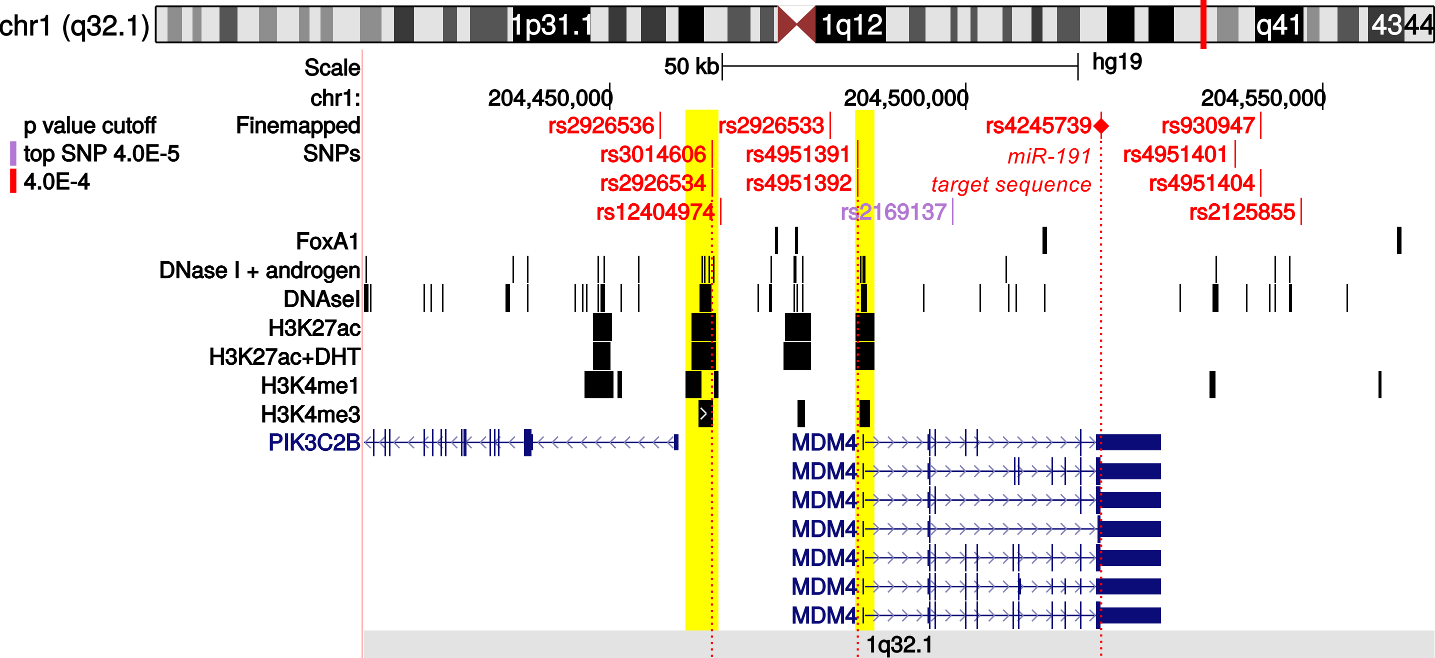
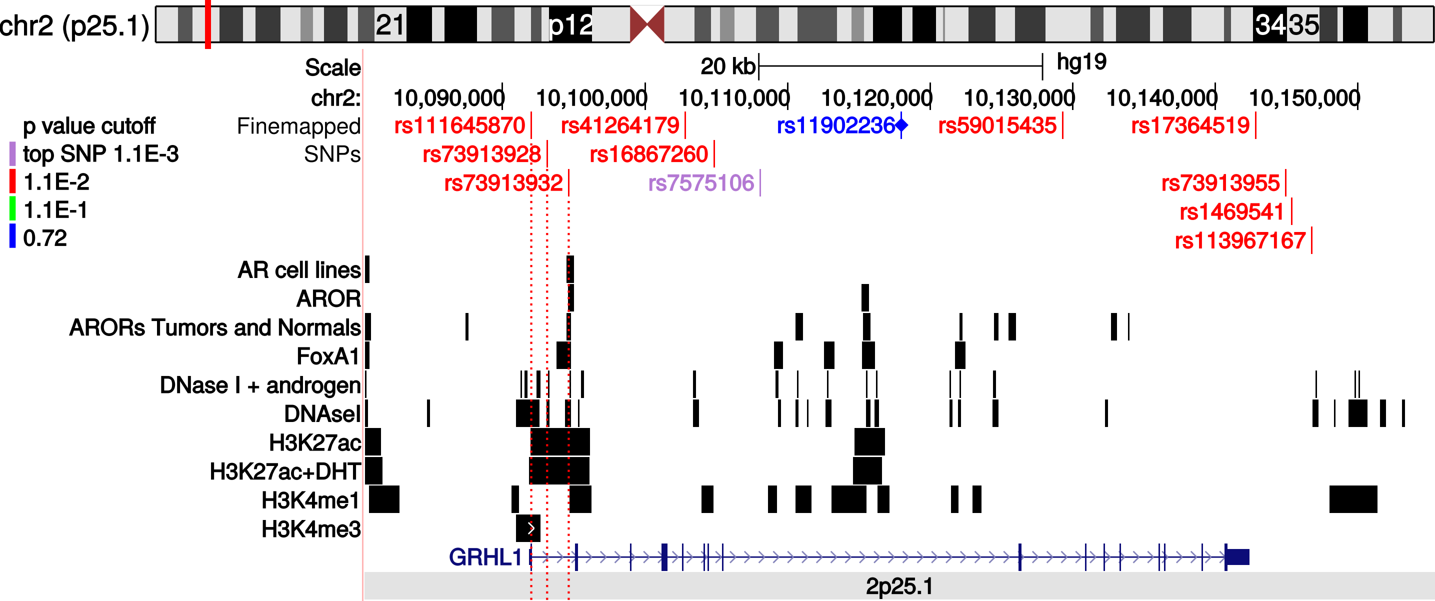
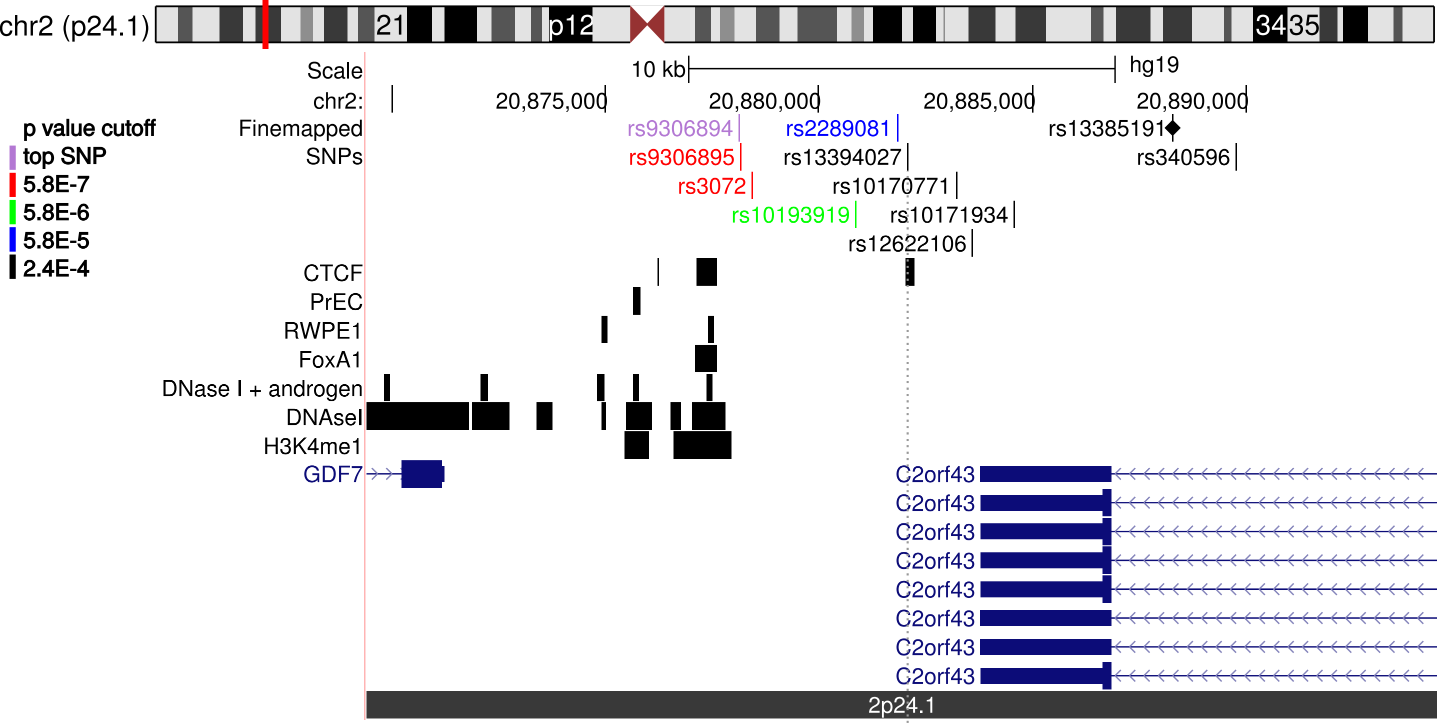

chr1 (q32.1)
1p31.1
1q12
q41
43
44
Scale
50 kb
hg19
chr1:
204,450,000
204,500,000
204,550,000
p value cutoff
top SNP 4.0E-5
4.0E-4
Finemapped
SNPs
rs2926536
rs2926533
rs4245739
rs930947
rs3014606
rs4951391
miR-191
rs4951401
rs2926534
rs4951392
target sequence
rs4951404
rs12404974
rs2169137
rs2125855
FoxA1
DNase I + androgen
DNAseI
H3K27ac
H3K27ac+DHT
H3K4me1
H3K4me3
PIK3C2B
MDM4
MDM4
MDM4
MDM4
MDM4
MDM4
MDM4
1q32.1


chr2 (p25.1)
21
p12
34
35
Scale
20 kb
hg19
chr2:
10,090,000
10,100,000
10,110,000
10,120,000
10,130,000
10,140,000
10,150,000
p value cutoff
top SNP 1.1E-3
1.1E-2
1.1E-1
0.72
Finemapped SNPs
rs111645870
rs41264179
rs11902236
rs59015435
rs17364519
rs73913928
rs16867260
rs73913932
rs7575106
rs73913955
rs1469541
rs113967167
AR cell lines
AROR
ARORs Tumors and Normals
FoxA1
DNase I + androgen
DNAseI
H3K27ac
H3K27ac+DHT
H3K4me1
H3K4me3
GRHL1
2p25.1


chr2 (p24.1)
21
p12
3435
Scale
10 kb
hg19
chr2:
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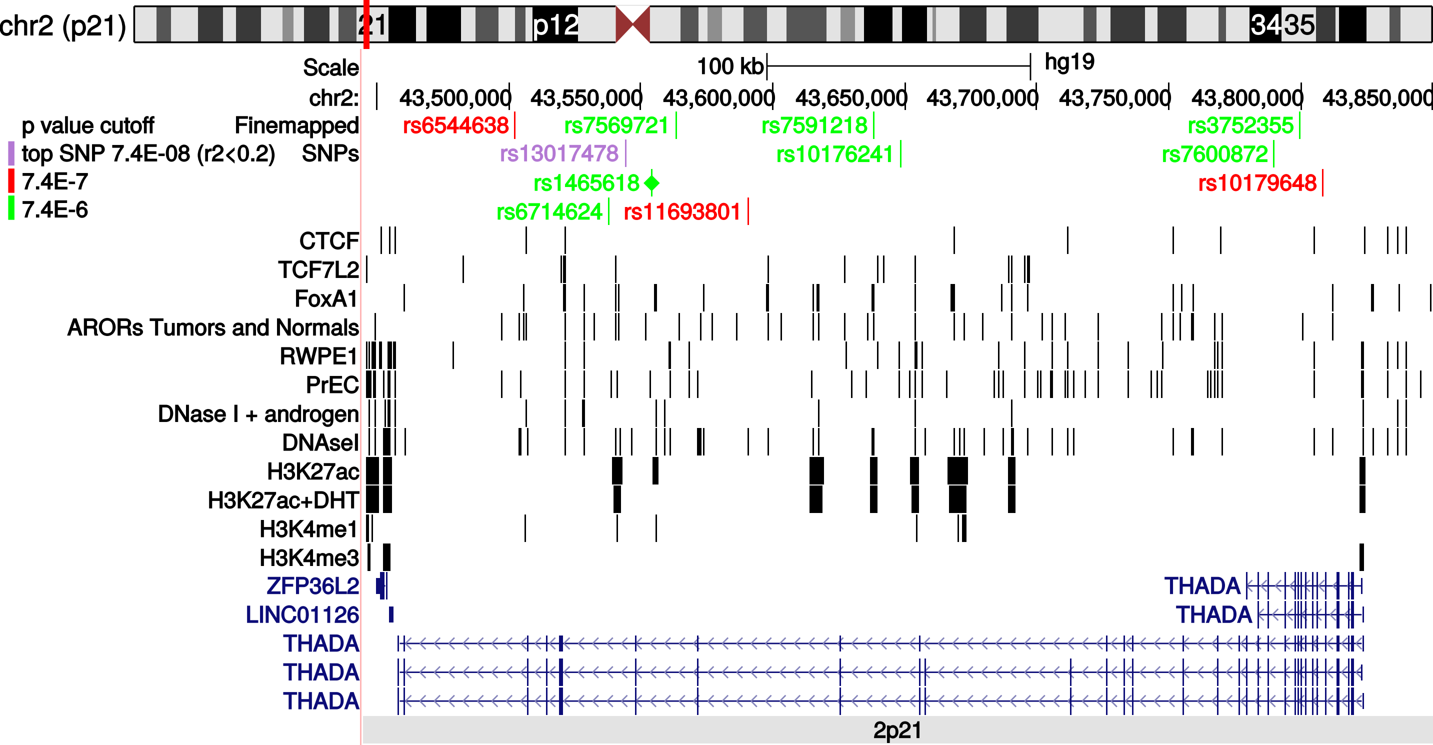
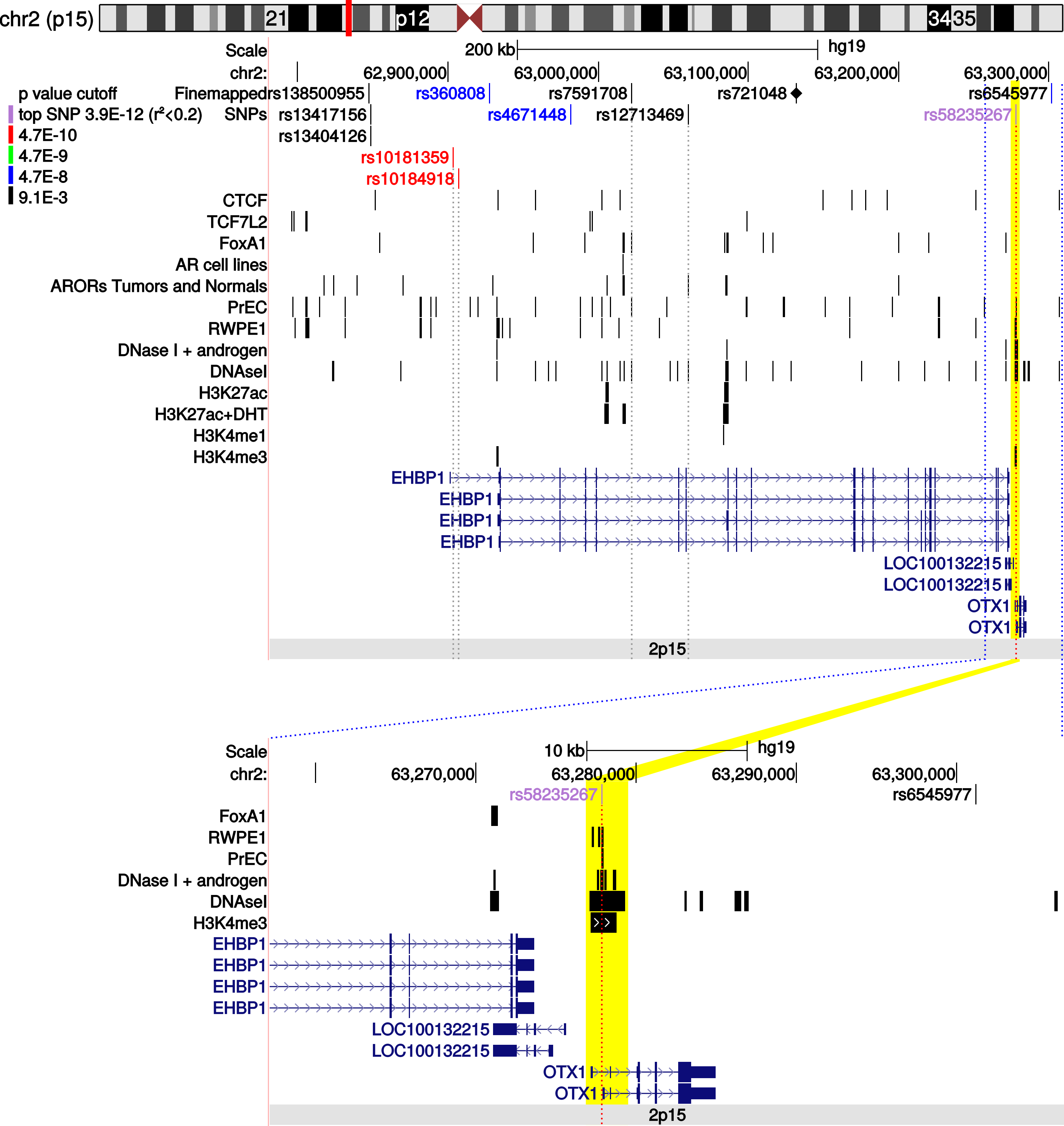
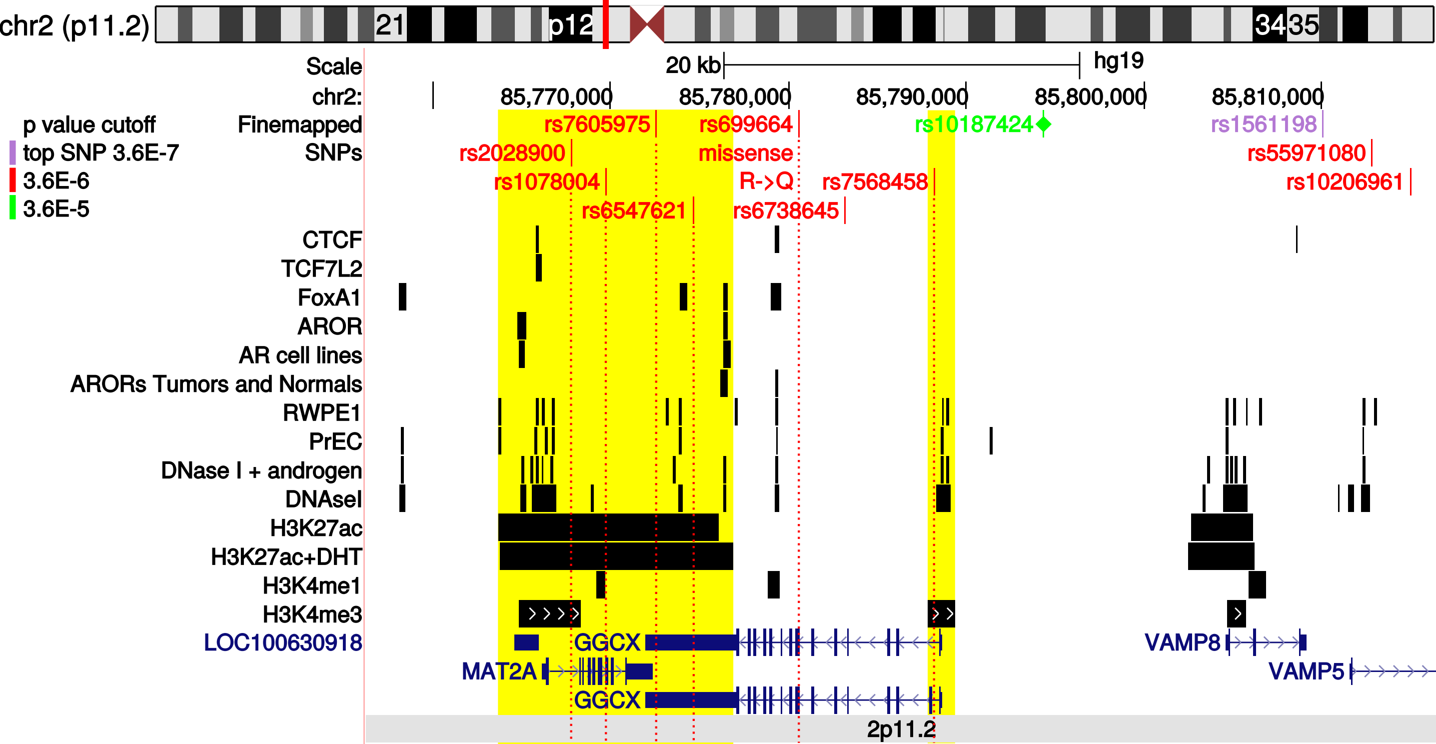
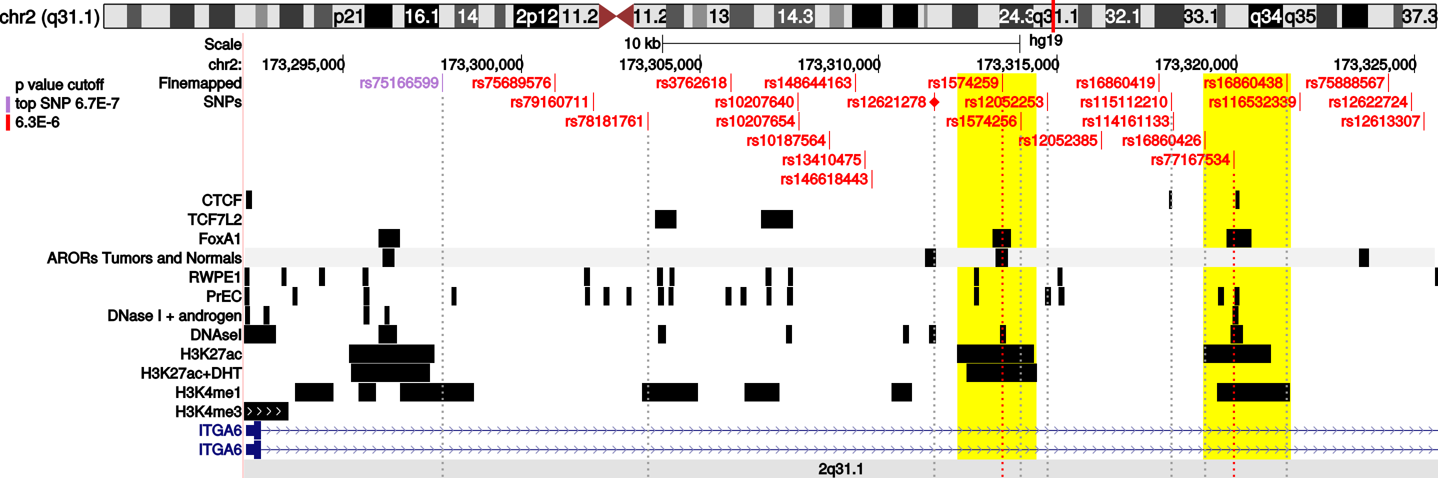
20,880,000
20,885,000
20,890,000
p value cutoff
top SNP
5.8E-7
5.8E-6
5.8E-5
2.4E-4
Finemapped
SNPs
rs9306894
rs2289081
rs13385191
rs9306895
rs13394027
rs340596
rs3072
rs10170771
rs10193919
rs10171934
rs12622106
CTCF
PrEC
RWPE1
FoxA1
DNase I + androgen
DNAseI
H3K4me1
GDF7
C2orf43
C2orf43
C2orf43
C2orf43
C2orf43
C2orf43
C2orf43
C2orf43
2p24.1


chr2 (p21)
21
p12
3435
Scale
100 kb
hg19
chr2:
43,500,000
43,550,000
43,600,000
43,650,000
43,700,000
43,750,000
43,800,000
43,850,000
p value cutoff
top SNP 7.4E-08 (r2<0.2)
7.4E-7
7.4E-6
Finemapped SNPs
rs6544638
rs7569721
rs7591218
rs3752355
rs13017478
rs10176241
rs7600872
rs1465618
rs10179648
rs6714624
rs11693801
CTCF
TCF7L2
FoxA1
ARORs Tumors and Normals
RWPE1
PrEC
DNase I + androgen
DNAseI
H3K27ac
H3K27ac+DHT
H3K4me1
H3K4me3
ZFP36L2
LINC01126
THADA
THADA
THADA
THADA
THADA
2p21


chr2 (p15)
21
p12
3435
Scale
200 kb
hg19
chr2:
62,900,000
63,000,000
63,100,000
63,200,000
63,300,000
p value cutoff
top SNP 3.9E-12 (r²<0.2)
4.7E-10
4.7E-9
4.7E-8
9.1E-3
Finemapped SNPs
rs138500955
rs360808
rs7591708
rs721048
rs6545977
rs13417156
rs4671448
rs12713469
rs58235267
rs13404126
rs10181359
rs10184918
CTCF
TCF7L2
FoxA1
AR cell lines
ARORs Tumors and Normals
PrEC
RWPE1
DNase I + androgen
DNAseI
H3K27ac
H3K27ac+DHT
H3K4me1
H3K4me3
EHBP1
EHBP1
EHBP1
EHBP1
LOC100132215
LOC100132215
OTX1
OTX1
2p15
Scale
10 kb
hg19
chr2:
63,270,000
63,280,000
63,290,000
63,300,000
rs58235267
rs6545977
FoxA1
RWPE1
PrEC
DNase I + androgen
DNAseI
H3K4me3
EHBP1
EHBP1
EHBP1
EHBP1
LOC100132215
LOC100132215
OTX1
OTX1
2p15


chr2 (p11.2)
21
p12
3435
Scale
20 kb
hg19
chr2:
85,770,000
85,780,000
85,790,000
85,800,000
85,810,000
p value cutoff
top SNP 3.6E-7
3.6E-6
3.6E-5
Finemapped SNPs
rs7605975
rs699664
rs10187424
rs1561198
rs2028900
missense
rs55971080
rs1078004
R->Q
rs7568458
rs10206961
rs6547621
rs6738645
CTCF
TCF7L2
FoxA1
AROR
AR cell lines
ARORs Tumors and Normals
RWPE1
PrEC
DNase I + androgen
DNAseI
H3K27ac
H3K27ac+DHT
H3K4me1
H3K4me3
LOC100630918
GGCX
MAT2A
GGCX
VAMP8
VAMP5
2p11.2


