

FIG. 1

	FileName	Sample	Cy3	Cy5	QBD_ID	Controls	Client_ID	YOB	CAG size	1st_Medical	Disease duration	SBMAFRS	No
1	SG19158648_258640710027_S001_CGH_1201_Sep17.txt	5	SMBA	pHC	SBMA0001	pHC	UCH0081	1943	37	64	13	43	1
2	SG19158648_258640710026_S001_CGH_1201_Sep17.txt	4	SMBA	pHC	SBMA0003	pHC	UCH0169	1974	49	95	11	36	3
3	SG19158648_258640710025_S001_CGH_1201_Sep17.txt	3	SMBA	pHC	SBMA0004	pHC	UCH0179	1969	46	46	5	50	4
4	SG19158648_258640710023_S001_CGH_1201_Sep17.txt	1	SMBA	pHC	SBMA0006	pHC	UCH0189	1967	45	42	11	34	6
5	SG19158648_258640710024_S001_CGH_1201_Sep17.txt	2	SMBA	pHC	SBMA0007	pHC	UCH0190	1951	45	63	6	47	7
6	SG19158648_258640710003_S001_CGH_1201_Sep17.txt	11	SMBA	pHC	SBMA0008	pHC	UCH0206	1939	40	66	21	32	8
7	SG19158648_258640710029_S001_CGH_1201_Sep17.txt	7	SMBA	pHC	SBMA0009	pHC	UCH0210	1955	UN	59	6	42	9
8	SG19158648_258640710030_S001_CGH_1201_Sep17.txt	8	SMBA	pHC	SBMA0010	pHC	UCH0213	1950	39	60	10	43	10
9	SG19158648_258640710002_S001_CGH_1201_Sep17.txt	10	SMBA	pHC	SBMA0014	pHC	UCH0292	1958	UN	57	5	40	14
10	SG19158648_258640710028_S001_CGH_1201_Sep17.txt	6	SMBA	pHC	SBMA0015	pHC	UCH0307	1950	UN	57	13	26	15
11	SG19158648_258640710004_S001_CGH_1201_Sep17.txt	12	SMBA	pHC	SBMA0016	pHC	UCH0309	1956	UN	52	12	UN	16
12	SG19158648_258640710001_S001_CGH_1201_Sep17.txt	9	SMBA	pHC	SBMA0018	pHC	UCH0312	1969	UN	48	3	50	18

