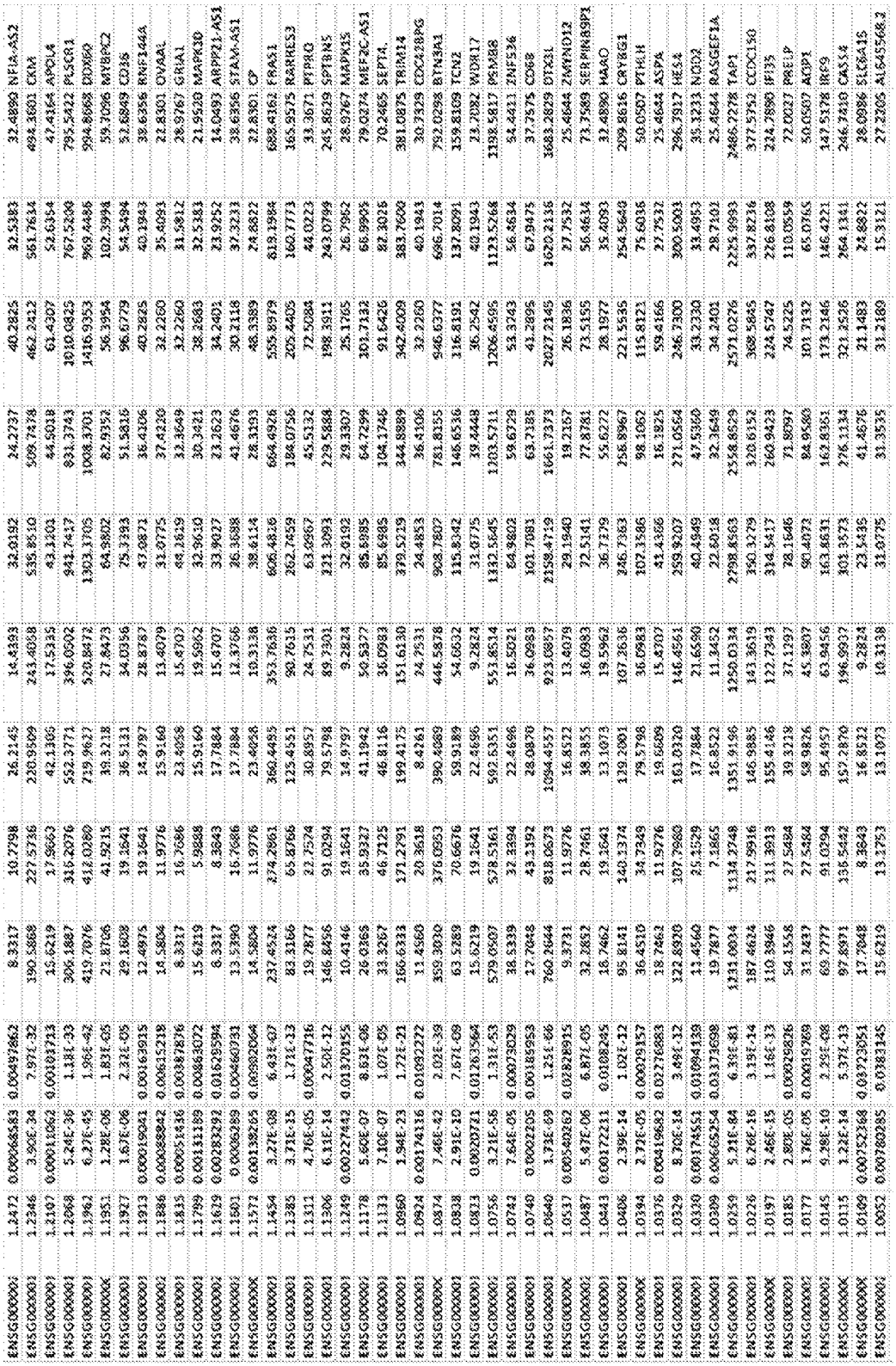
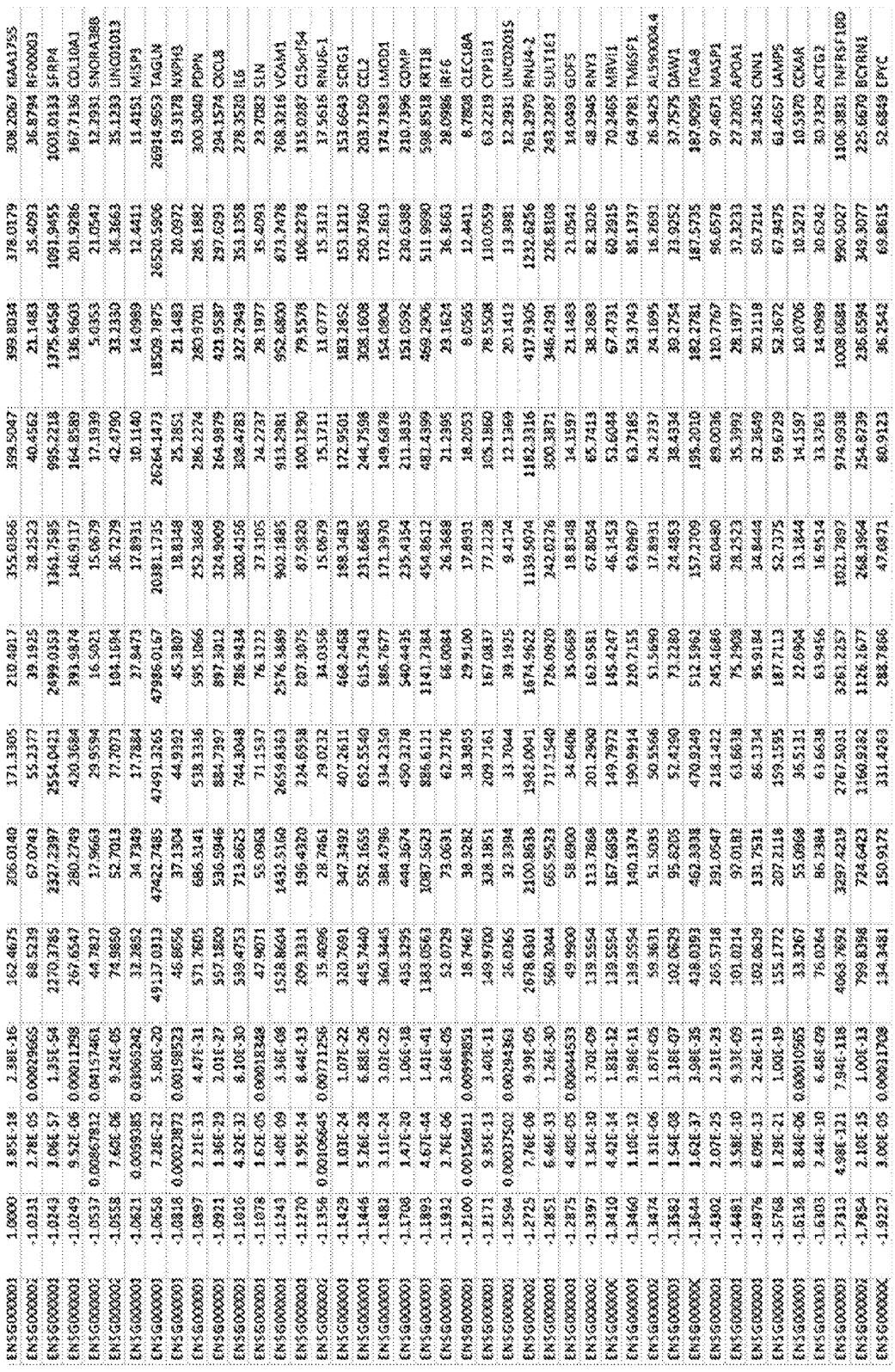


FIG. 24D



ENSG00000003	1.9800	3.85E-18	2.39E-16	162.4675	206.0140	171.3305	210.4817	355.0365	399.5047	399.8834	378.0179	308.2267	KIAA1755
ENSG00000004	-1.0131	2.78E-05	0.000294665	88.5239	67.0743	55.2377	39.1925	38.2523	40.4562	21.1483	35.4093	36.8794	RP2000003
ENSG00000005	-1.0249	3.06E-57	1.35E-54	2270.3765	2327.2397	2554.0421	2499.0353	1861.7585	995.2218	1375.6458	1691.9455	1601.0133	SFRP4
ENSG00000006	-1.0249	9.52E-08	0.000211258	267.6547	260.2749	420.3684	393.9874	146.9117	164.8389	136.9603	201.9286	167.7136	CD1084
ENSG00000007	-1.0537	0.002867812	0.041574461	44.7817	17.9663	29.9594	16.5921	15.8679	17.1939	5.0353	21.0542	12.2931	SNORA38B
ENSG00000008	-1.0558	7.66E-06	9.24E-05	74.9850	52.7013	77.7073	104.1894	36.7279	42.4790	33.2330	36.3663	35.1233	LINC01013
ENSG00000009	-1.0621	0.00599385	0.03963242	32.2852	34.7349	17.7884	17.8473	17.8931	10.1140	14.0989	12.4411	11.4151	MSP3
ENSG00000010	-1.0658	7.28E-22	5.80E-20	49137.0313	47422.7485	47491.3265	47986.0157	20381.1735	26264.1473	18503.7875	26520.5806	26814.9653	TAGLN
ENSG00000011	-1.0818	0.000023872	0.001598533	46.8856	37.1304	44.9392	45.3807	18.8348	25.2851	21.1483	20.0372	19.3178	NKPK3
ENSG00000012	-1.0897	2.21E-33	4.47E-31	571.7605	686.3141	538.3338	595.1866	252.3868	286.2274	283.9701	285.1882	300.3040	PDPN
ENSG00000013	-1.0921	1.36E-29	2.01E-27	557.1820	536.5946	884.7397	897.2812	324.9009	264.9879	421.9587	297.6293	294.1574	CXCL8
ENSG00000014	-1.1016	4.32E-32	8.10E-30	539.4753	713.8625	744.3048	788.9434	303.4156	328.4783	327.2943	353.1358	278.3533	IL6
ENSG00000015	-1.1078	1.62E-05	0.000218348	47.9071	55.0968	71.1537	76.3212	27.3105	24.2237	28.1977	35.4093	23.7882	SIX
ENSG00000016	-1.1243	1.40E-09	3.36E-08	1518.8664	1432.5160	2659.6303	2576.3689	902.1685	913.2981	952.6850	671.9478	768.3216	VCAM1
ENSG00000017	-1.1279	1.95E-14	8.44E-13	209.3331	196.4320	324.6938	287.4075	87.5820	100.1890	79.1578	166.2278	115.0287	C15orf54
ENSG00000018	-1.1356	0.002106645	0.037211256	35.4096	28.7461	29.0232	34.0356	15.0679	15.1711	11.0777	15.3111	17.5616	RNU6-1
ENSG00000019	-1.1429	1.03E-24	1.07E-22	320.7691	347.3492	407.2611	468.2468	198.3483	172.9501	183.2852	153.1212	153.6643	SCRG1
ENSG00000020	-1.1446	5.26E-28	6.88E-26	445.7440	552.1655	632.5548	615.7343	231.8685	244.7598	208.1608	250.7360	203.7150	CCL2
ENSG00000021	-1.1482	3.11E-24	3.03E-22	360.3445	384.4796	334.2159	385.7877	171.3970	149.6878	154.0804	172.3613	174.7383	LMCD1
ENSG00000022	-1.1708	1.47E-20	1.06E-18	435.3295	448.3674	450.3178	540.4435	235.4354	211.3835	151.0592	230.6388	210.7396	COMP
ENSG00000023	-1.1893	4.67E-44	1.41E-41	1383.0563	1087.5623	886.6121	1141.7384	454.8612	482.4399	469.2936	511.9990	598.8518	KRT18
ENSG00000024	-1.1932	2.76E-06	3.66E-05	52.0729	73.0631	62.7176	66.0884	26.3668	21.2395	28.1624	36.3663	28.0986	IRF6
ENSG00000025	-1.2100	0.001356811	0.009998851	38.7462	38.9282	38.3855	29.9100	17.8931	18.2053	8.0565	12.4411	8.7828	CLEC18A
ENSG00000026	-1.2171	9.35E-13	3.40E-11	149.9700	328.1851	209.7161	167.0837	77.2128	105.1860	78.5508	110.0559	63.2219	CYP1B1
ENSG00000027	-1.2594	0.000375402	0.00294363	26.0365	32.3394	33.7044	39.1925	9.4174	12.1369	20.1412	13.3981	12.2931	LINC02015
ENSG00000028	-1.2725	7.76E-06	9.39E-05	2678.6301	2100.8638	1981.6941	1674.6622	1133.5974	1182.3116	417.9305	1232.6256	761.2879	RNU4-2
ENSG00000029	-1.2851	6.46E-33	1.26E-30	580.3044	655.9523	717.1540	726.0970	242.8276	300.3871	346.4291	226.8108	263.2287	SULT1E1
ENSG00000030	-1.2875	4.40E-05	0.000344533	49.9900	58.6900	34.6406	35.0689	18.8348	14.1597	21.1483	21.0542	14.0493	GOS2
ENSG00000031	-1.3397	1.34E-10	3.70E-09	139.5554	113.7868	201.2900	162.9581	67.8054	65.7413	38.7683	82.3026	48.2945	RNF3
ENSG00000032	-1.3410	4.42E-14	1.83E-12	139.5554	167.6858	149.7972	145.4247	46.1453	53.6048	67.4731	60.2815	70.2465	MRVI1
ENSG00000033	-1.3460	1.10E-12	3.88E-11	139.5554	140.1374	190.9914	220.7135	63.8967	63.7169	53.3743	85.1737	64.9781	TMEM71
ENSG00000034	-1.3474	1.31E-06	1.67E-05	59.3831	51.5035	50.5566	51.5690	17.8931	24.2237	24.1895	16.2691	35.3425	AL590004.4
ENSG00000035	-1.3582	1.54E-08	3.18E-07	102.0629	95.8205	52.4290	73.2280	24.4853	38.4334	30.2754	23.9252	37.7575	DAW1
ENSG00000036	-1.3644	1.62E-37	3.98E-35	428.0393	462.3838	470.8249	512.3962	157.2709	195.2018	182.2781	187.5735	187.9285	ITGA8
ENSG00000037	-1.4302	2.07E-25	2.31E-23	265.5718	291.0547	218.1422	245.4686	83.6480	89.0036	110.7767	96.6578	97.4671	MASP1
ENSG00000038	-1.4481	3.58E-10	9.33E-09	101.0214	97.0182	63.6638	75.1958	28.2523	35.3992	28.1977	37.3233	27.2265	APOA1
ENSG00000039	-1.4976	6.09E-13	2.26E-11	102.0629	131.7531	86.1374	98.9184	34.8444	32.3649	32.2118	50.7214	34.2452	CNN1
ENSG00000040	-1.5768	1.28E-21	1.00E-19	155.1772	207.2118	159.1595	187.7113	52.7375	59.6729	52.3672	67.9475	61.4657	LAMP5
ENSG00000041	-1.6136	8.84E-06	0.000109565	33.3267	55.0968	36.5131	22.6964	13.1844	14.1597	10.0706	10.5271	10.5370	CCKAR
ENSG00000042	-1.6303	3.44E-10	6.48E-09	76.0264	86.2384	63.6638	63.9456	16.9514	33.3763	14.0989	20.6342	30.7329	ACTG2
ENSG00000043	-1.7313	4.58E-121	7.34E-118	4063.7692	3297.4219	2767.5031	3261.2257	1021.7897	974.9338	1008.8884	990.5027	1106.3831	TNFRSF10D
ENSG00000044	-1.7854	2.10E-15	1.00E-13	799.8398	724.6423	3160.8282	1126.1677	268.3964	254.8739	236.6534	349.3077	225.6679	BCYRN1
ENSG00000045	-1.9227	3.00E-05	0.000211708	134.3481	150.9172	331.4263	288.7666	47.6971	80.9123	36.2542	69.8615	52.6849	EPYC