chr2 (q31.1)
p21
16.1
14
2p12
11.2
11.2
13
14.3
24.3
q31.1
32.1
33.1
q34
q35
37.3
Scale
10 kb
hg19
chr2:
173,295,000
173,300,000
173,305,000
173,310,000
173,315,000
173,320,000
173,325,000
p value cutoff
top SNP 6.7E-7
6.3E-6
Finemapped SNPs
rs75166599
rs75689576
rs79160711
rs78181761
rs3762618
rs10207640
rs10207654
rs10187564
rs13410475
rs146618443
rs148644163
rs12621278
rs1574259
rs12052253
rs1574256
rs12052385
rs16860419
rs115112210
rs114161133
rs16860426
rs77167534
rs16860438
rs116532339
rs75888567
rs12622724
rs12613307
CTCF
TCF7L2
FoxA1
ARORs Tumors and Normals
RWPE1
PrEC
DNase I + androgen
DNAseI
H3K27ac
H3K27ac+DHT
H3K4me1
H3K4me3
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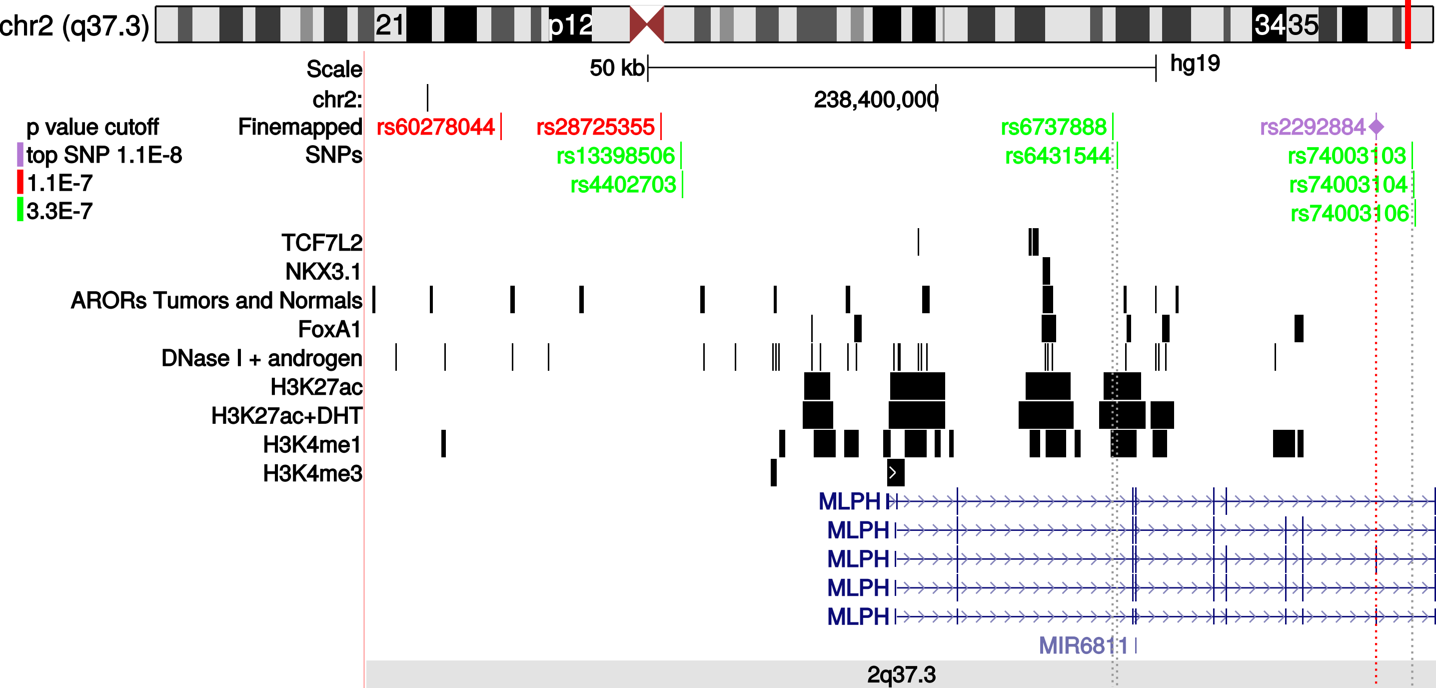
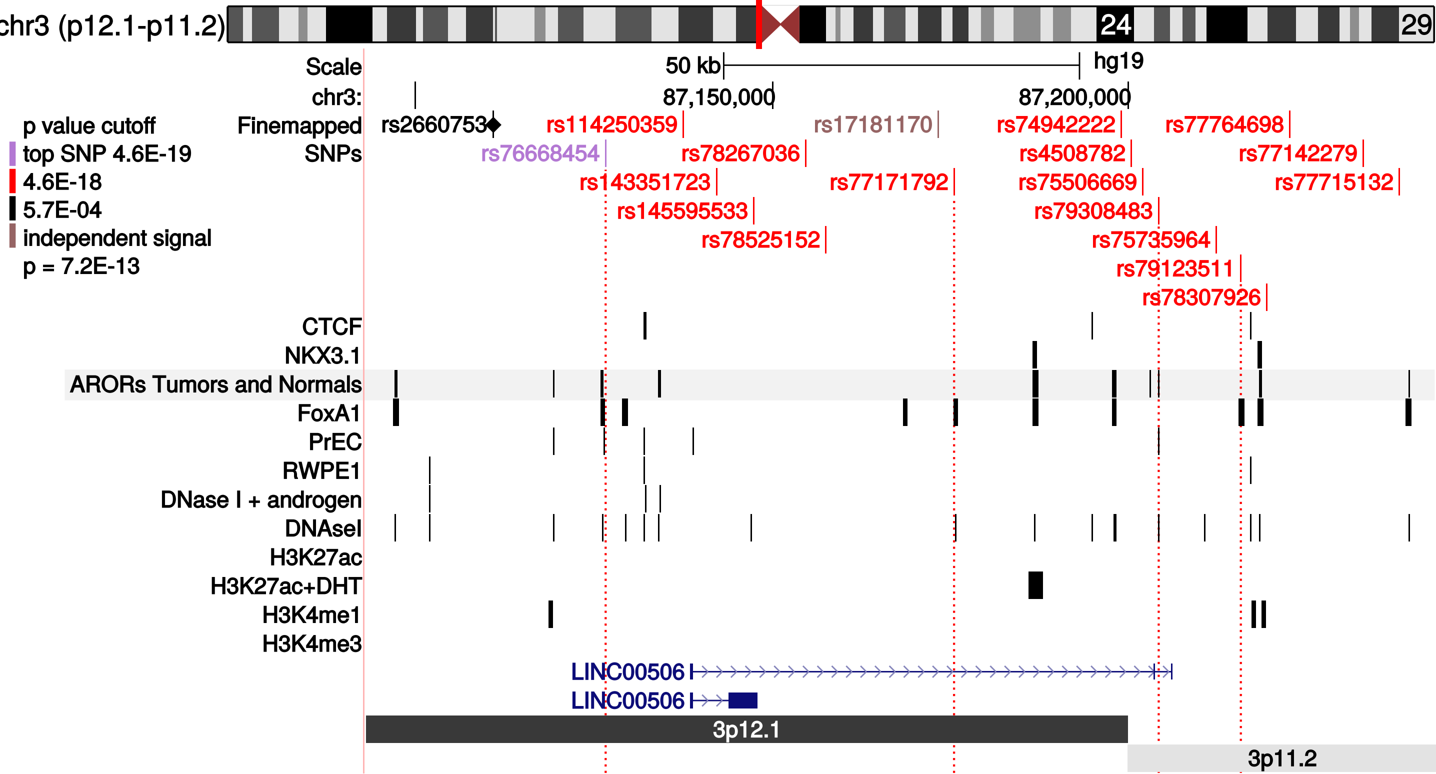
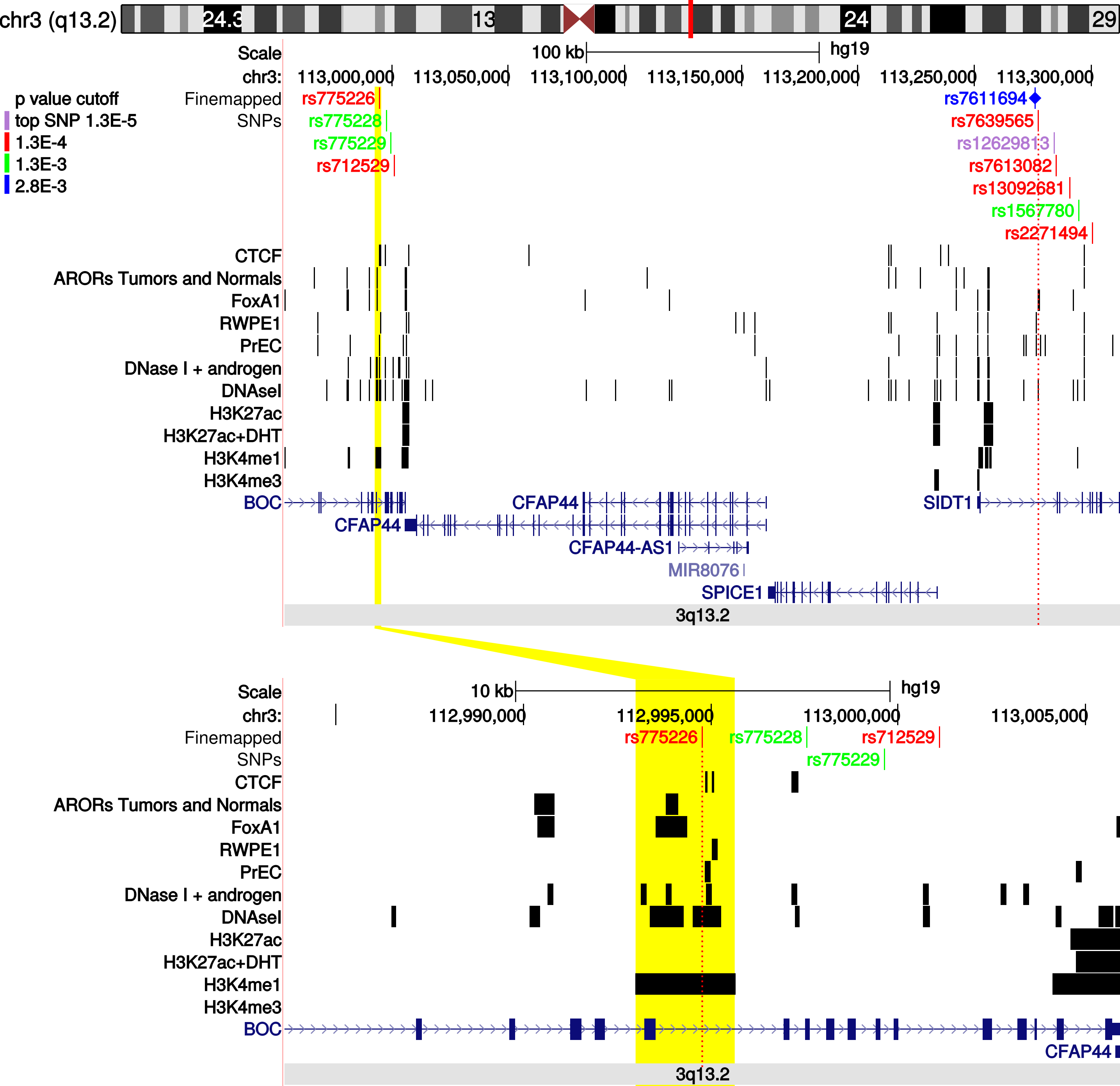
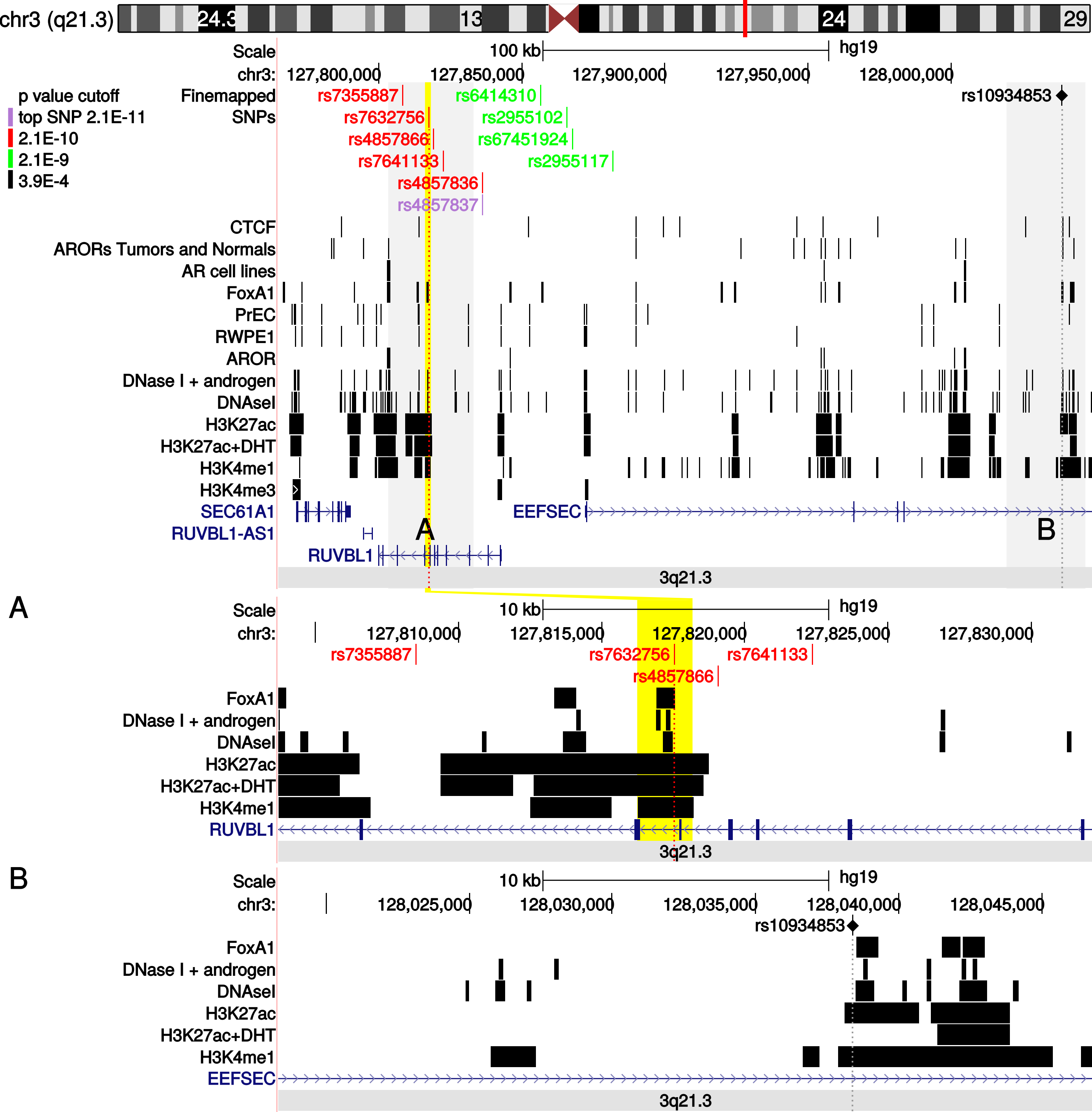
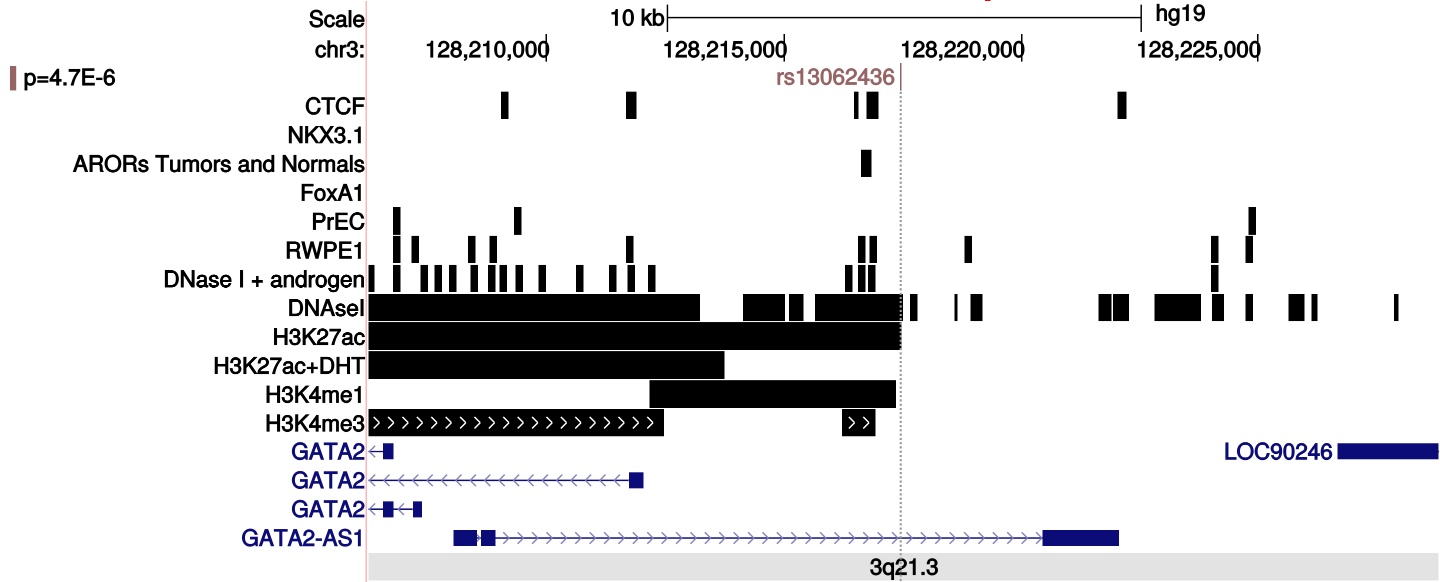
ITGA6
2q31.1


chr2 (q37.3)
21
p12
34
35
Scale
50 kb
hg19
chr2:
238,400,000
p value cutoff
top SNP 1.1E-8
1.1E-7
3.3E-7
Finemapped
SNPs
rs60278044
rs28725355
rs6737888
rs2292884
rs13398506
rs6431544
rs74003103
rs4402703
rs74003104
rs74003106
TCF7L2
NKX3.1
ARORs Tumors and Normals
FoxA1
DNase I + androgen
H3K27ac
H3K27ac+DHT
H3K4me1
H3K4me3
MLPH
MLPH
MLPH
MLPH
MLPH
MIR6811
2q37.3


chr3 (p12.1-p11.2)
24
29
Scale
50 kb
hg19
chr3:
87,150,000
87,200,000
p value cutoff
top SNP 4.6E-19
4.6E-18
5.7E-04
independent signal
p = 7.2E-13
Finemapped
SNPs
rs2660753
rs114250359
rs17181170
rs74942222
rs77764698
rs76668454
rs78267036
rs4508782
rs77142279
rs143351723
rs77171792
rs75506669
rs77715132
rs145595533
rs79308483
rs78525152
rs75735964
rs79123511
rs78307926
CTCF
NKX3.1
ARORs Tumors and Normals
FoxA1
PrEC
RWPE1
DNase I + androgen
DNAseI
H3K27ac
H3K27ac+DHT
H3K4me1
H3K4me3
LINC00506
LINC00506
3p12.1
3p11.2


chr3 (q13.2)
24.3
13
24
29
Scale
100 kb
hg19
chr3:
113,000,000
113,050,000
113,100,000
113,150,000
113,200,000
113,250,000
113,300,000
p value cutoff
top SNP 1.3E-5
1.3E-4
1.3E-3
2.8E-3
Finemapped SNPs
rs775226
rs775228
rs775229
rs712529
rs7611694
rs7639565
rs12629813
rs7613082
rs13092681
rs1567780
rs2271494
CTCF
ARORs Tumors and Normals
FoxA1
RWPE1
PrEC
DNase I + androgen
DNaseI
H3K27ac
H3K27ac+DHT
H3K4me1
H3K4me3
BOC
CFAP44
CFAP44
CFAP44-AS1
MIR8076
SPICE1
SIDT1
3q13.2
Scale
10 kb
hg19
chr3:
112,990,000
112,995,000
113,000,000
113,005,000
Finemapped SNPs
rs775226
rs775228
rs712529
rs775229
CTCF
ARORs Tumors and Normals
FoxA1
RWPE1
PrEC
DNase I + androgen
DNaseI
H3K27ac
H3K27ac+DHT
H3K4me1
H3K4me3
BOC
CFAP44
3q13.2


chr3 (q21.3)
24.3
13
24
29
Scale
100 kb
hg19
chr3:
127,800,000
127,850,000
127,900,000
127,950,000
128,000,000
p value cutoff
top SNP 2.1E-11
2.1E-10
2.1E-9
3.9E-4
Finemapped SNPs
rs7355887
rs7632756
rs4857866
rs7641133
rs4857836
rs4857837
rs6414310
rs2955102
rs67451924
rs2955117
rs10934853
CTCF
ARORs Tumors and Normals
AR cell lines
FoxA1
PrEC
RWPE1
AROR
DNase I + androgen
DNAseI
H3K27ac
H3K27ac+DHT
H3K4me1
H3K4me3
SEC61A1
RUVBL1-AS1
RUVBL1
EEFSEC
A
B
3q21.3
A
Scale
10 kb
hg19
chr3:
127,810,000
127,815,000
127,820,000
127,825,000
127,830,000
rs7355887
rs7632756
rs7641133
rs4857866
FoxA1
DNase I + androgen
DNAseI
H3K27ac
H3K27ac+DHT
H3K4me1
RUVBL1
3q21.3
B
Scale
10 kb
hg19
chr3:
128,025,000
128,030,000
128,035,000
128,040,000
128,045,000
rs10934853
FoxA1
DNase I + androgen
DNAseI
H3K27ac
H3K27ac+DHT
H3K4me1
EEFSEC
3q21.3


Scale
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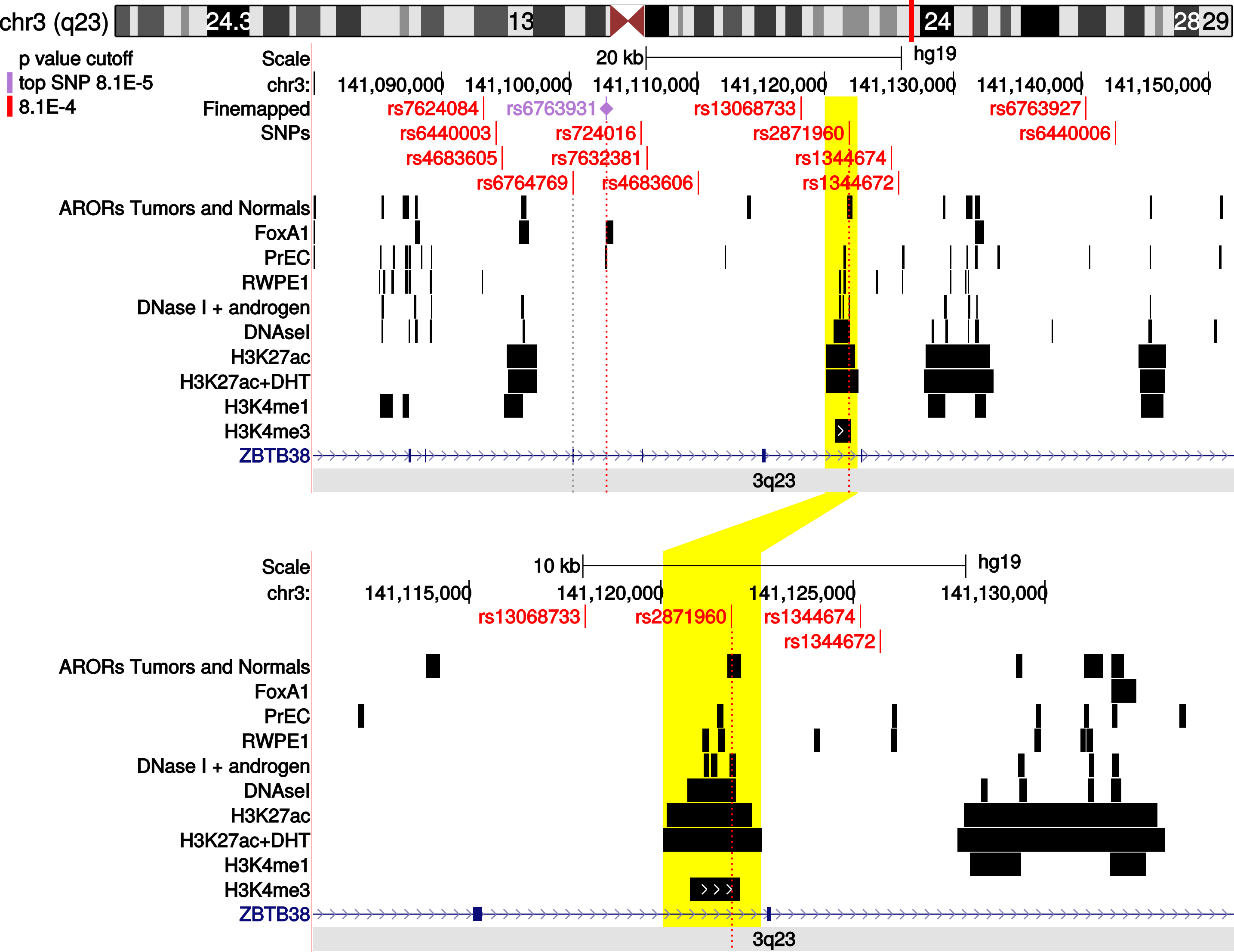
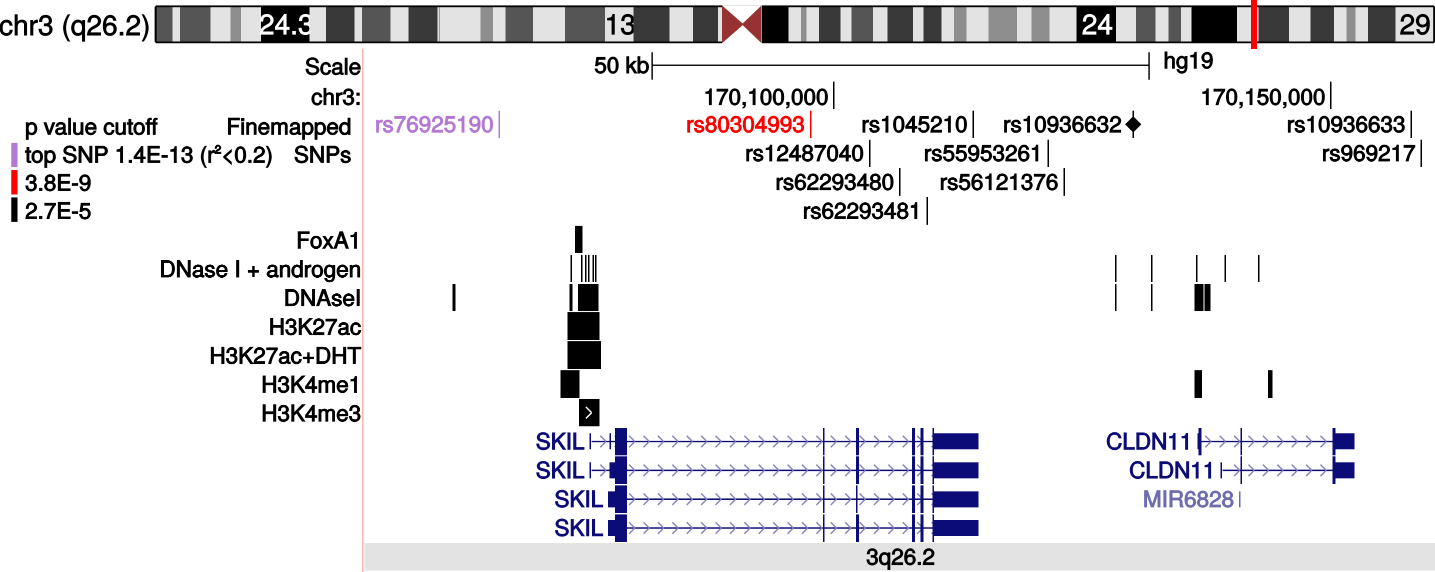
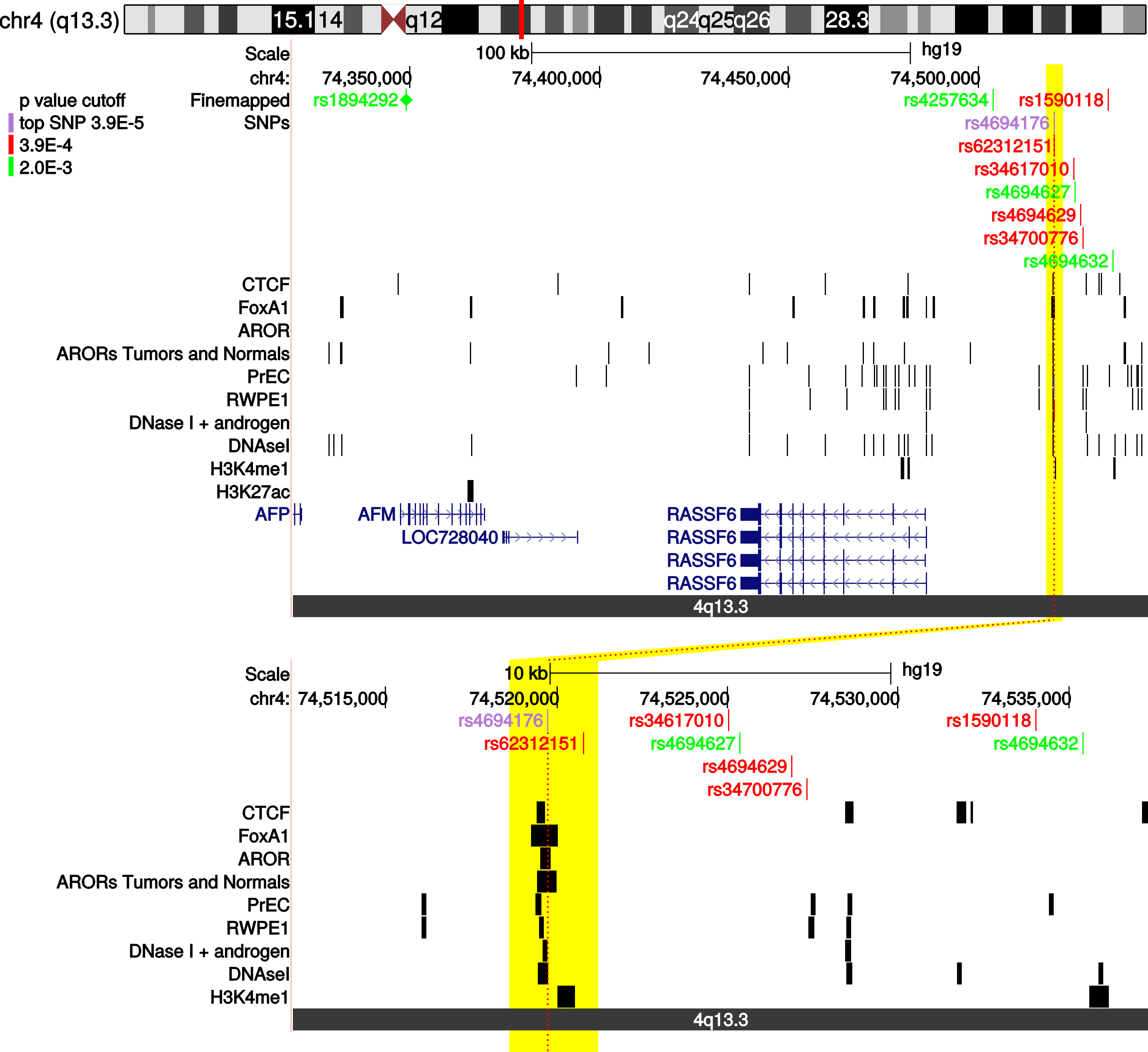
hg19
chr3:
128,210,000
128,215,000
128,220,000
128,225,000
p=4.7E-6
rs13062436
CTCF
NKX3.1
ARORs Tumors and Normals
FoxA1
PrEC
RWPE1
DNase I + androgen
DNAseI
H3K27ac
H3K27ac+DHT
H3K4me1
H3K4me3
GATA2
LOC90246
GATA2
GATA2
GATA2-AS1
3q21.3