FIG. 2

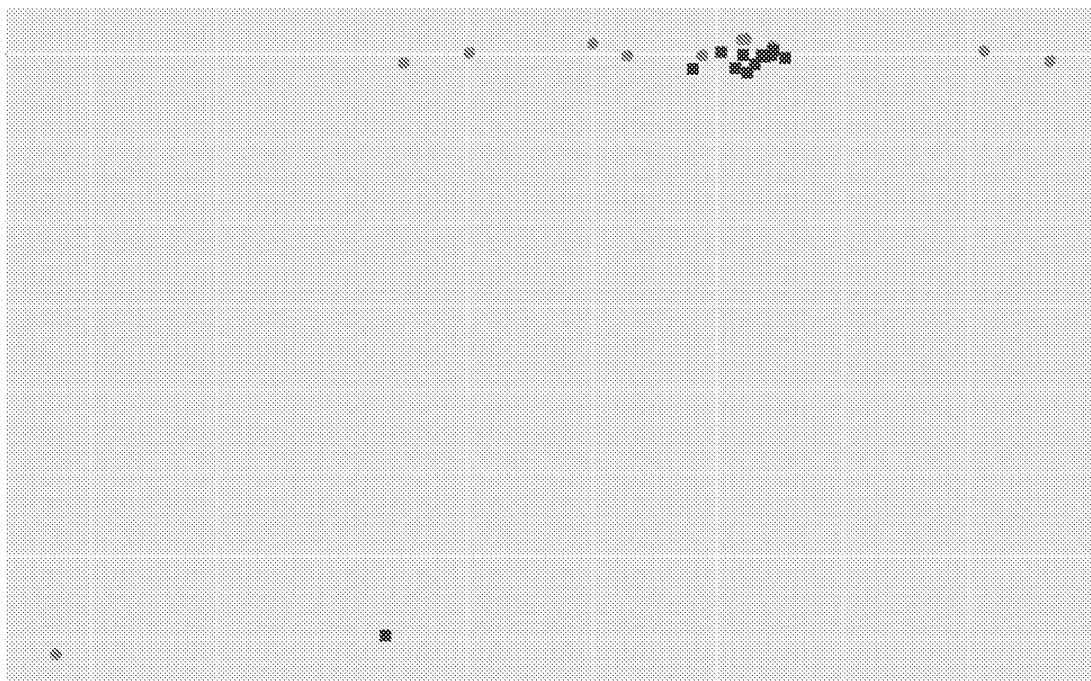


FIG. 3

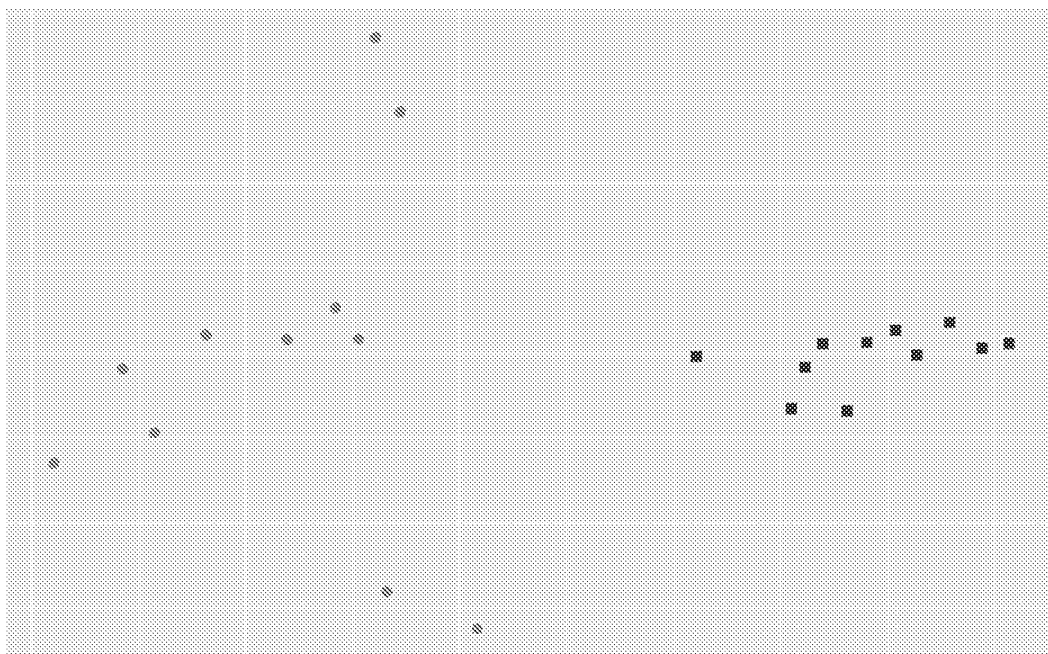


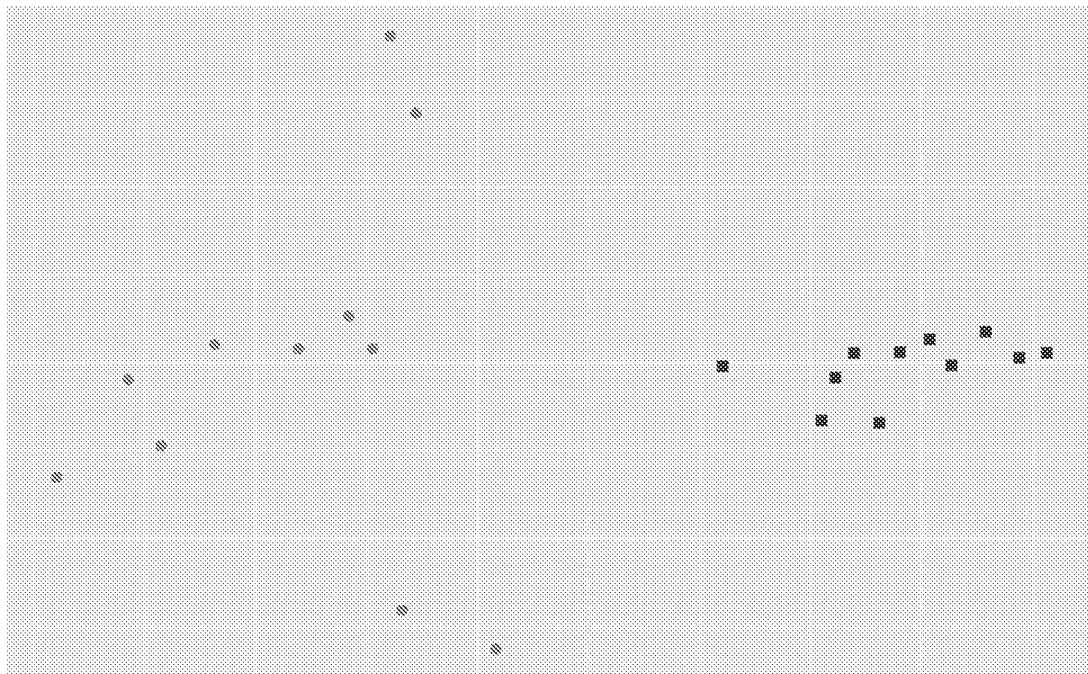
FIG. 4

FIG. 5

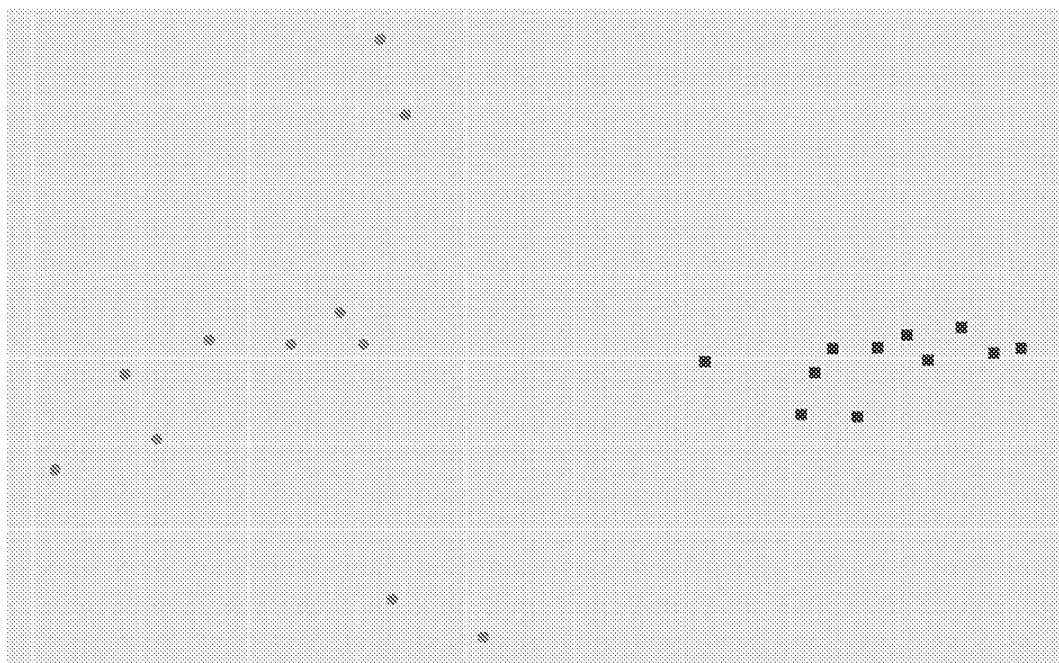


FIG. 6

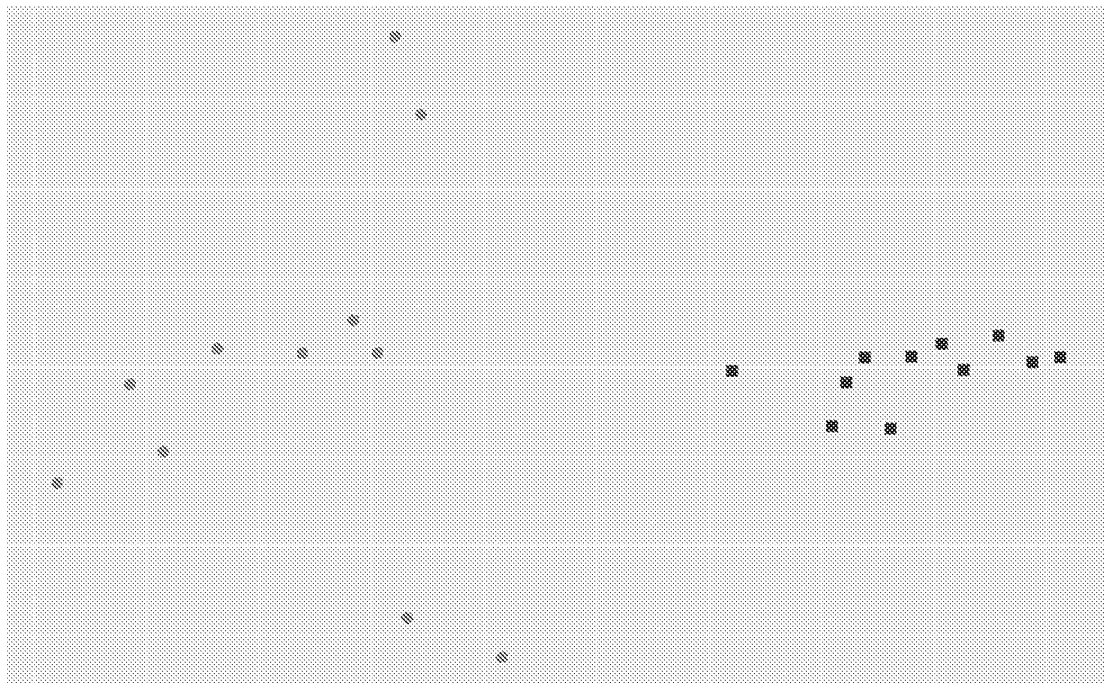


FIG. 7

Top 40 CCSs in Present in
SBMA

1	probe	FC
2	Hg38_2_351357305_15	2.283
3	Hg38_13_41466343_41	2.007
4	Hg38_20_23380285_23	1.878
5	Hg38_1_209333922_20	1.87
6	Hg38_1_84316044_843	1.87
7	Hg38_5_377834278_17	1.832
8	Hg38_11_77781318_77	1.798
9	Hg38_8_48489318_484	1.794
10	Hg38_8_33042243_330	1.788
11	Hg38_11_7823466_782	1.776
12	Hg38_2_242078290_24	1.776
13	Hg38_4_64204633_642	1.771
14	Hg38_6_344636123_14	1.767
15	Hg38_9_4737538_4739	1.767
16	Hg38_22_47207724_47	1.765
17	Hg38_16_31853018_31	1.764
18	Hg38_10_6735453_674	1.764
19	Hg38_14_26683688_26	1.76
20	Hg38_11_63024617_63	1.758
21	Hg38_11_35823665_55	1.726
22	Hg38_2_20793146_207	1.716
23	Hg38_1_314264796_11	1.702
24	Hg38_3_350148357_15	1.692
25	Hg38_3_3070802_3073	1.684
26	Hg38_X_126618971_12	1.682
27	Hg38_17_3298600_330	1.682
28	Hg38_2_728849719_22	1.682