FIG. 24D, continued

Table 32: Significant DEGs following targeting of dCas9-repressor to DUX4

ID	log2FoldChange	pvalue	padj	Mock-Expt 1	Mock-Expt 2	Mock-Expt 3	Mock-Expt 4	Mock-Expt 5	HP1g-Expt 2	HP1g-Expt 4	HP1g-Expt 5	HP1g-Expt 3	HP1g-Expt 1	Gene.name
ENSG00000001	5.4191	5.19E-45	3.49E-42	32.9515	14.0381	30.0270	58.7013	15.9246	1085.7322	1577.2222	1478.6639	1076.4012	788.9979	BST2
ENSG00000001	5.4129	1.52E-56	1.78E-53	198.6243	112.3648	169.4738	370.2699	120.4312	6574.8883	7492.3633	7646.9656	6686.7915	5579.9814	IFI27
ENSG00000001	4.8429	4.53E-38	2.03E-35	2117.3333	1182.2090	868.4719	3689.1528	1020.1819	43798.6265	51838.6323	50191.9816	44633.2190	35298.7482	IFI6
ENSG00000001	4.8220	5.90E-27	1.06E-24	1.8886	2.8054	3.4646	5.4186	1.9966	66.8633	105.9661	112.7317	73.0081	55.6532	CMPK2
ENSG00000001	4.3284	2.53E-39	1.23E-36	38.1884	47.1179	36.9563	279.9682	62.7039	922.2886	2548.8798	1890.1345	1245.8174	1101.3457	IFI44L
ENSG00000001	3.9484	4.69E-41	6.48E-38	42.1047	27.0735	25.4074	99.3407	36.8261	486.8816	958.1569	793.8189	541.0086	539.9333	OAS2
ENSG00000001	3.6226	1.50E-29	3.62E-27	80.5481	75.1041	57.7441	335.0491	85.5957	887.2650	1858.3113	1610.1842	1111.0332	978.3239	MX1
ENSG00000001	3.5843	1.06E-106	2.84E-103	45.7660	31.6044	30.0270	72.2478	35.8308	386.3121	540.9850	541.1122	408.0965	517.4767	OAS3
ENSG00000001	3.3808	3.71E-53	3.33E-48	45.7660	36.6980	34.6463	125.3303	65.6888	453.8637	833.2284	721.4828	565.3446	415.9341	OAS1
ENSG00000001	3.3803	1.27E-29	3.11E-27	141.8745	77.2096	63.5186	304.3438	108.4876	979.6000	1811.4632	1546.3029	1201.6732	964.6548	IFITM1
ENSG00000001	3.3671	7.50E-32	2.24E-29	10.0665	6.0163	9.2391	30.7953	8.9577	71.1086	186.2773	156.8849	128.2321	74.2042	RSAD2
ENSG00000001	3.2709	1.49E-52	1.42E-49	28.3749	28.8762	18.4781	25.2857	23.6872	208.8191	339.0916	321.2853	234.0003	143.5266	HERC5
ENSG00000001	3.0636	8.94E-21	1.26E-18	23.7983	18.8490	15.0135	62.3137	34.9295	128.4199	291.1260	248.9491	179.7122	189.8886	MX2
ENSG00000001	2.9701	7.70E-30	3.94E-27	71.3949	36.6980	32.3357	133.6594	57.7274	378.8919	673.7215	563.6584	382.8244	377.8557	HERC6
ENSG00000001	2.9496	7.40E-86	1.71E-82	5317.6892	4078.6696	4225.7164	4694.3002	4284.7638	33753.1547	40081.9687	40791.9583	33299.1733	27490.7877	HLA-B
ENSG00000001	2.9492	3.49E-34	1.31E-31	18.3864	18.8490	9.2391	24.3836	17.9154	95.5190	182.9310	186.3467	120.7441	104.4717	HERC5
ENSG00000001	2.7449	6.26E-28	3.46E-25	69.5643	65.1769	40.4209	143.5925	65.6888	351.2975	738.3388	631.2974	456.7685	341.7299	EPSTI1
ENSG00000001	2.7118	1.87E-09	6.85E-08	11.8991	1.0927	5.7744	1.8062	11.9436	26.5390	59.1179	43.2138	34.6320	31.2439	RTP4
ENSG00000001	2.6803	1.16E-17	1.22E-15	8.2379	9.8245	5.7744	39.7363	14.9295	54.1274	111.5423	109.9134	102.0241	65.4169	OAS1
ENSG00000001	2.6263	4.02E-73	7.21E-70	48.5119	67.1824	72.7576	77.6664	51.7556	362.9720	587.5220	453.1393	352.8724	284.1240	CFB
ENSG00000001	2.5747	6.39E-27	1.34E-24	186.7233	186.5083	166.3021	343.6646	167.2103	939.2698	2260.9827	1761.4325	1206.5094	893.3324	IFIT1
ENSG00000001	2.5249	7.70E-223	1.24E-218	5999.0021	5719.5252	5476.4545	5754.5365	5107.8764	33861.4708	34696.8082	36102.3204	31446.8272	26199.9450	HLA-C
ENSG00000001	2.5035	1.71E-21	2.53E-19	65.9039	66.1796	32.3357	146.3018	80.6152	315.2126	616.6344	496.0194	389.3764	238.0295	IFI44
ENSG00000001	2.4994	3.42E-21	4.97E-19	18.3864	17.6463	10.3939	16.2558	13.9342	72.1699	97.0427	103.3374	82.3681	77.1333	C2
ENSG00000001	2.4857	3.51E-40	1.81E-37	34.7821	28.0762	23.3367	41.5425	36.8261	232.4295	166.1995	232.0394	198.4322	181.3812	HLA-G
ENSG00000001	2.3492	6.63E-34	2.28E-31	309.1247	241.6560	198.6899	530.2500	263.7543	1199.2936	1988.8170	1849.7390	1371.2415	1116.9687	IFI44
ENSG00000001	2.3441	2.91E-73	5.87E-70	146.4511	118.3112	112.0236	332.7553	108.4876	664.3874	660.3363	774.3810	630.8647	480.3746	HLA-H
ENSG00000001	2.3267	3.88E-66	6.26E-63	78.7175	87.2368	91.2357	117.4027	72.6569	464.8589	482.9825	518.5657	378.1444	393.4776	HCG4P5
ENSG00000001	2.3195	9.67E-29	2.20E-26	215.1060	139.3763	146.6703	198.6814	141.3315	740.6026	886.7692	968.5530	783.4969	629.7594	HLA-F
ENSG00000001	2.2108	6.16E-08	1.78E-06	12.8345	5.8136	3.4646	10.8372	4.9766	26.5390	41.1710	37.5772	33.6960	27.3384	HCG4P7
ENSG00000001	2.1967	8.90E-09	2.87E-07	5.4919	6.0163	12.7037	7.2248	8.9577	27.5944	49.0791	53.5475	29.8530	28.3837	SCO2A
ENSG00000001	2.1841	6.56E-31	1.71E-28	169.3341	162.4489	130.5018	318.7934	157.2373	573.1138	1321.7881	1069.0721	735.6998	591.6810	IFIT3
ENSG00000001	2.1639	8.99E-23	1.47E-20	32.9515	20.0544	28.6721	25.2857	21.9966	135.8492	101.5044	120.2471	112.3201	108.3772	OTOF
ENSG00000001	2.1176	6.58E-13	3.99E-11	9.1532	14.0381	16.1684	16.2558	13.9342	44.5755	74.7340	77.0333	48.6721	37.6859	ETV7
ENSG00000001	2.1022	3.12E-40	1.68E-37	602.2809	627.7039	615.5526	601.4629	517.3337	2611.4648	2915.7418	3153.6687	2263.2585	1940.0496	MDK
ENSG00000001	2.0932	4.04E-22	6.26E-20	77.4545	24.6653	18.4781	31.6084	24.8825	165.6709	127.1594	97.7068	101.0881	104.4717	AL671883.2
ENSG00000001	2.0678	3.66E-13	2.36E-11	15.5604	30.0817	16.1684	16.2558	8.9577	76.4152	80.3112	79.8516	65.5201	52.7240	HLA-J
ENSG00000001	2.0389	7.43E-16	6.62E-14	13.7296	18.8490	19.8330	18.9660	19.9960	64.7406	89.2735	85.4882	66.4561	61.5114	ODF3B
ENSG00000001	2.0307	4.18E-10	1.74E-08	14.6463	11.8299	3.4646	16.2558	21.8966	56.2501	64.6851	63.8813	49.6084	36.1257	TNFSF10
ENSG00000001	2.0101	2.42E-07	5.91E-06	4.5766	6.0163	12.7037	10.8372	5.9718	27.5944	44.6173	31.9406	33.7666	20.5038	PATL2

FIG. 24E

ENSG00000001	1.9259	3.07E-153	8.61E-150	1549.6134	1494.0555	1368.5362	1915.4695	1355.5977	5579.3695	6429.3557	6110.0570	5718.9664	5305.0349	LYRE
ENSG00000001	1.6772	4.67E-17	4.48E-15	530.8851	436.3840	347.6197	1143.3213	468.7860	1618.5157	2677.0392	2415.2762	1803.6740	1539.7374	ISG15
ENSG00000001	1.8647	2.88E-29	6.83E-27	37.5381	46.1252	48.5051	53.2817	51.7556	161.3209	192.9699	212.3113	164.7362	134.7392	APOL3
ENSG00000001	1.8119	8.07E-07	1.79E-05	8.2379	9.0245	5.7744	14.4496	8.8577	32.6610	41.2710	39.4561	25.2730	23.4329	H6ST2
ENSG00000001	1.7338	9.35E-38	4.08E-35	166.3881	145.3947	155.9092	166.1699	136.3560	494.5759	604.5647	615.3171	556.9206	335.8717	PTN
ENSG00000001	1.7145	2.02E-33	6.73E-31	1183.3184	1537.1725	1629.5397	1403.4113	1259.6537	4133.7778	4462.8474	4341.8880	4383.2929	3540.9666	LGALS3BP
ENSG00000001	1.7072	1.93E-42	1.11E-39	160.3179	146.3974	132.8115	189.6565	174.1774	591.1562	584.4869	589.0230	542.8646	396.4067	PSMB9
ENSG00000001	1.6984	1.05E-32	3.46E-30	70.4796	86.2341	101.6297	92.1119	77.6334	265.3304	316.7830	308.1333	236.8883	258.7384	SERPING1
ENSG00000001	1.6984	6.76E-08	1.85E-06	20.1370	12.6327	13.8586	11.7403	12.9389	43.5142	55.7716	54.4870	32.7600	42.9603	HLA-U
ENSG00000001	1.6956	5.29E-54	5.34E-51	181.7332	142.3865	138.5859	186.9412	186.1210	569.9298	538.7541	545.8092	519.4806	523.3350	TYMP
ENSG00000001	1.6706	7.30E-25	1.35E-22	37410.9165	28792.7987	27356.8651	36281.9373	30156.5756	93407.9897	120037.3201	116213.7098	102773.8512	76915.5946	B2M
ENSG00000001	1.6486	1.04E-06	2.14E-05	11.8991	16.0435	6.9293	10.8372	14.9295	40.3302	32.3476	35.6984	24.3360	38.5823	LTK
ENSG00000001	1.6452	1.14E-59	1.53E-56	187.6404	185.5035	189.4008	235.7084	205.0317	565.6845	762.9562	743.0897	613.8887	481.3510	APOL1
ENSG00000001	1.6380	9.01E-15	6.83E-13	42.1847	25.0680	26.9623	33.4146	32.8449	105.0709	82.5420	91.1248	92.6641	126.9383	KREMEN2
ENSG00000001	1.6203	2.96E-06	5.59E-05	17.3911	10.8272	9.2391	9.0510	12.9389	36.0849	39.0402	37.5772	35.5680	30.2875	GGA3
ENSG00000001	1.6034	2.24E-124	9.03E-121	9147.7001	8750.7533	8762.0962	8720.3083	8475.9694	27048.8464	27422.8198	29987.5662	26163.1013	23075.9371	HLA-A
ENSG00000001	1.5934	1.50E-116	4.83E-113	1567.9418	1512.1045	1678.0448	2005.7793	1762.6752	5205.9956	5860.4849	5699.5258	4899.9635	4061.7042	C1R
ENSG00000001	1.5852	2.21E-32	6.99E-30	103.6351	83.2259	87.7711	93.0190	83.6145	247.2885	292.2434	289.3446	248.0403	262.6439	SLC15A3
ENSG00000001	1.5622	5.13E-18	5.57E-16	75.0362	53.1443	49.4209	98.4876	49.7650	147.3237	261.0113	217.9479	180.9922	140.5975	TLR3
ENSG00000001	1.5137	4.33E-32	2.36E-30	43.9353	31.0844	42.7307	29.8022	31.8496	134.6228	122.6976	100.5191	90.7921	83.9679	PSMB8-AS1
ENSG00000001	1.5002	7.04E-24	1.23E-21	110.7336	77.2096	77.3772	152.6235	103.5111	369.5757	401.3559	325.9824	279.8643	198.2094	IFIT2
ENSG00000001	1.4589	7.49E-06	0.00012642	30.0685	19.0537	10.3939	11.7403	17.9154	33.9623	41.1710	57.3053	32.7600	23.3857	ADAR1B
ENSG00000001	1.4372	6.29E-33	2.07E-30	153.8430	140.3811	180.1617	182.4257	127.3983	421.3447	486.2510	466.3210	393.1204	370.0447	USP18
ENSG00000001	1.4162	2.38E-09	8.43E-08	23.7981	30.0817	36.9563	33.4146	23.8872	68.9859	81.4266	74.2150	67.3921	102.3190	C3
ENSG00000001	1.4107	4.24E-05	0.00057616	13.7258	10.0272	18.4781	14.4496	8.9577	44.1755	26.7704	25.3646	30.6880	47.8422	MAPK13
ENSG00000001	1.4038	2.15E-43	1.28E-40	572.9858	514.3963	574.3168	539.1491	535.4711	1288.4446	1784.6828	1728.5524	1330.0575	1085.7246	BTN3A2
ENSG00000001	1.3861	1.69E-05	0.00026108	10.9838	8.0218	16.1684	22.5774	14.9295	25.4737	49.0791	39.4561	32.7600	39.0548	GBP4
ENSG00000001	1.3790	4.46E-06	7.97E-05	20.1370	19.0517	15.0135	27.9960	10.9463	28.7170	59.1179	48.6504	57.0961	45.8894	LY75
ENSG00000001	1.3545	9.31E-19	1.08E-16	115.3303	77.2096	87.7711	106.5655	96.5440	247.1883	268.8193	285.5869	285.5283	184.5342	ANGPTL7
ENSG00000001	1.3493	2.54E-31	1.27E-29	40.2740	31.0844	36.9563	36.1239	36.7321	107.3939	109.3124	118.3683	83.3841	99.8025	ACSM5
ENSG00000001	1.3442	9.43E-51	8.03E-48	443.9258	377.0234	382.2852	559.0173	459.8283	881.9584	1472.3715	1330.2338	1111.9632	901.1906	PARP9
ENSG00000001	1.3394	0.00019159	0.00215806	8.2379	11.0299	15.0135	9.9341	13.9342	33.9623	26.7704	29.1224	26.2880	29.2811	AL022315.1
ENSG00000001	1.3315	8.56E-07	1.88E-05	21.0523	17.0463	26.9623	19.8681	31.8496	56.2501	75.8494	82.6699	39.3120	42.9603	CASP1
ENSG00000001	1.3186	0.00059665	0.00569984	8.2379	10.0272	10.3939	9.9341	10.9463	21.1264	36.8093	23.4658	24.3360	19.5374	TMEM229B
ENSG00000001	1.3156	2.60E-46	1.53E-43	537.4294	538.4072	460.7983	721.5748	537.4617	1186.3926	1725.5748	1679.3077	1323.5855	1112.0868	SAMHD1
ENSG00000001	1.3098	0.00023892	0.00261709	13.7258	11.0299	5.7744	17.1589	12.9389	23.3491	31.2321	40.3955	23.4880	30.2875	IL15RA
ENSG00000001	1.2821	8.97E-22	1.37E-19	142.7898	94.2559	111.1785	117.4017	121.4265	320.5192	262.1268	263.9800	289.2243	294.9644	CMPK2
ENSG00000001	1.2737	1.05E-37	4.45E-35	336.8375	329.8955	347.6197	331.4947	338.4488	749.2932	967.0824	924.3998	799.3449	640.4995	BTN3A3
ENSG00000001	1.2655	4.86E-50	3.92E-47	1197.2375	993.6873	1141.0243	1627.3815	1439.2829	3010.9698	3828.1660	3521.9156	2872.5872	2193.9061	CIS