chr3 (q23)
24.3
13
24
28
29
p value cutoff
top SNP 8.1E-5
8.1E-4
Scale
20 kb
hg19
chr3:
141,090,000
141,100,000
141,110,000
141,120,000
141,130,000
141,140,000
141,150,000
Finemapped SNPs
rs7624084
rs6763931
rs13068733
rs6763927
rs6440003
rs724016
rs2871960
rs6440006
rs4683605
rs7632381
rs1344674
rs6764769
rs4683606
rs1344672
ARORs Tumors and Normals
FoxA1
PrEC
RWPE1
DNase I + androgen
DNaseI
H3K27ac
H3K27ac+DHT
H3K4me1
H3K4me3
ZBTB38
3q23
Scale
10 kb
hg19
chr3:
141,115,000
141,120,000
141,125,000
141,130,000
rs13068733
rs2871960
rs1344674
rs1344672
ARORs Tumors and Normals
FoxA1
PrEC
RWPE1
DNase I + androgen
DNaseI
H3K27ac
H3K27ac+DHT
H3K4me1
H3K4me3
ZBTB38
3q23


chr3 (q26.2)
24.3
13
24
29
Scale
50 kb
hg19
chr3:
170,100,000
170,150,000
p value cutoff
top SNP 1.4E-13 (r²<0.2)
3.8E-9
2.7E-5
Finemapped SNPs
rs76925190
rs80304993
rs1045210
rs10936632
rs10936633
rs12487040
rs55953261
rs969217
rs62293480
rs56121376
rs62293481
FoxA1
DNase I + androgen
DNAseI
H3K27ac
H3K27ac+DHT
H3K4me1
H3K4me3
SKIL
SKIL
SKIL
SKIL
CLDN11
CLDN11
MIR6828
3q26.2


chr4 (q13.3)
15.1
14
q12
q24
q25
q26
28.3
Scale
100 kb
hg19
chr4:
74,350,000
74,400,000
74,450,000
74,500,000
p value cutoff
top SNP 3.9E-5
3.9E-4
2.0E-3
Finemapped
SNPs
rs1894292
rs4257634
rs1590118
rs4694176
rs62312151
rs34617010
rs4694627
rs4694629
rs34700776
rs4694632
CTCF
FoxA1
AROR
ARORs Tumors and Normals
PrEC
RWPE1
DNase I + androgen
DNAseI
H3K4me1
H3K27ac
AFP
AFM
LOC728040
RASSF6
RASSF6
RASSF6
RASSF6
4q13.3
Scale
10 kb
hg19
chr4:
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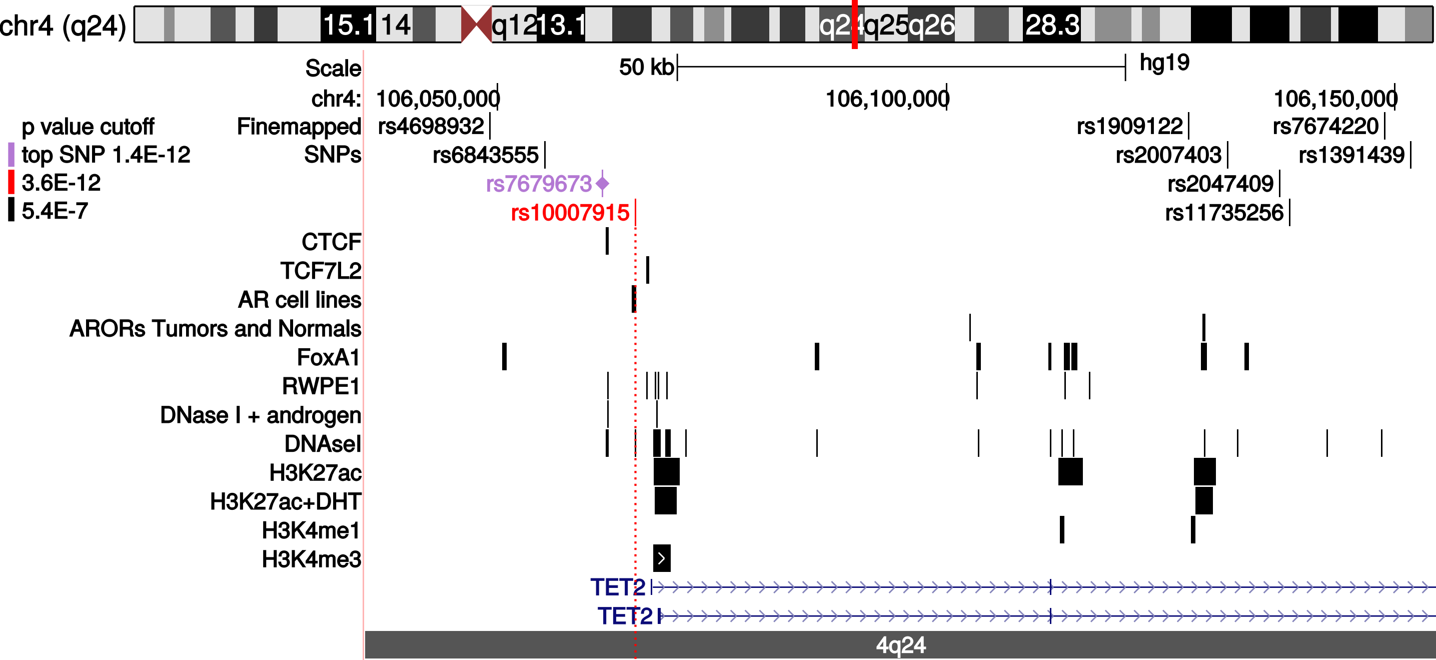
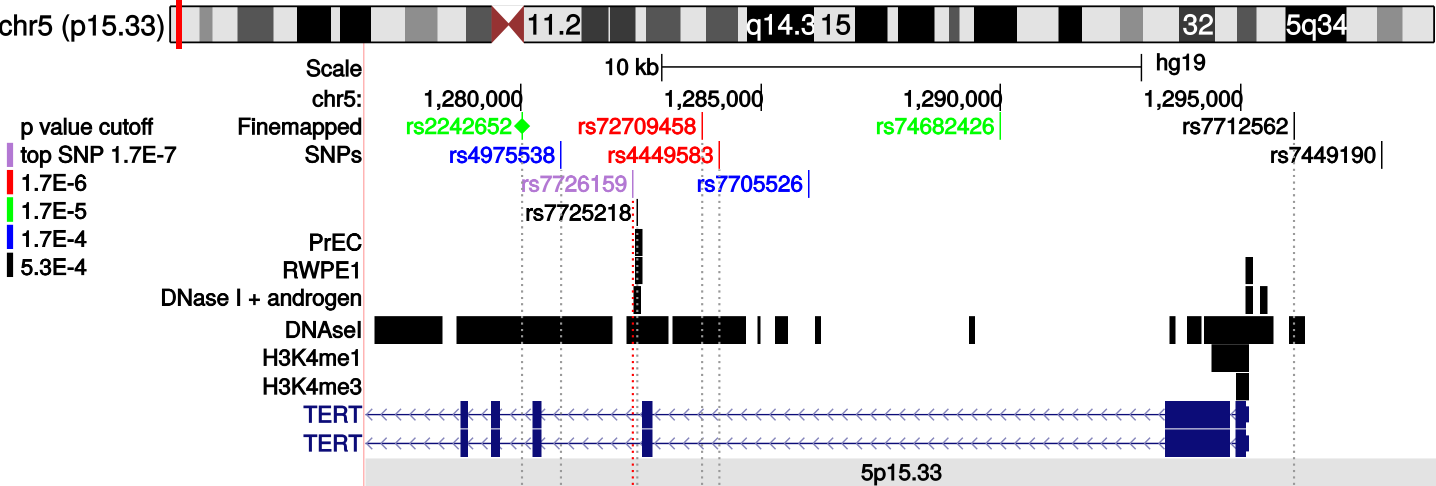
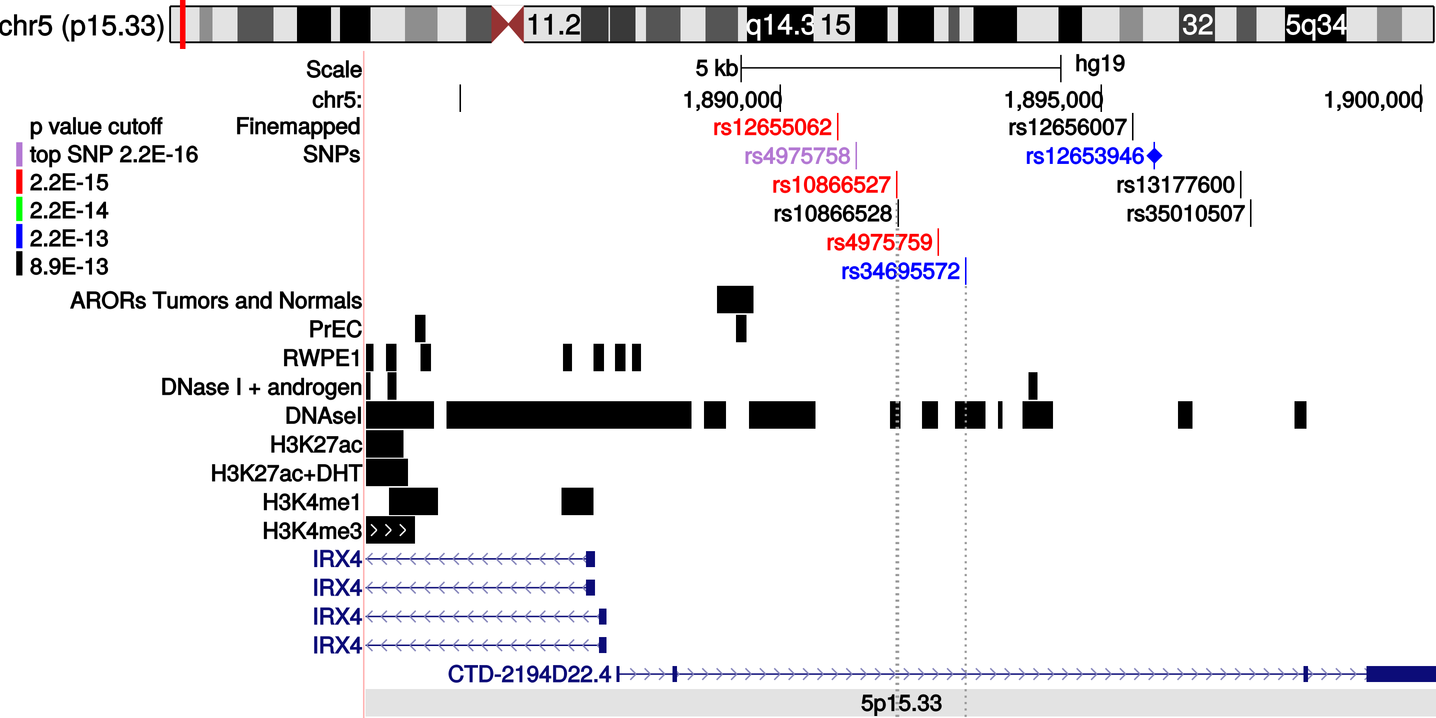
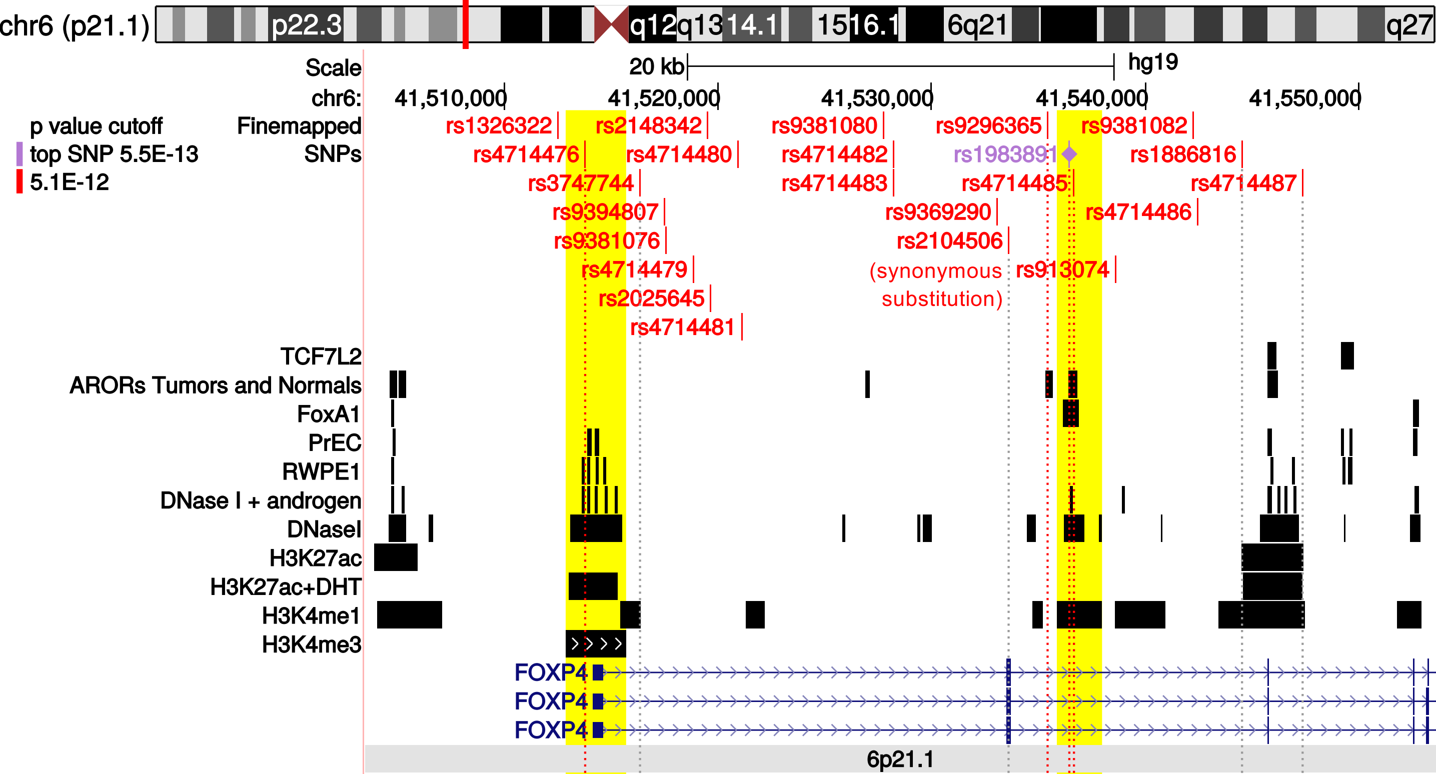
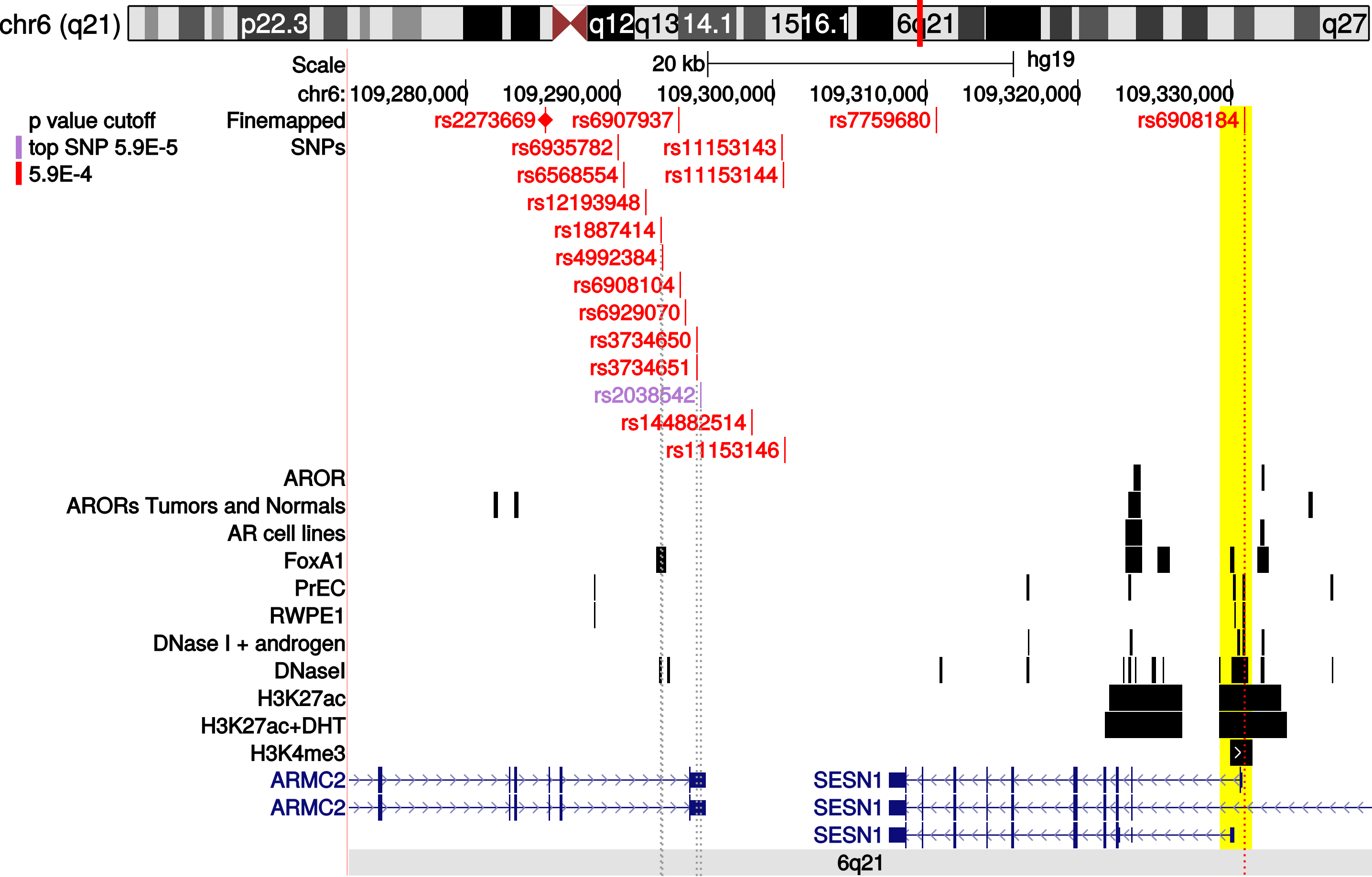
74,525,000
74,530,000
74,535,000
rs4694176
rs34617010
rs1590118
rs62312151
rs4694627
rs4694632
rs4694629
rs34700776
CTCF
FoxA1
AROR
ARORs Tumors and Normals
PrEC
RWPE1
DNase I + androgen
DNAseI
H3K4me1
4q13.3

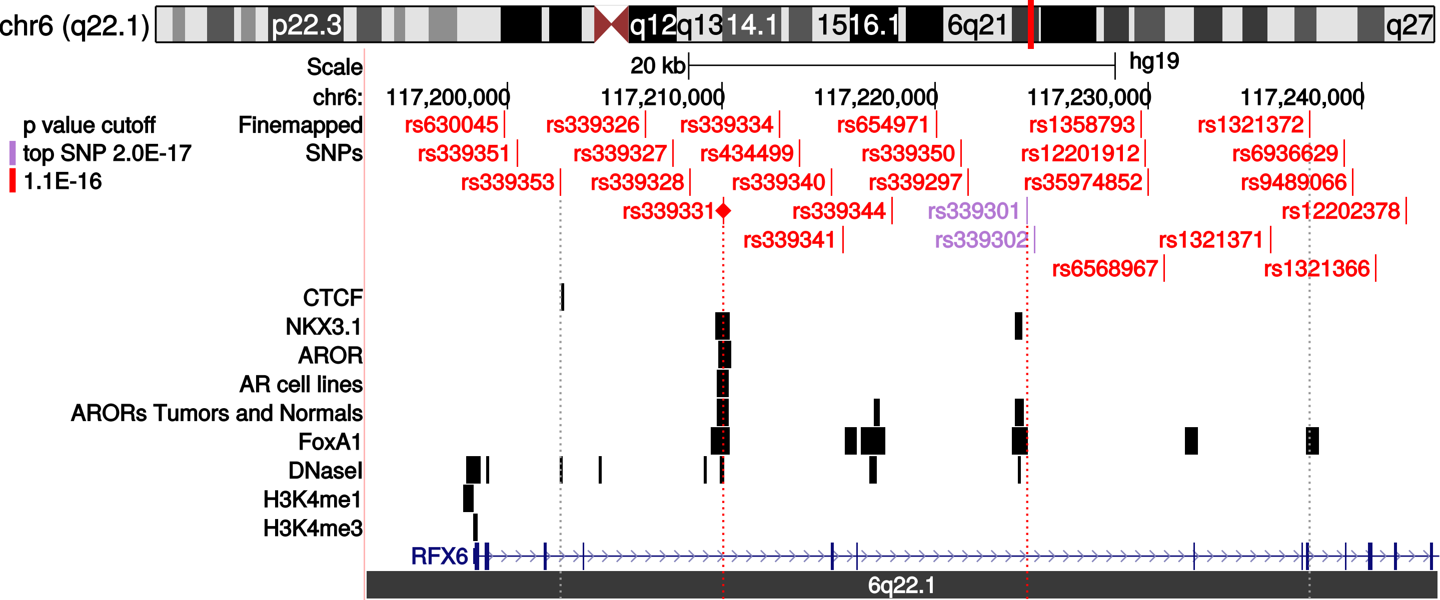

chr4 (q24)
15.1
14
q12
13.1
q24
q25
q26
28.3
Scale
50 kb
hg19
chr4:
106,050,000
106,100,000
106,150,000
p value cutoff
top SNP 1.4E-12
3.6E-12
5.4E-7
Finemapped
SNPs
rs4698932
rs6843555
rs7679673
rs10007915
rs1909122
rs2007403
rs2047409
rs11735256
rs7674220
rs1391439
CTCF
TCF7L2
AR cell lines
ARORs Tumors and Normals
FoxA1
RWPE1
DNase I + androgen
DNAseI
H3K27ac
H3K27ac+DHT
H3K4me1
H3K4me3
TET2
TET2
4q24

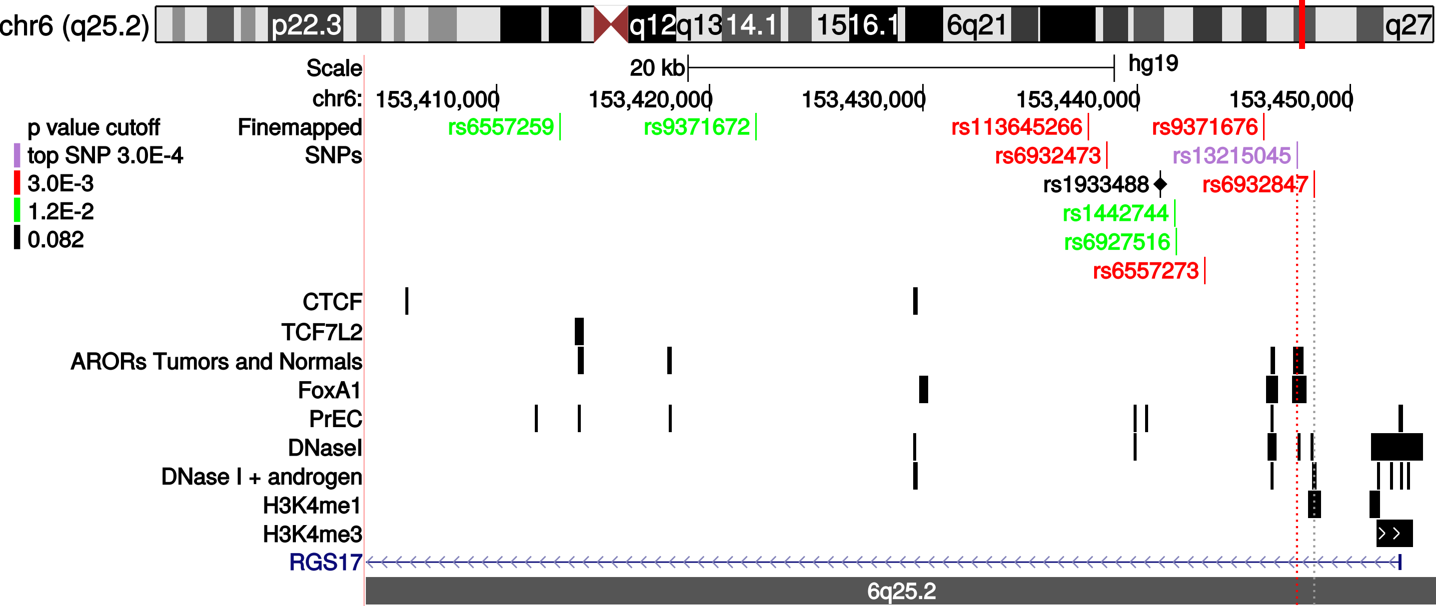

chr5 (p15.33)
11.2
q14.3
15
32
5q34
Scale
10 kb
hg19
chr5:
1,280,000
1,285,000
1,290,000
1,295,000
p value cutoff
top SNP 1.7E-7
1.7E-6
1.7E-5
1.7E-4
5.3E-4
Finemapped
SNPs
rs2242652
rs72709458
rs74682426
rs7712562
rs4975538
rs4449583
rs7449190
rs7726159
rs7705526
rs7725218
PrEC
RWPE1
DNase I + androgen
DNAseI
H3K4me1
H3K4me3
TERT
TERT
5p15.33