29	Hg38_6_341949437_14	1.681
30	Hg38_2_221629362_22	1.679
31	Hg38_18_8164330_816	1.675
32	Hg38_X_83389647_833	1.67
33	Hg38_2_38740634_387	1.666
34	Hg38_2_389562432_16	1.664
35	Hg38_X_51609399_516	1.658
36	Hg38_1_96786343_967	1.657
37	Hg38_13_76879860_76	1.653
38	Hg38_12_10235418_10	1.647
39	Hg38_3_351888504_15	1.643
40	Hg38_8_81036889_810	1.641
41	Hg38_21_25447238_25	1.639

Top 40 CCSs in Absent in
SBMA

1	probe	FC
2	Hg38_3_300733023_300742761	-1.862
3	Hg38_3_300750954_300758578	-1.807
4	Hg38_5_350272362_350278699	-1.745
5	Hg38_3_300862282_300875484	-1.739
6	Hg38_5_350008962_350014465	-1.715
7	Hg38_5_350272362_350278699	-1.708
8	Hg38_12_69346683_69349534_8	-1.633
9	Hg38_8_343073684_343079751	-1.62
10	Hg38_1_32214585_32217213_32	-1.612
11	Hg38_X_46498682_46508989_46	-1.611
12	Hg38_10_8256256_8258992_853	-1.604
13	Hg38_6_3027907_3030237_3148	-1.598
14	Hg38_7_27204432_27205465_27	-1.597
15	Hg38_7_25370684_25382177_25	-1.596
16	Hg38_6_2898813_2902737_3148	-1.59
17	Hg38_5_350036868_350040595	-1.579
18	Hg38_7_25370684_25382177_25	-1.578
19	Hg38_8_342863175_342868397	-1.578