FIG. 24E, continued

ENSG00000001	1.2571	2.34E-12	1.33E-10	73.1355	60.1633	54.2795	69.5385	52.7555	123.1133	198.5471	162.5215	146.0162	116.1882	LINC01358	
ENSG00000001	1.1795	4.70E-15	3.73E-13	84.2094	141.3838	87.7711	76.7633	86.5810	210.1417	234.2409	235.7971	211.5362	286.0143	SPTBN5	
ENSG00000001	1.2289	1.13E-34	4.46E-32	635.2315	540.4671	483.8959	842.5899	610.1185	1132.4363	1981.0890	1765.1962	1405.8726	1086.7812	DDX58	
ENSG00000001	1.2216	1.35E-23	2.30E-21	143.7851	118.3212	103.9385	155.3337	141.3325	297.1781	311.2058	338.8607	291.0983	310.4860	HES4	
ENSG00000001	1.2185	0.00045723	0.00045723	13.7298	11.0239	10.3919	17.1589	12.9389	32.5910	31.2321	27.2435	38.3759	23.4329	APOL5	
ENSG00000001	1.2136	9.27E-20	1.17E-17	152.6583	91.2447	101.8297	111.0810	116.4508	261.0812	249.8570	262.1012	264.6683	281.1949	ILDR2A	
ENSG00000001	1.2136	2.18E-45	1.53E-42	1649.9133	1228.3342	1238.0344	2138.5346	1570.6764	3882.5499	4683.7031	4280.9853	3358.3716	2871.5977	PARP14	
ENSG00000001	1.2034	0.00159951	0.01398837	14.6451	13.0354	26.5623	7.2248	5.9718	28.6557	23.4241	28.1829	25.2739	37.1021	PLEKHG4B	
ENSG00000001	1.2009	3.53E-29	8.22E-27	302.9707	286.7784	241.3705	292.6036	304.5616	681.3686	719.4543	763.7571	652.3927	492.6911	TPPP3	
ENSG00000001	1.1983	3.53E-09	1.22E-07	53.0885	34.0925	45.0404	59.6044	44.7885	55.1887	126.0439	160.6426	82.3681	137.6683	WISP2	
ENSG00000001	1.1937	7.29E-11	3.43E-09	488.5447	486.3301	608.5233	986.1823	1048.0502	1667.3365	1936.3917	1816.8589	1702.5859	1918.3694	NPAT	
ENSG00000001	1.1833	0.00116479	0.01498822	7.3226	6.0218	6.0842	17.1589	14.9295	16.9811	29.0013	31.6012	20.5929	25.3857	ARMC1-AS1	
ENSG00000001	1.1766	1.56E-08	4.82E-07	52.1732	32.0871	45.0404	45.1548	34.8355	95.5130	107.0816	93.5431	95.4721	79.8863	SEPT4	
ENSG00000001	1.1721	0.00024701	0.00226929	16.4757	21.0572	9.2391	15.3527	13.9248	43.5142	33.4630	34.7589	33.6990	29.2911	C1QTNF7	
ENSG00000001	1.1610	1.77E-06	3.52E-05	23.7983	28.0762	18.4781	35.2268	33.8449	64.7866	72.5031	68.5784	58.0321	44.9133	CD36	
ENSG00000001	1.1596	8.17E-34	2.80E-31	410.0530	294.8091	304.8891	332.8275	382.1950	633.6091	1125.4719	981.7050	821.8089	733.2548	PLSCR1	
ENSG00000001	1.1579	1.12E-40	6.22E-38	508.6022	404.0569	397.2797	694.4819	502.6262	875.5905	1527.0277	1374.3871	903.2410	947.6861	DDX60	
ENSG00000001	1.1557	1.08E-24	1.96E-22	172.0860	160.4355	165.1482	192.3597	146.3090	387.3824	370.3237	378.5906	371.5284	351.4936	TRIM14	
ENSG00000001	1.1514	3.14E-25	5.97E-23	368.8736	183.4981	219.4277	213.1310	234.8907	543.3967	435.6189	442.4718	355.9846	707.8691	CKM	
ENSG00000001	1.1513	0.00330754	0.02337759	9.1532	8.0218	18.4781	10.8372	8.9577	28.6557	27.8858	18.7886	20.5929	24.4093	CD1943	
ENSG00000001	1.1482	0.00211409	0.01638433	13.7298	17.0463	8.0842	9.0310	14.9295	30.7783	40.1536	19.7280	27.1449	22.4565	CIQL1	
ENSG00000001	1.1090	0.00059569	0.00259396	20.1370	18.0490	11.5488	18.9559	14.9295	30.7783	54.6562	46.0321	29.0159	24.4093	ASPA	
ENSG00000001	1.1557	1.08E-24	1.96E-22	172.0860	160.4355	165.1482	192.3597	146.3090	387.3824	370.3237	378.5906	371.5284	351.4936	TRIM14	
ENSG00000001	1.1514	3.14E-25	5.97E-23	368.8736	183.4981	219.4277	213.1310	234.8907	543.3967	435.6189	442.4718	355.9846	707.8691	CKM	
ENSG00000001	1.1513	0.00330754	0.02337759	9.1532	8.0218	18.4781	10.8372	8.9577	28.6557	27.8858	18.7886	20.5929	24.4093	CD1943	
ENSG00000001	1.1482	0.00211409	0.01638433	13.7298	17.0463	8.0842	9.0310	14.9295	30.7783	40.1536	19.7280	27.1449	22.4565	CIQL1	
ENSG00000001	1.1090	0.00059569	0.00259396	20.1370	18.0490	11.5488	18.9559	14.9295	30.7783	54.6562	46.0321	29.0159	24.4093	ASPA	
ENSG00000001	1.1082	1.76E-17	1.79E-15	100.6851	105.2885	107.4841	148.5142	118.4406	260.0238	282.2045	285.5869	240.5523	189.4180	IFI35	
ENSG00000001	1.1026	3.53E-12	1.96E-10	100.6851	80.2177	63.5186	121.6158	87.5863	193.1666	221.9732	217.9479	184.3922	150.3612	RARRES3	
ENSG00000001	1.0965	1.58E-05	0.00024725	25.6289	35.0953	24.2525	23.4805	23.8872	53.0661	63.5797	45.0927	57.0961	63.4641	ATP2A1	
ENSG00000001	1.0939	0.00142016	0.01184899	19.2217	11.0239	19.6310	8.1279	23.8872	37.1463	29.6013	23.4858	42.1299	38.0785	CDC42EP5	
ENSG00000001	1.0848	3.14E-05	0.000447	21.0523	32.0871	25.4074	25.2857	26.8731	44.5755	66.9260	78.9122	55.2241	37.1021	GSN1	
ENSG00000001	1.0818	1.33E-05	0.00021145	46.6813	36.0980	28.8721	42.4456	15.9248	56.2581	88.1192	69.5179	70.2001	66.3333	SLC1A2	
ENSG00000001	1.0711	0.0028473	0.02067784	15.5604	13.0354	11.5488	10.8372	10.9483	22.2878	30.1167	20.6575	25.2739	32.1202	AC084860.3	
ENSG00000001	1.0697	0.00299817	0.02153647	13.8145	15.0408	10.3919	11.7405	10.9483	28.6557	29.6013	21.6069	25.2739	23.4329	STEAP4	
ENSG00000001	1.0679	1.21E-08	3.81E-07	45.7660	62.1688	48.5851	49.6704	66.6851	126.2973	116.8050	106.1557	88.9201	133.7829	UTS2R	
ENSG00000001	1.0658	0.00044256	0.00344875	11.8991	17.0463	15.0135	21.6343	23.8872	27.5944	46.8482	45.0927	35.5680	31.2439	AC093788.1	
ENSG00000001	1.0553	0.00016658	0.00288289	27.4596	15.0408	17.3212	40.6284	16.9201	40.3302	50.1945	53.5475	45.8641	43.9367	APOL4	
ENSG00000001	1.0508	5.99E-06	0.00010385	25.5443	52.1415	26.5623	37.9301	33.8308	63.6793	85.8883	84.5488	64.5841	65.3932	PREP	
ENSG00000001	1.0504	1.01E-30	1.42E-28	337.7528	228.6206	264.4682	347.6925	341.3877	629.3638	557.7185	610.6299	671.1128	656.1215	FRAS1	
ENSG00000001	1.0491	0.00025434	0.00550298	21.0523	15.0408	24.2525	15.3527	15.9248	43.4529	26.7784	36.6378	38.3759	44.9131	AL365181.3	
ENSG00000001	1.0458	0.00123351	0.01054672	14.6451	17.0463	13.8586	16.2558	16.9201	31.8397	32.3476	48.8504	31.6048	21.4882	AC026376.1	
ENSG00000001	1.0425	0.00288543	0.01974602	15.5604	11.0239	12.7037	17.1589	12.9389	29.7170	28.6550	35.6984	29.0159	23.4329	TTC4P3	
ENSG00000001	1.0416	1.66E-30	7.33E-09	59.4957	54.1470	66.9832	74.0540	84.6004	127.3586	130.5057	164.4094	152.5682	122.0464	SCT	
ENSG00000001	1.0407	3.61E-31	1.60E-28	388.0107	345.9390	362.6332	376.5915	438.9646	756.7224	897.9235	890.5803	718.8488	669.7906	BTN3A1	
ENSG00000001	1.0358	0.00026425	0.01924854	14.6451	15.0435	13.8586	16.2556	8.9577	41.3915	33.4630	23.4858	21.5280	24.4093	APOBR	
ENSG00000001	1.0304	2.69E-32	8.36E-30	313.1228	273.7431	285.2561	329.6305	339.3971	581.6043	670.3752	661.3592	575.6406	654.1687	HELZ2	
ENSG00000001	1.0215	0.00045036	0.02799582	14.6451	16.0435	16.1684	17.1589	6.9671	33.9623	24.5395	31.9466	30.8880	23.4802	GCH1	
ENSG00000001	1.0174	9.57E-07	2.08E-05	42.1047	36.0980	37.9301	43.7932	65.8019	87.0038	79.8516	77.6861	88.8498	VGLL2		
ENSG00000001	1.0165	2.68E-06	5.10E-05	33.8668	31.0844	36.9563	46.9611	33.8482	74.2915	101.5044	56.3658	69.2641	70.2987	FRZB	

FIG. 24F

ENSG00000	1.0120	3.52E-05	0.0004958	34.7821	17.0463	41.5758	27.0929	34.8355	39.2689	80.3112	72.3362	64.5841	54.6768	CD68
ENSG00000	1.0118	3.93E-24	7.04E-22	677.3362	557.5133	557.8094	571.6606	534.4758	1195.0483	1249.2849	1297.3537	1172.8093	942.1173	PSMB8
ENSG00000	1.0116	5.31E-06	1.48E-05	59.4957	67.1824	87.7711	92.1159	61.7086	342.2171	133.8539	135.4016	120.7441	149.3848	IRF9
ENSG00000	1.0109	0.00383114	0.0262152	12.8145	10.0272	17.3232	13.5465	13.9342	21.2264	27.8858	36.6378	26.2080	24.4991	GBP2
ENSG00000	1.0081	7.02E-06	0.00011902	38.6128	31.0844	32.3367	31.5115	34.8355	53.0661	73.6186	66.6996	65.5201	79.0861	ATP8B3
ENSG00000	-1.0016	1.09E-38	5.16E-36	41587.5280	47309.4180	45725.2763	45830.5178	46307.2585	27611.9366	18402.4133	20197.3389	25786.8289	22121.6424	TAGLN
ENSG00000	-1.0144	0.0025751	0.0190892	30.2055	32.0871	19.6330	37.9301	37.8214	20.1651	15.6161	17.8492	15.9120	8.7873	CSTA
ENSG00000	-1.0299	0.00960152	0.0977346	18.3064	18.0490	36.9583	37.0370	28.8637	16.9811	16.7315	8.4549	10.2960	14.6456	CLEC18A
ENSG00000	-1.0340	6.07E-23	9.99E-21	767.0375	519.4899	688.3102	717.5624	759.4134	345.9999	290.0126	321.2853	361.2964	358.3282	IL6
ENSG00000	-1.0574	0.00020675	0.0029096	56.7498	48.1306	56.5893	33.4146	33.8402	21.2264	24.5995	18.7685	16.6480	27.9384	GDF5
ENSG00000	-1.0700	1.23E-08	3.87E-07	121.7375	99.2695	116.6432	135.4646	126.4039	67.9246	45.7328	53.4284	66.4561	50.7713	SMOX
ENSG00000	-1.0990	9.42E-07	2.06E-05	82.3787	87.2368	69.2930	71.3447	84.8604	33.9623	42.3865	45.0927	40.2480	24.4093	IL27RA
ENSG00000	-1.1368	4.70E-34	1.68E-31	873.2145	1331.6146	1048.6336	855.2312	1101.7964	541.2741	453.9812	412.4101	467.0645	484.2801	GBT18
ENSG00000	-1.1432	3.95E-05	0.0005437	33.8668	50.1361	70.4479	60.5075	63.6992	32.7359	29.0013	20.6675	35.5680	29.2911	IRF6
ENSG00000	-1.1500	9.72E-22	1.47E-19	518.9860	536.4562	517.3875	853.4270	865.9105	285.4956	303.3978	283.7081	311.6883	261.6675	CXCL8
ENSG00000	-1.1564	1.51E-29	3.62E-27	521.7315	428.1648	532.4010	629.4589	594.1937	230.1417	254.3187	220.7662	257.4033	257.5157	CCL2
ENSG00000	-1.1568	2.65E-10	1.14E-08	182.1485	134.3647	135.1213	184.2319	212.9941	96.5803	52.4354	71.3957	74.8803	84.9443	TMEM71
ENSG00000	-1.1884	6.38E-08	1.73E-06	2388.0878	1471.8956	1381.2399	2566.6997	2486.2578	932.9018	915.7705	831.3961	894.8170	797.6953	VCAM1
ENSG00000	-1.1905	3.13E-22	4.90E-20	409.1477	308.8383	334.9160	392.8474	451.8659	154.9530	197.4316	168.1581	173.1602	136.6930	SCRG1
ENSG00000	-1.2158	0.00091837	0.0082081	25.6289	27.0735	24.2525	30.7053	25.8778	11.6745	7.8080	12.2126	12.1680	13.6691	OVOL2
ENSG00000	-1.2289	3.76E-07	8.91E-06	58.5804	72.1960	50.8148	74.9571	100.5252	24.4104	35.6939	34.7589	36.5040	20.5038	LINC01013
ENSG00000	-1.2294	2.84E-08	8.38E-07	58.5804	97.2640	93.5455	61.4106	72.6569	39.2689	31.2321	35.6984	35.5680	21.4801	APOA1
ENSG00000	-1.2319	7.42E-20	9.42E-18	275.5111	346.9417	370.7174	322.4058	373.2373	146.5859	122.6976	113.6711	169.4162	166.9595	LMOD1
ENSG00000	-1.2433	3.01E-36	1.25E-33	474.1353	539.4643	642.1149	691.7726	700.6908	267.4531	285.5308	248.9491	298.5943	188.4396	SULT1E1
ENSG00000	-1.2603	1.11E-06	2.33E-05	43.9353	46.1252	53.1246	68.6354	73.6532	24.4104	25.6330	24.4252	22.4640	21.4802	SLN
ENSG00000	-1.2631	3.51E-06	6.43E-05	49.4272	57.1553	49.6620	48.7623	49.7650	16.9811	22.3087	28.1829	19.6560	19.5274	AL589004.4
ENSG00000	-1.2681	4.40E-08	1.48E-07	78.4796	98.2667	127.0371	83.0850	92.5628	50.9434	32.2476	31.9405	36.5040	42.9603	CNN1
ENSG00000	-1.2725	1.14E-11	5.97E-10	86.0400	134.3647	161.6836	144.4958	140.3372	61.5567	62.4642	34.7589	70.2001	47.8422	MRVI1
ENSG00000	-1.2727	1.66E-17	1.78E-15	179.4026	201.5471	169.4038	216.7434	209.8553	71.1086	74.7340	95.7614	93.6001	73.2278	CISorf54
ENSG00000	-1.2870	2.98E-20	3.91E-18	165.6728	255.6941	280.6365	210.4217	236.6812	132.5091	78.0803	80.7910	116.0641	82.9916	MASP1
ENSG00000	-1.3112	1.08E-06	2.32E-05	45.7660	73.1987	61.1516	61.4106	61.7086	23.3491	16.7315	24.4252	28.0800	39.0548	ACTG2
ENSG00000	-1.3399	0.00031689	0.0017420	19.2217	25.6680	31.1818	32.5115	37.8214	9.5319	14.5006	12.2126	10.2960	9.7637	LINC02015
ENSG00000	-1.3654	1.12E-30	2.88E-28	414.6396	412.1187	445.7848	454.2380	494.6638	205.8864	155.0452	147.4905	182.5202	173.7941	ITGA8
ENSG00000	-1.4236	1.12E-19	1.38E-17	158.3502	149.4056	199.7947	153.5266	181.1445	73.2312	58.1945	42.2744	71.1361	41.6076	LAMP5
ENSG00000	-1.4364	1.55E-96	1.79E-53	623.3324	770.6934	698.7041	1119.8408	1086.8569	258.9625	337.9762	259.2829	263.0163	236.2818	SCYRN1
ENSG00000	-1.4756	1.98E-124	9.03E-121	3112.0653	3912.6205	3179.3925	2669.5559	3147.1366	1052.8312	956.3488	963.8559	1057.6812	960.7493	TNFRSF10D
ENSG00000	-1.7049	7.35E-07	1.65E-05	196.7936	129.3511	145.5152	319.6965	278.6838	65.8019	61.3488	46.0321	80.4961	60.5339	EPYC
ENSG00000	-1.7843	1.09E-06	2.32E-05	21.9677	32.0871	53.1246	35.2208	21.8966	10.6132	7.8080	7.5154	15.9120	5.8582	CCKAR

FIG. 24F, continued

Table 52: Significant DEGs following targeting of dCas9-repressors to *DUX4*

ID	log2FoldChan	pvalue	padj	Mock-Expt 1	Mock-Expt 2	Mock-Expt 3	HP1a-Expt 1	Mock-Expt 4	HP1a-Expt 3	HP1a-Expt 5	HP1a-Expt 2	HP1a-Expt 4	Gene.name
ENSG0000001	4.4242	8.51E-09	3.29E-07	181.2561	14.3073	59.7335	934.9313	16.1769	1314.4005	847.4331	868.6690	1385.1328	BST2
ENSG0000001	4.1208	2.33E-25	1.31E-22	11.6939	2.0439	5.5157	92.7928	2.0221	96.3323	98.3022	62.3320	126.1929	CMPK2
ENSG0000001	3.8863	8.09E-06	0.00015258	2250.1098	114.4588	376.9864	5837.1925	122.3375	6899.5324	4999.8552	6182.8017	7039.7620	IFI27
ENSG0000001	3.4271	1.52E-13	1.54E-11	16.5664	6.1317	31.2357	154.9465	9.0995	138.0763	138.4700	87.5300	255.3904	RSAD2
ENSG0000001	3.4058	3.78E-06	7.87E-05	20172.0545	1204.8831	3755.2749	40029.9824	1036.3302	46213.8088	35859.2999	41084.7305	45399.4039	IFI6
ENSG0000001	3.1948	1.21E-07	3.69E-06	385.9032	48.0318	284.9780	1351.6235	63.6864	1584.1309	1483.0079	976.0922	1978.0116	IFI44L
ENSG0000001	2.9729	8.23E-07	2.05E-05	250.4453	27.5927	101.1212	681.0642	37.4090	736.4068	644.8966	429.6928	933.4270	OAS2
ENSG0000001	2.7316	1.47E-07	4.39E-06	187.1031	31.6806	73.5427	502.4818	36.3979	488.0836	460.1562	368.6870	621.9508	OAS3
ENSG0000002	2.6960	1.05E-20	3.47E-18	62.3677	28.6147	25.7400	249.4901	24.2653	232.2678	264.3991	159.1455	266.4073	HCP5
ENSG0000001	2.6902	5.95E-07	1.54E-05	463.8596	76.6465	341.0543	1371.7578	86.9506	1401.0996	1329.6225	909.7816	1742.6641	MX1
ENSG0000001	2.6379	2.19E-31	3.03E-28	38.9798	18.3952	24.8107	173.3300	18.1990	158.4131	210.1634	86.2038	203.3108	HERC5
ENSG0000001	2.6300	3.37E-09	1.39E-07	213.4145	36.7903	127.7805	637.2940	66.7296	744.9697	556.7635	387.2540	886.3550	OAS1
ENSG0000002	2.4774	4.29E-09	1.73E-07	12283.5143	4156.2845	4778.4379	33802.8424	4352.5868	38583.2214	32373.6384	30165.9179	37035.6791	HLA-B
ENSG0000001	2.4540	4.13E-08	1.41E-06	15.5919	1.0220	1.8386	41.1440	12.1326	42.8143	41.5242	31.8291	38.0582	ATF4
ENSG0000001	2.4154	1.31E-08	3.07E-05	537.9215	78.6804	309.7987	1207.1818	110.2049	1401.0996	1191.1858	795.7274	1427.1818	IFITM1
ENSG0000003	2.3743	1.06E-10	5.76E-09	9.7450	6.1317	7.3543	59.5275	9.0995	34.2515	62.7100	25.1980	48.0735	SCN2A
ENSG0000001	2.3697	9.54E-06	0.00017579	86.7301	18.3952	63.4306	206.5953	15.1658	221.5643	205.0788	159.1455	267.4088	MX2
ENSG0000001	2.3414	5.75E-20	1.68E-17	26.3114	17.3732	16.5471	107.6747	14.1548	96.3323	113.5560	67.6368	108.1623	C2
ENSG0000001	2.2639	5.70E-13	5.18E-11	120.8374	68.4709	79.0584	331.7780	52.5748	524.4758	348.2950	293.0929	452.6920	CFB
ENSG0000001	2.2320	1.64E-07	4.87E-06	200.7460	36.7903	136.0540	456.9608	58.6411	508.4204	478.7997	318.2909	566.8666	HERC6
ENSG0000002	2.1455	2.26E-12	1.83E-10	12303.4686	5829.2222	5857.6772	30822.0924	5388.7384	36098.9188	29004.2445	29171.3655	34792.1882	HLA-C
ENSG0000001	2.0928	7.97E-07	2.00E-05	38.0053	9.1976	40.4485	119.9303	15.1658	88.8398	103.3868	67.6368	147.2251	OASL
ENSG0000001	2.0882	4.60E-08	1.54E-06	215.3635	66.4270	146.1661	489.3507	66.7296	601.5416	458.4613	366.0346	621.9508	EPSTI1
ENSG0000002	2.0081	2.21E-44	1.12E-40	167.6132	88.9099	119.5069	482.3475	73.8069	476.3096	517.7816	358.0773	479.7334	HCG4P5
ENSG0000001	1.9751	3.38E-21	1.16E-18	944.2860	639.7428	612.2431	2799.5414	525.7480	3045.1706	2588.0506	2144.4853	3017.6131	MDK
ENSG0000001	1.9576	1.17E-13	1.22E-11	173.4602	67.4489	148.9240	423.6954	81.8954	490.2243	481.3420	331.5331	540.8268	IFIH1
ENSG0000002	1.9485	4.76E-11	2.87E-09	252.3943	120.5903	135.1347	562.0092	110.2049	617.5970	526.7982	599.4480	653.9998	HLA-H