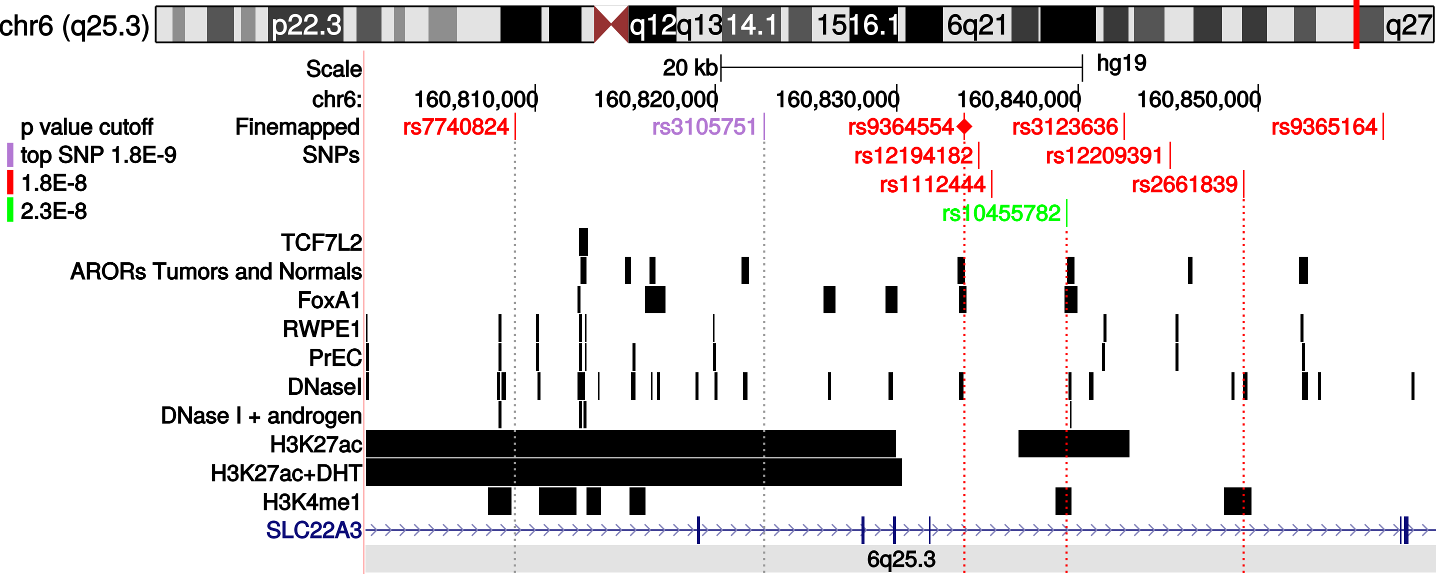

chr5 (p15.33)
11.2
q14.3
15
32
5q34
Scale
5 kb
hg19
chr5:
1,890,000
1,895,000
1,900,000
p value cutoff
top SNP 2.2E-16
2.2E-15
2.2E-14
2.2E-13
8.9E-13
Finemapped SNPs
rs12655062
rs12656007
rs4975758
rs12653946
rs10866527
rs13177600
rs10866528
rs35010507
rs4975759
rs34695572
ARORs Tumors and Normals
PrEC
RWPE1
DNase I + androgen
DNAseI
H3K27ac
H3K27ac+DHT
H3K4me1
H3K4me3
IRX4
IRX4
IRX4
IRX4
CTD-2194D22.4
5p15.33

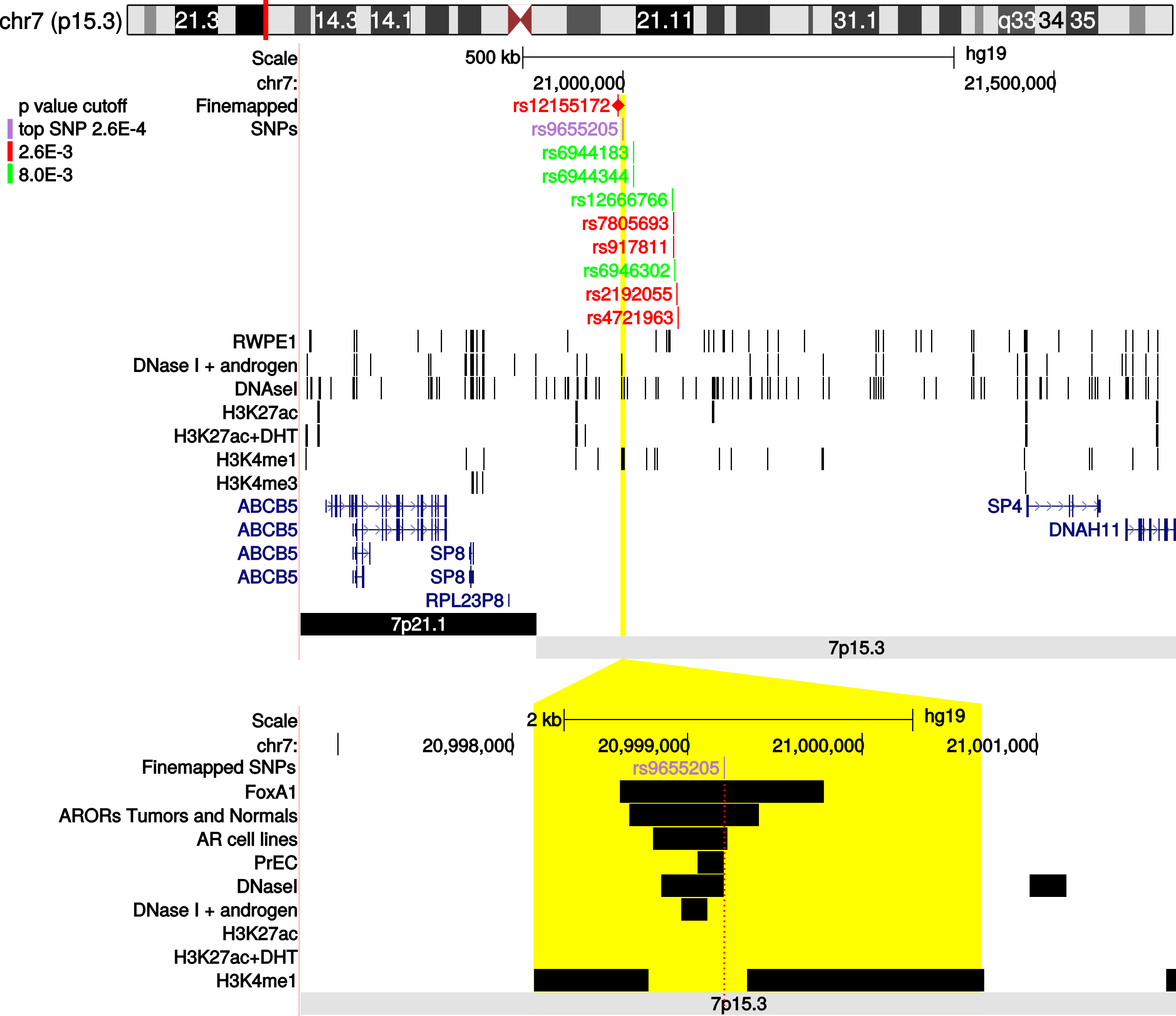

chr6 (p21.1)
p22.3
q12
q13
14.1
15
16.1
6q21
q27
Scale
20 kb
hg19
chr6:
41,510,000
41,520,000
41,530,000
41,540,000
41,550,000
p value cutoff
top SNP 5.5E-13
5.1E-12
Finemapped SNPs
rs1326322
rs2148342
rs9381080
rs9296365
rs9381082
rs4714476
rs4714480
rs4714482
rs1983891
rs1886816
rs3747744
rs4714483
rs4714485
rs4714487
rs9394807
rs9369290
rs4714486
rs9381076
rs2104506
rs4714479
(synonymous substitution)
rs913074
rs2025645
rs4714481
TCF7L2
ARORs Tumors and Normals
FoxA1
PrEC
RWPE1
DNase I + androgen
DNaseI
H3K27ac
H3K27ac+DHT
H3K4me1
H3K4me3
FOXP4
FOXP4
FOXP4
6p21.1

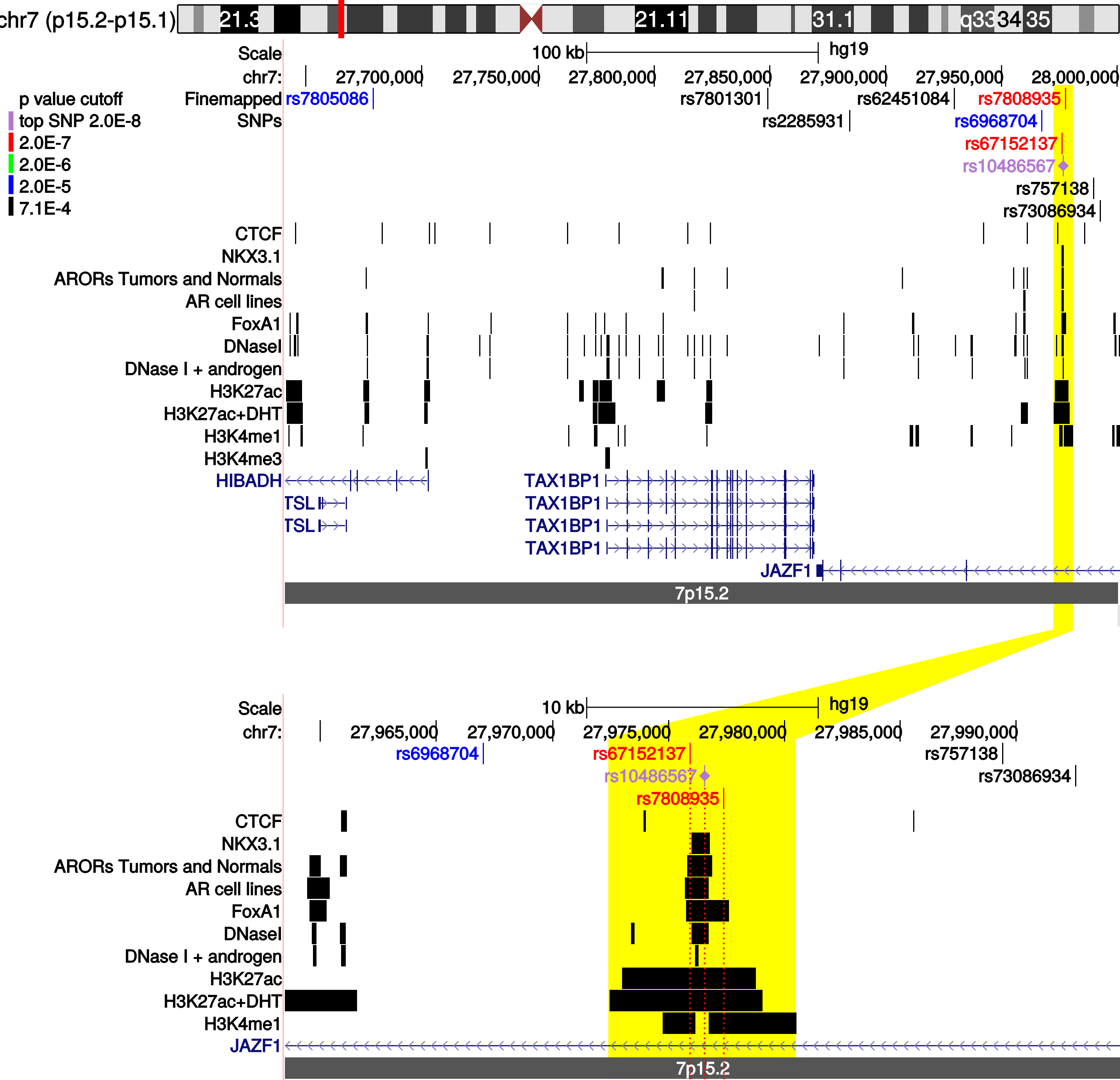

chr6 (q21)
p22.3
q12
q13
14.1
15
16.1
6q21
q27
Scale
20 kb
hg19
chr6:
109,280,000
109,290,000
109,300,000
109,310,000
109,320,000
109,330,000
p value cutoff
top SNP 5.9E-5
5.9E-4
Finemapped SNPs
rs2273669
rs6907937
rs7759680
rs6908184
rs6935782
rs11153143
rs6568554
rs11153144
rs12193948
rs1887414
rs4992384
rs6908104
rs6929070
rs3734650
rs3734651
rs2038542
rs144882514
rs11153146
AROR
ARORs Tumors and Normals
AR cell lines
FoxA1
PrEC
RWPE1
DNase I + androgen
DNaseI
H3K27ac
H3K27ac+DHT
H3K4me3
ARMC2
ARMC2
SESN1
SESN1
SESN1
6q21

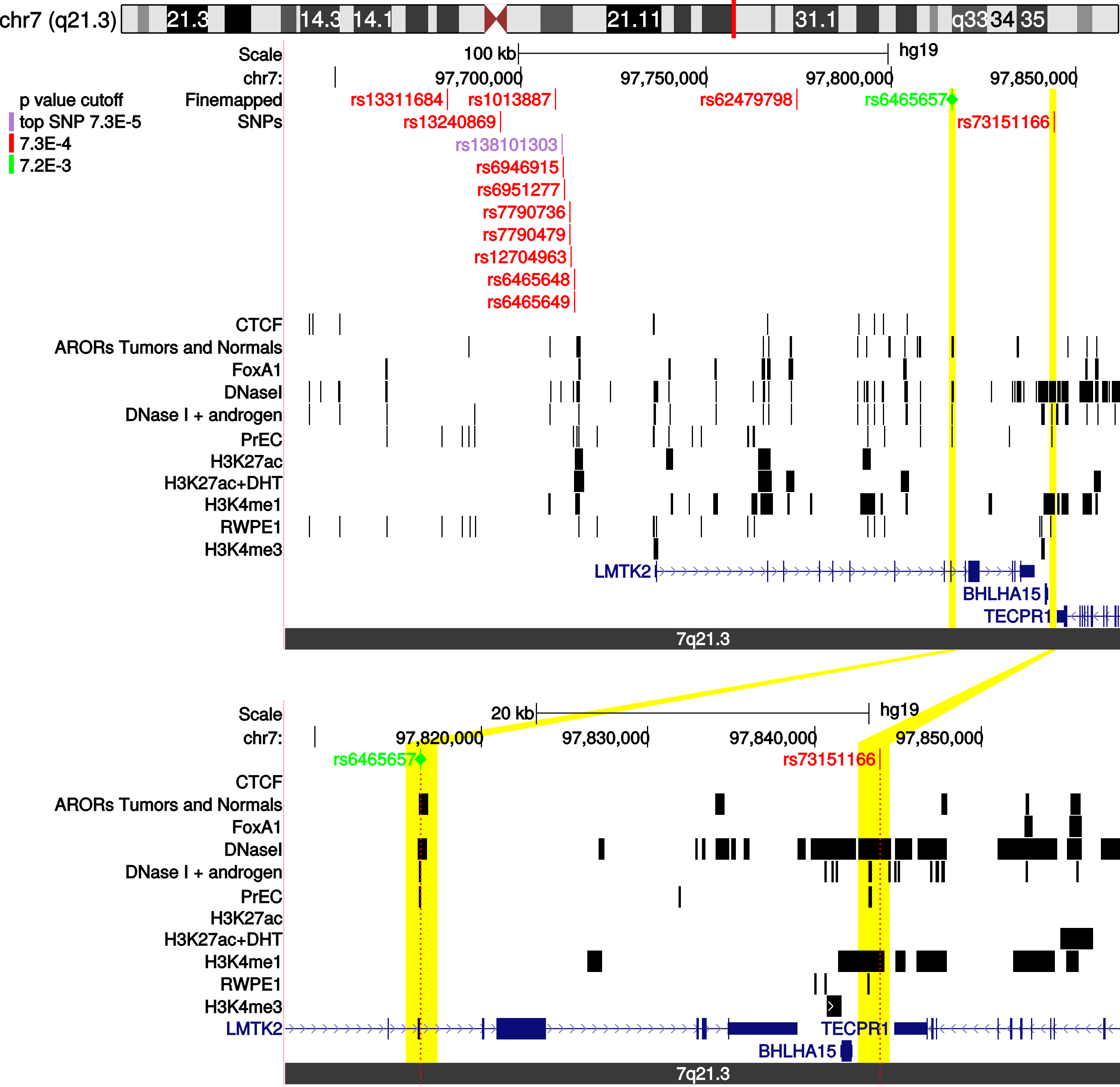

chr6 (q22.1)
p22.3
q12
q13
14.1
15
16.1
6q21
q27
Scale
20 kb
hg19
chr6:
117,200,000
117,210,000
117,220,000
117,230,000
117,240,000
p value cutoff
top SNP 2.0E-17
1.1E-16
Finemapped SNPs
rs630045
rs339326
rs339334
rs654971
rs1358793
rs1321372
rs339351
rs339327
rs434499
rs339350
rs12201912
rs6936629
rs339353
rs339328
rs339340
rs339297
rs35974852
rs9489066
rs339331
rs339344
rs339301
rs12202378
rs339341
rs339302
rs1321371
rs6568967
rs1321366
CTCF
NKX3.1
AROR
AR cell lines
ARORs Tumors and Normals
FoxA1
DNaseI
H3K4me1
H3K4me3
RFX6
6q22.1

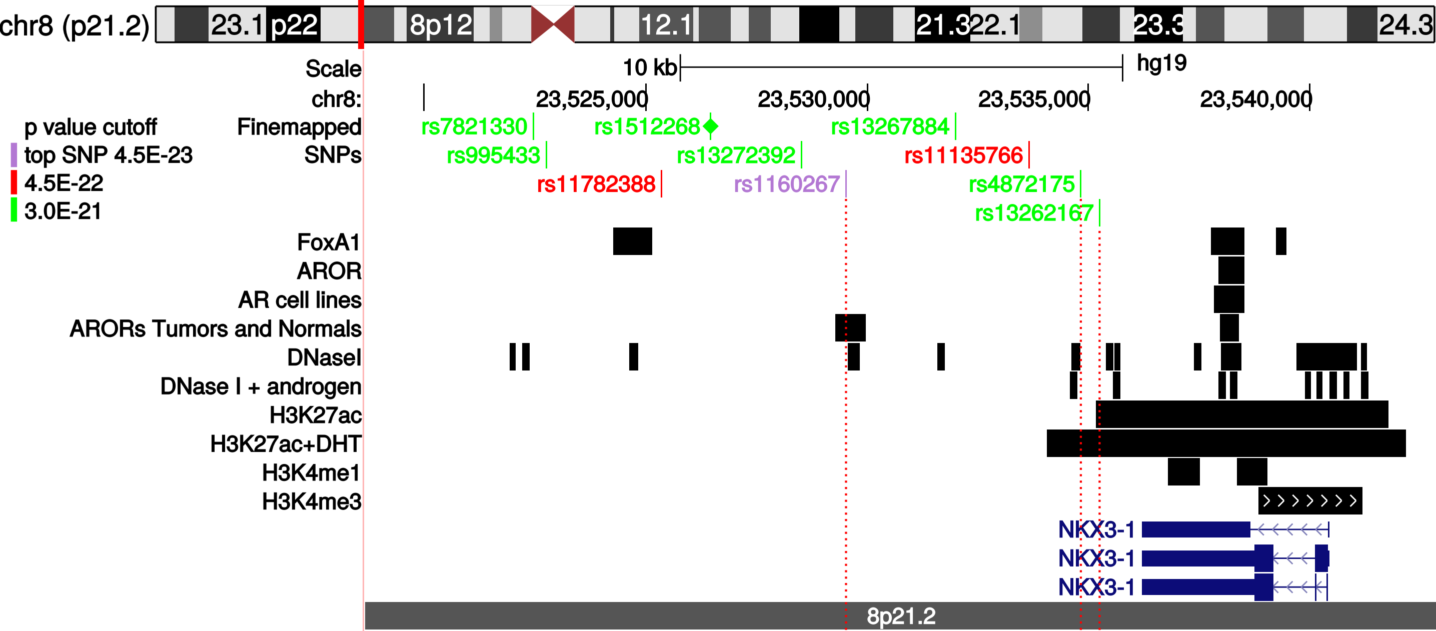

chr6 (q25.2)
p22.3
q12
q13
14.1
15
16.1
6q21
q27
Scale
20 kb
hg19
chr6:
153,410,000
153,420,000
153,430,000
153,440,000
153,450,000
p value cutoff
top SNP 3.0E-4
3.0E-3
1.2E-2
0.082
Finemapped SNPs
rs6557259
rs9371672
rs113645266
rs9371676
rs6932473
rs13215045
rs1933488
rs6932847
rs1442744
rs6927516
rs6557273
CTCF
TCF7L2
ARORs Tumors and Normals
FoxA1
PrEC
DNaseI
DNase I + androgen
H3K4me1
H3K4me3
RGS17
6q25.2

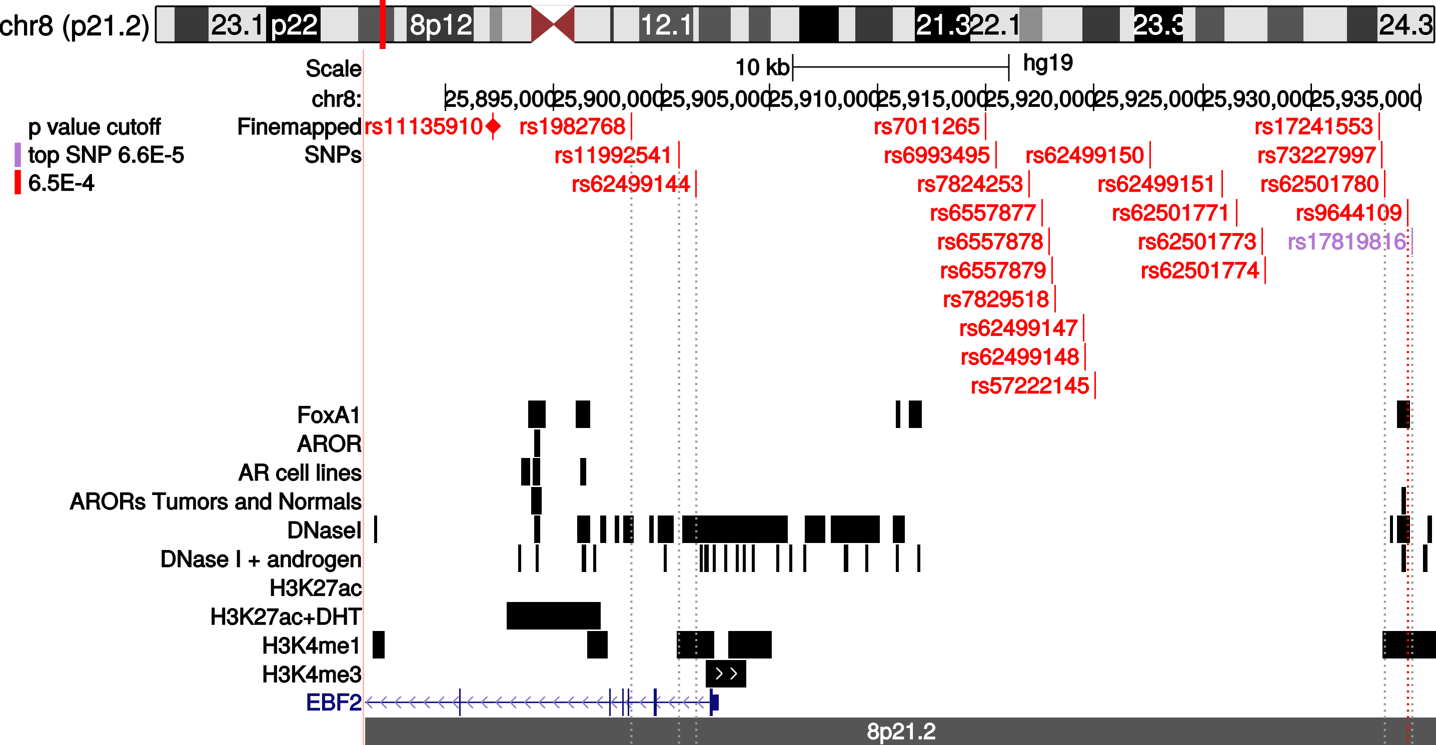

chr6 (q25.3)
p22.3
q12
q13
14.1
15
16.1
6q21
q27
Scale
20 kb
hg19
chr6:
160,810,000
160,820,000
160,830,000
160,840,000
160,850,000
p value cutoff
top SNP 1.8E-9
1.8E-8
2.3E-8
Finemapped SNPs
rs7740824
rs3105751
rs9364554
rs3123636
rs9365164
rs12194182
rs12209391
rs1112444
rs2661839
rs10455782
TCF7L2
ARORs Tumors and Normals
FoxA1
RWPE1
PrEC
DNaseI
DNase I + androgen
H3K27ac
H3K27ac+DHT
H3K4me1
SLC22A3
6q25.3

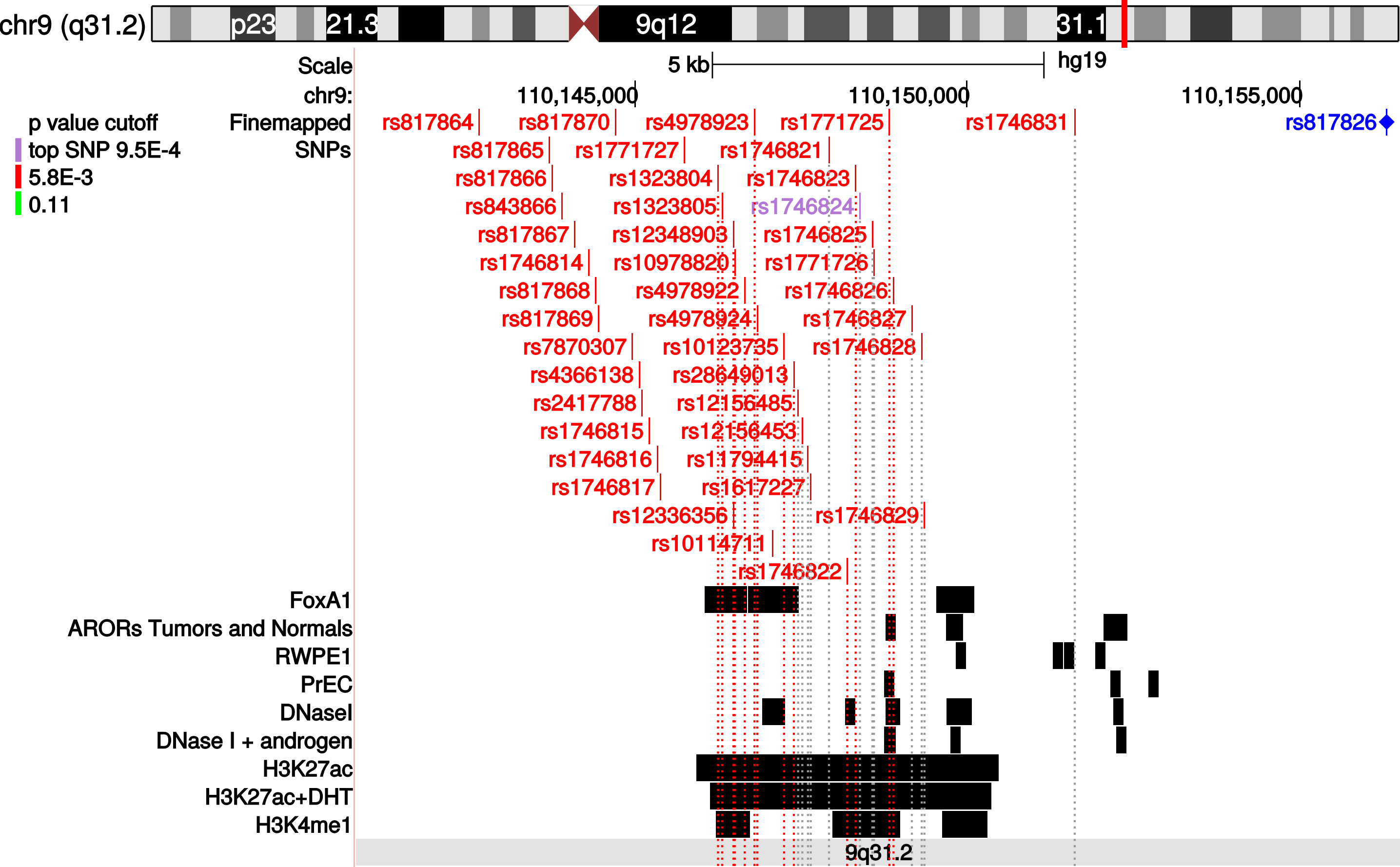

chr7 (p15.3)
21.3
14.3
14.1
21.11
31.1
q33
34
35
Scale
500 kb
hg19
chr7:
21,000,000
21,500,000
p value cutoff
top SNP 2.6E-4
2.6E-3
8.0E-3
Finemapped SNPs
rs12155172
rs9655205
rs6944183
rs6944344
rs12666766
rs7805693
rs917811
rs6946302
rs2192055
rs4721963
RWPE1
DNase I + androgen
DNAseI
H3K27ac
H3K27ac+DHT
H3K4me1
H3K4me3
ABCB5
ABCB5
ABCB5
ABCB5
SP8
SP8
RPL23P8
SP4
DNAH11
7p21.1
7p15.3
Scale
2 kb
hg19
chr7:
20,998,000
20,999,000
21,000,000
21,001,000
Finemapped SNPs
rs9655205
FoxA1
ARORs Tumors and Normals
AR cell lines
PrEC
DNaseI
DNase I + androgen
H3K27ac
H3K27ac+DHT
H3K4me1
7p15.3