20	Hg38_5_350194890_350198093	-1.576
21	Hg38_3_300862282_300875484	-1.572
22	Hg38_8_26561792_26565691_26	-1.571
23	Hg38_7_27153628_27154280_27	-1.57
24	Hg38_3_300677572_300682389	-1.568
25	Hg38_9_84621528_84639678_84	-1.564
26	Hg38_X_46498682_46508989_46	-1.563
27	Hg38_7_25274699_25276258_25	-1.563
28	Hg38_6_3146778_3149848_3232	-1.557
29	Hg38_Y_7774814_7781345_7903	-1.557
30	Hg38_6_47291785_47297630_47	-1.556
31	Hg38_5_350272362_350278699	-1.555
32	Hg38_6_2891780_2893777_3148	-1.555
33	Hg38_13_33481982_33488531_3	-1.549
34	Hg38_6_3045545_3051391_3148	-1.549
35	Hg38_8_26561792_26565691_26	-1.548
36	Hg38_6_2860707_2865436_3148	-1.544
37	Hg38_7_27250080_27251352_27	-1.544
38	Hg38_12_114767229_114770912	-1.54
39	Hg38_7_22390272_22396878_22	-1.539
40	Hg38_12_91718135_91726240_5	-1.538
41	Hg38_10_8256256_8258992_853	-1.537

FIG. 8

This is a snapshot of the genomic regions regulated through 3D genomic architecture, mapping to the top EpiSwitch CCSs present in the SMBA patients

The coding regions associated to the significant CCSs were used for subsequent pathway analysis.