FIG. 24G

ENSG00000202	1.9375	1.91E-11	1.26E-09	326.4560	142.0515	202.2415	744.9686	143.5696	925.8603	686.4208	653.8227	866.3244	HLA-F	
ENSG00000201	1.9301	1.46E-05	0.00025425	640.2435	190.0833	553.4089	1252.7028	169.8570	1439.6325	1392.3325	1069.2476	1786.7314	IFIT1	
ENSG00000202	1.9172	1.34E-06	3.12E-05	77.9596	28.6147	42.2871	135.8219	37.4090	214.0717	126.2675	214.8464	163.2496	HLA-G	
ENSG00000201	1.8686	1.09E-10	5.86E-09	339.1244	165.5565	324.5072	871.9022	159.7465	962.2525	951.5148	562.3140	1226.8756	IFIT3	
ENSG00000201	1.8631	1.46E-28	1.70E-25	69.1892	47.0099	54.2378	211.8477	52.5748	238.6900	187.2827	169.7552	237.3322	APOL3	
ENSG00000201	1.8505	6.91E-09	2.73E-07	671.4273	246.2908	519.3954	1398.8953	267.9293	1601.2567	1494.0245	1169.7192	1841.8157	IFI44	
ENSG00000201	1.8482	2.96E-13	2.88E-11	28.2604	20.4391	25.7489	79.6617	22.2432	108.1062	60.1577	98.1397	85.1301	OTOF	
ENSG00000202	1.8204	9.41E-09	3.60E-07	26.3114	12.2634	11.9507	49.0226	13.1437	68.5030	54.2357	47.7436	65.0995	HLA-U	
ENSG00000201	1.8192	5.29E-10	2.56E-08	15.5919	11.2415	16.5471	57.7767	22.2432	71.7140	61.8626	30.3029	70.1072	TNFSF10	
ENSG00000200	1.7825	1.98E-09	8.66E-08	19.4899	14.3073	16.5471	62.1537	14.1548	61.0104	56.7780	35.8077	70.1072	ETV7	
ENSG00000202	1.7190	1.02E-08	3.88E-07	23.3879	30.6586	16.5471	63.0291	9.0995	71.7140	49.1511	64.9844	65.0995	HLA-J	
ENSG00000201	1.6412	2.24E-10	1.11E-08	29.2349	18.3952	19.3050	75.2847	20.2211	61.0104	75.4215	64.9844	73.1118	ODF3B	
ENSG00000201	1.6361	5.57E-46	4.23E-42	224.1339	148.1832	169.1482	552.3798	138.5144	528.7572	579.6442	476.1102	560.8574	PTN	
ENSG00000201	1.6031	1.02E-27	8.63E-25	107.1945	87.8880	93.7670	321.2732	78.8622	285.7858	267.7869	220.1512	329.5037	SERPING1	
ENSG00000202	1.5564	4.78E-13	4.45E-11	46.7758	31.6806	30.3364	109.4255	32.3537	124.1616	107.6240	103.4446	86.1317	PSMB8-AS1	
ENSG00000202	1.5432	2.66E-05	0.00094271	68.2147	24.5269	32.1749	88.4158	25.2763	124.1616	107.6240	103.4446	115.1761	AL671883.2	
ENSG00000201	1.5369	1.02E-06	2.45E-05	3115.4617	1522.7106	1949.8012	5408.2447	1377.0534	6234.8396	4582.5797	5795.5477	6571.0454	IFI6E	
ENSG00000201	1.4811	1.17E-37	2.96E-34	320.6090	169.0614	219.9331	661.8053	208.2771	776.0101	681.3362	534.4636	744.1376	APOL1	
ENSG00000201	1.4571	7.68E-27	5.55E-24	124.7354	78.6904	155.3590	318.6470	105.1496	351.0777	321.8720	213.5202	392.6002	IFIT2	
ENSG00000202	1.4341	4.96E-05	0.00073306	9.7450	19.4171	11.9507	48.1472	18.1990	50.3069	34.7448	29.1767	34.0321	ADRA2B	
ENSG00000202	1.4171	1.65E-14	1.96E-12	13077.7281	8916.5873	8876.6057	26047.6401	8610.1346	30415.3139	23284.0712	24450.0497	28470.5240	HLA-A	
ENSG00000202	1.4115	1.59E-12	1.33E-10	79.9086	34.7464	60.6727	166.3267	45.4974	192.6646	122.8778	103.4446	161.2465	WISP2	
ENSG00000201	1.4000	2.30E-12	1.86E-10	53387.7297	28835.4370	36912.2310	94168.0623	30633.9208	108822.3024	96104.8430	91239.4268	105170.7787	B2M	
ENSG00000201	1.3925	4.59E-08	1.54E-06	142.2763	84.8221	94.6862	268.7490	82.9064	281.5043	211.7057	236.0658	342.5236	SLC15A3	
ENSG00000201	1.3876	1.54E-14	1.85E-12	91.6026	54.1635	100.2019	218.8510	50.9527	183.0313	228.8069	132.6212	233.3567	TLR3	
ENSG00000201	1.3798	6.48E-08	2.12E-06	2342.6869	1566.6546	1428.5672	3781.7444	1278.9831	4562.9393	3580.4048	4754.4711	4794.3193	LGALS3BP	
ENSG00000201	1.3520	9.88E-08	3.09E-06	39.9543	17.3732	20.2142	76.1601	32.3537	72.7844	71.1844	53.0485	83.1271	CASP1	
ENSG00000201	1.3306	3.06E-05	0.00047974	19.4899	8.1756	22.9821	48.1472	13.1658	49.2365	39.8294	25.1980	46.0704	GBP1	
ENSG00000201	1.3126	0.00053778	0.00551694	1091.4348	444.5497	1163.8135	1766.5649	476.2084	2246.6830	1320.3007	1560.9519	2502.8262	ISG15	
ENSG00000202	1.2974	1.04E-09	4.78E-08	319.6345	145.1174	190.2918	615.4089	189.0671	544.8126	464.3933	446.9335	547.8375	TYMP	
ENSG00000201	1.2763	2.73E-13	2.69E-11	859.5049	524.2521	548.8125	1470.6784	543.9470	1696.5186	1552.4974	1299.6860	1583.4206	BTN3A2	
ENSG00000202	1.2705	1.33E-06	3.09E-05	20.4644	43.9440	43.2063	74.4093	25.2763	77.0658	88.9805	59.6796	85.1301	NLGN4Y-AS1	

FIG. 24G, continued

ENSG00000003	1.2585	1.79E-07	5.28E-06	39.9543	25.5488	84.0135	83.1634	33.3648	79.2065	60.1677	90.1824	85.1301	KREMEN2		
ENSG00000004	1.2492	9.88E-08	3.08E-06	338.1499	148.2052	193.0496	540.1241	176.9344	560.8680	477.9523	417.7569	566.8668	PSMB9		
ENSG00000005	1.2319	4.39E-06	8.94E-05	3278.2025	1541.1057	2041.7296	4549.4736	1790.5764	5898.7470	4754.9470	4705.4012	5394.2494	C1R		
ENSG00000001	1.2065	0.00031215	0.00135522	13.4839	12.2634	14.7065	34.2750	28.3095	42.8143	31.6934	34.4815	37.0566	RNF144A		
ENSG00000002	1.2062	3.05E-12	2.40E-10	69.1892	61.3172	70.7849	137.4384	52.5788	142.3577	157.6226	145.8834	152.2327	LINC01358		
ENSG00000002	1.2004	0.00725428	0.04542305	8.7705	22.4830	8.2736	82.2680	7.0774	8.5629	33.8973	33.1553	14.0214	XIST		
ENSG00000001	1.1934	5.10E-06	0.00031022	29.2349	37.8123	22.0628	70.8077	16.1769	56.7280	59.3203	67.6358	46.0704	ZNF536		
ENSG00000001	1.1599	8.62E-06	0.00016156	27.2859	29.6366	23.9014	63.0291	23.2582	42.8143	63.5535	58.3533	69.1855	EPHA7		
ENSG00000001	1.1586	3.85E-28	3.58E-25	474.5793	336.2227	337.3772	811.4993	333.6478	905.5235	861.8394	697.5877	925.4147	BTN3A3		
ENSG00000001	1.1455	3.92E-05	0.00080038	31.1839	17.3732	27.5785	66.5307	35.3869	58.7290	41.5242	72.9417	67.1026	CD68		
ENSG00000001	1.1378	0.00068449	0.00617011	13.6429	18.3952	19.3050	35.8516	15.1858	39.6013	33.8873	25.1980	46.0704	ASPA		
ENSG00000001	1.1164	6.45E-12	4.75E-10	898.4847	538.3499	734.5079	1510.9470	545.9691	1516.6983	1582.1576	1136.5639	1734.6518	SAMHD1		
ENSG00000006	1.1132	0.00127642	0.01144338	16.5664	14.3073	22.9821	29.7837	10.1105	41.7440	28.8127	26.5242	42.0643	CP		
ENSG00000006	1.0980	0.00276503	0.02115004	14.6174	17.3732	16.5471	63.0291	9.0995	20.3368	43.2191	25.1980	25.0383	SLC6A15		
ENSG00000001	1.0955	1.18E-05	0.00021252	25.3369	28.6147	33.8521	70.0323	33.3648	64.2215	85.5907	54.3747	61.0934	CD36		
ENSG00000001	1.0911	2.64E-07	7.44E-06	56.5207	31.6806	47.8028	147.6678	34.3758	87.7694	109.3185	62.3320	84.1286	FRZB		
ENSG00000001	1.0872	2.18E-13	2.17E-11	97.4495	78.6984	108.4755	202.2183	98.0722	216.2125	195.7570	220.1512	181.2771	ANGPTL7		
ENSG00000001	1.0829	7.64E-07	3.92E-05	50.6738	32.7025	45.9642	104.1731	35.3869	84.5583	82.2010	71.6155	103.1577	SEPT4		
ENSG00000001	1.0712	2.99E-09	1.26E-07	75.0361	62.3392	58.8342	150.5695	53.5859	139.1466	134.7419	102.1188	145.2220	TCN2		
ENSG00000001	1.0649	1.71E-10	9.07E-09	721.1266	384.2545	563.0368	1047.8584	467.1069	1184.8871	1165.2205	937.6321	1306.9981	PARP9		
ENSG00000001	1.0625	1.46E-10	7.42E-09	67.2402	70.5148	85.4934	161.0743	79.8733	201.2274	137.2842	152.5144	131.2006	HIST3H2B		
ENSG00000001	1.0526	1.82E-13	1.83E-11	2241.3394	1251.8929	2176.8644	3555.0148	1575.2219	3965.6791	4038.8660	2973.3680	4309.5882	PARP14		
ENSG00000001	1.0523	0.00227541	0.01808071	17.5408	11.2415	17.4664	38.5178	13.1437	38.5329	34.7448	17.2408	31.0490	APOL6		
ENSG00000001	1.0381	0.00027918	0.00219324	19.4894	13.4171	30.3364	43.7702	24.2653	52.4476	38.9819	55.7028	42.0643	PTPRO		
ENSG00000001	1.0273	0.00033925	0.00278052	323.5325	143.0735	185.6954	372.9220	129.4149	416.3695	415.2422	327.5744	456.6981	USP18		
ENSG00000001	1.0251	1.11E-15	1.65E-13	214.3890	183.5125	195.8075	359.7910	148.6249	404.5956	311.8554	375.3181	383.5864	TRIM14		
ENSG00000001	1.0190	1.03E-07	3.21E-06	1938.2713	1012.7356	1656.5496	2589.4444	1461.9839	3732.3409	2852.4597	2778.4147	3369.0587	C1S		
ENSG00000001	1.0173	2.38E-11	1.53E-09	89.6536	144.0954	78.1391	196.9659	87.9617	174.4685	191.5199	213.5202	206.3154	SPTBN5		
ENSG00000001	1.0146	2.04E-12	1.66E-10	850.7342	550.8329	857.6919	1372.6332	619.7780	1562.7238	1391.4851	1259.9017	1665.5462	DDX58		
ENSG00000001	1.0132	1.38E-23	5.97E-22	332.3039	292.2787	297.8480	649.5496	309.3825	758.8843	581.3391	523.8539	618.9462	TPPP3		
ENSG00000001	1.0109	1.11E-12	9.66E-11	169.5622	94.0197	128.8612	256.4933	105.1496	233.3382	309.3131	237.3920	249.3812	CRYBG1		
ENSG00000001	-1.0097	1.09E-27	8.67E-25	693.8407	1357.1541	870.5619	369.4204	1119.2366	501.9982	311.6079	724.1119	452.6920	KRT18		
ENSG00000001	-1.0089	7.31E-11	4.19E-09	1509.4934	1500.2276	2611.6857	938.4329	2525.6125	1060.7255	998.2782	836.8400	985.5066	VCAM1		
ENSG00000002	-1.0064	4.69E-05	0.00069797	95.5085	57.2294	99.2827	40.2686	115.2601	54.5883	30.5076	59.6796	38.0582	AC009403.2		
ENSG00000001	-1.0018	8.28E-55	1.26E-50	37480.0670	48216.7832	46631.5968	20368.8957	47840.2917	21683.9273	16817.3094	26491.0905	21143.3236	TAGLN		
ENSG00000001	-1.0013	0.00074223	0.00238842	40.9258	51.0977	61.5920	29.7617	64.7074	24.6183	27.9653	29.1757	20.0306	IRF6		
ENSG00000001	-1.0001	7.83E-08	2.52E-06	124.7314	110.3710	157.1976	45.5210	159.7465	92.0509	36.4396	72.9417	81.1240	INHBE		
ENSG00000001	-1.0593	0.00238185	0.01693369	29.2349	32.7025	38.6099	7.8786	38.4200	23.5479	11.0166	18.5670	20.0306	CSTA		

FIG. 24H

ENSG0000000	-1.0617	2.92E-08	1.03E-06	124.7354	101.1734	137.8926	59.5275	128.4038	61.0104	54.2357	71.6155	49.0730	SMLR	
ENSG0000001	-1.0773	2.89E-15	3.84E-13	240.7004	353.5959	328.1844	136.5630	379.1452	179.8203	140.6739	156.4931	122.1944	LMOD1	
ENSG0000001	-1.0875	0.0001262	0.0016456	53.5972	36.7903	56.9956	20.1343	61.6743	33.1811	21.1858	25.1980	22.0337	EN2	
ENSG0000001	-1.0982	0.00171291	0.01441957	34.1073	20.4391	41.3678	26.2621	51.5637	18.1961	16.3012	13.2621	13.0199	GPRC5C	
ENSG0000001	-1.1027	0.00048425	0.00511832	39.9543	43.9440	40.4485	18.3835	39.4311	27.8293	15.2538	19.8932	14.0214	RNU6-33P	
ENSG0000001	-1.1073	3.12E-06	6.64E-05	64.3167	99.1295	62.5113	28.0129	73.8069	35.3218	22.8807	53.0485	30.0459	APOA1	
ENSG0000001	-1.1306	4.99E-19	1.23E-16	363.4868	549.8109	704.1715	175.0898	711.7819	252.6047	197.4519	355.4249	253.3874	SULT1E1	
ENSG0000001	-1.1308	8.37E-16	1.26E-13	287.4761	262.6420	412.7585	163.7005	386.2226	153.0613	131.3521	163.1241	138.2128	COL10A1	
ENSG0000001	-1.1389	4.03E-27	3.08E-24	819.5306	561.0524	528.5883	302.8897	583.3781	280.4340	305.0759	298.3978	263.4027	PDPN	
ENSG0000001	-1.1463	0.00134436	0.01191164	628.5495	147.1613	205.9196	133.9368	163.7907	119.8802	172.0289	128.6426	76.1164	CYP1B1	
ENSG0000001	-1.1471	8.44E-18	1.66E-15	277.7312	314.7616	399.6885	134.8122	459.0185	161.6242	131.3521	196.2794	157.2404	SCRG1	
ENSG0000001	-1.1759	5.76E-06	0.00011368	62.3677	47.0059	69.8656	28.8883	74.8180	38.5329	33.0499	38.5670	24.0367	SLN	
ENSG0000001	-1.1788	3.24E-12	2.54E-10	1898.3170	2628.4641	1946.1241	814.1355	1641.9515	926.9307	548.2892	1243.9871	835.2785	RNU4-2	
ENSG0000001	-1.1919	1.45E-19	3.99E-17	279.6802	420.0228	462.3998	144.4416	502.4938	168.0463	158.4700	224.1299	165.2526	ITGA8	
ENSG0000001	-1.2196	1.76E-10	9.24E-09	93.5516	136.9418	187.5339	48.1472	216.3655	70.6437	60.1677	70.2893	62.0949	TMEM71	
ENSG0000001	-1.2272	9.32E-05	0.00126936	27.2859	58.2513	49.6413	13.1311	50.5527	13.9147	16.9487	19.8932	28.0429	AL590004.4	
ENSG0000001	-1.2375	1.24E-07	3.77E-06	62.3677	100.1514	84.5741	28.0129	94.0280	24.6183	22.8807	57.0271	43.0658	CNN1	
ENSG0000001	-1.2422	9.82E-06	0.0001805	52.6228	74.6026	62.5113	21.0097	62.6853	22.4775	11.8641	51.7223	27.0413	ACTG2	
ENSG0000001	-1.3645	7.06E-20	2.02E-17	150.0723	260.5981	214.1932	53.3996	240.6308	85.6287	51.6934	108.7494	96.1470	MASP1	
ENSG0000001	-1.3652	7.33E-16	1.12E-13	154.9448	132.2711	156.2783	53.3996	184.0118	57.7994	60.1677	70.2893	69.1056	LAMP5	
ENSG0000001	-1.3887	2.67E-08	9.52E-07	1644.9482	3987.6622	2717.4033	1088.1269	3196.9523	1042.5294	1019.4620	1168.7135	910.3918	TNFRSF10D	
ENSG0000001	-1.5471	2.28E-18	4.94E-16	462.8853	784.8602	1139.9121	231.9820	1104.0708	308.2633	227.1121	232.0872	347.3313	BCYRN1	
ENSG0000001	-1.5746	1.51E-13	1.54E-11	107.1945	136.9418	197.6460	36.7670	159.7465	48.1661	27.1179	83.5514	47.0720	RNY3	
ENSG0000001	-1.7897	2.92E-05	0.00046188	178.3327	131.8320	325.4265	74.4093	283.0951	48.1661	68.6421	68.8562	45.0689	EPYC	

