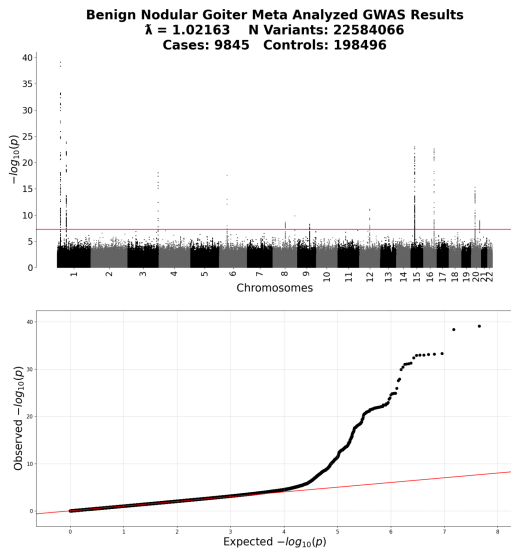


# **Global multi-ancestry genome-wide analyses identify genes and biological pathways associated with thyroid cancer and benign thyroid diseases**

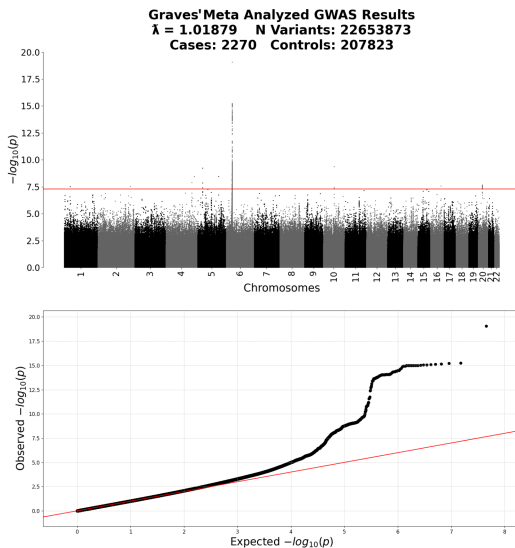
In the format provided by the  
authors and unedited

Supplementary Figure 1. Manhattan and quartile-quartile (QQ) plots for ancestry stratified inverse-variance weighted meta-analysis results. Manhattan plots show the  $-\log_{10}(\text{p-value})$  (y-axis) of each meta-analyzed SNP vs their genomic coordinate (x-axis). Genome wide significance,  $-\log_{10}(5\text{e-}8)$ , is marked by a red horizontal line. QQ plots are displayed in the lower half of the figure.

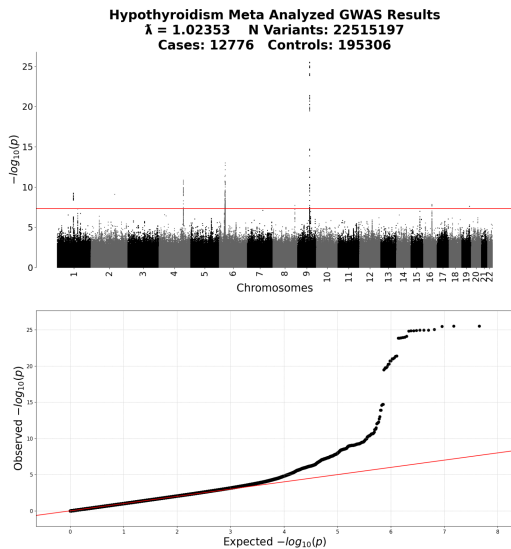




African Ancestry

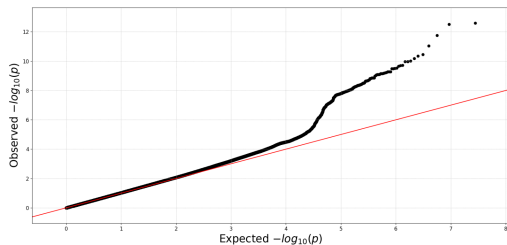
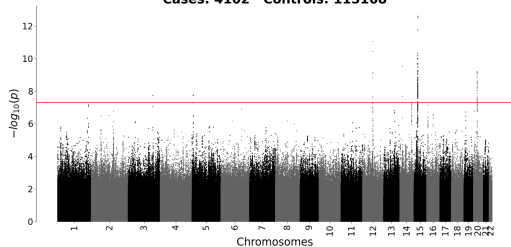