Dist ~ Linear distance to the coding region within 3D Genomic long-range interactions from the anchoring sites of identified EpiSwitch CCSs

S	probe	XC	Gene	Distance
2	Hg38_2_151	2.883	WDR	0
3	Hg38_2_151	2.883	WDR1	0
4	Hg38_2_151	2.883	TNFAIP6	0
5	Hg38_13_41	2.007	WDR1	0
6	Hg38_13_41	2.007	WDR2	5488
7	Hg38_13_41	2.007	KAR1B	89314
8	Hg38_20_23	1.878	CS11	0
9	Hg38_20_23	1.878	CS18	0
10	Hg38_20_23	1.878	CS11	0
11	Hg38_20_23	1.878	KAR1B	0
12	Hg38_1_843	1.87	DNASE2B	0
13	Hg38_1_843	1.87	DNASE	0
14	Hg38_1_843	1.87	WDR1	0
15	Hg38_1_843	1.87	KAR1B	0
16	Hg38_1_843	1.87	KAR1B	0
17	Hg38_1_208	1.87	DNASE2B	163086
18	Hg38_1_208	1.87	DNASE2B	194191
19	Hg38_1_208	1.87	DNASE2B	254740
20	Hg38_5_173	1.872	DNASE2B	0
21	Hg38_5_173	1.872	DNASE2B	54881
22	Hg38_11_77	1.798	DNASE2B	0
23	Hg38_11_77	1.798	DNASE2B	0
24	Hg38_11_77	1.798	DNASE2B	0
25	Hg38_8_484	1.794	DNASE2B	0
26	Hg38_8_484	1.794	DNASE2B	201207
27	Hg38_8_484	1.794	DNASE2B	337828
28	Hg38_8_339	1.798	DNASE2B	121227
29	Hg38_8_339	1.798	DNASE2B	213789
30	Hg38_8_339	1.798	DNASE2B	235153
31	Hg38_11_78	1.778	DNASE2B	0
32	Hg38_11_78	1.778	DNASE2B	294094
33	Hg38_11_78	1.778	DNASE2B	32980
34	Hg38_2_242	1.778	DNASE2B	204408
35	Hg38_2_242	1.778	DNASE2B	213781
36	Hg38_2_242	1.778	DNASE2B	268878
37	Hg38_4_842	1.771	DNASE2B	0
38	Hg38_4_842	1.771	DNASE2B	969601
39	Hg38_4_842	1.771	DNASE2B	3120301
40	Hg38_9_473	1.767	DNASE2B	0
41	Hg38_9_473	1.767	DNASE2B	0
42	Hg38_9_473	1.767	DNASE2B	0