FIG. 24H, continued

Significant DEGs following targeting of dSaCas9-repressors to *DUX4*

ID	log2FoldChange	pvalue	padj	Mock-Expt 1	Mock-Expt 2	Mock-Expt 3	Mock-Expt 4	Mock-Expt 5	KRAB-Expt 5	KRAB-Expt 1	KRAB-Expt 4	KRAB-Expt 3	KRAB-Expt 2	Gene.name
ENSG00000229807	6.0850	2.25E-09	7.37E-08	0.8962	10.7583	13.1876	1.0196	26.5246	219.9086	571.0243	1299.2865	1405.3073	56.4540	XIST
ENSG00000130303	4.4989	6.37E-34	4.23E-31	3.5847	17.6044	1.7583	9.1762	10.2018	216.4364	205.7448	168.4650	189.4188	362.4290	BST2
ENSG00000134321	4.0526	2.75E-11	1.31E-09	0.8962	8.8022	0.8792	8.1566	10.2018	163.1953	101.2220	90.5500	68.5516	50.5115	RSAD2
ENSG00000165949	3.9749	3.85E-33	2.38E-30	74.3823	90.9563	26.3752	105.0161	120.3811	1255.7939	1256.4735	1158.1970	1236.6344	1200.3898	IFI27
ENSG00000137959	3.7236	8.50E-15	6.71E-13	64.5244	174.0883	38.6836	148.8577	156.0873	2565.9862	1838.5001	1494.0742	973.2520	814.1258	IFI44L
ENSG00000126709	3.4711	1.55E-21	2.84E-19	1418.6406	1365.8603	349.0512	1600.7301	1614.9450	14765.1268	12548.2310	12298.6996	15719.9592	15290.1140	IFI6
ENSG00000111335	3.3093	3.84E-24	2.82E-12	113.8139	170.1762	43.9586	239.5997	228.5200	2195.6138	1859.4047	1583.5712	1152.7489	1045.8842	OAS2
ENSG00000134326	3.2793	3.99E-07	7.67E-06	0.0000	5.8681	3.5167	10.1957	18.5632	105.3246	88.0192	65.3802	56.8257	49.5210	CMPK2
ENSG00000157601	3.2060	3.86E-11	1.80E-09	39.4316	155.5058	33.4085	85.8399	120.3811	1259.2661	1021.0222	840.2193	496.9889	481.3444	MX1
ENSG00000089127	2.8574	9.56E-19	1.27E-16	39.4316	40.0990	27.2543	77.4876	68.3116	495.9731	418.0910	384.3108	266.0884	247.6052	OAS1
ENSG00000136531	2.8052	9.44E-15	7.42E-13	3.5847	7.8242	7.0334	9.1762	8.1634	89.1209	51.7113	42.1163	37.8838	28.7222	SCN2A
ENSG00000282851	2.6943	1.53E-14	1.55E-14	3.5847	6.8462	2.6375	9.1762	10.2018	46.2965	34.1074	42.1163	46.9037	35.6551	BISPR
ENSG00000162654	2.6811	3.80E-17	4.06E-15	5.3770	7.8242	5.2750	8.1566	9.1616	68.2874	38.5084	44.2221	37.8838	39.6168	GBP4
ENSG00000136646	2.6659	3.66E-09	1.14E-07	8.9617	17.6044	3.5167	25.4893	26.5246	144.6767	116.6254	98.9732	82.9835	74.2815	HERC5
ENSG00000185885	2.5838	1.19E-18	1.54E-16	24.1966	43.8792	21.9793	44.8612	48.9686	277.7793	290.4632	224.2691	191.2228	150.5439	IFITM1
ENSG00000206337	2.5624	1.54E-47	3.06E-44	31.3660	30.3188	18.4626	36.7046	55.0897	237.2698	192.5419	189.5232	190.3208	197.0937	HCP5
ENSG00000166278	2.4811	1.94E-30	8.27E-28	11.6502	14.6704	14.9459	17.3327	22.4439	97.2228	102.3223	93.7087	82.3955	68.3390	C2
ENSG00000183486	2.4643	1.02E-12	6.11E-11	25.0928	61.6155	26.3752	51.9982	38.7668	337.9648	248.1529	249.3388	158.7510	133.7068	MX2
ENSG00000133106	2.4315	4.51E-37	4.04E-34	34.9507	53.7913	36.0460	40.7829	46.9282	319.4462	244.2532	242.1685	157.8490	182.2374	EPSTI1
ENSG00000135114	2.4297	4.85E-12	2.61E-10	5.3770	18.5825	3.5167	7.1370	10.2018	71.7597	48.4105	53.6982	33.3738	32.6839	OAS1
ENSG00000111331	2.4061	4.06E-09	1.25E-07	250.0320	223.9675	78.2463	394.5749	358.0827	1937.5106	1552.4379	1462.4870	1012.9398	948.8230	OAS3
ENSG00000139644	2.4048	3.97E-13	2.51E-11	110.2292	133.9893	56.2670	149.8775	130.5829	939.8199	705.2535	631.7438	417.6234	380.3215	HERC6
ENSG00000185745	2.3795	3.17E-12	1.76E-10	86.0325	154.5278	67.6962	119.2901	125.4820	914.3568	663.4444	608.5799	336.4439	353.5802	IFIT1
ENSG00000119917	2.2859	6.06E-10	2.28E-08	94.9543	113.4508	54.5086	110.1139	130.5829	788.1987	585.3274	547.5113	257.9704	276.3274	IFIT3
ENSG00000146604	2.2833	1.13E-10	4.86E-09	9.8579	3.9121	4.3959	10.1957	5.1009	24.3057	37.4081	42.1163	37.8838	20.7988	RGR
ENSG00000204632	2.2499	2.31E-29	9.64E-27	28.6775	20.5385	11.4292	32.6263	40.8071	130.7877	130.9285	131.6133	110.9453	127.7643	HLA-G
ENSG00000137965	2.2287	1.34E-20	2.24E-18	96.7886	198.5389	111.6548	143.7598	154.0470	879.6344	756.9647	650.6962	535.7847	478.3732	IFI44
ENSG00000206341	2.1873	1.55E-18	1.99E-16	14.3388	8.8022	9.6709	25.4893	21.4238	60.1855	66.0144	63.1744	91.1014	77.2528	HLA-H
ENSG00000177989	2.1723	4.64E-12	2.51E-10	4.4809	11.7363	8.7917	6.1174	6.1211	33.5650	34.1074	36.8517	27.0598	36.6456	ODF3B
ENSG00000234745	2.0519	2.84E-15	2.43E-13	2532.5826	1570.7069	1417.2248	3132.1292	3730.7937	10341.4916	9939.5632	9860.4684	10785.1476	10418.2348	HLA-B
ENSG00000229474	2.0385	5.72E-08	1.38E-06	1.7923	7.8242	9.6709	5.0979	8.1634	28.9353	20.9045	38.9575	27.9618	16.8372	PATL2
ENSG00000214872	2.0363	3.12E-06	4.83E-05	2.6885	1.9560	7.9125	10.1957	1.0202	19.6760	27.5060	16.8465	16.2359	17.8276	SMTNL1
ENSG00000121858	2.0320	1.02E-06	1.78E-05	0.0000	7.8242	4.3959	8.1566	11.2226	31.1502	29.7065	23.1639	13.5299	29.7126	TNFSF10
ENSG00000196139	1.9712	5.21E-06	7.52E-05	5.3770	5.8681	1.7583	9.1762	7.1413	34.7224	30.8067	24.2168	9.9219	14.8563	TMEM229B
ENSG00000168062	1.8807	1.30E-06	2.21E-05	3.5847	5.8681	5.2750	10.1957	4.0807	12.7316	20.9045	30.5343	22.5499	18.8180	BATF2
ENSG00000204525	1.8583	1.22E-19	1.91E-17	3599.0275	2851.9186	2505.6384	4658.4305	5961.0393	13781.3251	13376.7113	13623.3559	14249.7082	13766.8470	HLA-C
ENSG00000171004	1.8580	8.32E-06	0.00013596	9.8579	2.9341	3.5167	10.1957	4.0807	21.9909	34.1074	26.3227	18.0399	10.8946	HS6ST2
ENSG00000010030	1.8474	8.36E-10	3.05E-08	8.9617	7.8242	14.0667	5.0979	12.2421	32.4076	44.0096	41.0833	26.1578	31.6935	ETV7
ENSG00000115267	1.8211	1.00E-09	3.60E-08	69.0055	66.5056	32.5294	105.0356	86.7152	291.6683	314.6685	280.0731	189.4188	197.0937	IFIH1
ENSG00000182961	1.7896	1.95E-10	8.06E-09	15.2349	14.6704	9.6709	16.3132	12.2421	68.2874	49.5108	47.3808	45.0997	25.7509	LGALS9
ENSG00000110492	1.7818	5.04E-26	1.46E-23	890.7952	686.5730	595.1993	986.9470	1136.4791	3219.9250	2927.7372	3000.7832	2825.9486	3792.9862	MDK
ENSG00000233030	1.7411	1.13E-05	0.00014688	1.7923	5.8681	8.7917	4.0783	7.1413	20.8334	16.5036	14.7407	24.3539	15.8467	AC243772.2
ENSG00000149131	1.7099	5.87E-72	5.26E-68	1156.9583	1272.4095	1038.3018	1442.6962	1592.4990	4512.7561	4364.6499	4375.8790	3999.4434	4009.2228	SERPING1
ENSG00000105894	1.6792	2.39E-19	3.43E-17	46.6010	27.3847	18.4626	31.6068	36.7264	109.9543	91.3199	109.5023	107.3373	96.0708	PTN

FIG. 24I

ENSG00000247317	1.6682	1.41E-06	2.37E-05	8.0655	6.8462	4.3959	8.1565	10.2018	32.4076	29.7065	17.8994	20.7459	18.8180	LY6E-DT
ENSG00000128284	1.6630	1.05E-17	1.24E-15	24.1966	28.3627	22.8585	24.4698	45.9080	90.2783	92.4201	80.0209	110.9453	84.1858	APOL3
ENSG00000187608	1.6303	6.50E-05	0.000866194	29.5737	79.2200	18.4626	24.4698	40.8071	144.6767	168.3366	106.4494	92.0034	62.2049	ISG15
ENSG00000196482	1.6122	0.000580478	0.004174921	1.7923	4.8901	8.7917	8.1566	8.1614	28.9353	25.3055	27.3756	8.1180	7.9234	ESRRG
ENSG00000113525	1.6117	2.30E-06	3.67E-05	4.4809	7.8242	6.1541	7.1370	14.2825	31.2502	24.2053	23.1639	24.3539	17.8276	ILS
ENSG00000243649	1.6017	7.15E-27	2.33E-24	41.2239	48.9012	37.8044	42.8221	34.8361	121.5284	133.1290	107.3965	128.9852	131.7259	CFB
ENSG00000100918	1.5980	6.94E-18	8.29E-16	18.8196	40.0990	39.5627	27.5285	30.6054	98.3802	84.7184	98.9732	107.3373	84.1858	RECQ
ENSG00000109832	1.5850	1.89E-06	3.08E-05	6.2732	9.7802	7.0334	7.1370	9.1816	17.3612	20.9045	21.0581	30.6678	26.7414	DDX25
ENSG00000274286	1.5787	1.24E-07	2.69E-06	8.0655	13.6923	10.5501	5.0979	10.2018	25.4631	28.6962	31.5872	27.0598	29.7126	ADRA2B
ENSG00000041353	1.5786	1.14E-09	4.07E-08	21.5081	28.3627	24.6168	33.6459	33.6659	148.1490	82.5180	76.8522	65.9456	50.5115	RAB27B
ENSG00000151322	1.5728	2.01E-06	3.26E-05	6.2732	8.8022	11.4292	7.1370	5.1009	18.5186	20.9045	24.2168	26.1578	25.7509	NPAS3
ENSG00000160932	1.5666	1.87E-72	3.34E-68	655.9980	657.9905	478.2694	576.0589	618.2283	1714.1297	1842.5011	1721.5020	1974.4658	1617.3569	LY6E
ENSG00000128045	1.5234	2.02E-05	0.000224393	8.0655	3.9121	4.3959	7.1370	12.2421	20.8334	20.9045	15.7936	24.3539	19.8084	RASL11B
ENSG00000177294	1.5217	0.000119461	0.001104798	2.6885	8.8022	3.5167	4.0783	12.2421	18.5186	15.4034	15.7936	20.7459	17.8276	FBXO39
ENSG00000162958	1.5208	4.65E-10	1.79E-08	20.6120	36.1889	21.9793	16.3132	30.6054	93.7505	83.6182	89.1796	49.6097	51.5019	FRZB
ENSG00000272235	1.5052	3.51E-06	5.35E-05	9.5847	9.7802	12.3084	12.2349	9.1816	37.0372	28.6962	20.0052	24.3539	23.7761	AL590438.1
ENSG00000135235	1.4751	0.009303441	0.016102506	119.1909	82.1540	58.0253	175.3666	136.7040	515.0491	430.1936	397.9986	123.5732	121.8217	GPNMB
ENSG00000176945	1.4694	1.64E-05	0.000204	8.9617	4.8901	12.3084	4.0783	8.1614	21.9909	25.3055	20.0052	18.9419	21.7893	MUC20
ENSG00000259954	1.4607	0.000140038	0.001266349	5.3770	10.7583	10.5501	1.0196	11.2220	18.5186	16.5036	29.4814	16.2359	26.7414	IL21R-AS1
ENSG00000170011	1.4519	9.43E-05	0.000901349	6.2732	6.8462	4.3959	6.1174	9.1816	20.8334	13.2029	24.2168	16.2359	14.8563	MYRIP
ENSG00000115155	1.4476	1.62E-08	4.44E-07	51.0818	28.3627	17.5834	33.6459	39.7870	57.8707	118.8259	126.3488	92.0034	69.3294	DTOF
ENSG00000143520	1.4348	1.23E-11	6.21E-10	16.1311	22.4946	20.2209	19.3719	25.5045	60.1855	44.8096	57.9099	62.2376	54.4731	FLG2
ENSG00000258461	1.4304	2.79E-08	7.24E-07	11.6502	16.6264	11.4292	13.2545	13.3623	39.3521	36.3079	35.7888	37.8838	28.7222	AC012651.1
ENSG00000204642	1.4297	1.47E-22	2.97E-20	75.2785	66.5056	44.8378	87.6833	93.8564	201.3900	194.7424	180.0470	200.2428	209.9692	HLA-F
ENSG00000259461	1.4196	0.000364614	0.002864963	2.6885	5.8661	16.7043	6.1174	5.1009	16.2038	23.1050	14.7407	21.6479	22.7797	AC012404.1
ENSG00000199053	1.4195	0.000338188	0.002676091	5.3770	6.8462	8.7917	2.0391	10.2018	16.2038	19.8043	15.7936	26.1578	10.8946	MIR324
ENSG00000279320	1.4189	0.000475484	0.003575728	3.5847	5.8681	9.6709	5.0979	10.2018	32.4076	15.4034	16.8465	18.0399	9.9042	AC069528.2
ENSG00000226614	1.4176	0.000544515	0.003963018	6.2732	15.6484	5.2750	4.0783	7.1413	34.7224	18.7841	17.8994	21.6479	9.9042	AL356176.2
ENSG00000228236	1.4074	1.12E-07	2.48E-06	10.7541	22.4946	19.3418	10.1957	9.1816	40.5095	31.9069	41.0533	39.6878	38.6264	TXNP5
ENSG00000052524	1.4011	8.29E-05	0.000811138	6.2732	4.8901	10.5501	6.1174	7.1413	20.8334	20.9045	13.6878	19.8439	17.8276	LTK
ENSG00000164342	1.3794	3.88E-19	5.48E-17	62.7521	62.5935	47.4753	49.9591	85.6950	196.7603	161.7352	142.1424	153.3391	147.5727	TLR3
ENSG00000196296	1.3774	1.95E-23	4.21E-21	58.2542	73.3518	73.8504	61.1744	57.1300	189.8159	192.5419	162.1476	136.2012	164.4098	ATP2A1
ENSG00000245466	1.3565	1.12E-07	2.48E-06	8.9617	12.7143	17.5834	18.3523	18.3632	37.0372	48.4105	32.6401	34.2758	41.5977	AL357153.1
ENSG00000254413	1.3359	2.83E-06	4.45E-05	8.9617	17.6044	22.8585	7.1370	15.3027	31.2502	29.7065	33.6930	42.3937	44.5689	CHKB-CPT1B
ENSG00000250740	1.3355	1.73E-08	4.69E-07	23.3005	21.5165	13.1876	23.4502	25.5045	67.1300	60.5132	57.9099	50.5117	33.6743	AC109361.2
ENSG00000260258	1.3329	4.38E-06	6.47E-05	8.0655	22.4946	18.4626	6.1174	14.2825	40.5095	37.4081	35.7888	34.2758	27.7318	AC007346.1
ENSG00000137752	1.3316	0.000197753	0.001700073	5.3770	7.8242	8.7917	10.1957	13.2623	28.9353	30.8067	21.0581	23.4519	9.9042	CASP1
ENSG00000259336	1.3264	0.000128738	0.001348709	5.3770	9.7802	5.2750	5.0979	11.2220	12.7316	16.5036	20.0052	17.1379	24.7665	AC021231.1
ENSG00000163624	1.3235	0.000472422	0.003559154	4.4809	14.6704	11.1001	10.1957	3.0605	24.3057	18.7841	24.2168	31.5698	35.6551	CDS1
ENSG00000242068	1.3217	0.001129458	0.007771293	8.9617	6.8462	8.7917	7.1370	2.0404	18.5186	20.9045	7.3703	23.4519	14.8563	AC106734.3
ENSG00000155511	1.3212	6.23E-07	1.15E-05	26.8852	15.6484	14.9459	31.6068	30.6054	77.5467	78.1170	61.0686	36.0798	46.5496	GRIA1
ENSG00000273079	1.3178	2.07E-05	0.000249789	9.8579	6.8462	7.0334	13.2545	17.3430	33.5650	27.5060	29.4814	24.3539	19.8084	GRIN2B
ENSG00000259529	1.3165	2.15E-07	4.43E-06	10.7541	17.6044	22.8585	13.2545	16.3229	33.5650	44.8096	45.2750	31.5698	47.5402	AL136295.5
ENSG00000139497	1.3155	1.82E-14	1.40E-12	46.6010	33.2528	27.2543	54.0374	49.9888	101.8524	97.9213	121.0842	103.7294	98.0516	USP18
ENSG00000166710	1.3150	1.79E-17	2.03E-15	23255.6685	18780.0208	16942.5182	29150.6208	26401.2057	65885.7758	53549.7545	55488.1671	54136.8046	55880.5234	B2M
ENSG00000132530	1.2971	1.39E-26	4.46E-24	102.1636	164.3081	152.9759	119.2901	141.8048	389.1039	360.8785	317.9777	314.7961	297.1262	XAF1
ENSG00000236230	1.2946	0.000719652	0.005007741	11.6502	2.9341	8.7917	11.2153	5.1009	11.5741	30.8067	16.8465	20.7459	17.8276	AL356108.1