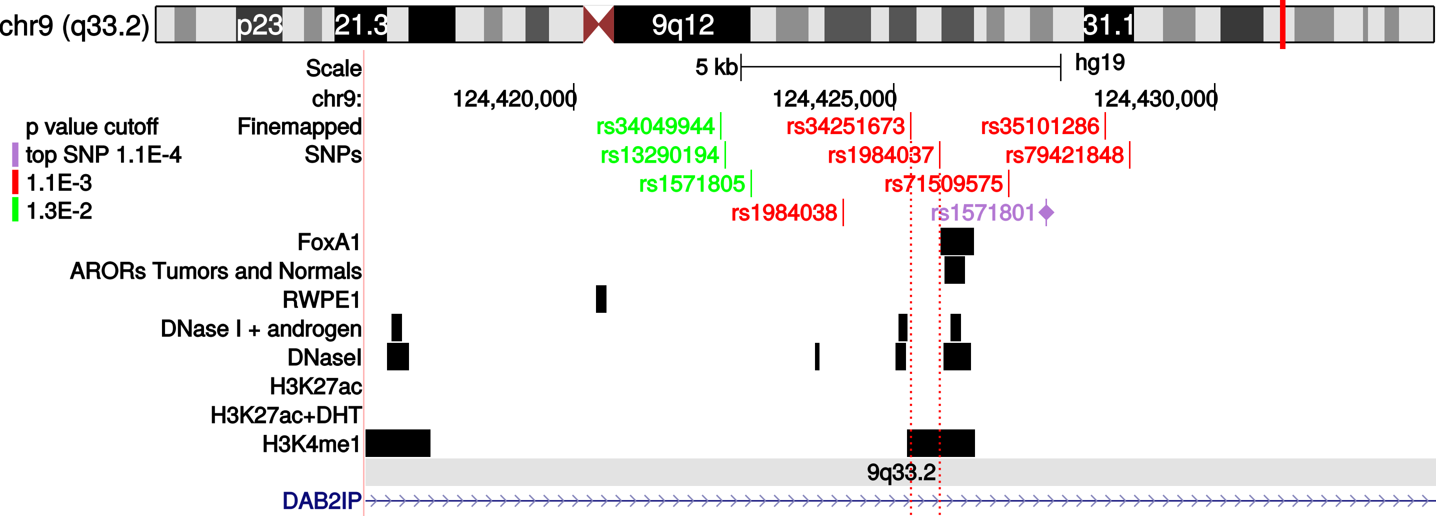

chr7 (p15.2-p15.1)
21.3
21.11
31.1
q33
34
35
Scale
100 kb
hg19
chr7:
27,700,000
27,750,000
27,800,000
27,850,000
27,900,000
27,950,000
28,000,000
p value cutoff
top SNP 2.0E-8
2.0E-7
2.0E-6
2.0E-5
7.1E-4
Finemapped
SNPs
rs7805086
rs7801301
rs62451084
rs7808935
rs2285931
rs6968704
rs67152137
rs10486567
rs757138
rs73086934
CTCF
NKX3.1
ARORs Tumors and Normals
AR cell lines
FoxA1
DNaseI
DNase I + androgen
H3K27ac
H3K27ac+DHT
H3K4me1
H3K4me3
HIBADH
TSL
TSL
TAX1BP1
TAX1BP1
TAX1BP1
TAX1BP1
JAZF1
7p15.2
Scale
10 kb
hg19
chr7:
27,965,000
27,970,000
27,975,000
27,980,000
27,985,000
27,990,000
rs6968704
rs67152137
rs757138
rs10486567
rs73086934
rs7808935
CTCF
NKX3.1
ARORs Tumors and Normals
AR cell lines
FoxA1
DNaseI
DNase I + androgen
H3K27ac
H3K27ac+DHT
H3K4me1
JAZF1
7p15.2

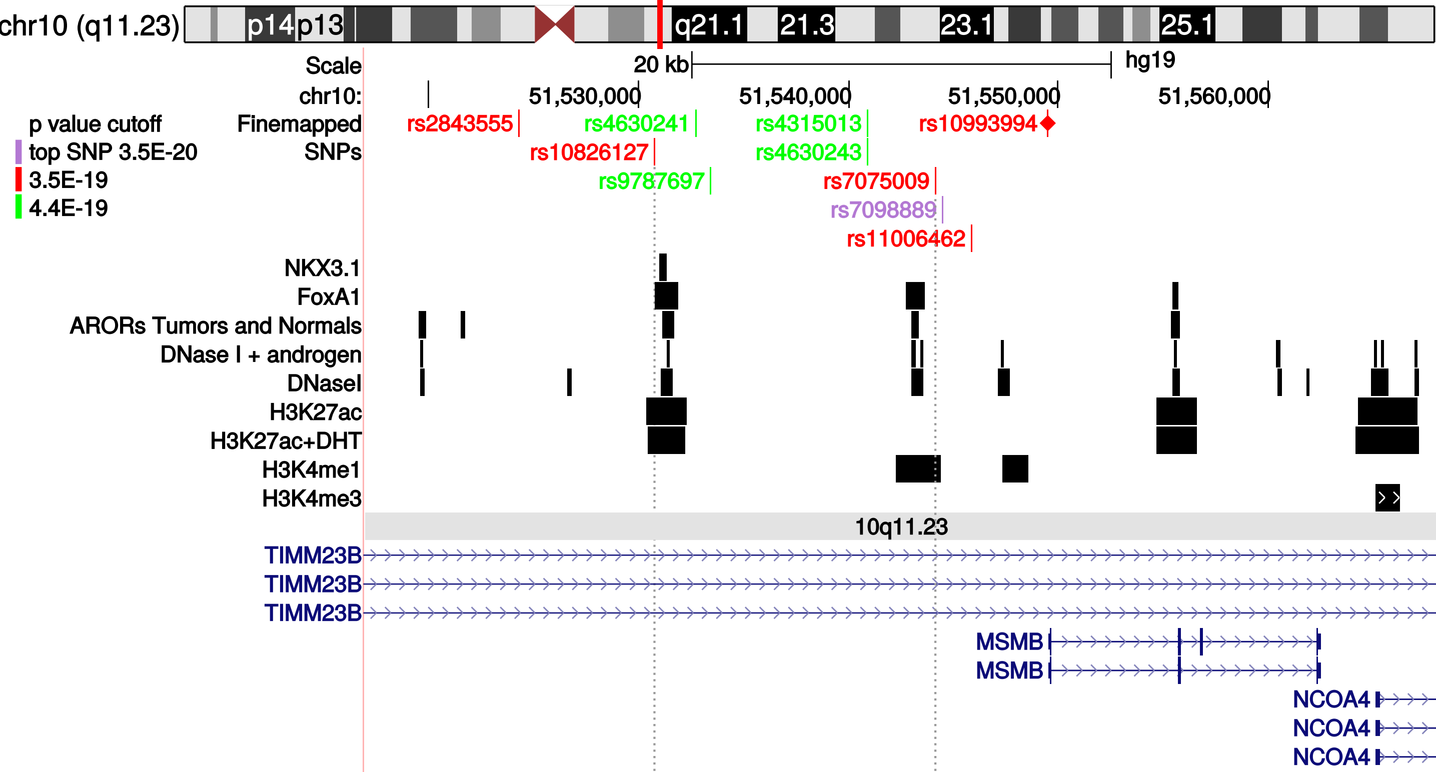

chr7 (q21.3)
21.3
14.3
14.1
21.11
31.1
q33
34
35
Scale
100 kb
hg19
chr7:
97,700,000
97,750,000
97,800,000
97,850,000
p value cutoff
top SNP 7.3E-5
7.3E-4
7.2E-3
Finemapped SNPs
rs13311684
rs1013887
rs62479798
rs6465657
rs13240869
rs73151166
rs138101303
rs6946915
rs6951277
rs7790736
rs7790479
rs12704963
rs6465648
rs6465649
CTCF
ARORs Tumors and Normals
FoxA1
DNaseI
DNase I + androgen
PrEC
H3K27ac
H3K27ac+DHT
H3K4me1
RWPE1
H3K4me3
LMTK2
BHLHA15
TECPR1
7q21.3
Scale
20 kb
hg19
chr7:
97,820,000
97,830,000
97,840,000
97,850,000
rs6465657
rs73151166
CTCF
ARORs Tumors and Normals
FoxA1
DNaseI
DNase I + androgen
PrEC
H3K27ac
H3K27ac+DHT
H3K4me1
RWPE1
H3K4me3
LMTK2
TECPR1
BHLHA15
7q21.3

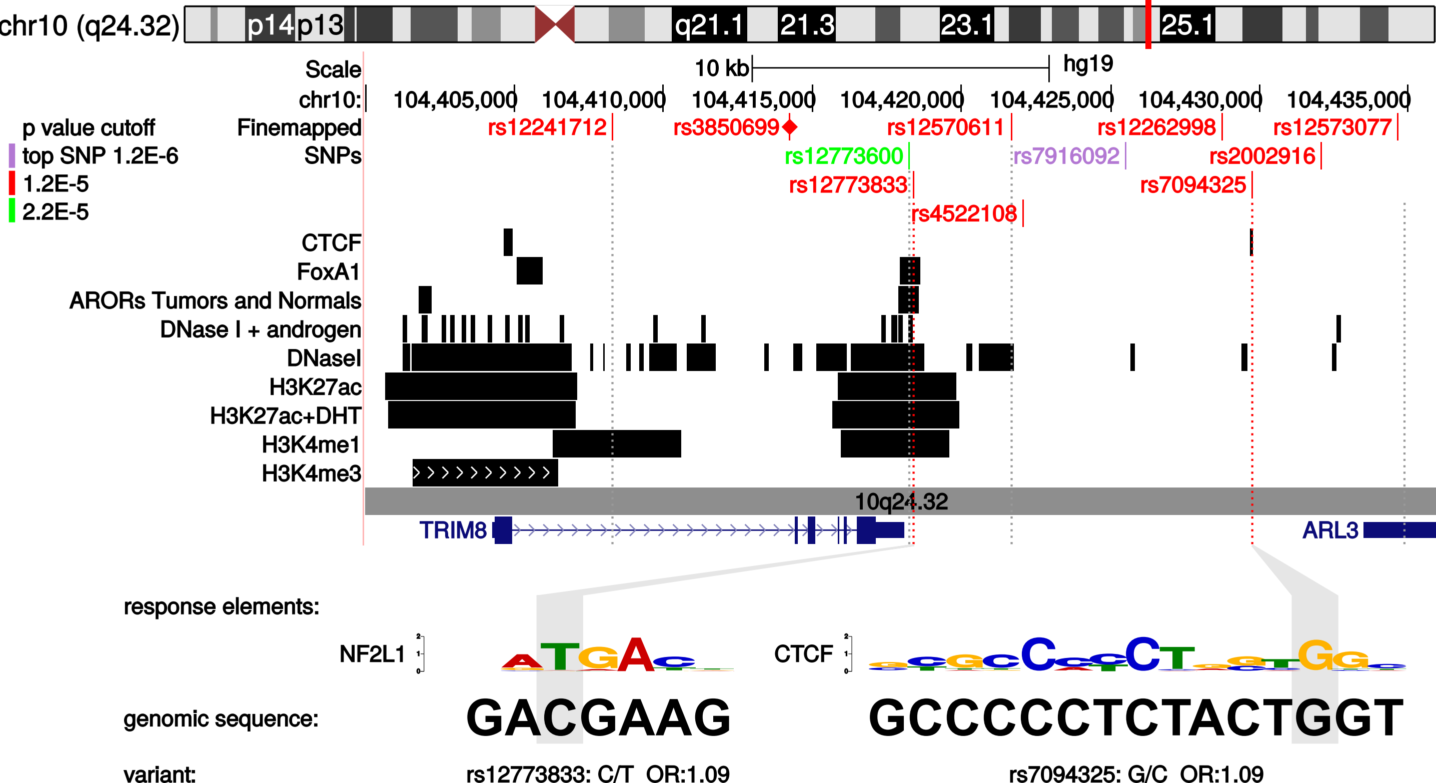

chr8 (p21.2)
23.1
p22
8p12
12.1
21.3
22.1
23.3
24.3
Scale
10 kb
hg19
chr8:
23,525,000
23,530,000
23,535,000
23,540,000
p value cutoff
top SNP 4.5E-23
4.5E-22
3.0E-21
Finemapped
SNPs
rs7821330
rs1512268
rs13267884
rs995433
rs13272392
rs11135766
rs11782388
rs1160267
rs4872175
rs13262167
FoxA1
AROR
AR cell lines
ARORs Tumors and Normals
DNaseI
DNase I + androgen
H3K27ac
H3K27ac+DHT
H3K4me1
H3K4me3
NKX3-1
NKX3-1
NKX3-1
8p21.2

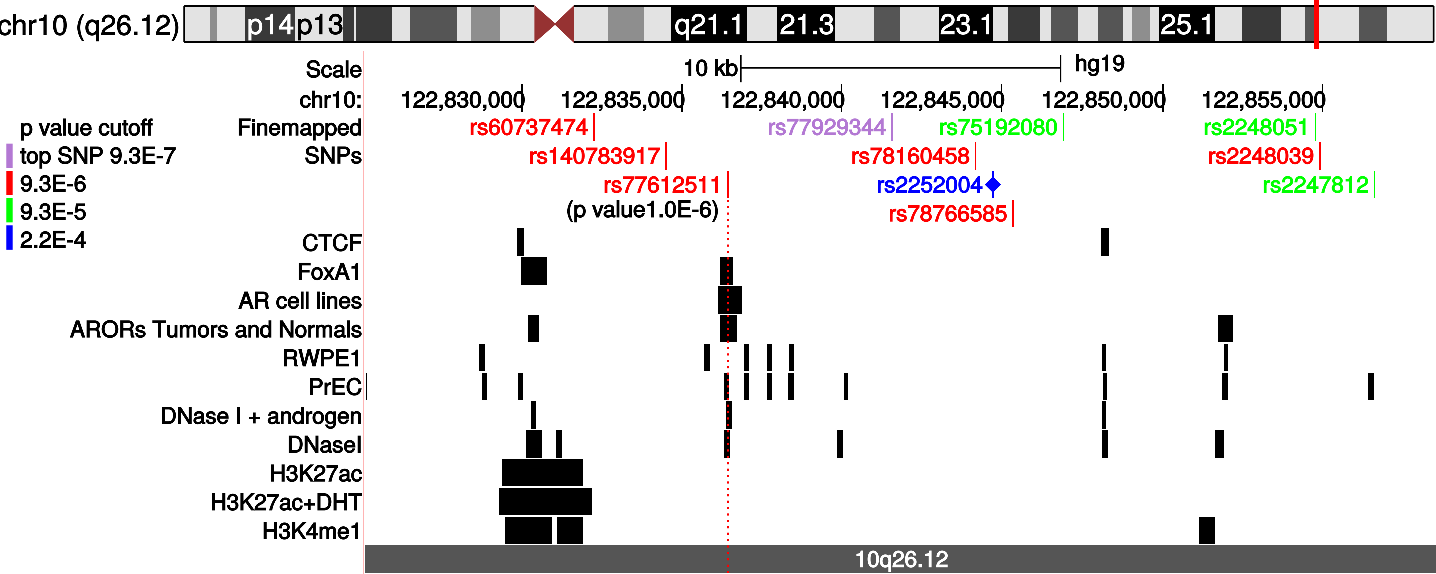

chr8 (p21.2)
23.1
p22
8p12
12.1
21.3
22.1
23.3
24.3
Scale
10 kb
hg19
chr8:
25,895,000
25,900,000
25,905,000
25,910,000
25,915,000
25,920,000
25,925,000
25,930,000
25,935,000
p value cutoff
top SNP 6.6E-5
6.5E-4
Finemapped SNPs
rs11135910
rs1982768
rs11992541
rs62499144
rs7011265
rs6993495
rs7824253
rs6557877
rs6557878
rs6557879
rs7829518
rs62499147
rs62499148
rs57222145
rs62499150
rs62499151
rs62501771
rs62501773
rs62501774
rs17241553
rs73227997
rs62501780
rs9644109
rs17819816
FoxA1
AROR
AR cell lines
ARORs Tumors and Normals
DNaseI
DNase I + androgen
H3K27ac
H3K27ac+DHT
H3K4me1
H3K4me3
EBF2
8p21.2

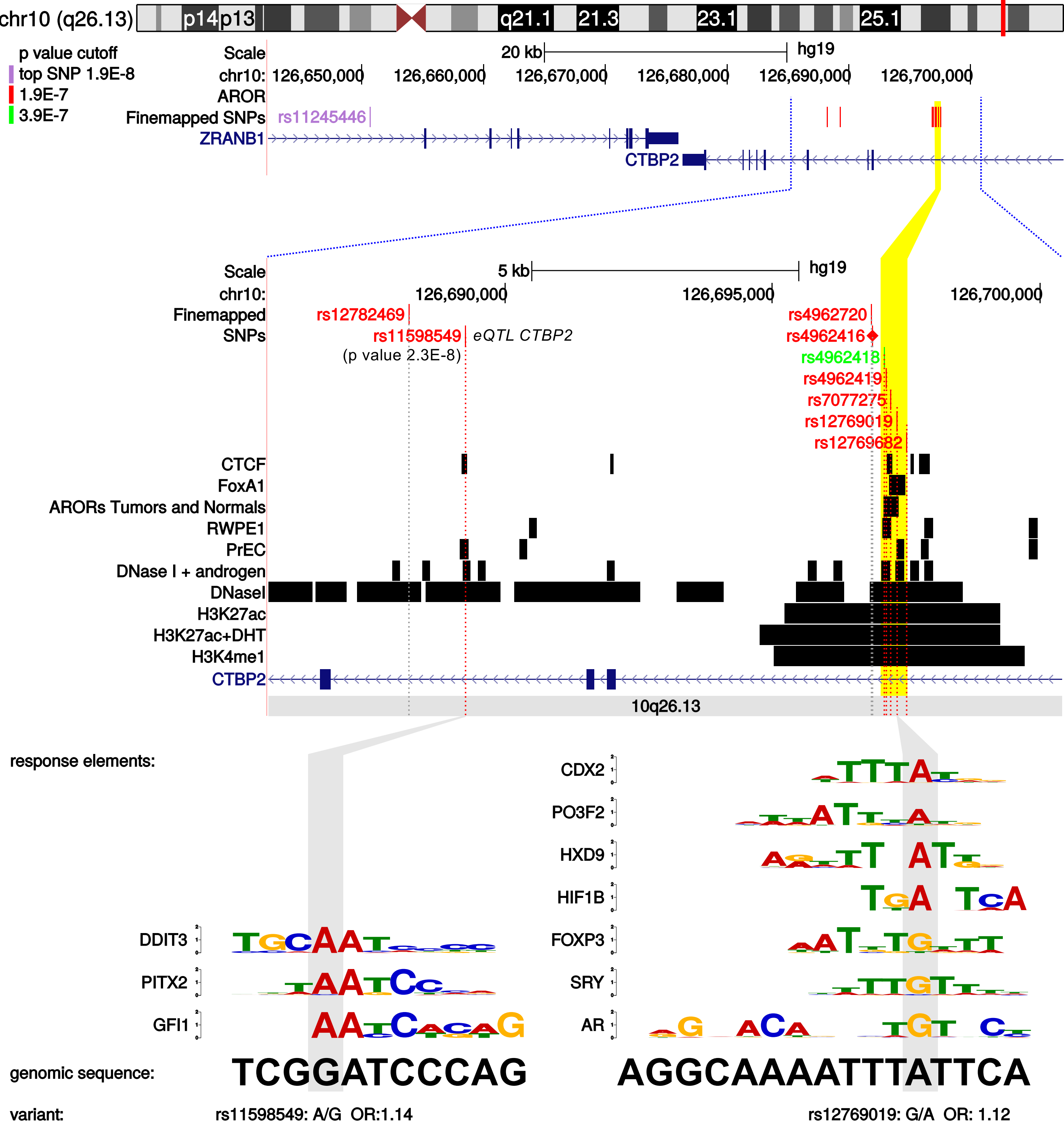

chr9 (q31.2)
p23
21.3
9q12
31.1
Scale
5 kb
hg19
chr9:
110,145,000
110,150,000
110,155,000
p value cutoff
top SNP 9.5E-4
5.8E-3
0.11
Finemapped
SNPs
rs817864
rs817870
rs4978923
rs1771725
rs1746831
rs817826
rs817865
rs1771727
rs1746821
rs817866
rs1323804
rs1746823
rs843866
rs1323805
rs1746824
rs817867
rs12348903
rs1746825
rs1746814
rs10978820
rs1771726
rs817868
rs4978922
rs1746826
rs817869
rs4978924
rs1746827
rs7870307
rs10123735
rs1746828
rs4366138
rs28649013
rs2417788
rs12156485
rs1746815
rs12156453
rs1746816
rs11794415
rs1746817
rs1617227
rs12336356
rs1746829
rs10114711
rs1746822
FoxA1
ARORs Tumors and Normals
RWPE1
PrEC
DNaseI
DNase I + androgen
H3K27ac
H3K27ac+DHT
H3K4me1
9q31.2

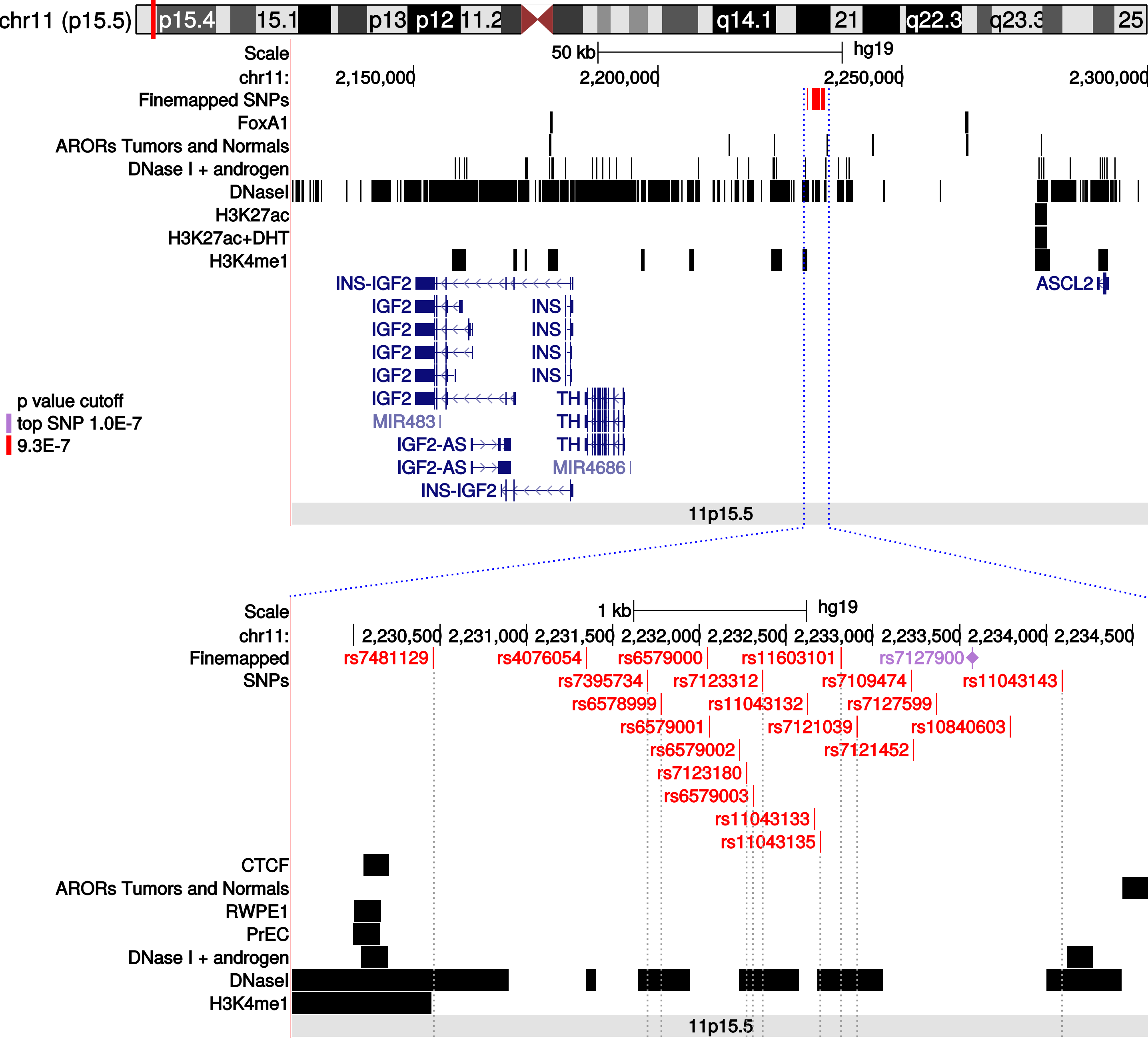

chr9 (q33.2)
p23
21.3
9q12
31.1
Scale
5 kb
hg19
chr9:
124,420,000
124,425,000
124,430,000
p value cutoff
top SNP 1.1E-4
1.1E-3
1.3E-2
Finemapped
SNPs
rs34049944
rs13290194
rs1571805
rs1984038
rs34251673
rs1984037
rs71509575
rs1571801
rs35101286
rs79421848
FoxA1
ARORs Tumors and Normals
RWPE1
DNase I + androgen
DNaseI
H3K27ac
H3K27ac+DHT
H3K4me1
9q33.2
DAB2IP

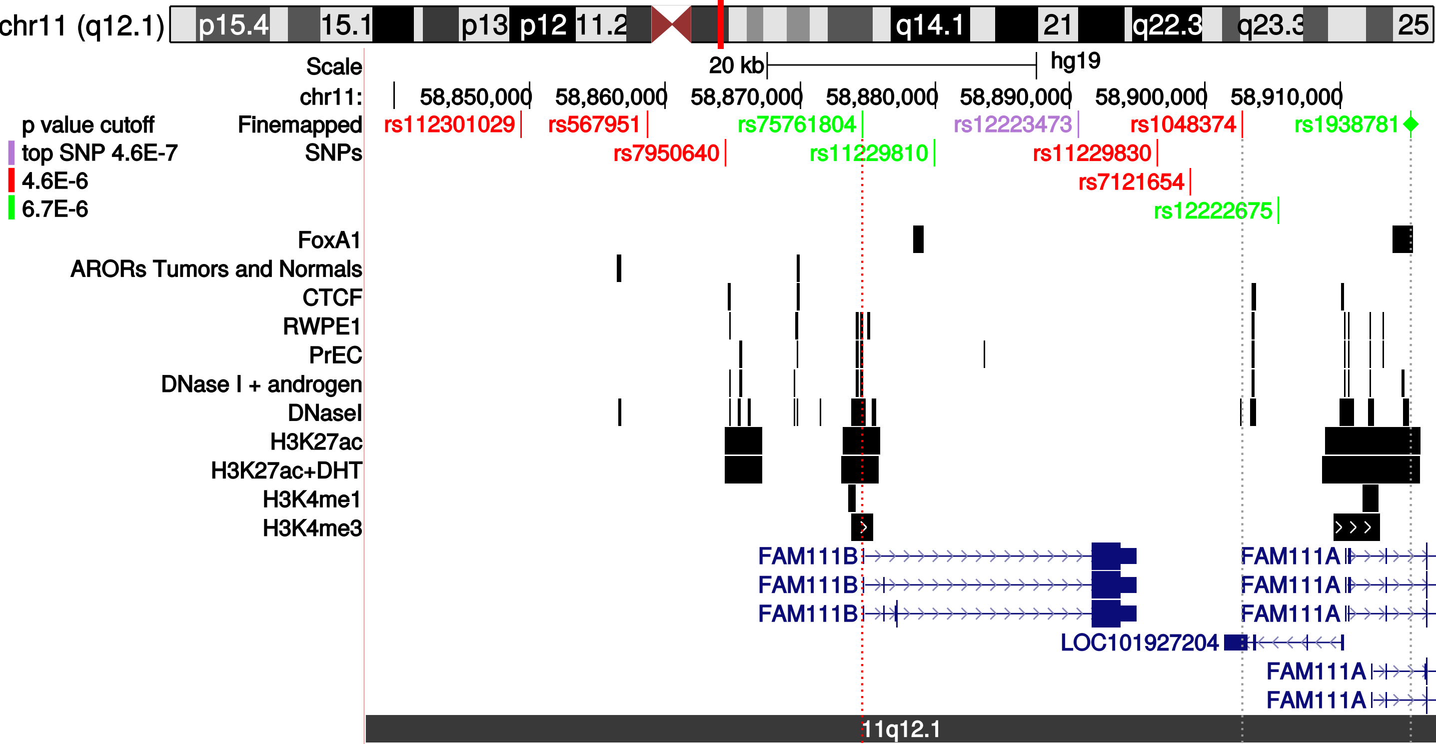

chr10 (q11.23)
p14
p13
q21.1
21.3
23.1
25.1
Scale
20 kb
hg19
chr10:
51,530,000
51,540,000
51,550,000
51,560,000
p value cutoff
top SNP 3.5E-20
3.5E-19
4.4E-19
Finemapped
SNPs
rs2843555
rs4630241
rs4315013
rs10993994
rs10826127
rs4630243
rs9787697
rs7075009
rs7098889
rs11006462
NKX3.1
FoxA1
ARORs Tumors and Normals
DNase I + androgen
DNaseI
H3K27ac
H3K27ac+DHT
H3K4me1
H3K4me3
10q11.23
TIMM23B
TIMM23B
TIMM23B
MSMB
MSMB
NCOA4
NCOA4
NCOA4