FIG. 9

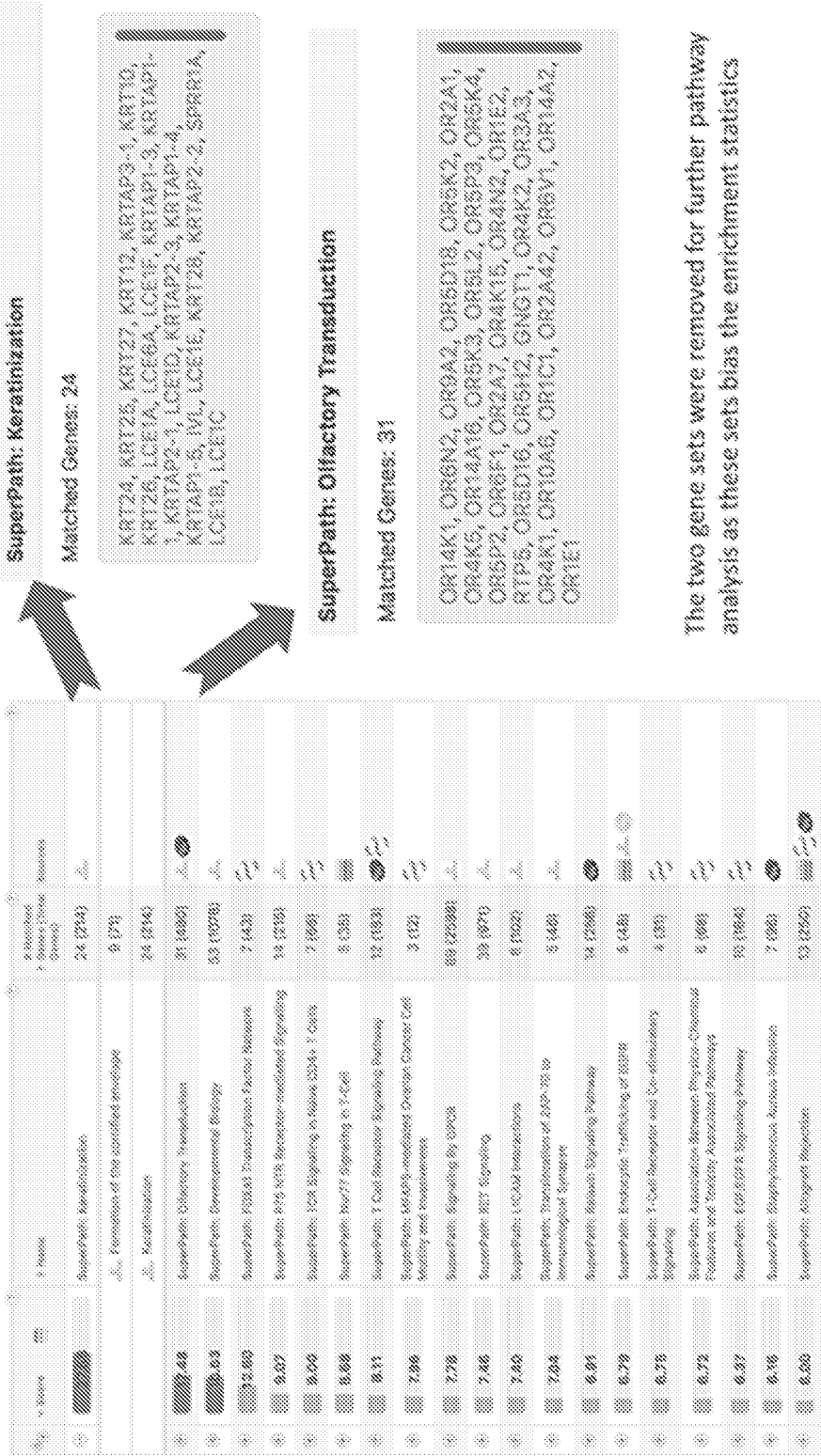


FIG. 10

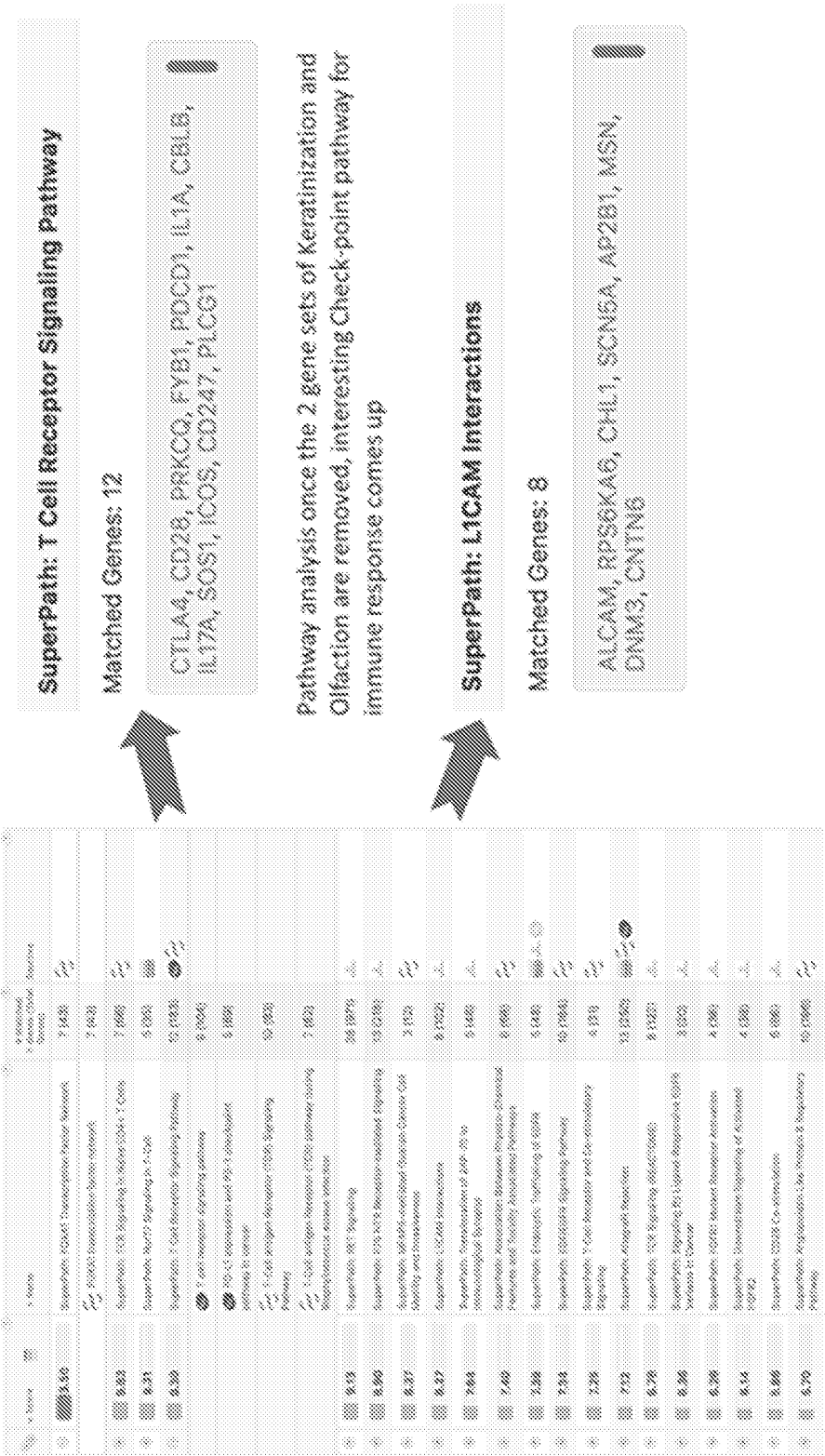


FIG. 12

This is a snapshot of the genomic regions regulated through 3D genomic architecture, mapping to the top EpiSwitch CCSs absent in the SMBA patients

The coding regions associated to the significant CCSs were used for subsequent pathway analysis.

Dist – Linear distance to the coding region within 3D Genomic long-range interactions from the anchoring sites of identified EpiSwitch CCSs

1	probe	FC	Gene	Distance
2	hg38.3.100	-1.862	ABRBP	0
3	hg38.3.100	-1.862	CPH128	37543
4	hg38.3.100	-1.862	YIG	0
5	hg38.3.100	-1.867	ABRBP	0
6	hg38.3.100	-1.867	CPH128	38478
7	hg38.3.100	-1.867	YIG	3069
8	hg38.5.100	-1.745	ABRBP	0
9	hg38.5.100	-1.745	CPH128	28157
10	hg38.5.100	-1.745	YIG	0
11	hg38.3.100	-1.739	ABRBP	0
12	hg38.3.100	-1.739	CPH128	32082