FIG. 24I, continued

ENSG00000224081	1.2878	6.88E-06	9.66E-05	11.6502	16.6264	21.9793	10.1957	10.2018	48.6114	31.9069	37.9046	32.4718	23.7701	SLC44A3-AS1
ENSG00000237352	1.2780	8.67E-11	3.79E-09	30.4695	28.3627	20.2209	38.7438	28.5650	52.5931	67.1146	67.3860	64.0416	63.3865	LINC01358
ENSG00000138496	1.2779	1.89E-23	4.14E-21	582.5115	707.1115	505.5237	666.8010	641.6924	1824.0840	1796.6910	1550.9311	1208.6726	1145.9167	PARP9
ENSG00000277829	1.2710	1.77E-18	2.24E-16	51.0818	74.3298	74.7296	62.1940	66.3116	175.9269	173.8378	163.2005	162.3590	118.8505	AL031651.2
ENSG00000169116	1.2703	1.68E-08	4.57E-07	35.8469	33.2528	30.7710	30.5872	30.6054	112.2691	73.7160	96.8674	61.3356	46.5498	PARM1
ENSG00000261916	1.2686	0.000180638	0.001573164	4.4805	9.7802	8.7917	12.2349	8.1614	17.3612	23.1050	22.1110	26.1578	14.8563	AC027796.1
ENSG00000259158	1.2662	3.29E-12	1.81E-10	21.5081	48.9012	41.3211	36.7046	34.6861	90.2763	99.0716	75.8093	87.4935	87.1570	ADAM20P1
ENSG00000101347	1.2618	3.65E-24	8.50E-22	596.8507	624.9575	487.9403	683.1141	589.6633	1833.3453	1615.1515	1403.5242	1199.6526	1101.3478	SAMHD1
ENSG00000183549	1.2589	1.50E-06	2.51E-05	8.9617	21.5165	15.8251	16.3132	23.4641	49.7668	31.9069	32.6401	39.6878	50.5115	ACSM5
ENSG00000183018	1.2524	0.000545944	0.003969558	10.7541	9.7802	6.1542	2.0391	10.2018	18.5186	15.4034	22.1110	15.3339	21.7895	SPNS2
ENSG00000249715	1.2492	0.000763141	0.005254617	8.0655	4.8901	6.1542	6.1174	11.2220	19.6760	13.2029	17.8994	23.4519	11.8850	FERMT3
ENSG00000280875	1.2472	1.58E-09	5.46E-08	17.0273	38.1429	30.7710	31.6068	48.9886	84.4912	69.3151	73.7034	73.0616	92.1091	AL359740.1
ENSG00000237928	1.2458	2.85E-06	4.46E-05	14.3388	10.7583	19.3418	13.2545	13.2623	40.5095	39.6086	33.6930	32.4718	23.7701	NFIA-AS2
ENSG00000213928	1.2425	2.07E-16	2.05E-14	46.6810	77.2659	47.4753	53.0178	55.0897	149.5193	146.3318	133.7191	114.5533	122.8122	RF9
ENSG00000235812	1.2404	0.000849765	0.005746846	3.5847	6.8462	10.5501	6.1174	14.2825	18.5186	14.3031	27.3756	14.4319	22.7797	ADAM21P1
ENSG00000206503	1.2403	6.59E-33	3.81E-30	2822.9424	2312.0492	1987.8073	2939.4299	3248.2491	6767.2125	6371.4867	6171.0844	6188.5839	6002.9396	HLA-A
ENSG00000260326	1.2395	2.18E-06	3.51E-05	10.7541	15.6484	16.7043	15.2936	19.3834	42.8243	49.5108	28.4285	32.4718	30.7030	PHBP21
ENSG00000231549	1.2363	1.18E-07	2.58E-06	13.4476	18.5825	21.9793	21.4110	18.3632	52.0836	49.5108	45.2750	32.4718	42.5881	ATP5MDP1
ENSG00000279883	1.2344	1.07E-05	1.86E-05	14.3388	19.5605	14.0667	14.2740	11.2220	40.5095	36.3079	29.4814	32.4718	34.6647	AC010480.1
ENSG00000108679	1.2343	2.03E-47	3.63E-44	8180.2598	7440.8082	6408.2827	9267.9215	9013.2792	20040.6185	19217.8826	19014.4366	18533.2799	18025.6558	LGALS3BP
ENSG00000174844	1.2258	1.22E-05	0.000158262	7.1694	12.7113	13.1876	16.3132	12.2421	23.1483	30.8067	28.4285	27.9618	32.6839	DNAH12
ENSG00000064135	1.2205	1.84E-07	3.88E-06	16.1311	40.0990	35.1669	19.3719	19.3834	67.1300	53.9117	60.0157	71.2576	51.5015	DLX3
ENSG00000274995	1.2192	0.000448812	0.003396987	4.4805	8.8022	8.7917	6.1174	13.2623	21.9909	15.4034	20.0052	22.5499	15.8467	AC013564.1
ENSG00000259151	1.2154	0.000335251	0.002662255	4.4805	5.8681	9.6709	14.2740	10.2018	20.8334	23.1050	16.8465	18.0399	23.7701	CAP2P1
ENSG00000260277	1.2136	0.002879244	0.015581129	4.4805	13.6923	9.6709	4.0783	4.0807	16.5186	14.3031	13.6878	11.7259	25.7509	AC009019.1
ENSG00000232282	1.2126	0.000136638	0.001240606	7.1694	13.6923	8.7917	10.1957	17.3430	28.9353	39.6086	22.1110	20.7459	20.7988	MTND1P32
ENSG00000226627	1.2103	3.83E-07	7.43E-06	16.1311	19.5605	19.3418	11.2153	22.4439	50.9262	44.0096	35.7988	36.7858	36.6456	RF00432
ENSG00000245904	1.2065	9.31E-05	0.000899317	11.6502	5.8681	13.1876	20.3915	9.1816	26.9353	29.7065	34.7459	27.0598	18.8180	SHANK2-AS1
ENSG00000230417	1.2021	8.59E-06	0.000116671	16.1311	16.6264	12.3084	12.2349	13.2623	27.7779	47.3103	27.3756	31.5698	28.7222	AC025164.1
ENSG00000100342	1.2004	9.20E-14	6.27E-12	94.9943	79.2200	61.5420	119.2901	103.0381	234.9550	253.0551	215.8458	182.2029	165.4002	LINC00595
ENSG00000100342	1.1981	1.21E-22	2.46E-20	104.8521	110.5167	93.1922	115.2118	111.1995	248.8439	202.4441	209.5284	278.7163	283.2603	APOL1
ENSG00000259922	1.1968	7.99E-05	0.000788576	7.1694	15.6484	7.0334	14.2740	10.2018	25.4631	27.5060	23.1639	21.6479	25.7509	AC023825.1
ENSG00000235829	1.1960	0.004660511	0.022938688	5.3770	6.8462	3.5167	7.1370	14.2825	19.6760	27.5060	17.8994	10.8239	8.9138	TBCAP2
ENSG00000165339	1.1958	1.19E-14	9.24E-13	51.0818	39.1210	52.7503	41.8025	63.2511	105.3246	137.5199	112.6610	105.7294	109.9367	TCN2
ENSG00000101342	1.1944	0.000742592	0.005149014	7.1694	8.8022	9.6709	10.1957	5.1009	25.4631	25.3055	13.6878	15.3339	14.8563	TLDC2
ENSG00000181516	1.1929	8.21E-06	0.000112479	8.9617	16.6264	13.1876	14.2740	15.3017	23.1483	34.1074	30.5343	33.3738	33.6743	DRS2H1
ENSG00000198597	1.1920	1.57E-06	2.63E-05	18.8196	21.5165	14.0667	14.2740	11.2220	40.5095	31.9069	35.7988	33.3738	41.5977	ZNF536
ENSG00000159403	1.1778	5.14E-38	5.70E-35	1285.1109	1243.0688	969.7764	1384.5806	1518.0760	2962.9791	2971.7468	2934.4501	2862.9304	2741.4944	CIR
ENSG00000109511	1.1759	2.51E-05	0.000294198	12.5464	19.5605	25.4960	12.2349	24.4843	56.7133	36.3079	46.3279	50.5117	23.7701	ANXA10
ENSG00000137628	1.1757	6.70E-26	1.85E-23	300.2177	367.7371	262.8723	341.5571	360.1231	832.1805	849.3949	751.8281	628.6901	623.9650	DDX60
ENSG00000243650	1.1718	0.000723748	0.005027808	11.6502	5.8681	20.2209	9.1762	9.1816	40.5095	17.6038	17.8994	24.3539	27.7316	RN7SL834P
ENSG00000243811	1.1708	4.54E-06	6.67E-05	25.0928	22.4946	8.7917	16.3132	22.4439	32.4076	36.3079	50.5395	47.8057	45.5599	APOBEC3D
ENSG00000160525	1.1646	2.01E-22	3.96E-20	74.3823	76.2859	80.0046	102.9769	95.8968	174.7695	196.9429	208.4755	199.3408	179.2661	PRR26
ENSG00000107201	1.1583	2.66E-26	8.21E-24	444.5014	463.5835	394.7481	551.5892	511.1096	1266.5254	1143.1488	1079.2291	881.2486	907.2255	DDX58
ENSG00000237813	1.1572	0.000101906	0.000971124	10.7541	8.8022	19.3418	10.1957	11.2220	32.4076	19.8043	33.6930	26.1578	23.7701	AC002066.1
ENSG00000137877	1.1568	3.45E-09	1.09E-07	21.5081	31.2968	31.6502	45.8808	51.0089	68.2874	83.6182	75.8093	87.4935	95.1762	SPTBN5
ENSG00000110446	1.1532	2.60E-25	6.74E-23	179.2344	135.9454	123.9632	176.3862	134.6636	351.8538	335.6733	352.7236	337.3459	290.1933	SLC15A3

FIG. 24J

ENSG00000259224	1.1454	9.99E-05	0.000948209	8.9617	7.8242	23.7376	12.2349	13.2623	27.7779	26.4057	29.4814	34.2758	28.7222 SLC35G6
ENSG00000119922	1.1424	3.99E-10	1.55E-08	25.9890	44.9891	27.2543	43.8417	44.8879	83.3338	84.7184	92.6558	70.3596	79.2337 IFIT2
ENSG00000111305	1.1387	7.54E-06	0.000104793	17.0273	21.5165	15.8251	22.4306	19.3834	43.9817	48.4105	54.7511	23.4519	43.5977 GSG1
ENSG00000190638	1.1385	0.001073135	0.006961203	6.2732	3.9121	13.1976	9.1762	12.2421	13.8890	18.7041	25.2698	21.6479	18.8180 SLC47A2
ENSG00000155330	1.1383	0.001150279	0.009208377	3.5847	10.7583	10.5501	8.1566	7.1413	21.9909	17.6038	15.7936	12.6279	20.7988 IRGJK
ENSG00000277420	1.1364	0.000418943	0.003214997	8.9617	14.6704	10.5501	10.1957	6.1211	26.6205	14.3031	18.9523	25.2558	25.7509 AC245407.2
ENSG00000150637	1.1361	2.18E-14	1.65E-12	57.3550	72.3738	81.7630	59.1353	68.3520	187.5010	143.0311	120.0313	161.4579	134.6972 CD226
ENSG00000255321	1.1360	0.000921055	0.006117545	7.1694	8.8022	11.4292	16.3132	7.1413	32.4076	16.5036	13.6878	27.0598	21.7693 AC068389.4
ENSG00000153064	1.1345	2.19E-05	0.000262568	12.5464	10.7583	22.8585	14.2740	13.2623	31.2502	25.3055	38.9575	33.3738	35.6743 BANK1
ENSG00000137874	1.1339	0.001270441	0.008017648	10.7541	5.8681	6.1542	11.2153	8.1614	15.0464	12.1026	24.2168	22.5499	17.8276 SLC14A2
ENSG00000236532	1.1300	0.001680642	0.010054123	5.3770	12.7143	6.1542	6.1174	12.2421	21.9909	20.9045	21.0581	18.0399	10.8946 LINC01695
ENSG00000197315	1.1275	1.15E-10	4.92E-09	47.4971	44.9891	36.0460	26.5089	44.8879	93.7505	99.0216	68.4389	86.5915	90.1283 HRNR
ENSG00000225963	1.1274	4.52E-05	0.000485364	13.4426	13.6923	18.4626	15.2936	14.2825	35.8798	19.8043	46.3279	27.0598	35.6551 AC009950.1
ENSG00000204176	1.1274	8.29E-09	2.40E-07	33.1584	61.6155	47.4793	23.4502	45.9080	92.5931	83.6182	80.0209	104.6314	101.0229 SYT15
ENSG00000207444	1.1271	0.001575682	0.009557281	8.0655	5.8681	10.5501	6.1174	11.2220	24.3057	14.3031	25.2698	14.4319	13.8659 SNORD56B
ENSG00000150627	1.1263	0.000289393	0.002363	11.6502	8.8022	12.3084	14.2740	17.3430	35.8798	35.2077	32.6401	23.4519	13.8659 WDR17
ENSG00000227766	1.1260	1.28E-06	2.17E-05	25.9890	14.6704	22.8585	39.7634	26.5246	42.8243	52.8115	57.9099	73.9635	55.4827 HCG4P5
ENSG00000092068	1.1253	1.47E-09	5.15E-08	52.8742	55.7474	49.2336	60.1548	58.1502	152.7786	129.8283	151.6185	86.5915	83.1953 SLC7A8
ENSG00000117501	1.1219	5.19E-05	0.000545153	17.0273	7.8242	20.2209	8.1566	18.3632	34.7224	30.8067	27.3756	31.5698	32.6839 MROH9
ENSG00000155846	1.1218	0.006783606	0.036099911	14.3388	3.9121	6.1542	23.4502	5.1009	15.0464	35.2077	25.2698	22.5499	16.8372 PPARGC1B
ENSG00000187934	1.1209	0.002130747	0.012201082	34.0545	118.3409	109.8173	36.7046	84.6748	146.9915	171.6374	151.6185	205.6547	156.4865 SAMD11
ENSG00000166689	1.1208	2.79E-10	1.13E-08	43.9124	44.0111	65.9379	27.5285	52.0291	115.7414	110.0239	94.7616	98.3174	92.1091 PLEKHA7
ENSG00000171502	1.1189	8.89E-06	0.000119829	18.8196	27.3847	33.4085	21.4110	17.3430	60.1855	67.1146	40.0104	59.5316	31.6935 COL24A1
ENSG00000273233	1.1183	0.001983972	0.011474257	6.2732	8.8022	10.5501	8.1566	5.1009	20.8934	9.9022	21.0581	16.2359	16.8372 AC097724.1
ENSG00000232751	1.1169	0.000877646	0.005891404	8.0655	7.8242	10.5501	5.0979	10.2018	17.3612	19.8043	16.8465	17.1379	19.8084 AL645568.3
ENSG00000271444	1.1166	1.45E-05	0.000183594	12.5464	14.6704	15.8251	13.2545	16.3229	35.8798	26.4057	34.7459	27.0598	33.6743 AC092757.3
ENSG00000269481	1.1165	0.000964279	0.006368801	7.1694	8.8022	11.4292	7.1370	14.2825	32.4076	23.1050	18.9523	14.4319	17.8276 AC010319.4
ENSG00000227215	1.1125	0.000532083	0.003884534	6.2732	10.7583	10.5501	11.2153	11.2220	26.6205	25.3055	13.6878	23.4519	18.8180 AL355613.1
ENSG00000108381	1.1121	7.79E-08	1.82E-06	20.6120	27.3847	36.0460	27.5285	26.5246	76.3893	67.1146	57.9099	48.7077	50.5115 ASPA
ENSG00000230699	1.1109	0.001979415	0.011455294	5.3770	7.8242	7.9125	6.1174	17.3430	23.1483	23.1050	15.7936	19.8439	13.8659 AL645608.3
ENSG00000224769	1.1093	0.005615599	0.026484162	8.9617	8.8022	12.3084	5.0979	4.0807	13.8890	14.3031	20.0052	27.9618	8.9138 MUC20P1
ENSG00000239922	1.1069	9.04E-07	1.60E-05	23.3005	17.6044	21.9793	25.4893	27.5448	68.2874	46.2101	36.8517	43.2957	55.4636 AC092958.1
ENSG00000107954	1.1065	9.54E-06	0.000127648	12.5464	10.7583	18.4626	18.3523	21.4238	34.7224	37.4081	38.9575	30.6678	33.6743 NEURL1
ENSG00000130649	1.1059	1.26E-05	0.000162794	12.5464	18.5825	18.4626	17.3327	19.3834	50.9262	37.4081	38.9575	33.3738	25.7509 CYP2E1
ENSG00000149633	1.1049	5.40E-38	5.70E-35	428.3703	429.3526	499.4777	388.4574	409.0917	969.9127	953.9076	687.6001	1012.0378	750.7389 KIAA1755
ENSG00000134532	1.1040	7.53E-10	2.79E-08	31.3660	38.1429	33.4085	30.5872	24.4843	78.7041	64.9141	67.1215	66.7478	68.3390 SOX5
ENSG00000229106	1.1025	4.13E-07	7.95E-06	25.0928	11.7363	22.8585	24.4698	29.5852	53.2410	47.3103	49.4866	48.7077	45.5593 AL162408.1
ENSG00000132815	1.0998	0.003967588	0.020065202	3.5847	7.8242	6.1542	9.1762	18.3632	21.9909	16.5036	15.7936	14.4319	26.7414 PDE6A
ENSG00000280248	1.0997	2.64E-05	0.000307813	17.0273	21.5165	14.9459	14.2740	12.2421	27.7779	34.1074	48.4337	28.8638	32.6839 AC124319.4
ENSG00000103522	1.0975	3.06E-17	3.29E-15	215.9775	348.1766	347.2728	209.0125	313.1949	606.4848	627.1365	560.1462	672.8879	603.1853 IL21R
ENSG00000173193	1.0975	3.20E-25	7.98E-23	1105.8765	1169.7170	508.1844	1286.7015	1140.5598	2819.4598	2681.2836	2459.5893	2028.5855	2017.4369 PARP14
ENSG00000258676	1.0965	0.001739637	0.010327762	6.2732	10.7583	7.0334	7.1370	9.1816	16.2038	22.0048	18.9523	17.1379	11.8850 AC091544.2
ENSG00000068976	1.0951	0.000177395	0.001154718	19.7158	11.7363	14.9459	12.2349	9.1816	28.9353	20.9045	37.9046	36.0798	21.7893 PYGM
ENSG00000198313	1.0934	2.21E-16	2.17E-14	221.3545	232.7698	210.1220	271.2065	277.4886	639.1053	612.8334	531.7177	413.1135	398.1491 PLSCR1
ENSG00000144452	1.0870	0.001303414	0.008199753	8.9617	7.8242	7.0334	9.1762	20.4036	26.6205	22.0048	18.9523	28.8638	15.8467 ABCA12
ENSG00000279645	1.0868	0.002675089	0.014680223	3.5847	8.8022	6.1542	10.1957	12.2421	13.8890	23.1050	15.7936	15.3339	17.8276 AC016251.1
ENSG00000201341	1.0849	0.004897092	0.023751111	8.0655	1.9560	7.0334	15.2936	10.2018	21.9909	15.4034	24.2168	12.6279	15.8467 RNU6-421P