**African Ancestry**

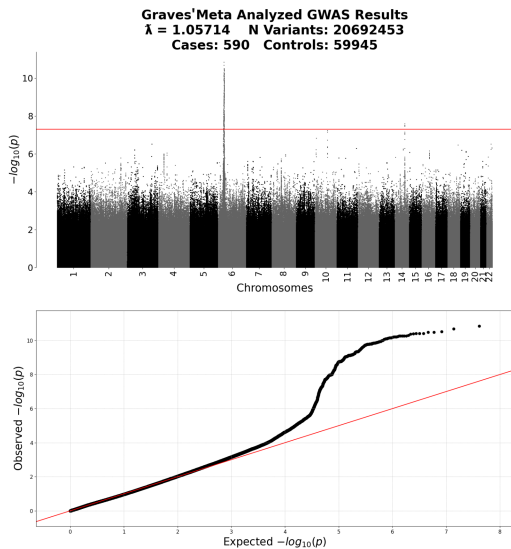


African Ancestry

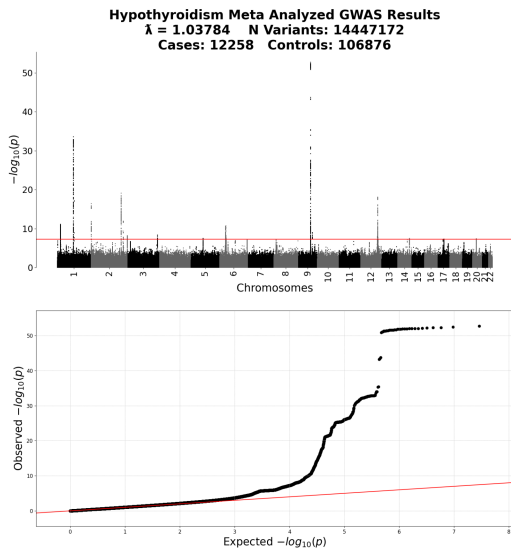
**Benign Nodular Goiter Meta Analyzed GWAS Results**  
 **$\lambda = 1.03784$  N Variants: 13941186**  
**Cases: 4102 Controls: 115168**