13	hg38.3.100	-1.739	YIG	33317
14	hg38.5.100	-1.715	ABRBP	0
15	hg38.5.100	-1.715	CPH128	0
16	hg38.5.100	-1.715	YIG	0
17	hg38.5.100	-1.715	ABRBP	0
18	hg38.5.100	-1.715	CPH128	0
19	hg38.5.100	-1.715	YIG	0
20	hg38.5.100	-1.708	ABRBP	0
21	hg38.5.100	-1.708	CPH128	0
22	hg38.5.100	-1.708	YIG	0
23	hg38.12.00	-1.693	ABRBP	0
24	hg38.12.00	-1.693	CPH128	0
25	hg38.12.00	-1.693	YIG	0
26	hg38.8.100	-1.62	ABRBP	0
27	hg38.8.100	-1.62	CPH128	0
28	hg38.8.100	-1.62	YIG	0
29	hg38.3.100	-1.612	ABRBP	0
30	hg38.3.100	-1.612	CPH128	0
31	hg38.3.100	-1.612	YIG	0
32	hg38.8.100	-1.612	ABRBP	0
33	hg38.8.100	-1.612	CPH128	0
34	hg38.8.100	-1.612	YIG	0
35	hg38.10.02	-1.604	ABRBP	449443
36	hg38.10.02	-1.604	CPH128	283059
37	hg38.10.02	-1.604	YIG	288030
38	hg38.6.100	-1.598	ABRBP	0
39	hg38.6.100	-1.598	CPH128	0
40	hg38.6.100	-1.598	YIG	0
41	hg38.7.275	-1.597	ABRBP	0