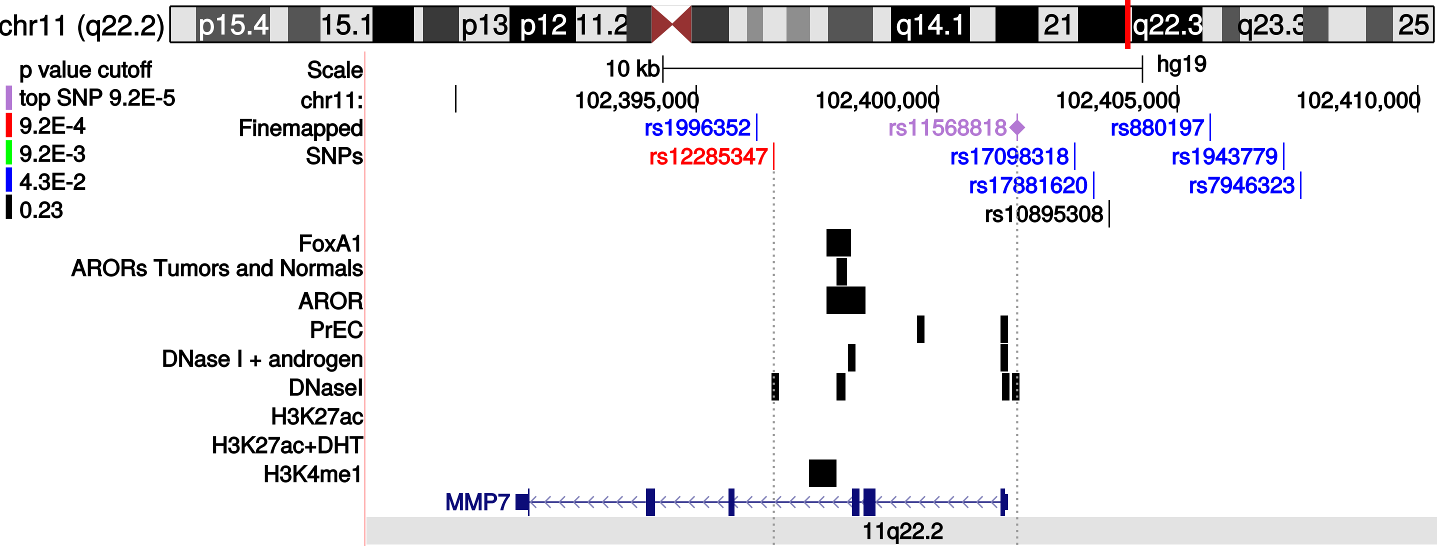

chr10 (q24.32)
p14
p13
q21.1
21.3
23.1
25.1
Scale
10 kb
hg19
chr10:
104,405,000
104,410,000
104,415,000
104,420,000
104,425,000
104,430,000
104,435,000
p value cutoff
top SNP 1.2E-6
1.2E-5
2.2E-5
Finemapped
SNPs
rs12241712
rs3850699
rs12570611
rs12262998
rs12573077
rs12773600
rs7916092
rs2002916
rs12773833
rs7094325
rs4522108
CTCF
FoxA1
ARORs Tumors and Normals
DNase I + androgen
DNaseI
H3K27ac
H3K27ac+DHT
H3K4me1
H3K4me3
10q24.32
TRIM8
ARL3
response elements:
NF2L1
CTCF
genomic sequence:
GACGAAG
GCCCCCCTCTACTGGT
variant:
rs12773833: C/T OR:1.09
rs7094325: G/C OR:1.09


chr10 (q26.12)
p14
p13
q21.1
21.3
23.1
25.1
Scale
10 kb
hg19
chr10:
122,830,000
122,835,000
122,840,000
122,845,000
122,850,000
122,855,000
p value cutoff
top SNP 9.3E-7
9.3E-6
9.3E-5
2.2E-4
Finemapped SNPs
rs60737474
rs77929344
rs75192080
rs2248051
rs140783917
rs78160458
rs2248039
rs77612511
rs2252004
rs2247812
(p value1.0E-6)
rs78766585
CTCF
FoxA1
AR cell lines
ARORs Tumors and Normals
RWPE1
PrEC
DNase I + androgen
DNaseI
H3K27ac
H3K27ac+DHT
H3K4me1
10q26.12


chr10 (q26.13)
p14 p13 q21.1 21.3 23.1 25.1
p value cutoff
top SNP 1.9E-8
1.9E-7
3.9E-7
Scale
20 kb
hg19
chr10: 126,650,000 126,660,000 126,670,000 126,680,000 126,690,000 126,700,000
AROR
Finemapped SNPs
rs11245446
ZRANB1
CTBP2
Scale
5 kb
hg19
chr10: 126,690,000 126,695,000 126,700,000
Finemapped SNPs
rs12782469
rs11598549
eQTL CTBP2
(p value 2.3E-8)
rs4962720
rs4962416
rs4962418
rs4962419
rs7077275
rs12769019
rs12769682
CTCF
FoxA1
ARORs Tumors and Normals
RWPE1
PrEC
DNase I + androgen
DNaseI
H3K27ac
H3K27ac+DHT
H3K4me1
CTBP2
10q26.13
response elements:
CDX2
PO3F2
HXD9
HIF1B
DDIT3
FOXP3
PITX2
SRY
GFI1
AR
genomic sequence:
TCGGATCCCAG
AGGCAAAATTTATTCA
variant:
rs11598549: A/G OR:1.14
rs12769019: G/A OR: 1.12


chr11 (p15.5)
p15.4
15.1
p13
p12
11.2
q14.1
21
q22.3
q23.3
25
Scale
50 kb
hg19
chr11:
2,150,000
2,200,000
2,250,000
2,300,000
Finemapped SNPs
FoxA1
ARORs Tumors and Normals
DNase I + androgen
DNaseI
H3K27ac
H3K27ac+DHT
H3K4me1
INS-IGF2
IGF2
INS
TH
MIR483
IGF2-AS
MIR4686
ASCL2
11p15.5
p value cutoff
top SNP 1.0E-7
9.3E-7
Scale
1 kb
hg19
chr11:
2,230,500
2,231,000
2,231,500
2,232,000
2,232,500
2,233,000
2,233,500
2,234,000
2,234,500
Finemapped SNPs
rs7481129
rs4076054
rs6579000
rs11603101
rs7127900
rs7395734
rs7123312
rs7109474
rs11043143
rs6578999
rs11043132
rs7127599
rs6579001
rs7121039
rs10840603
rs6579002
rs7121452
rs7123180
rs6579003
rs11043133
rs11043135
CTCF
ARORs Tumors and Normals
RWPE1
PrEC
DNase I + androgen
DNaseI
H3K4me1
11p15.5


chr11 (q12.1)
p15.4
15.1
p13
p12
11.2
q14.1
21
q22.3
q23.3
25
Scale
20 kb
hg19
chr11:
58,850,000
58,860,000
58,870,000
58,880,000
58,890,000
58,900,000
58,910,000
p value cutoff
top SNP 4.6E-7
4.6E-6
6.7E-6
Finemapped
SNPs
rs112301029
rs567951
rs75761804
rs12223473
rs1048374
rs1938781
rs7950640
rs11229810
rs11229830
rs7121654
rs12222675
FoxA1
ARORs Tumors and Normals
CTCF
RWPE1
PrEC
DNase I + androgen
DNaseI
H3K27ac
H3K27ac+DHT
H3K4me1
H3K4me3
FAM111B
FAM111B
FAM111B
FAM111A
FAM111A
FAM111A
LOC101927204
FAM111A
FAM111A
11q12.1


chr11 (q22.2)
p15.4
15.1
p13
p12
11.2
q14.1
21
q22.3
q23.3
25
p value cutoff
top SNP 9.2E-5
9.2E-4
9.2E-3
4.3E-2
0.23
Scale
10 kb
hg19
chr11:
102,395,000
102,400,000
102,405,000
102,410,000
Finemapped
SNPs
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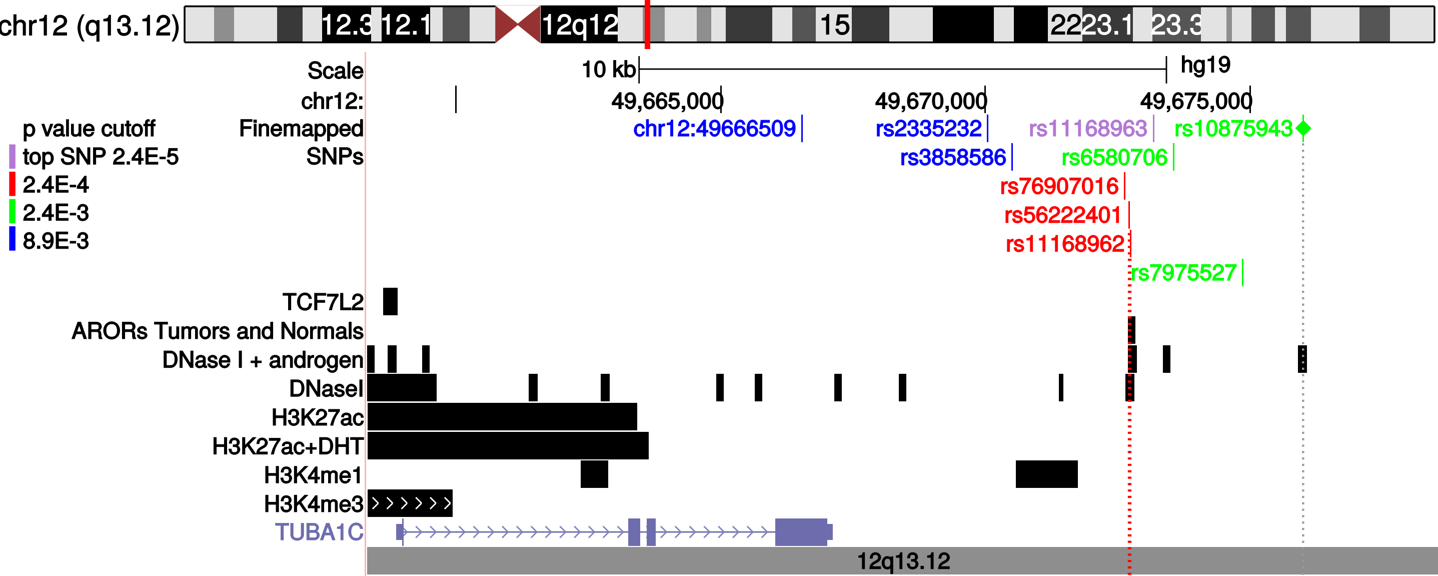
rs11568818
rs880197
rs12285347
rs17098318
rs1943779
rs17881620
rs7946323
rs10895308
FoxA1
ARORs Tumors and Normals
AROR
PrEC
DNase I + androgen
DNaseI
H3K27ac
H3K27ac+DHT
H3K4me1
MMP7
11q22.2


chr12 (q13.12)
12.3
12.1
12q12
15
22
23.1
23.3
Scale
10 kb
hg19
chr12:
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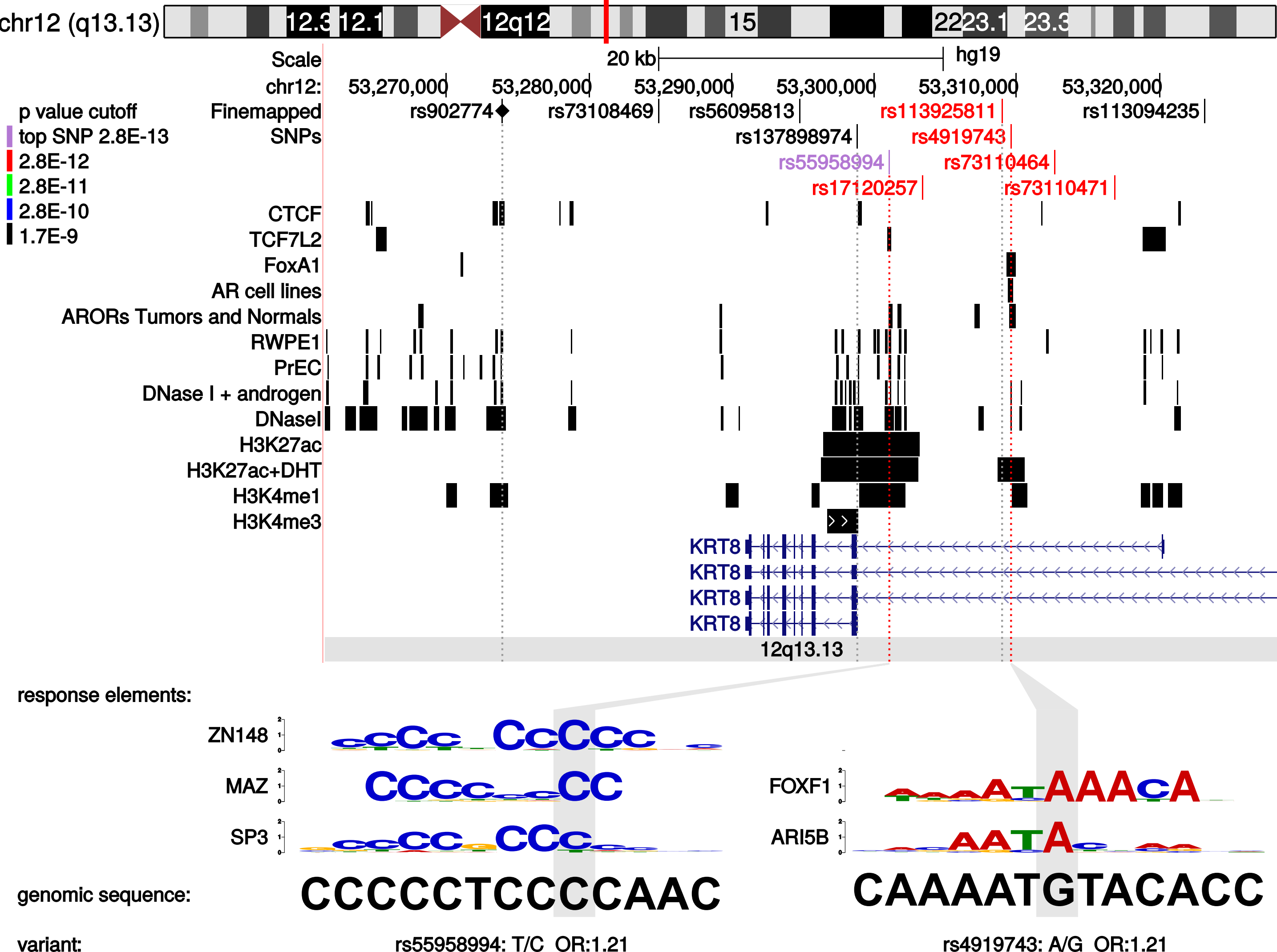
49,670,000
49,675,000
p value cutoff
top SNP 2.4E-5
2.4E-4
2.4E-3
8.9E-3
Finemapped SNPs
chr12:49666509
rs2335232
rs11168963
rs10875943
rs3858586
rs6580706
rs76907016
rs56222401
rs11168962
rs7975527
TCF7L2
ARORs Tumors and Normals
DNase I + androgen
DNaseI
H3K27ac
H3K27ac+DHT
H3K4me1
H3K4me3
TUBA1C
12q13.12


chr12 (q13.13)
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12.1
12q12
15
22
23.1
23.3
Scale
20 kb
hg19
chr12:
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53,280,000
53,290,000
53,300,000
53,310,000
53,320,000
p value cutoff
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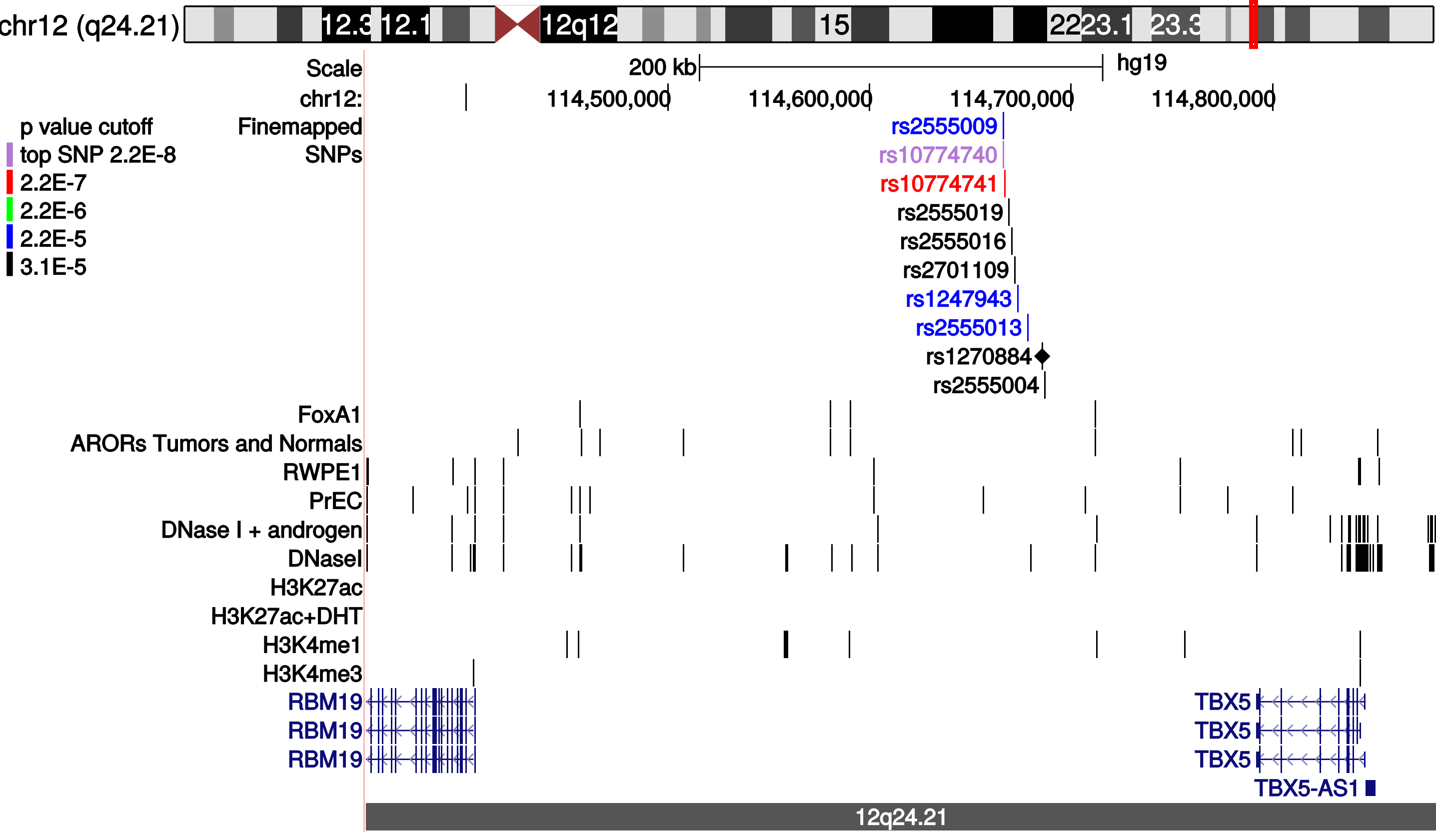
2.8E-12
2.8E-11
2.8E-10
1.7E-9
Finemapped SNPs
rs902774
rs73108469
rs56095813
rs113925811
rs113094235
rs137898974
rs4919743
rs55958994
rs73110464
rs17120257
rs73110471
CTCF
TCF7L2
FoxA1
AR cell lines
ARORs Tumors and Normals
RWPE1
PrEC
DNase I + androgen
DNaseI
H3K27ac
H3K27ac+DHT
H3K4me1
H3K4me3
KRT8
KRT8
KRT8
KRT8
12q13.13
response elements:
ZN148
MAZ
SP3
FOXF1
ARI5B
genomic sequence:
CCCCCTCCCCAAC
CAAAATGTACACC
variant:
rs55958994: T/C OR:1.21
rs4919743: A/G OR:1.21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12.3
12.1
12q12
15
22
23.1
23.3
Scale
200 kb
hg19
chr12:
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114,700,000
114,800,000
p value cutoff
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2.2E-7
2.2E-6
2.2E-5
3.1E-5
Finemapped SNPs
rs2555009
rs10774740
rs10774741
rs2555019
rs2555016
rs2701109
rs1247943
rs2555013
rs1270884
rs2555004
FoxA1
ARORs Tumors and Normals
RWPE1
PrEC
DNase I + androgen
DNaseI
H3K27ac
H3K27ac+DHT
H3K4me1
H3K4me3
RBM19
RBM19
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TBX5
TBX5
TBX5
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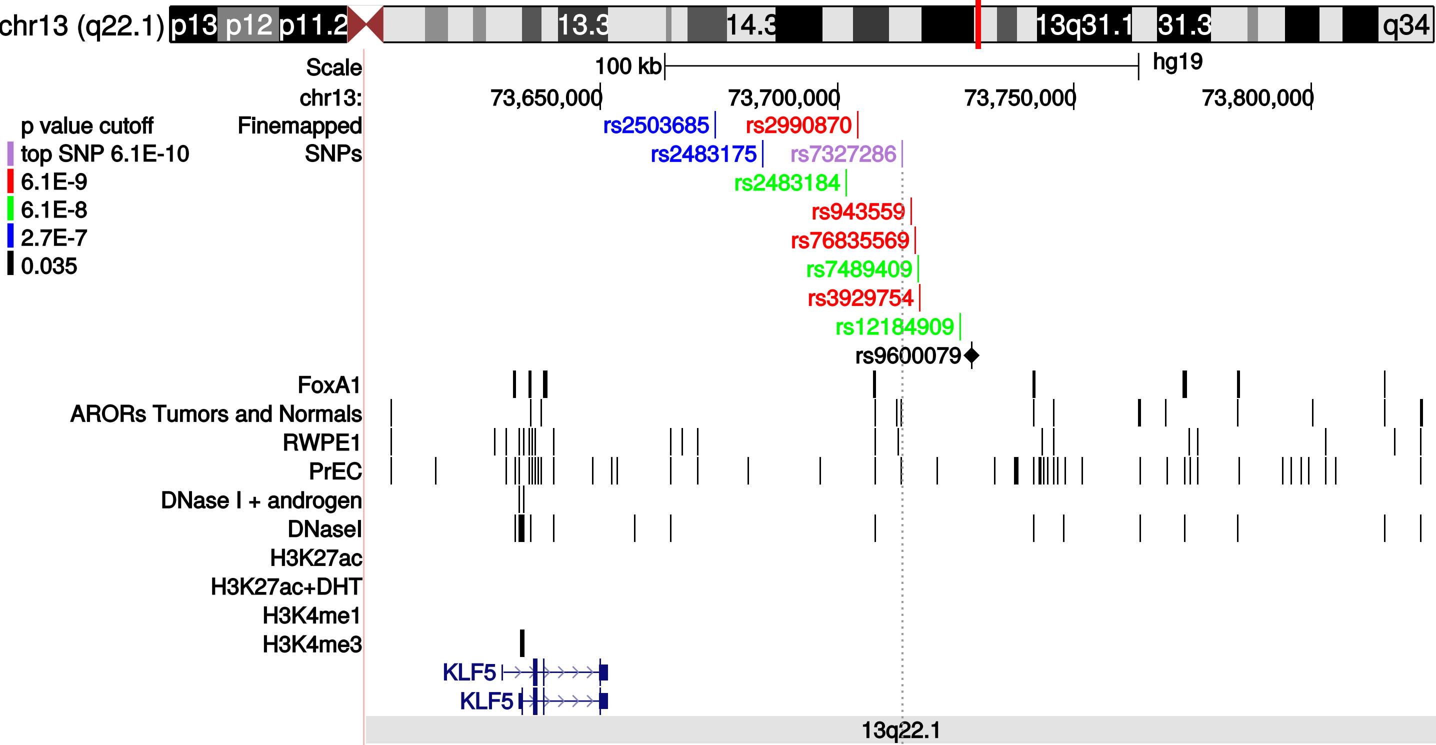
12q24.21


chr13 (q22.1)
p13
p12
p11.2
13.3
14.3
13q31.1
31.3
q34
Scale
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hg19
chr13:
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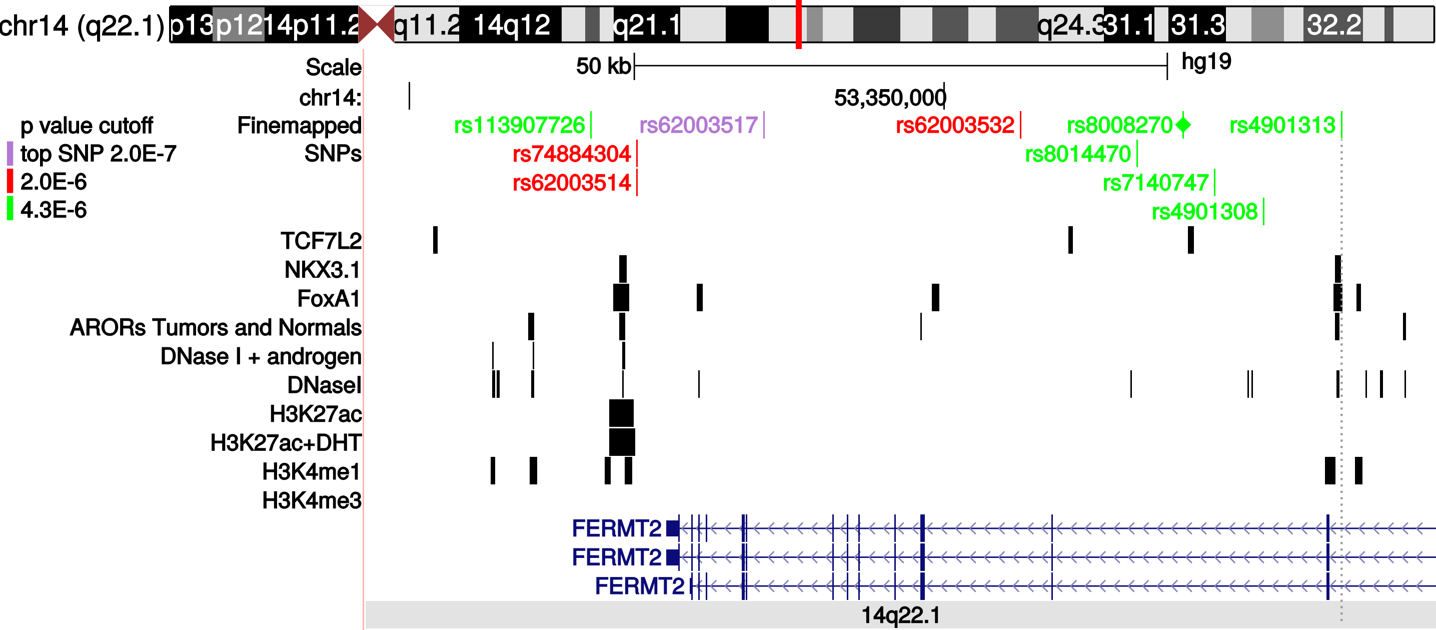
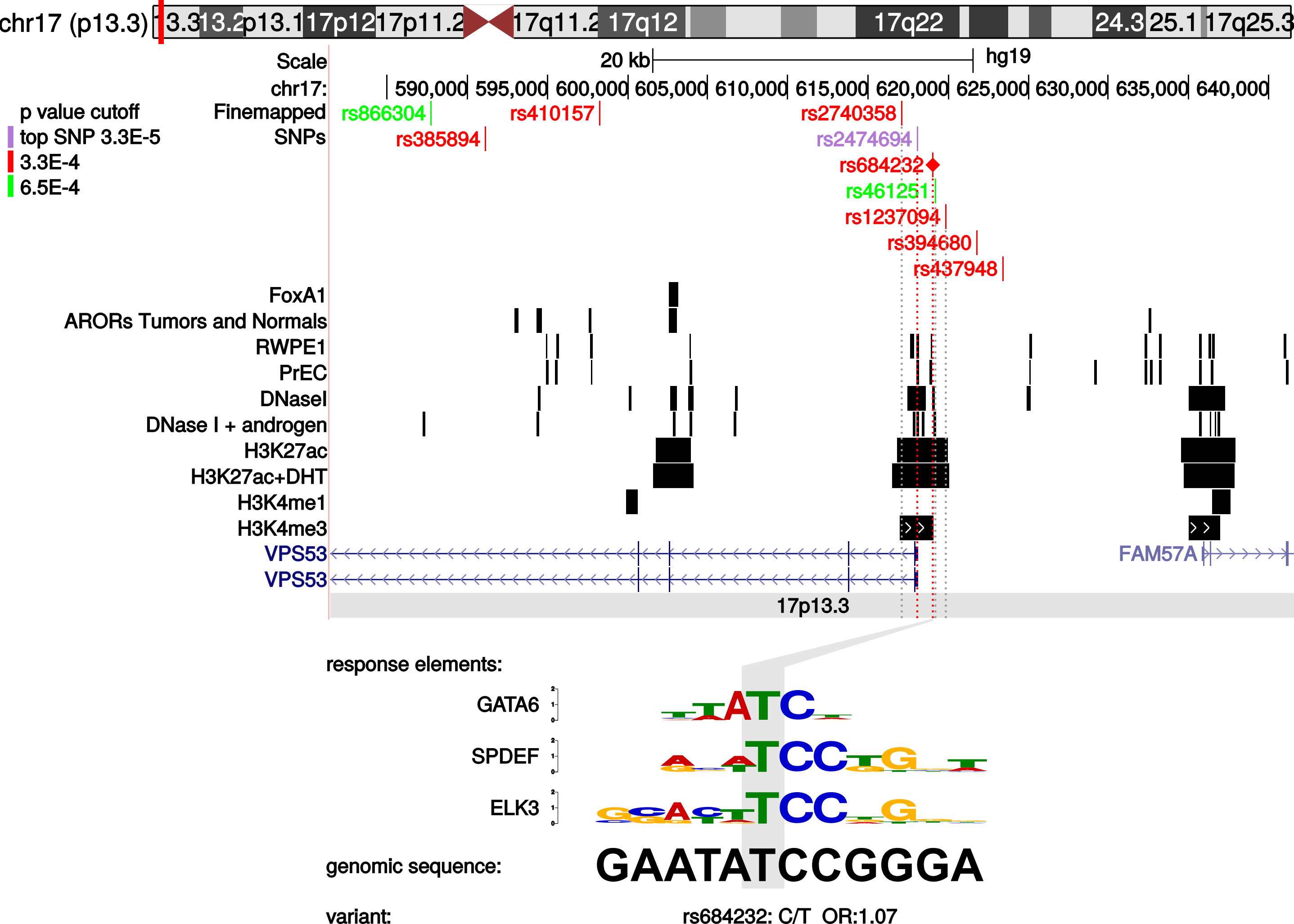
73,700,000
73,750,000
73,800,000
p value cutoff
top SNP 6.1E-10
6.1E-9
6.1E-8
2.7E-7
0.035
Finemapped SNPs
rs2503685
rs2990870
rs2483175
rs7327286
rs2483184
rs943559
rs76835569
rs7489409
rs3929754
rs12184909
rs9600079
FoxA1
ARORs Tumors and Normals
RWPE1
PrEC
DNase I + androgen
DNaseI
H3K27ac
H3K27ac+DHT
H3K4me1
H3K4me3
KLF5
KLF5
13q22.1