FIG. 24J, continued

ENSG00000236756	1.0823	0.00616993	0.028449617	4.4809	11.7363	12.3084	8.1566	3.0605	11.5741	11.0024	20.0052	23.4519	17.8276	DNAJC9-AS1
ENSG00000180481	1.0792	0.0010759905	0.008976647	7.1694	13.6923	24.6168	13.2545	5.1009	27.7779	27.5060	26.3227	32.4718	21.7893	GLRPR1L2
ENSG00000229531	1.0781	0.00378764	0.01930221	8.0655	6.8462	4.3959	10.1957	11.2220	21.9609	23.1050	11.5820	18.0399	10.8946	Z99127.1
ENSG00000271743	1.0734	0.00132599	0.008312596	16.1311	15.6484	6.1542	6.1174	8.1614	26.6205	22.0048	26.3227	18.0399	17.8276	AF287957.1
ENSG00000227544	1.0716	0.000647271	0.00458902	20.6120	12.7143	9.6709	15.2936	26.5246	20.8334	22.0048	49.4866	38.7858	45.5593	AC018647.1
ENSG00000237628	1.0715	0.0009520011	0.005117545	5.3770	6.8462	14.0667	11.2153	15.3027	24.3057	19.8043	18.9523	19.8439	27.7338	MTCO2P19
ENSG00000138678	1.0714	0.000381325	0.002976693	17.9234	8.8022	7.0834	20.3915	11.2220	31.2502	31.9069	21.0581	25.2558	27.7318	GPAT3
ENSG00000108387	1.0711	2.30E-07	4.66E-06	28.6775	32.2746	21.9793	21.4110	36.7264	43.9817	63.8139	52.6453	69.4536	64.3773	SEPT4
ENSG00000242067	1.0649	0.004316712	0.021503177	6.2732	10.7583	5.2750	9.1762	11.2220	13.8890	15.4034	10.5291	27.9618	19.8084	RPL9P28
ENSG00000202533	1.0627	0.005088813	0.024458781	1.7923	8.8022	14.9459	13.2545	7.1413	24.3057	19.8043	16.8465	13.5289	21.7893	RF00019
ENSG00000279561	1.0609	0.0008997755	0.005594956	8.9617	7.8242	8.7917	11.2153	18.3632	16.2038	20.9045	30.5343	25.2558	20.7988	AL845472.2
ENSG00000257964	1.0556	0.006226407	0.028629012	6.2732	5.8681	3.5167	13.2545	10.2018	19.6760	11.0024	12.6349	20.7459	15.8467	AC020612.3
ENSG00000143217	1.0549	0.000201536	0.001729762	16.1311	28.3627	29.8918	12.2349	14.2825	63.8578	28.6062	34.7459	39.6878	44.5689	NECTIN4
ENSG00000225140	1.0538	1.77E-06	2.92E-05	16.1311	24.4506	20.2209	19.3719	26.5246	39.3521	40.7089	51.5924	47.8057	40.6072	AL358216.1
ENSG00000214402	1.0505	3.77E-05	0.000415848	13.4426	22.4946	16.7043	15.2936	13.2623	32.4076	31.9069	40.0104	37.8838	25.7509	LCNL1
ENSG00000075275	1.0494	0.001248297	0.007894573	29.5737	10.7583	9.6709	18.3523	35.7063	35.8798	61.6134	53.6982	34.2758	29.7126	CELSR1
ENSG00000223956	1.0492	0.003364723	0.017643633	5.3770	7.8242	8.7917	7.1378	11.2220	23.1483	18.7041	11.5820	14.4319	15.8467	LINC01767
ENSG00000262003	1.0468	0.003259425	0.017186803	7.1694	7.8242	8.7917	17.3327	12.2421	16.2038	26.4057	18.9523	34.2758	12.8755	AC087392.1
ENSG00000232928	1.0468	1.81E-10	7.47E-09	57.3550	51.6353	50.9920	72.3897	90.7959	121.5284	145.2316	161.0947	119.9653	117.8601	DDX3P1
ENSG00000256609	1.0464	0.000107422	0.001005914	10.7541	14.6704	15.8251	11.2153	21.4238	26.6205	39.6086	27.3756	27.0598	31.6935	AC084880.3
ENSG00000210077	1.0444	0.011779242	0.048946708	24.1966	6.8462	14.9459	30.5872	4.0807	41.6669	28.6062	13.6878	48.7077	33.6743	MT-TV
ENSG00000248944	1.0438	0.002784783	0.015166002	9.8579	5.8681	9.6709	9.1762	8.1614	11.5741	24.2053	14.7407	21.6479	15.8467	AC004846.2
ENSG00000154065	1.0425	5.35E-09	1.61E-07	69.0053	82.1540	74.7295	60.1548	92.8363	199.0752	165.0359	181.0999	141.6131	95.0804	ANKRD29
ENSG00000254346	1.0415	0.003858857	0.019598268	5.3770	11.7363	7.9125	7.1378	7.1413	21.9609	12.1026	13.6878	16.2359	16.8372	MTND1P6
ENSG00000151692	1.0355	0.001505129	0.009219559	12.5464	12.7143	20.2209	26.5089	17.3430	33.5650	49.5108	58.9628	20.7459	20.7988	RNF1444
ENSG00000268316	1.0349	0.000401471	0.002446024	17.9234	16.6264	11.4292	7.1378	18.3632	26.6205	33.0072	33.6930	33.3738	19.8084	AL008727.1
ENSG00000267648	1.0337	0.000103044	0.000972026	18.8196	6.8462	18.4626	13.2545	23.4641	32.4076	29.7065	33.6930	36.0798	33.6743	AC060766.5
ENSG00000271723	1.0288	0.003222964	0.017050026	6.2732	10.7583	7.9125	8.1566	10.2018	11.5741	13.2029	20.0052	23.4519	18.8180	MROH7-TTC4
ENSG00000206052	1.0283	0.002306522	0.013008118	11.6502	7.8242	13.1876	5.0979	11.2220	24.3057	25.3055	18.9523	20.7459	11.8850	DOK6
ENSG00000226375	1.0277	2.97E-06	4.62E-05	18.8196	31.2968	26.3752	19.3719	33.6659	39.3521	55.0120	49.4866	51.4137	67.3486	AL022310.1
ENSG00000240095	1.0274	0.006666604	0.030180737	8.9617	13.6923	14.0667	5.0979	17.3430	15.0464	25.3055	12.6349	22.5499	44.5689	AC055758.1
ENSG00000249244	1.0271	3.70E-06	5.53E-05	19.7158	21.5165	24.6168	22.4306	18.3632	33.5650	42.9093	53.6982	39.6878	47.5402	AC110373.1
ENSG00000275850	1.0245	0.006900779	0.034827813	7.1694	8.8022	14.9459	11.2153	9.1816	24.3057	12.1026	28.4285	31.5698	7.9234	AC005912.2
ENSG00000230830	1.0189	0.003111286	0.016555343	3.5847	7.8242	14.9459	12.2349	16.3229	24.3057	26.4057	21.0581	25.2558	13.8659	ARPP21-AS1
ENSG00000227456	1.0158	6.93E-05	0.000700665	9.8579	20.5385	20.2209	31.6068	21.4238	33.5650	44.0096	49.4866	46.9037	33.6743	LINC00310
ENSG00000214243	1.0151	2.03E-05	0.000245239	17.0773	21.5165	14.9459	16.3332	16.3229	35.8798	38.5084	33.6930	33.3738	32.6839	AC004980.2
ENSG00000264176	1.0133	0.003213823	0.016986537	6.2732	7.8242	11.4292	10.1957	10.2018	16.2038	24.2053	21.0581	10.8239	20.7988	MAGOH2P
ENSG00000236064	1.0128	0.002899833	0.015659445	6.2732	17.6044	5.2750	12.2349	10.2018	26.6205	18.7041	22.1110	16.2359	19.8084	AL034399.2
ENSG00000270741	1.0110	0.001404969	0.008704204	10.7541	9.7802	12.3084	6.1174	12.2421	20.8334	27.5060	20.0052	19.8439	15.8467	PRELID3BP8
ENSG00000182326	1.0110	4.14E-33	2.47E-30	554.7305	664.0784	530.1405	642.3312	553.9346	1346.0722	1267.4759	1291.9161	1178.0047	1050.8363	C15
ENSG00000135333	1.0107	3.45E-05	0.000386093	17.0173	20.5385	12.3084	26.5089	26.5246	50.9252	36.3079	32.6401	46.9037	38.6264	EPHA7
ENSG00000196460	1.0103	2.38E-10	9.68E-09	85.1364	65.5276	60.6628	102.9769	93.8564	192.1307	182.6397	171.6237	153.3391	121.8217	RFX8
ENSG00000161425	1.0041	5.58E-06	7.98E-05	32.2622	36.1869	18.4626	24.4698	19.3834	67.1350	45.1098	48.4337	46.9037	55.4636	BPI
ENSG00000187229	1.0002	6.40E-08	1.52E-06	31.3660	27.3847	48.3544	44.8612	44.8879	77.5467	82.5180	75.8093	63.1396	95.0804	AC100800.1
ENSG00000249264	-1.0018	0.000858677	0.005796636	23.3065	20.5385	22.8565	17.3327	27.5448	10.4167	12.1026	9.4762	10.8239	12.8755	EEF1A1P9
ENSG00000152493	-1.0045	1.53E-18	1.97E-16	395.2119	381.4294	400.9023	391.5162	327.4774	219.9086	218.9477	206.3697	159.6530	144.6014	PDPN
ENSG00000065717	-1.0077	0.003248359	0.017138754	20.6120	33.3528	29.8918	28.3915	24.4843	9.2593	2.2005	16.8465	19.8439	14.8563	TLE2

FIG. 24K

ENSG00000117016	-1.0091	2.32E-06	3.70E-05	75.2785	44.9891	51.8711	62.1940	44.8879	27.7779	25.3055	27.3756	34.2758	23.7701	RIMS3
ENSG00000149591	-1.0096	2.50E-40	3.20E-37	4041.7366	3888.6242	3912.3142	3075.0331	3606.3319	1641.2127	1968.3284	1875.2263	1836.4607	1879.8184	TAGLN
ENSG00000187550	-1.0179	0.003772145	0.019252213	26.8852	22.4946	12.3084	29.5676	27.5448	3.4722	18.7041	11.5820	15.3339	8.9136	SBK2
ENSG00000280143	-1.0194	5.50E-14	3.93E-12	322.6220	254.2863	275.1807	215.1300	320.3361	98.3802	156.2340	142.1424	132.5932	154.5056	AP000892.3
ENSG00000136404	-1.0221	1.78E-05	0.000218922	46.6010	85.0881	105.5006	50.9787	85.6950	34.7224	28.6062	29.4814	46.9037	43.5785	TM6SF1
ENSG00000135069	-1.0394	5.92E-05	0.000611792	2589.0415	4103.7896	4131.2279	2714.1042	2871.8032	1237.2753	1201.4615	1254.0115	1946.5040	2343.3353	PSAT1
ENSG00000138829	-1.0404	1.74E-34	1.20E-31	1504.6731	1084.6288	1181.6068	1308.1126	1237.4768	650.4665	608.4324	626.4793	633.2001	553.6451	FBN2
ENSG00000275126	-1.0426	4.51E-06	6.63E-05	121.8794	67.4837	62.4212	49.9591	74.4730	42.8243	37.4081	31.5872	38.7858	32.6839	HIST1H4L
ENSG00000003989	-1.0437	2.20E-12	1.25E-10	158.6225	194.6268	129.2382	162.1122	210.1568	67.1300	82.5180	83.1796	100.1214	79.2337	SLC7A2
ENSG00000057294	-1.0485	1.32E-11	6.62E-10	81.5517	84.1101	87.9172	90.7420	93.8564	40.5095	40.7089	47.3808	44.1977	38.6264	PKP2
ENSG00000117507	-1.0552	6.15E-05	0.00063286	39.4316	28.3627	27.2543	36.7046	28.5650	11.5741	16.5036	11.5820	17.1379	19.8084	FMO6P
ENSG00000174640	-1.0686	0.004863447	0.023654037	10.7541	24.4506	21.1001	14.2740	17.3430	3.4722	11.0024	5.2645	12.6279	8.9138	SLCO2A1
ENSG00000183196	-1.0688	3.79E-06	5.69E-05	40.3277	50.8573	38.6836	41.8025	34.6861	26.6205	17.6038	18.9523	19.8439	15.8467	CHST6
ENSG00000207445	-1.0719	0.000844773	0.005724333	34.0545	22.4946	20.2209	17.3327	24.4843	11.5741	5.5012	10.5291	11.7259	16.8372	SNORD15B
ENSG00000173530	-1.0771	1.95E-17	2.18E-15	846.8827	1074.8486	1252.8197	777.9344	738.6094	446.7617	440.0958	401.1573	441.0753	495.2103	TNFRSF10D
ENSG00000099960	-1.0780	5.43E-15	4.39E-13	407.7584	287.5391	243.5306	300.7741	301.9729	128.4729	132.0287	186.3644	143.4171	139.6493	SLC7A4
ENSG00000135842	-1.0839	0.000144926	0.001305279	325.3105	551.6057	536.2947	311.9894	284.6299	168.9824	121.0263	162.1476	230.9106	264.4423	FAM129A
ENSG00000145777	-1.0926	6.71E-07	1.23E-05	47.4971	44.9891	45.7169	46.9004	36.7264	16.2038	19.8043	26.3227	21.6479	19.8084	TSLP
ENSG00000102981	-1.1098	0.000801897	0.005475203	25.0928	17.6044	19.3418	16.3132	23.4641	5.7871	12.1026	6.3174	12.6279	9.9042	PARD6A
ENSG00000196196	-1.1099	7.35E-05	0.000733292	45.7048	64.5496	50.9920	24.4698	39.7870	12.7316	16.5036	24.2168	18.9419	31.6935	HRCT1
ENSG00000123500	-1.1160	2.28E-06	3.65E-05	187.3000	399.0339	347.2728	228.3844	213.2174	144.6767	133.1290	138.9836	104.6314	113.8984	COL10A1
ENSG00000201558	-1.1218	7.81E-05	0.000772502	51.0818	27.3847	25.4960	43.8417	37.7466	18.5186	16.5036	26.3227	13.5299	10.8946	RNVU1-6
ENSG00000202354	-1.1221	5.79E-10	2.18E-08	126.3603	94.8683	100.2256	115.2118	96.9170	67.1300	58.3127	52.6453	39.6878	29.7126	RNY3
ENSG00000260604	-1.1276	0.000672593	0.004736691	27.7813	39.1210	41.3211	20.3915	17.3430	20.8334	9.9022	8.4233	18.0399	9.9042	AL590004.4
ENSG00000139269	-1.1406	7.45E-06	0.000103637	42.1201	59.6595	70.3337	49.9591	38.7668	25.4631	13.2029	16.8465	35.1778	26.7414	INHBE
ENSG00000154146	-1.1484	0.000429498	0.003281285	22.4043	24.4506	24.6168	26.5089	43.8677	16.2038	13.2029	21.0581	7.2160	6.9329	NRGN
ENSG00000163563	-1.1514	0.009322547	0.039130682	5.3770	27.3847	27.2543	8.1566	30.6054	8.1019	7.7017	11.5820	8.1180	8.9138	MNDA
ENSG00000104998	-1.1755	0.001264384	0.00798223	17.0273	30.3188	27.2543	15.2936	18.3632	10.4167	13.2029	8.4233	2.7060	13.8659	IL27RA
ENSG00000128965	-1.1894	0.00018474	0.001603435	116.5024	210.2752	205.7262	89.7225	113.2398	45.1391	52.8115	51.5924	81.1795	91.1187	CHAC1
ENSG00000111057	-1.1956	6.43E-05	0.000655437	200.7426	375.5613	330.5686	230.4236	190.7734	78.7041	94.6206	87.3912	138.0052	180.2566	KRT18
ENSG00000105664	-1.2043	0.01089539	0.044160576	154.1416	346.1766	390.3522	107.0552	147.9259	41.6669	73.7160	97.9203	130.7892	153.5152	COMP
ENSG00000181790	-1.2282	8.68E-07	1.54E-05	43.0163	33.2528	40.4419	38.7438	34.6861	16.2038	17.6038	8.4233	20.7459	17.8276	ADGRB1
ENSG00000026559	-1.2327	2.46E-07	4.97E-06	77.0708	106.6046	119.5674	69.3310	69.3722	21.9909	30.8067	30.5343	60.4336	42.5881	KCNG1
ENSG00000182492	-1.2495	3.63E-09	1.14E-07	6197.9269	8252.5683	7966.1750	5423.1105	4821.3647	2010.4276	2584.4625	2331.1348	3348.2034	3461.5202	BGN
ENSG00000164778	-1.2619	6.55E-11	2.91E-09	188.1962	107.5827	122.2049	194.7385	125.4820	76.3893	66.0144	71.5976	47.8057	47.5402	EN2
ENSG00000236824	-1.2881	7.54E-05	0.000750575	69.9014	58.6815	93.1922	22.4306	65.2914	18.5186	16.5036	17.8994	44.1977	28.7222	BCYRN1
ENSG00000162692	-1.3028	2.32E-37	2.19E-34	771.6043	873.3756	865.1050	624.9984	660.0556	278.9367	312.4680	292.7080	337.3459	315.9442	VCAM1
ENSG00000156453	-1.3492	4.44E-05	0.000477666	41.2239	77.2639	73.8504	36.7046	39.7870	5.7871	17.6038	21.0581	21.6479	38.6264	PCDH1
ENSG00000109193	-1.3606	0.000420454	0.003224557	222.2507	390.2317	449.2567	212.0713	189.7532	83.3338	78.1170	70.5447	134.3972	203.0362	SULT1E1
ENSG00000083782	-1.3619	0.000306261	0.002475921	85.1364	212.2313	184.6261	89.7225	111.1995	71.7597	59.4129	69.4918	25.2558	40.6072	EPYC
ENSG00000127241	-1.4161	4.37E-11	2.00E-09	110.2292	117.3629	136.2716	79.5267	73.4529	27.7779	37.4081	27.3756	49.6097	50.5115	MASP1
ENSG00000117595	-1.4180	4.81E-09	1.46E-07	41.2239	42.0550	54.5086	40.7829	39.7870	20.8334	13.2029	20.0032	11.7259	16.8372	IRF6
ENSG00000125965	-1.4542	0.000147118	0.001322367	38.5354	15.6484	12.3084	31.6068	38.7668	8.1019	12.1026	15.7936	8.1180	5.9425	GDF5
ENSG00000163394	-1.4649	3.79E-06	5.69E-05	53.7703	39.1210	22.8585	31.6068	20.4036	10.4167	14.3031	12.6349	12.6279	10.8946	CCKAR
ENSG00000130176	-1.5102	1.04E-09	3.74E-08	55.5627	46.9452	50.9920	49.9591	33.6659	10.4167	14.3031	21.0581	14.4319	22.7797	CNN1
ENSG00000125869	-1.8217	1.63E-08	4.44E-07	49.2895	59.6595	72.9713	26.5089	46.9282	11.5741	8.8019	7.3703	26.1578	16.8372	LAMP5
ENSG00000163017	-1.9177	1.44E-39	1.73E-36	180.1306	178.0004	144.1842	170.2687	156.0873	33.5650	41.8091	41.0633	48.7077	52.4923	ACTG2