FIG. 13

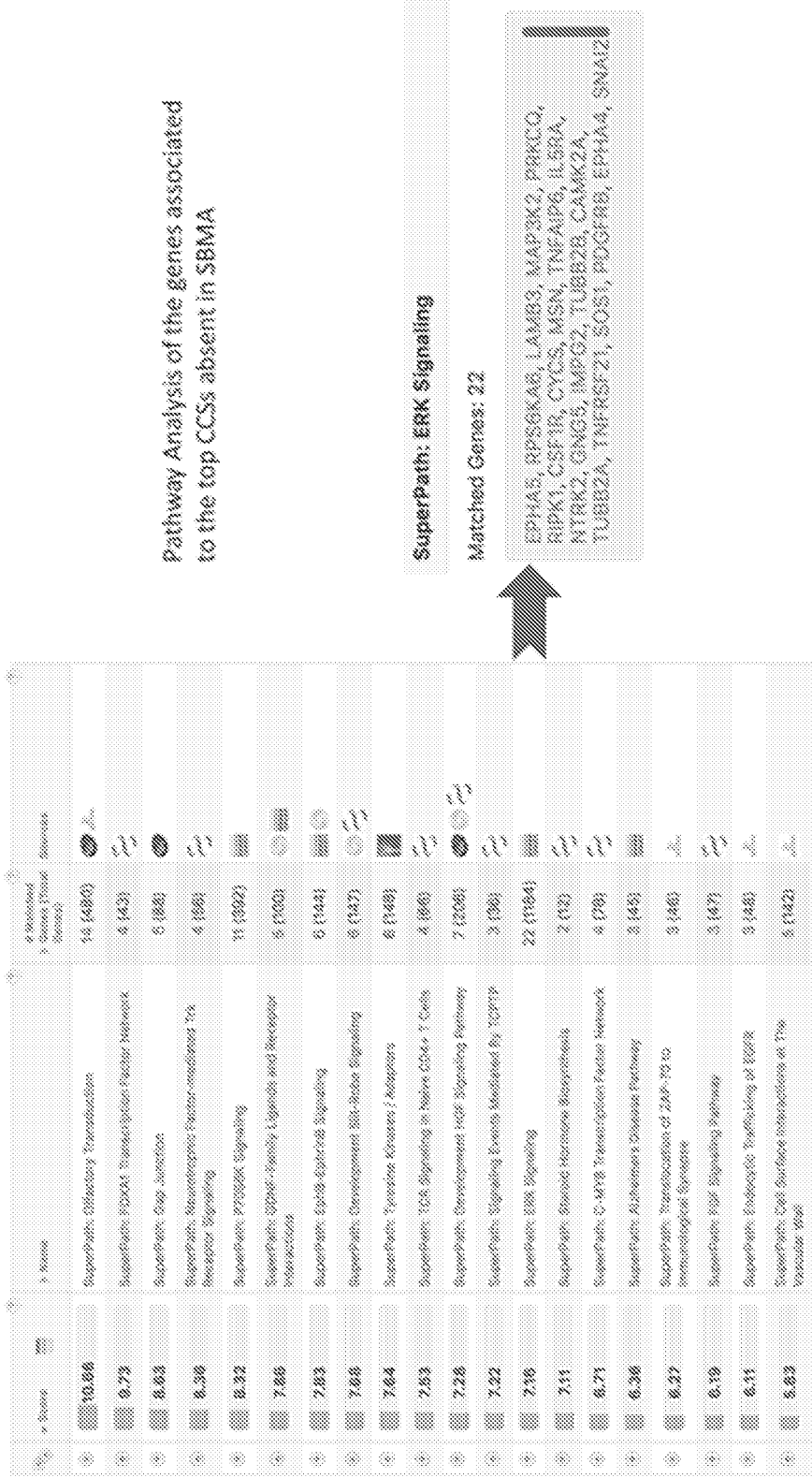


FIG. 14

	Breast Cancer	13 {1404}
	Alzheimer's Disease	16 {1665}
	Lung Cancer	16 {1278}
	Cervical Cancer	15 {1713}
	Neurodegenerative	15 {5905}
	Cervical Cancer	13 {1379}
	Neurodegenerative Conditions	9 {812}
	Viral Etiology	5 {127}
	Heavy Metal Induced Neurodegenerative Toxic Lesion 1:	11 {8433}
	Neurodegenerative Disease	11 {4023}
	Neurodegenerative Disease Type	10 {3121}
	Prostate Cancer	11 {1622}
	Endometriosis	13 {608}
	Melanoma	12 {422}
	Multiple Sclerosis	8 {849}
	Neurodegenerative Lesions :	9 {823}
	Leukemia, Acute Myeloid	8 {492}
	Acute Frontal Cortex Syndrome	4 {20}
	Myotonic Dystrophy Syndrome	7 {253}
		8 {125}

Muscular Dystrophy, Duchenne Type		
Matched Cases (10)		
Run on & Read Query Search by the Exact View in Matchcards Differentially Expressed Genes		
Case	Reads	Genes
1	955,882	ATG family member 8 binding protein
2	867,712	unclassified protein transcript/nucleic domain containing 12
3	147	myosin
4	11,866,124	ribonucleic protein 26, cytosolic
5	1,179,914	myosin
6	2,076,512	myosin heavy chain 2
7	6,016,12	myosin 2
8	5,076,12	myosin 2
9	9,276,12	myosin 2
10	5,016,12	myosin 2

FIG. 15