chr14 (q22.1)
p13
p12
14p11.2
q11.2
14q12
q21.1
q24.3
31.1
31.3
32.2
Scale
50 kb
hg19
chr14:
53,350,000
p value cutoff
top SNP 2.0E-7
2.0E-6
4.3E-6
Finemapped
SNPs
rs113907726
rs62003517
rs62003532
rs8008270
rs4901313
rs74884304
rs8014470
rs62003514
rs7140747
rs4901308
TCF7L2
NKX3.1
FoxA1
ARORs Tumors and Normals
DNase I + androgen
DNaseI
H3K27ac
H3K27ac+DHT
H3K4me1
H3K4me3
FERMT2
FERMT2
FERMT2
14q22.1


chr17 (p13.3)
13.3 13.2 p13.1 17p12 17p11.2 17q11.2 17q12 17q22 24.3 25.1 17q25.3
Scale
20 kb
hg19
chr17:
590,000 595,000 600,000 605,000 610,000 615,000 620,000 625,000 630,000 635,000 640,000
p value cutoff
top SNP 3.3E-5
3.3E-4
6.5E-4
Finemapped SNPs
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rs410157
rs2740358
rs385894
rs2474694
rs684232
rs461251
rs1237094
rs394680
rs437948
FoxA1
ARORs Tumors and Normals
RWPE1
PrEC
DNaseI
DNase I + androgen
H3K27ac
H3K27ac+DHT
H3K4me1
H3K4me3
VPS53
VPS53
FAM57A
17p13.3
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SPDEF
ELK3
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1
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genomic sequence:
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variant:
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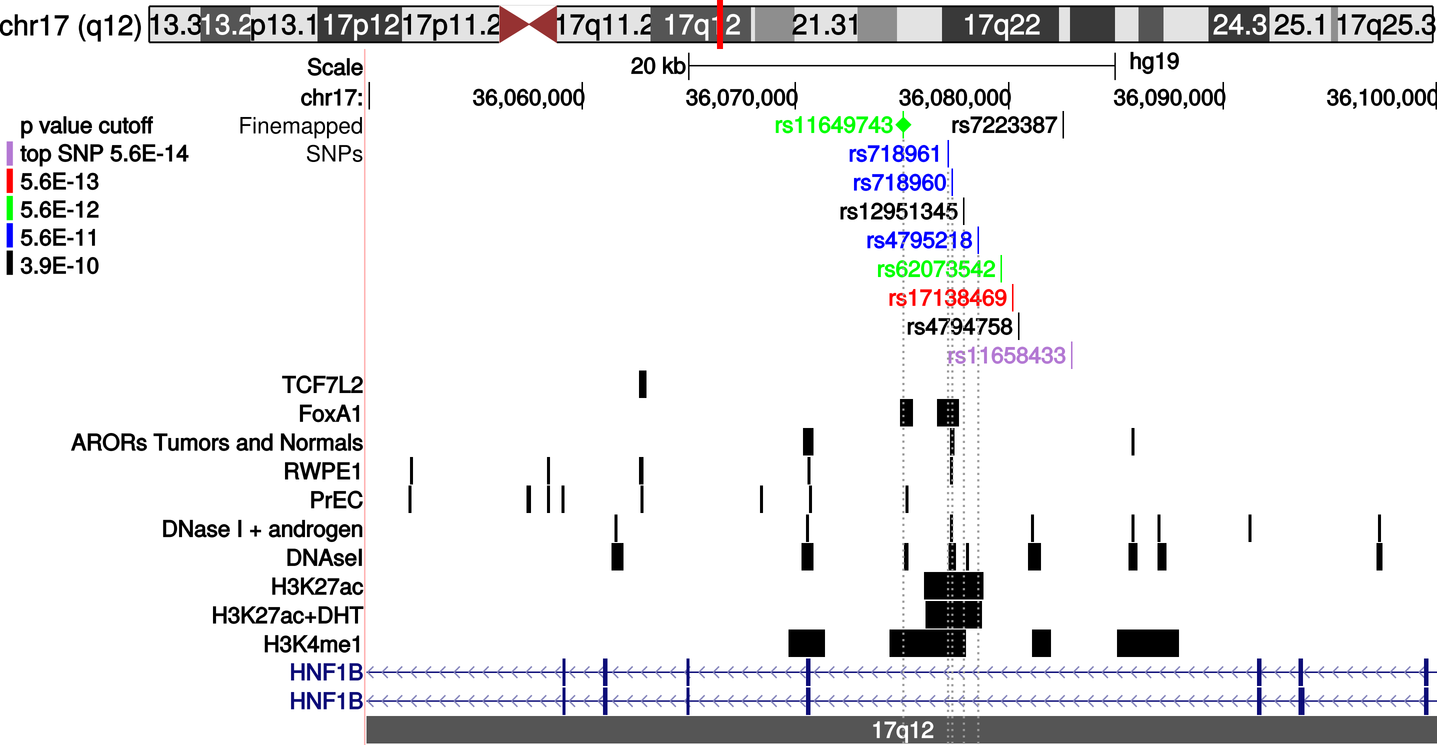
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17p12
17p11.2
17q11.2
17q12
21.31
17q22
24.3
25.1
17q25.3
Scale
20 kb
hg19
chr17:
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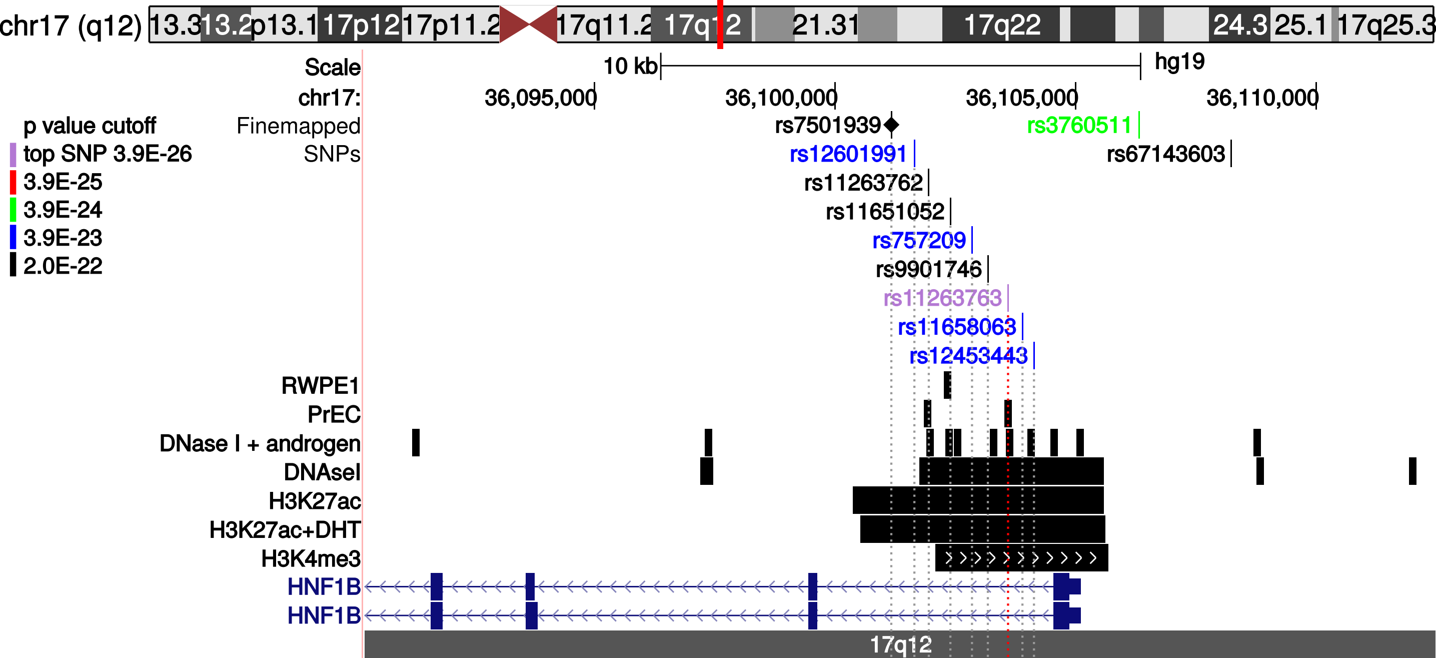
36,090,000
36,100,000
p value cutoff
top SNP 5.6E-14
5.6E-13
5.6E-12
5.6E-11
3.9E-10
Finemapped
SNPs
rs11649743
rs7223387
rs718961
rs718960
rs12951345
rs4795218
rs62073542
rs17138469
rs4794758
rs11658433
TCF7L2
FoxA1
ARORs Tumors and Normals
RWPE1
PrEC
DNase I + androgen
DNAseI
H3K27ac
H3K27ac+DHT
H3K4me1
HNF1B
HNF1B
17q12


chr17 (q12)
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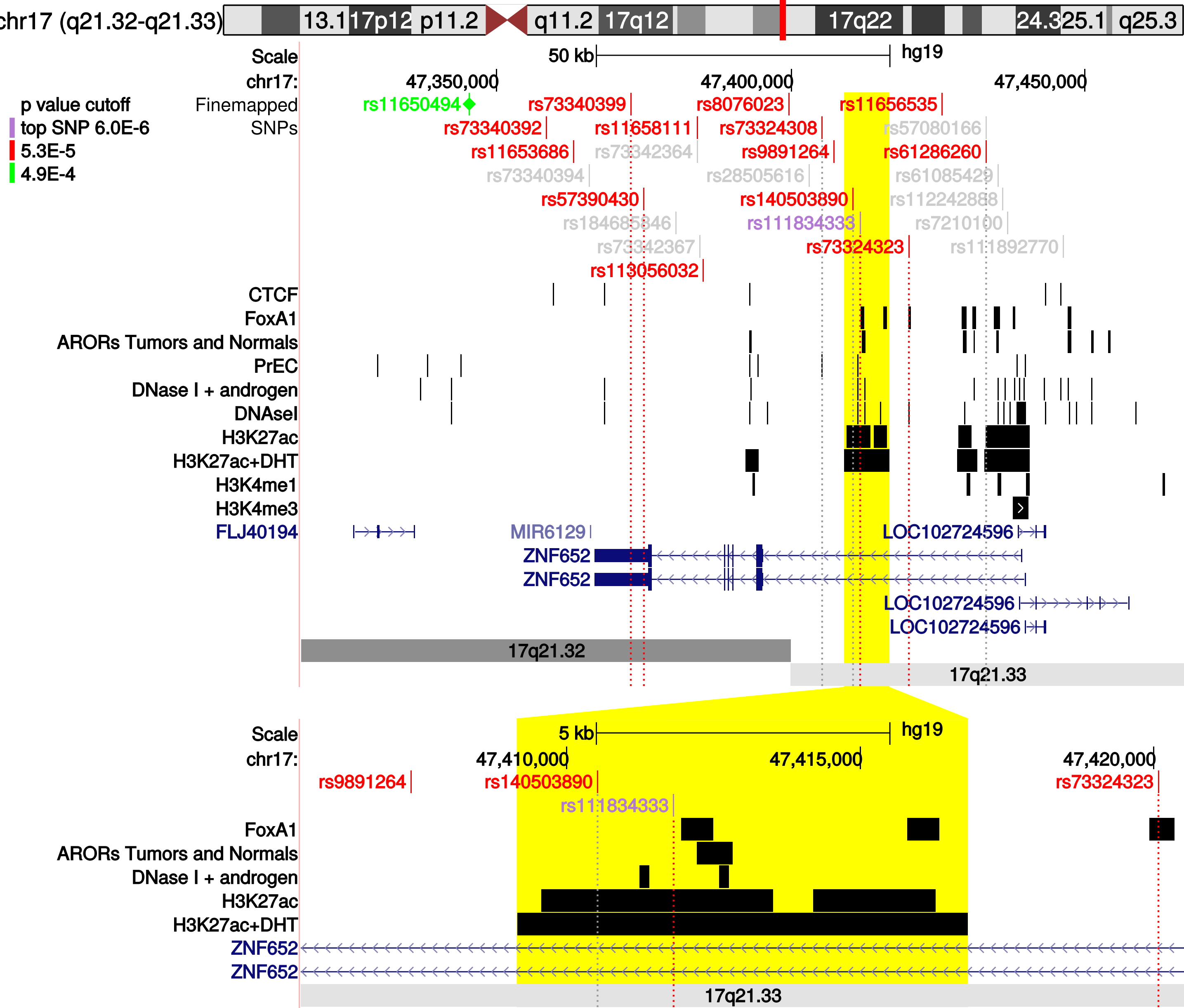
13.2
p13.1
17p12
17p11.2
17q11.2
17q12
21.31
17q22
24.3
25.1
17q25.3
Scale
10 kb
hg19
chr17:
36,095,000
36,100,000
36,105,000
36,110,000
p value cutoff
top SNP 3.9E-26
3.9E-25
3.9E-24
3.9E-23
2.0E-22
Finemapped
SNPs
rs7501939
rs3760511
rs12601991
rs67143603
rs11263762
rs11651052
rs757209
rs9901746
rs11263763
rs11658063
rs12453443
RWPE1
PrEC
DNase I + androgen
DNAseI
H3K27ac
H3K27ac+DHT
H3K4me3
HNF1B
HNF1B
17q12


chr17 (q21.32-q21.33)
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17p12
p11.2
q11.2
17q12
17q22
24.3
25.1
q25.3
Scale
50 kb
hg19
chr17:
47,350,000
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p value cutoff
top SNP 6.0E-6
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4.9E-4
Finemapped SNPs
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rs73340399
rs8076023
rs11656535
rs73340392
rs11658111
rs73324308
rs57080166
rs11653686
rs73342364
rs9891264
rs61286260
rs73340394
rs28505616
rs61085429
rs57390430
rs140503890
rs112242888
rs184685846
rs111834333
rs7210100
rs73342367
rs73324323
rs111892770
rs113056032
CTCF
FoxA1
ARORs Tumors and Normals
PrEC
DNase I + androgen
DNaseI
H3K27ac
H3K27ac+DHT
H3K4me1
H3K4me3
FLJ40194
MIR6129
LOC102724596
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LOC102724596
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Scale
5 kb
hg19
chr17:
47,410,000
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rs9891264
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rs73324323
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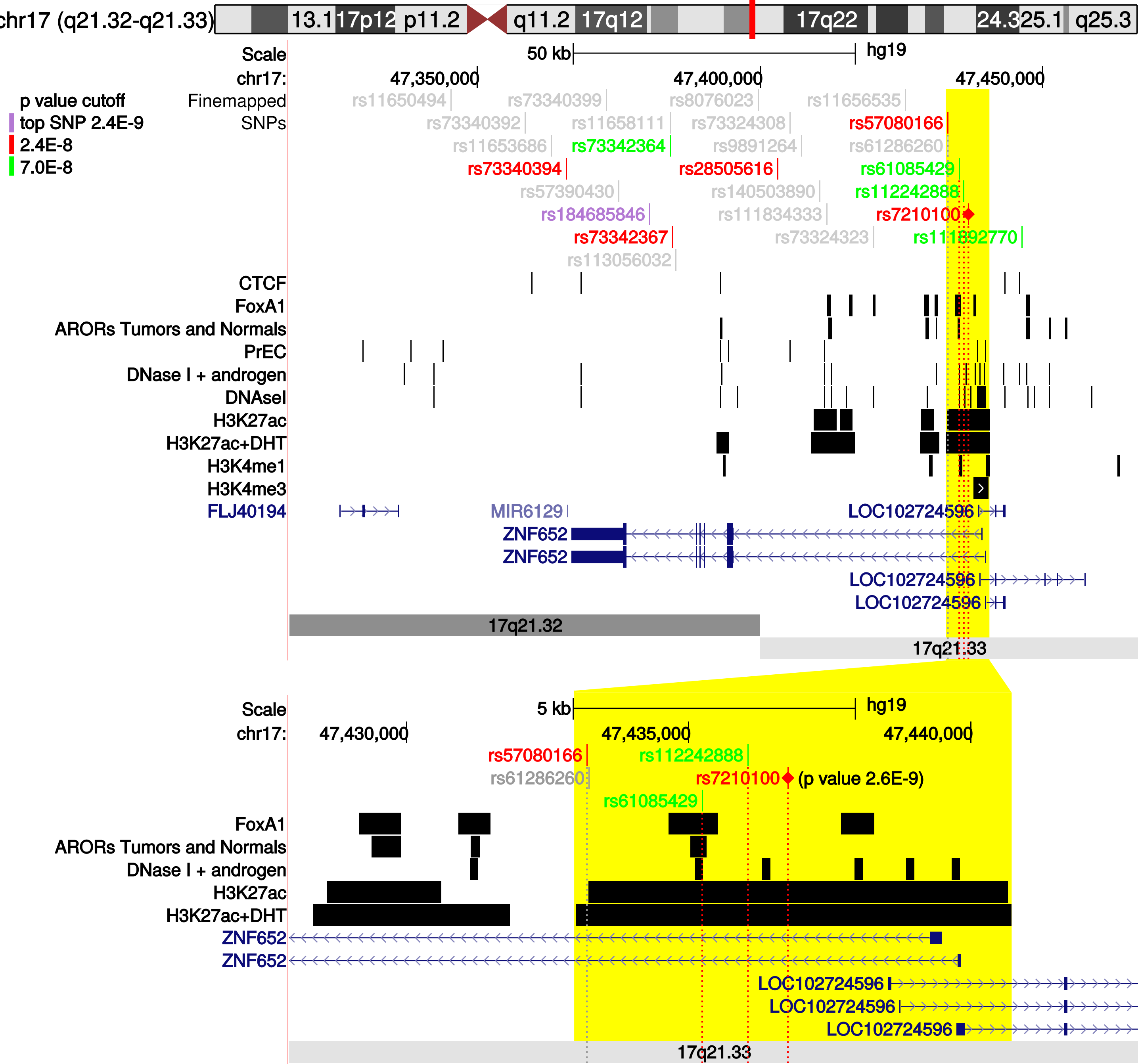
FoxA1
ARORs Tumors and Normals
DNase I + androgen
H3K27ac
H3K27ac+DHT
ZNF652
ZNF652
17q21.33


chr17 (q21.32-q21.33)
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17p12
p11.2
q11.2
17q12
17q22
24.3
25.1
q25.3
Scale
50 kb
hg19
chr17:
47,350,000
47,400,000
47,450,000
p value cutoff
top SNP 2.4E-9
2.4E-8
7.0E-8
Finemapped SNPs
rs11650494
rs73340399
rs8076023
rs11656535
rs73340392
rs11658111
rs73324308
rs57080166
rs11653686
rs73342364
rs9891264
rs61286260
rs73340394
rs28505616
rs61085429
rs57390430
rs140503890
rs112242888
rs184685846
rs111834333
rs7210100
rs73342367
rs73324323
rs111892770
rs113056032
CTCF
FoxA1
ARORs Tumors and Normals
PrEC
DNase I + androgen
DNAseI
H3K27ac
H3K27ac+DHT
H3K4me1
H3K4me3
FLJ40194
MIR6129
LOC102724596
ZNF652
ZNF652
LOC102724596
LOC102724596
17q21.32
17q21.33
Scale
5 kb
hg19
chr17:
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47,440,000
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rs112242888
rs61286260
rs7210100
(p value 2.6E-9)
rs61085429
FoxA1
ARORs Tumors and Normals
DNase I + androgen
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H3K27ac+DHT
ZNF652
ZNF652
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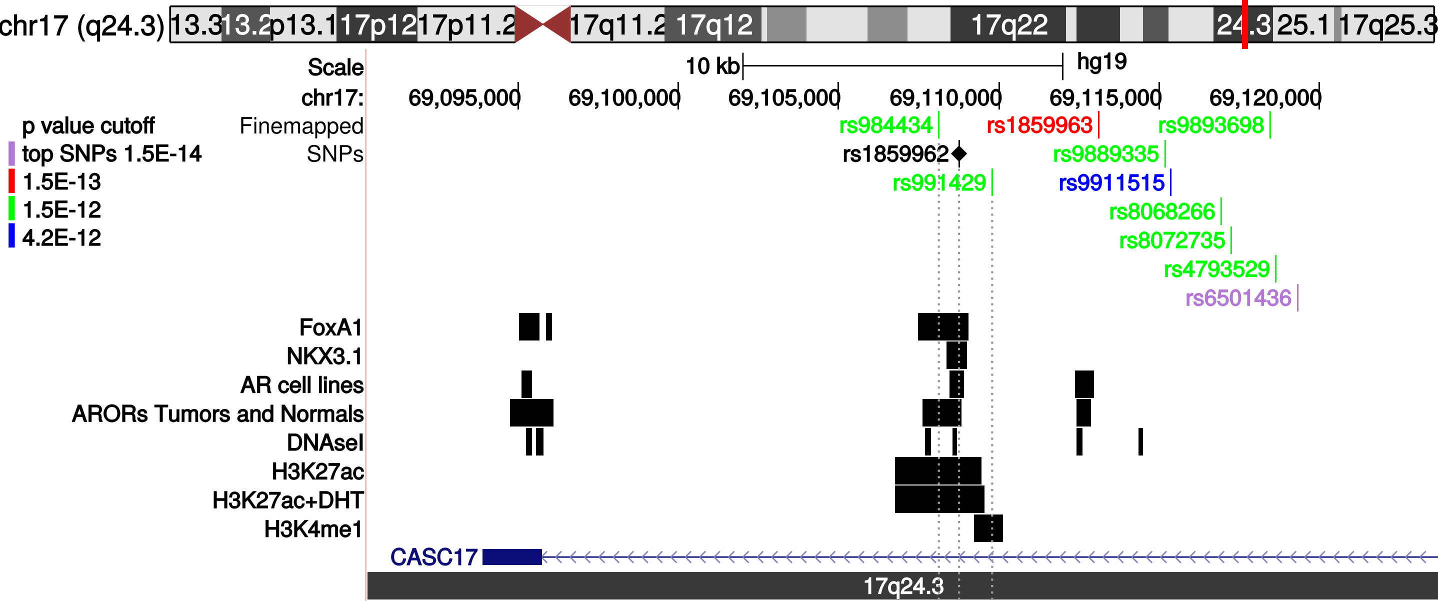
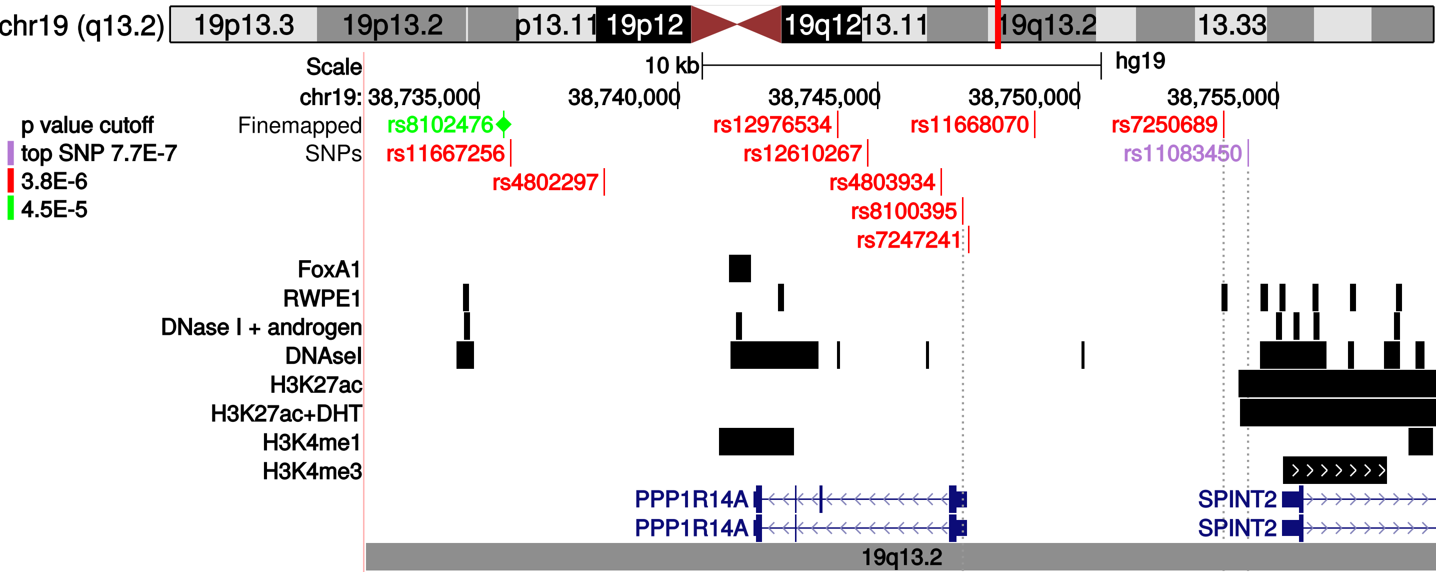
17q21.33