FIG. 24K, continued

Comparison of DEGs following targeting of dSaCas9-repressors to *DUX4*									
Common DEGs (that are associated with GO terms) in color among treatments after removing factors involved in response to virus						**Unique DEGs (that are associated with GO terms) among treatments**			
TRD + 6	**SET + 1**	**HP1γ + 5**	**HP1α + 2**	**KRAB + 6**		**TRD+6**	**SET+1**	**HP1γ+5**	**HP1α+2**	**KRAB+6**
ETV7	ETV7	ETV7	ETV7	ETV7	**Total unique DEGs:**	0	7	8	0	37
TYMP	TYMP	TYMP	TYMP	KCNG1			MYBPC2	COL9A2		KCNG1
ITGA8	SLC6A15	COL9A2	SLC6A15	PKP2			PTHLH	SCT		PKP2
EPYC	ITGA8	SCT	ITGA8	DUX3			CASS4	ATP6B3		DUX3
CKM	EPYC	ITGA8	EPYC	TLE2			HAAO	HELZ2		TLE2
TRIM14	MYBPC2	EPYC	TRIM14	PYGM			NXPH3	C1QL1		PYGM
SULT1E1	PTHLH	APOL4	ASPA	EPYC			RASGEF1A	ST8SIA6		REC8
CSTA	CASS4	CKM	SULT1E1	REC8			MEF2C-AS1	VGLL2		DDX25
DAW1	APOL4	TRIM14	CSTA	ASPA				OVCH2		FMO6P
CNN1	CKM	ASPA	COL10A1	SULT1E1						RASL11B
KREMEN2	TRIM14	SULT1E1	APOL5	DDX25						PDE6A
CMPK2	ASPA	CSTA	CNN1	FMO6P						IRS4
TM6SF1	SULT1E1	APOL5	KREMEN2	COL10A1						SOX5
SPTBN5	COL10A1	CNN1	CMPK2	RASL11B						PSAT1
FRAS1	DAW1	ATP6B3	TM6SF1	CNN1						GPAT3
GRIA1	APOL5	HELZ2	SPTBN5	PDE6A						FBN2
TPPP3	CNN1	C1QL1	TAGLN	IRS4						RGR
LY6E	KREMEN2	KREMEN2	GRIA1	CMPK2	common to 3 treatments					NPAS3
ACTG2	RARRES3	RARRES3	TPPP3	SOX5	common to 3 treatments					NRGN
CCKAR	CMPK2	CMPK2	LY6E	PSAT1	common to 4-5 treatments					LRGUK
LMOD1	CHRND	CHRND	FRZB	TM6SF1	unique to a treatment					PCDH1
SORG1	TM6SF1	TM6SF1	ACTG2	SPTBN5						CDS1
SLN	SPTBN5	SPTBN5	LMOD1	GPAT3						PLEKHA7
GPRC5C	FRAS1	FRAS1	SORG1	FBN2						PARM1
PARP14	TAGLN	ST8SIA6	EN2	RGR						MYRIP
ACSM5	PLEKHG4B	TAGLN	SLN	TAGLN						COL24A1
HES4	GRIA1	PLEKHG4B	GPRC5C	NPAS3						SLCO2A1
PRELP	TPPP3	GRIA1	PARP14	NRGN						DNAH12
	LY6E	TPPP3	ZNF536	GRIA1						MUC20
	HAAO	LY6E	XIST	LRGUK						OR52H1
	ACTG2	FRZB		PCDH1						CHST6
	CCKAR	ACTG2		LY6E						SBK2
	LMOD1	CCKAR		FRZB						RFX8
	SLN	LMOD1		ACTG2						ESRRG
	HS6ST2	SORG1		CCKAR						SMTNL1
	CDC42BPG	VGLL2		CDS1						FER1L5
	PARP14	SLN		EN2						CHKB-CPT1B
	MAPK15	HS6ST2		PLEKHA7						GRIN2B
	NXPH3	CDC42BPG		PARM1						
	ACSM5	PARP14		MYRIP						
	HES4	MAPK15		HS6ST2						
	PRELP	OVCH2		COL24A1						
	ZNF536	ACSM5		PARP14						
	RASGEF1A	HES4		SLCO2A1						
	PATL2	PRELP		DNAH12						
	XIST	PATL2		MUC20						
	MEF2C-AS1			OR52H1						
				CHST6						
				ACSM5						
				SBK2						
				RFX8						
				ESRRG						
				ZNF536						
				SMTNL1						
				PATL2						
				FER1L5						
				CHKB-CPT1B						
				GRIN2B						
				XIST						

FIG. 25

Changes in expression among developmental and myogenic DEGs following targeting of dSaCas9-repressors to *DUX4*.

		dSaCas9-TRD		dSaCas9-SET		dSaCas9-HP1γ		dSaCas9-HP1α	
Gene name	ID	log2FoldChange	padj	log2FoldChange	pvalue	padj	log2FoldChange	padj	log2FoldChange	padj
KREMEN2	ENSG00000131960	GO:0090090~neg	1.32E+00	5.54E-06	2.69E-07	1.37E+00	2.61E-11	7.97E-10	1.63E+00	9.01E-15	8.83E-13	1.25E+00	1.79E-07	5.22E-06
FRAS1	ENSG00000139759	GO:0030326~em	1.08E+00	2.15E-08	8.54E-10	1.14E+00	3.27E-08	6.43E-07	1.05E+00	1.01E-20	1.42E-18	0.75E+00	5.53E-11	3.28E-08
TRIM14	ENSG00000100785	GO:0051091~pos	1.04E+00	2.17E-10	3.93E-14	1.09E+00	1.94E-23	1.72E-21	1.15E+00	1.08E-24	1.98E-22	1.12E+00	1.11E-15	1.85E-13
FRZB	ENSG00000162998	GO:0061053~sor	0.84E+00	0.00627202	0.04776949	0.88E+00	0.00020507	0.00177403	1.09E+00	2.69E-06	5.19E-05	1.19E+00	2.84E-07	7.44E-06
COL9A2	ENSG00000049089	GO:0030198~ext	0.80E+00	0.00043858	NA	0.59E+00	0.01333E+00	NA	1.15E+00	0.00307542	0.02337503	0.58E+00	0.01600962	NA
TYMP	ENSG00000025708	GO:0030154~cel	1.02E+00	1.40E-41	2.38E-38	1.02E+00	3.11E-58	1.18E-47	1.66E+00	5.29E-54	5.34E-51	1.39E+00	1.04E-08	4.78E-08
CMPK2	ENSG00000134326	GO:0006165~nuc	4.47E+00	3.93E-21	1.40E-18	4.79E+00	8.61E-25	8.08E-23	4.82E+00	3.60E-27	1.08E-24	4.12E+00	2.33E-25	1.31E-22
SPTBN5	ENSG00000137877	GO:0030036~act	1.83E+00	5.73E-16	3.86E-08	1.71E+00	0.11E+00	2.30E-12	1.22E+00	4.70E-15	3.73E-13	1.01E+00	2.30E-11	1.83E-09
GRIA1	ENSG00000155511	GO:0044206~CO	1.10E+00	0.00163282	0.01916E+00	1.15E+00	0.00051E+00	0.00387E+00	1.36E+00	1.66E-05	0.00026E+00	1.33E+00	3.06E-05	0.00047E+00
TPPP3	ENSG00000165757	GO:0046785~mic	1.06E+00	1.83E-18	3.59E-16	1.22E+00	2.90E-49	1.06E-46	1.21E+00	3.51E-29	8.22E-27	1.01E+00	1.38E-23	5.97E-21
LY6E	ENSG00000160932	GO:0007166~cel	1.02E+00	1.23E-27	9.03E-25	1.08E+00	3.62E-228	1.15E-224	1.02E+00	1.07E-153	8.61E-150	1.59E+00	1.02E-08	2.44E-06
PARP14	ENSG00000173193	GO:0006355~reg	1.03E+00	9.53E-10	6.21E-08	1.33E+00	1.18E-67	1.57E-64	1.24E+00	2.18E-45	1.53E-42	1.05E+00	1.82E-13	1.80E-11
ACSM5	ENSG00000180549	GO:0006639~lipi	1.12E+00	3.16E-07	1.12E-05	1.46E+00	5.62E-12	1.65E-10	1.34E+00	2.54E-11	1.27E-09	0.95E+00	2.23E-05	0.00036E+00
PRELP	ENSG00000188783	GO:0007420~ant	1.00E+00	7.36E-06	0.00126429	1.01E+00	2.80E-06	0.00029E+00	1.08E+00	5.99E-06	0.00010E+00	0.79E+00	0.00082E+00	0.00094E+00
TMEM51	ENSG00000139404	GO:0008150~bio	1.11E+00	3.55E-06	2.03E-07	1.34E+00	1.10E-12	3.38E-11	1.15E+00	2.83E-10	1.14E-08	1.21E+00	1.78E-10	9.24E-08
ITGA8	ENSG00000077943	GO:0007420~bra	1.23E+00	4.55E-22	1.84E-19	1.30E+00	1.62E-37	3.38E-35	1.38E+00	1.12E-30	2.88E-28	1.19E+00	1.45E-19	3.96E-17
COL10A1	ENSG00000123500	GO:0061216~cel	0.86E+00	0.00096738	0.01080E+00	1.02E+00	9.52E-06	0.00011E+00	0.96E+00	4.79E-13	2.93E-11	1.19E+00	8.37E-16	1.26E-13
MYBPC2	ENSG00000086967	Fast Skeletal-Typ	0.87E+00	0.00103E+00	0.01124E+00	1.16E+00	1.28E-06	1.80E-04	0.79E+00	0.00178E+01	0.01430E+00	0.39E+00	0.18E+00	0.43326E+00
CKM	ENSG00000104879	Muscle creatine k	1.16E+00	5.30E-06	0.00314E+00	1.23E+00	3.90E-34	7.97E-32	1.15E+00	3.14E-25	5.97E-23	0.84E+00	0.04779E+00	0.19396E+00
MEF2C-AS1	ENSG00000249309	Myocyte-specific	0.92E+00	3.52E-05	0.00038E+00	1.11E+00	5.60E-07	8.53E-06	0.96E+00	4.15E-06	7.47E-05	0.77E+00	0.00050E+00	0.00534E+00
MYOD1	ENSG00000129152	Myogenic differe	0.46E+00	4.56E-06	0.00011E+00	0.46E+00	1.40E-10	3.40E-09	0.52E+00	0.00031E+00	0.00039E+00	0.46E+00	2.63E-16	3.42E-13
MYOG	ENSG00000122180	Myogenin	0.54E+00	1.49E-08	6.86E-07	0.64E+00	3.50E-23	3.58E-21	0.68E+00	6.24E-14	4.36E-12	0.31E+00	0.05E+00	0.23E+00
MYH1	ENSG00000109061	Myosin heavy ch	0.41E+00	9.55E-05	0.00157E+00	0.43E+00	9.65E-06	0.00011E+00	0.36E+00	0.00022E+00	0.00301E+00	0.32E+00	0.00114E+00	0.01124E+00
MEF2C	ENSG00000081189	Myocyte-specific	0.63E+00	0.00246E+00	0.02267E+00	0.81E+00	1.54E-16	8.38E-15	0.67E+00	2.40E-05	0.00035E+00	0.45E+00	0.00364E+00	0.00814E+00

FIG. 26A

			data consistent with this study				
Gene name	ID		[61]	[62]	[63]	[64]	[65]
KREMEN2	ENSG00000131650	GO:0090090~negative regulation of canonical Wnt signaling pathway	DUX4 expression leads to decrease in DUX4, enDUX4				
FRAS1	ENSG00000138759	GO:0036326~embryonic limb morphogenesis	DUX4 expres DUX4 knockdown leads to increase				
TRIM14	ENSG00000106785	GO:0051091~positive regulation of sequence-specific DNA binding transcription factor activity	DUX4 expres DUX4 knockdown leads to increase				
FRZB	ENSG00000162998	GO:0061053~somite development	DUX4 expression leads to increase in iD decreased in FSHD vs healthy				
COL9A2	ENSG00000049089	GO:0030198~extracellular matrix organization	DUX4 expression leads to (Dunbi overexpression leads to decrease of Col9a1 and Col9a3				
TYMP	ENSG00000025708	GO:0030154~cell differentiation	DUX4 expression leads to decrease in enDUX4, vDUX4				
CMPK2	ENSG00000194326	GO:0006165~nucleoside diphosphate phosphorylation	DUX4 expression leads to decrease in vDUX4				
SPTBN5	ENSG00000137877	GO:0030036~actin cytoskeleton organization	DUX4 expression leads to decrease in vDUX4				
GRIA1	ENSG00000155511	GO:0048208~COPII vesicle coating	DUX4 expression leads to decrease in DUX4, enDUX4, vDUX4 (but p values not sig)				
TPPP3	ENSG00000159713	GO:0046785~microtubule polymerization	DUX4 expression leads to decrease in DUX4				
LY6E	ENSG00000160932	GO:0007166~cell surface receptor signaling pathway	DUX4 expression leads to decrease in DUX4, enDUX4, vDUX4				
PARP14	ENSG00000173193	GO:0006355~regulation of transcription, DNA-templated	DUX4 expression leads to decrease in DUX4, enDUX4, vDUX4				
ACSM5	ENSG00000183549	GO:0006633~fatty acid biosynthetic process	DUX4 expression leads to decrease in DUX4, vDUX4				
PRELP	ENSG00000188783	GO:0007409~axonogenesis	DUX4 expression leads to decrease in DUX4				
TM6SF1	ENSG00000138404	GO:0008150~biological_process	DUX4 expression leads to increase in enDUX4				
ITGA8	ENSG00000077943	GO:0007420~brain development	DUX4 expression leads to (Dunbi overexpression leads to increase				
COL10A1	ENSG00000123500	GO:0051216~cartilage development	Dunbi overexpression leads to increase				
MYBPC2	ENSG00000086567	Fast Skeletal-Type Muscle Myosin-Binding-Protein C	DUX4 expression leads to decrease				
CKM	ENSG00000104879	Muscle creatine kinase					
MEF2C-AS1	ENSG00000248309	Myocyte-specific enhancer factor 2C antisense transcript 1					
MYOD1	ENSG00000129152	Myogenic differentiation 1					
MYOG	ENSG00000122180	Myogenin					
MYH1	ENSG00000109061	Myosin heavy chain 1					
MEF2C	ENSG00000081189	Myocyte-specific enhancer factor 2C					

FIG. 26B