chr17 (q24.3)
13.3
13.2
p13.1
17p12
17p11.2
17q11.2
17q12
17q22
24.3
25.1
17q25.3
Scale
10 kb
hg19
chr17:
69,095,000
69,100,000
69,105,000
69,110,000
69,115,000
69,120,000
p value cutoff
top SNPs 1.5E-14
1.5E-13
1.5E-12
4.2E-12
Finemapped SNPs
rs984434
rs1859963
rs9893698
rs1859962
rs9889335
rs991429
rs9911515
rs8068266
rs8072735
rs4793529
rs6501436
FoxA1
NKX3.1
AR cell lines
ARORs Tumors and Normals
DNAseI
H3K27ac
H3K27ac+DHT
H3K4me1
CASC17
17q24.3


chr19 (q13.2)
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19p13.2
p13.11
19p12
19q12
13.11
19q13.2
13.33
Scale
10 kb
hg19
chr19:
38,735,000
38,740,000
38,745,000
38,750,000
38,755,000
p value cutoff
top SNP 7.7E-7
3.8E-6
4.5E-5
Finemapped
SNPs
rs8102476
rs12976534
rs11668070
rs7250689
rs11667256
rs12610267
rs11083450
rs4802297
rs4803934
rs8100395
rs7247241
FoxA1
RWPE1
DNase I + androgen
DNAseI
H3K27ac
H3K27ac+DHT
H3K4me1
H3K4me3
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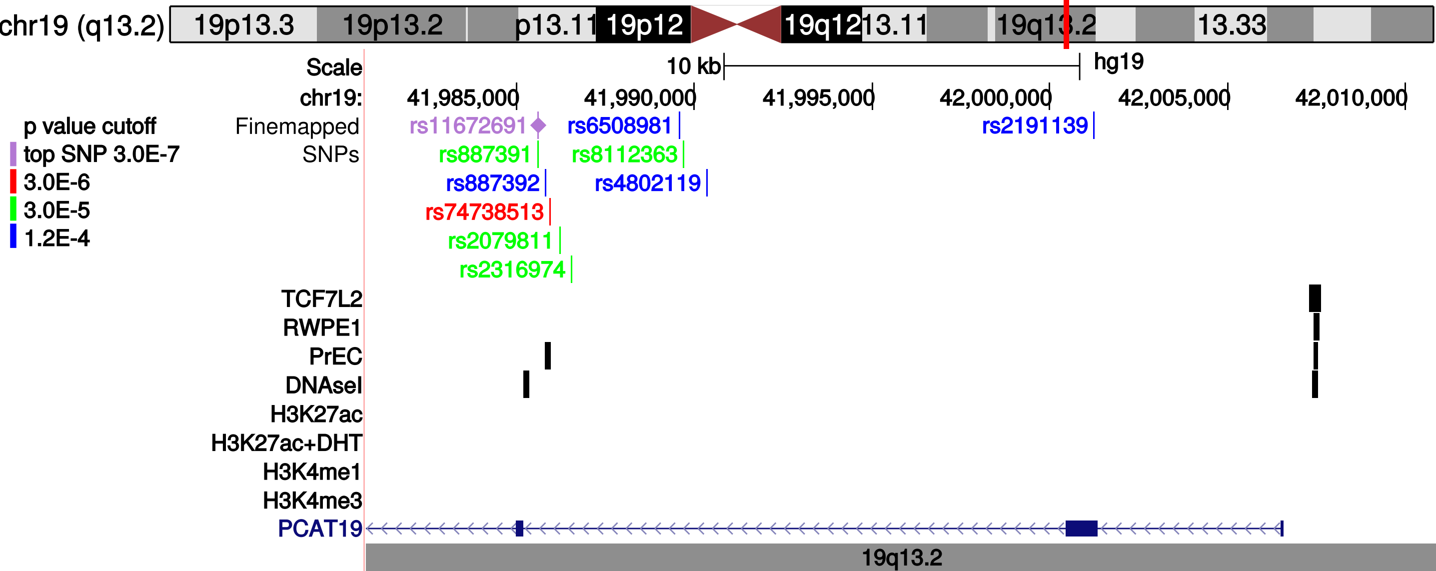
SPINT2
19q13.2


chr19 (q13.2)
19p13.3
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p13.11
19p12
19q12
13.11
19q13.2
13.33
Scale
10 kb
hg19
chr19:
41,985,000
41,990,000
41,995,000
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42,010,000
p value cutoff
top SNP 3.0E-7
3.0E-6
3.0E-5
1.2E-4
Finemapped SNPs
rs11672691
rs6508981
rs2191139
rs887391
rs8112363
rs887392
rs4802119
rs74738513
rs2079811
rs2316974
TCF7L2
RWPE1
PrEC
DNAseI
H3K27ac
H3K27ac+DHT
H3K4me1
H3K4me3
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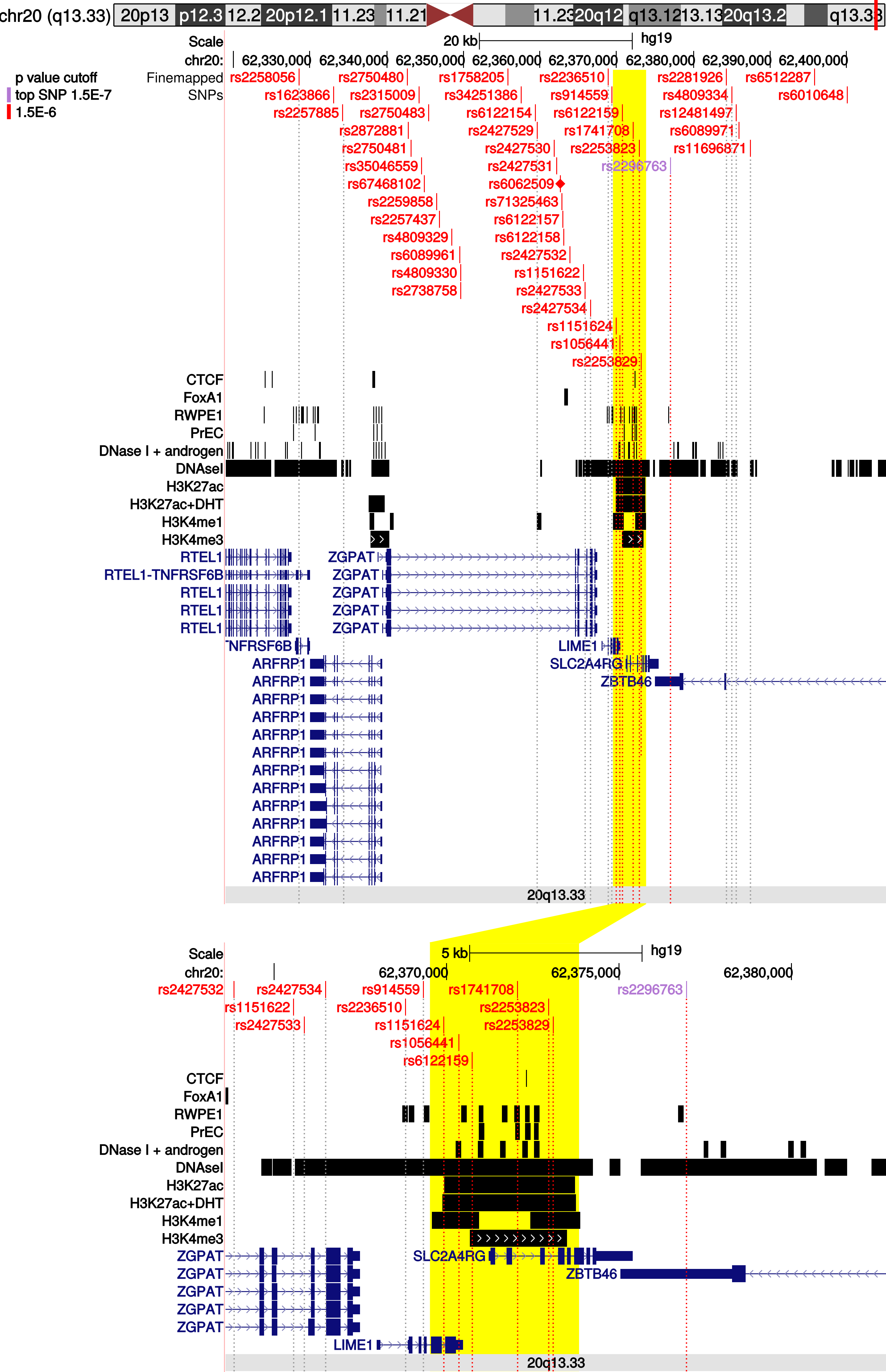
chr20 (q13.33)
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p12.3
12.2
20p12.1
11.23
11.21
11.23
20q12
q13.12
13.13
20q13.2
q13.33
Scale
20 kb
hg19
chr20:
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62,350,000
62,360,000
62,370,000
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62,390,000
62,400,000
p value cutoff
top SNP 1.5E-7
1.5E-6
Finemapped SNPs
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rs2257885
rs2750480
rs2315009
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rs35046559
rs67468102
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rs2257437
rs4809329
rs6089961
rs4809330
rs2738758
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rs34251386
rs6122154
rs2427529
rs2427530
rs2427531
rs6062509
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rs2296763
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rs12481497
rs6089971
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rs6512287
rs6010648
CTCF
FoxA1
RWPE1
PrEC
DNase I + androgen
DNaseI
H3K27ac
H3K27ac+DHT
H3K4me1
H3K4me3
RTEL1
RTEL1-TNFRSF6B
RTEL1
RTEL1
RTEL1
TNFRSF6B
ARFRP1
ZGPAT
ZGPAT
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LIME1
SLC2A4RG
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Scale
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hg19
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rs914559
rs2236510
rs1151624
rs1056441
rs6122159
rs1741708
rs2253823
rs2253829
rs2296763
CTCF
FoxA1
RWPE1
PrEC
DNase I + androgen
DNaseI
H3K27ac
H3K27ac+DHT
H3K4me1
H3K4me3
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ZGPAT
ZGPAT
ZGPAT
ZGPAT
SLC2A4RG
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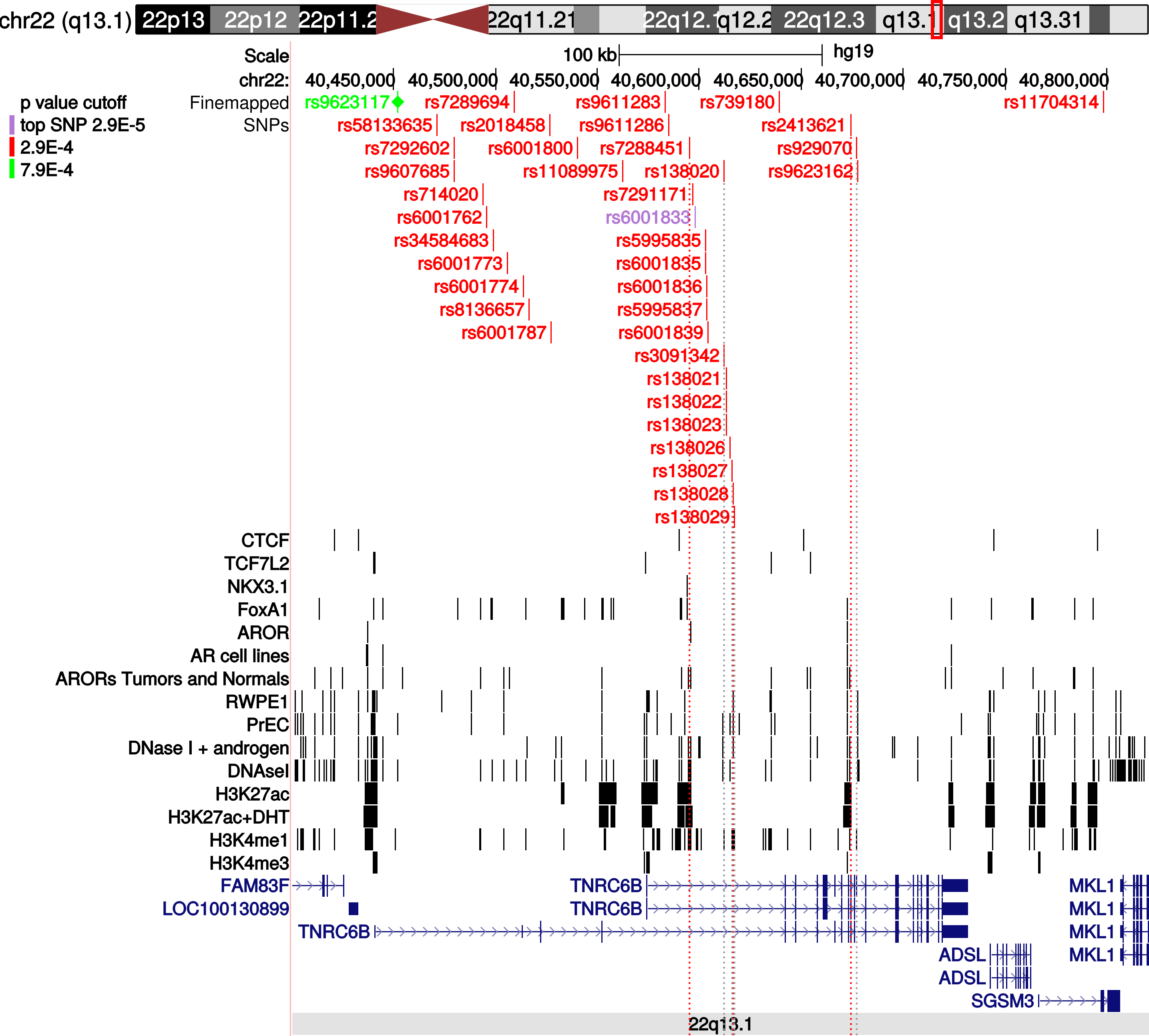
LIME1
20q13.33


chr22 (q13.1)
22p13
22p12
22p11.2
22q11.21
22q12.1
q12.2
22q12.3
q13.1
q13.2
q13.31
Scale
100 kb
hg19
chr22:
40,450,000
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40,700,000
40,750,000
40,800,000
p value cutoff
top SNP 2.9E-5
2.9E-4
7.9E-4
Finemapped SNPs
rs9623117
rs7289694
rs9611283
rs739180
rs11704314
rs58133635
rs2018458
rs9611286
rs2413621
rs7292602
rs6001800
rs7288451
rs929070
rs9607685
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rs7291171
rs6001762
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rs6001836
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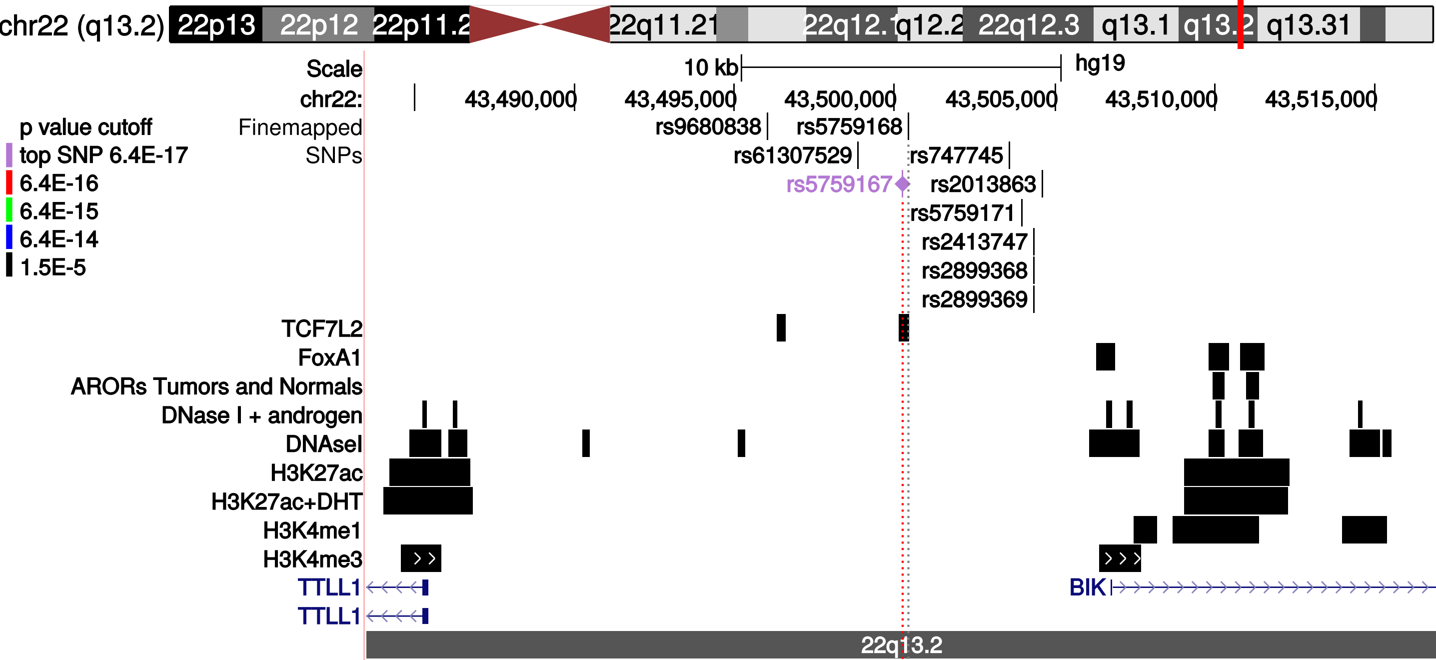
rs138023
rs138026
rs138027
rs138028
rs138029
CTCF
TCF7L2
NKX3.1
FoxA1
AROR
AR cell lines
ARORs Tumors and Normals
RWPE1
PrEC
DNase I + androgen
DNAseI
H3K27ac
H3K27ac+DHT
H3K4me1
H3K4me3
FAM83F
LOC100130899
TNRC6B
TNRC6B
TNRC6B
MKL1
MKL1
MKL1
MKL1
ADSL
ADSL
SGSM3
22q13.1


chr22 (q13.2)
22p13
22p12
22p11.2
22q11.21
22q12.1
q12.2
22q12.3
q13.1
q13.2
q13.31
Scale
10 kb
hg19
chr22:
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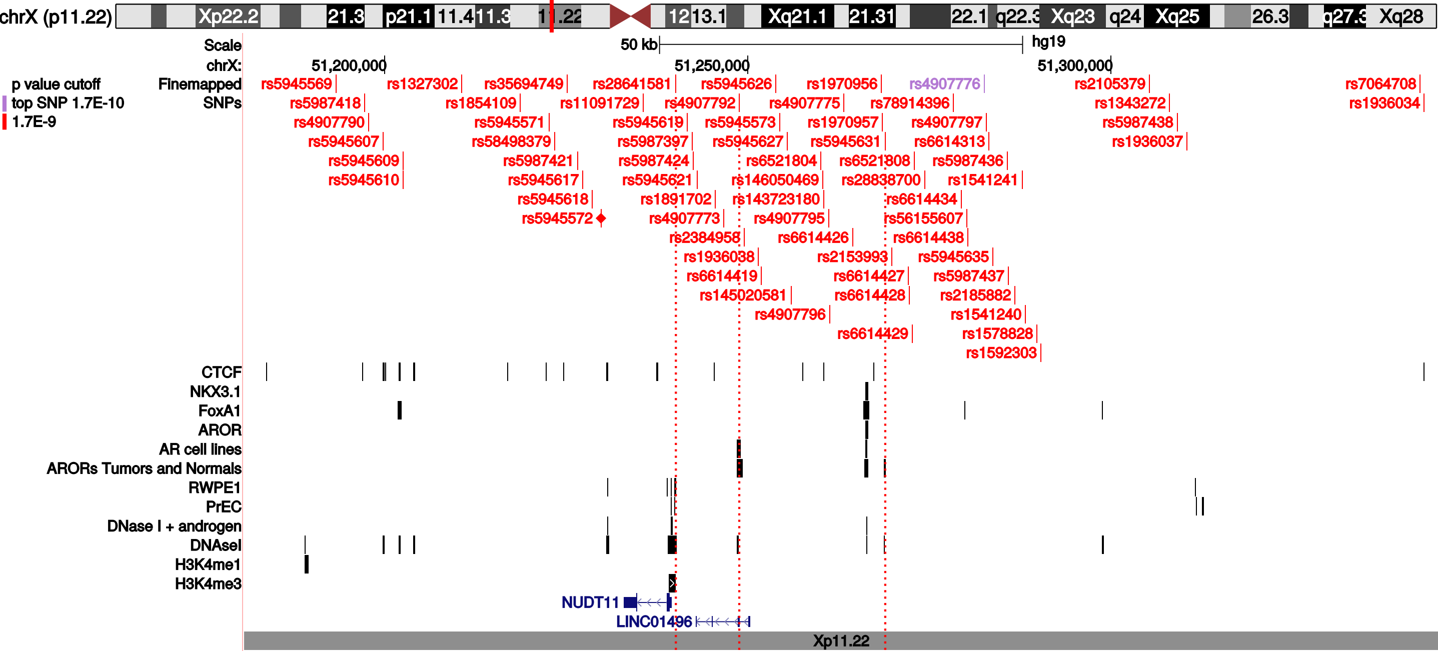
43,495,000
43,500,000
43,505,000
43,510,000
43,515,000
p value cutoff
top SNP 6.4E-17
6.4E-16
6.4E-15
6.4E-14
1.5E-5
Finemapped
SNPs
rs9680838
rs5759168
rs61307529
rs747745
rs5759167
rs2013863
rs5759171
rs2413747
rs2899368
rs2899369
TCF7L2
FoxA1
ARORs Tumors and Normals
DNase I + androgen
DNAseI
H3K27ac
H3K27ac+DHT
H3K4me1
H3K4me3
TTLL1
TTLL1
BIK
22q13.2


chrX (p11.22)
Xp22.2
21.3
p21.1
11.4
11.3
11.22
12
13.1
Xq21.1
21.31
22.1
q22.3
Xq23
q24
Xq25
26.3
q27.3
Xq28
Scale
50 kb
hg19
chrX:
51,200,000
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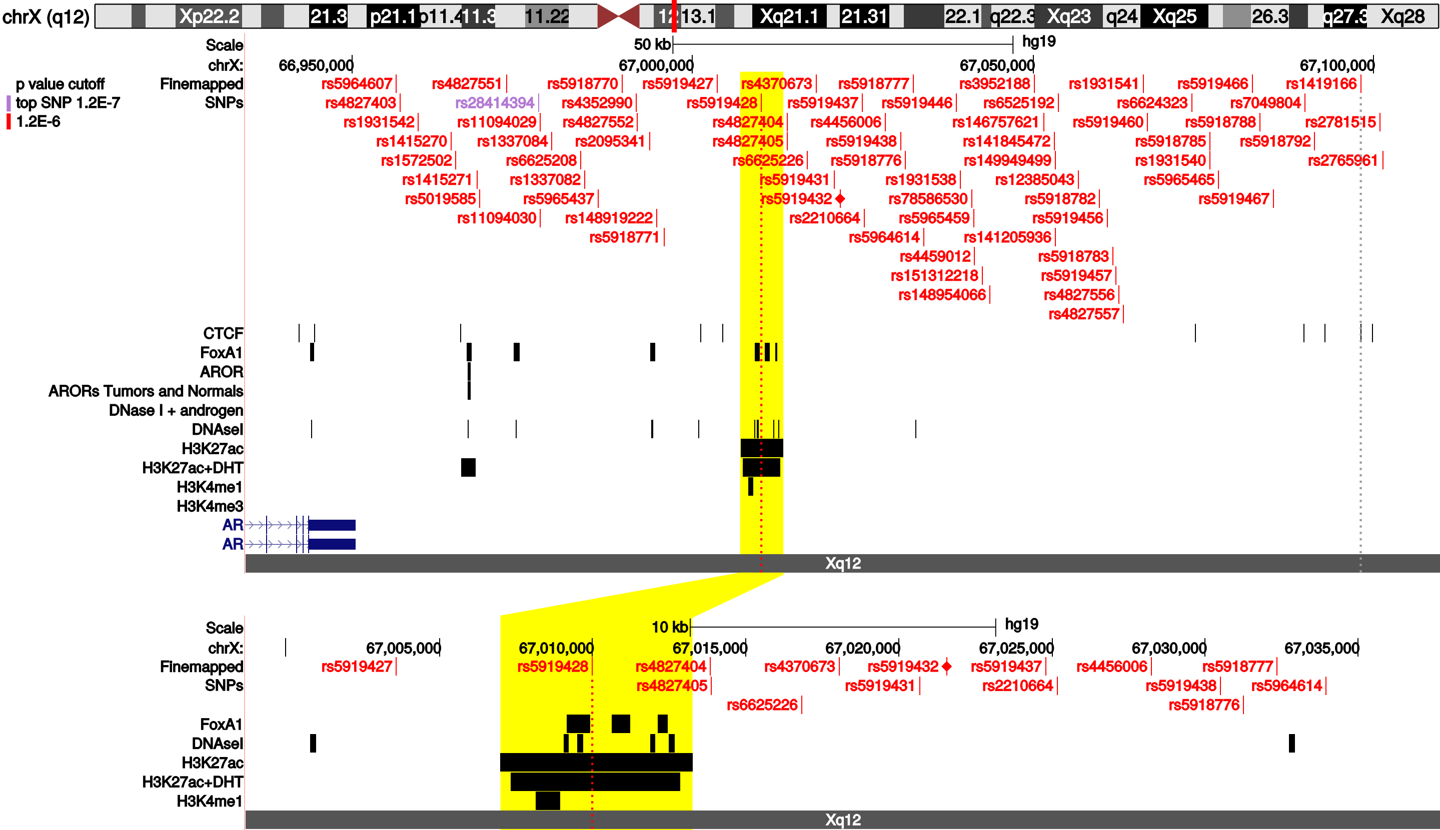
top SNP 1.7E-10
1.7E-9
Finemapped SNPs
rs5945569
rs1327302
rs35694749
rs28641581
rs5945626
rs1970956
rs4907776
rs2105379
rs7064708
rs5987418
rs1854109
rs11091729
rs4907792
rs4907775
rs78914396
rs1343272
rs1936034
rs4907790
rs5945571
rs5945619
rs5945573
rs1970957
rs4907797
rs5987438
rs5945607
rs58498379
rs5987397
rs5945627
rs5945631
rs6614313
rs1936037
rs5945609
rs5987421
rs5987424
rs6521804
rs6521808
rs5987436
rs5945610
rs5945617
rs5945621
rs146050469
rs28838700
rs1541241
rs5945618
rs1891702
rs143723180
rs6614434
rs5945572
rs4907773
rs4907795
rs56155607
rs2384958
rs6614426
rs6614438
rs1936038
rs2153993
rs5945635
rs6614419
rs6614427
rs5987437
rs145020581
rs6614428
rs2185882
rs4907796
rs1541240
rs6614429
rs1578828
rs1592303
CTCF
NKX3.1
FoxA1
AROR
AR cell lines
ARORs Tumors and Normals
RWPE1
PrEC
DNase I + androgen
DNAseI
H3K4me1
H3K4me3
NUDT11
LINC01496
Xp11.22


chrX (q12)
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21.3
p21.1
p11.4
11.3
11.22
12
13.1
Xq21.1
21.31
22.1
q22.3
Xq23
q24
Xq25
26.3
q27.3
Xq28
Scale
50 kb
hg19
chrX:
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67,000,000
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p value cutoff
top SNP 1.2E-7
1.2E-6
Finemapped SNPs
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rs4827551
rs5918770
rs5919427
rs4370673
rs5918777
rs3952188
rs1931541
rs5919466
rs1419166
rs4827403
rs28414394
rs4352990
rs5919428
rs5919437
rs5919446
rs6525192
rs6624323
rs7049804
rs1931542
rs11094029
rs4827552
rs4827404
rs4456006
rs146757621
rs5919460
rs5918788
rs2781515
rs1415270
rs1337084
rs2095341
rs4827405
rs5919438
rs141845472
rs5918785
rs5918792
rs1572502
rs6625208
rs6625226
rs5918776
rs149949499
rs1931540
rs2765961
rs1415271
rs1337082
rs5919431
rs1931538
rs12385043
rs5965465
rs5019585
rs5965437
rs5919432
rs78586530
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rs5919456
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rs5964614
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rs4459012
rs5918783
rs151312218
rs5919457
rs148954066
rs4827556
rs4827557
CTCF
FoxA1
AROR
ARORs Tumors and Normals
DNase I + androgen
DNAseI
H3K27ac
H3K27ac+DHT
H3K4me1
H3K4me3
AR
AR
Xq12
Scale
10 kb
hg19
chrX:
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67,010,000
67,015,000
67,020,000
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67,035,000
Finemapped SNPs
rs5919427
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rs4827404
rs4370673
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rs5919437
rs4456006
rs5918777
rs4827405
rs5919431
rs2210664
rs5919438
rs5964614
rs6625226
rs5918776
FoxA1
DNAseI
H3K27ac
H3K27ac+DHT
H3K4me1
Xq12