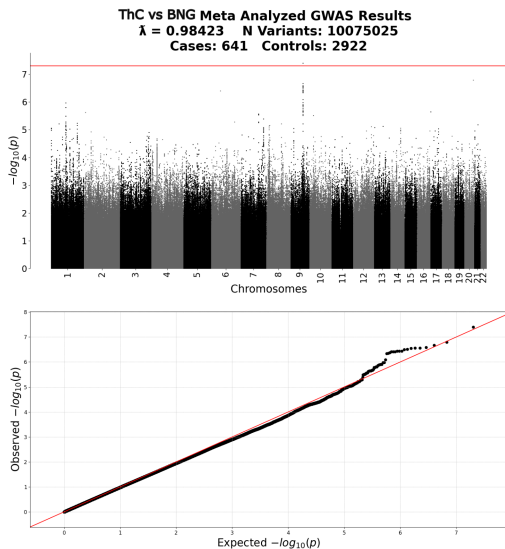
Admixed American Ancestry



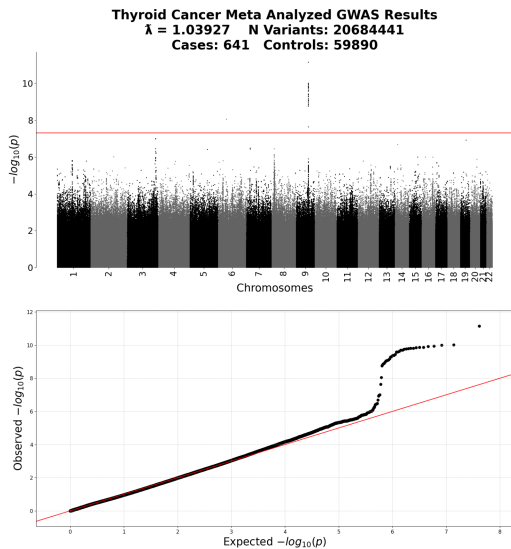
Admixed American Ancestry



Admixed American Ancestry

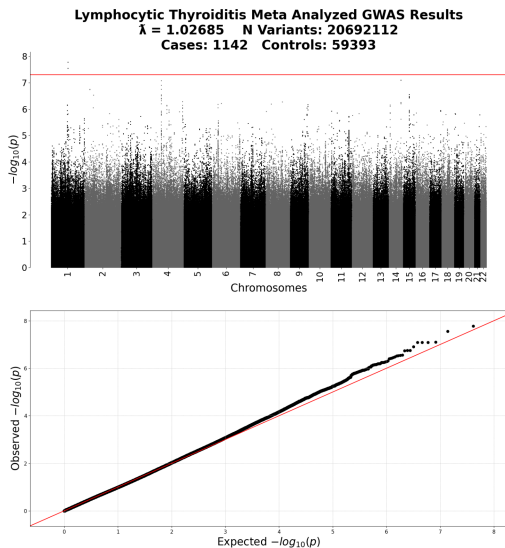


**Admixed American Ancestry**

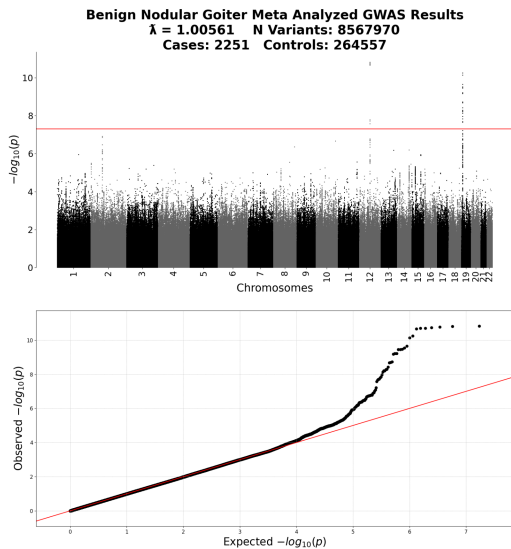


Admixed American Ancestry

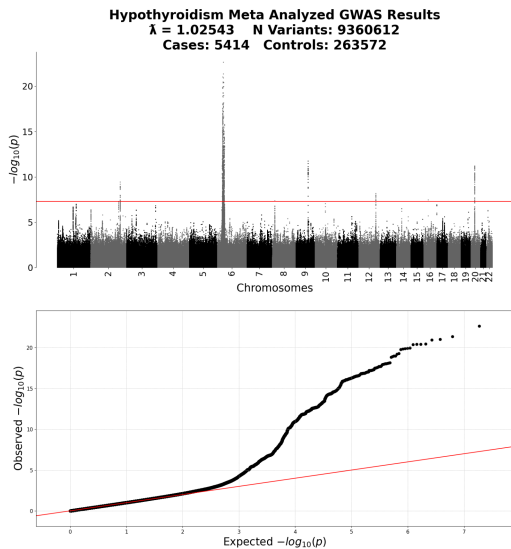




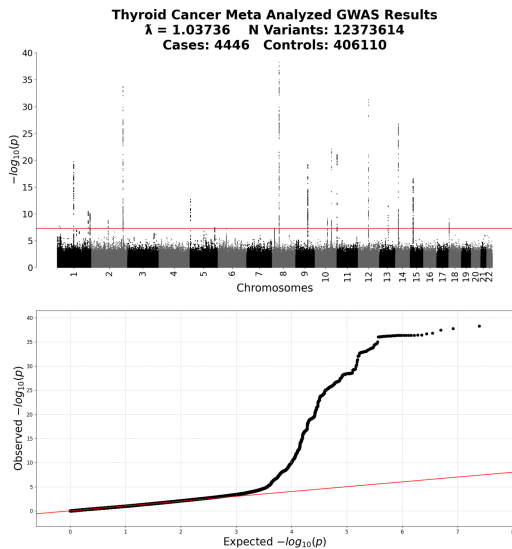
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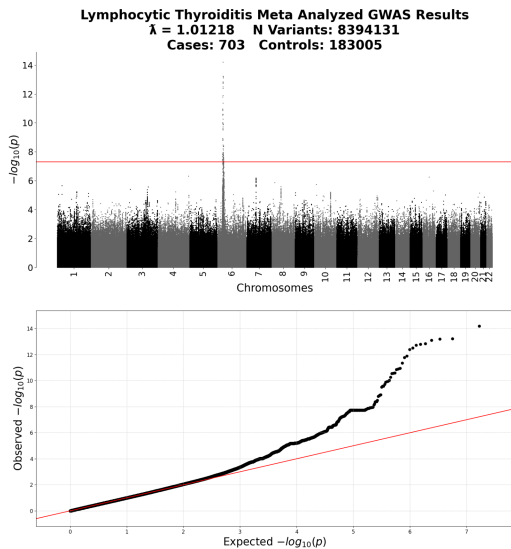
East Asian Ancestry



East Asian Ancestry

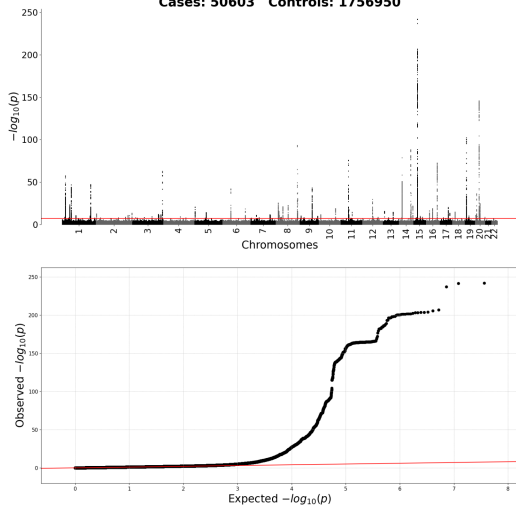


East Asian Ancestry

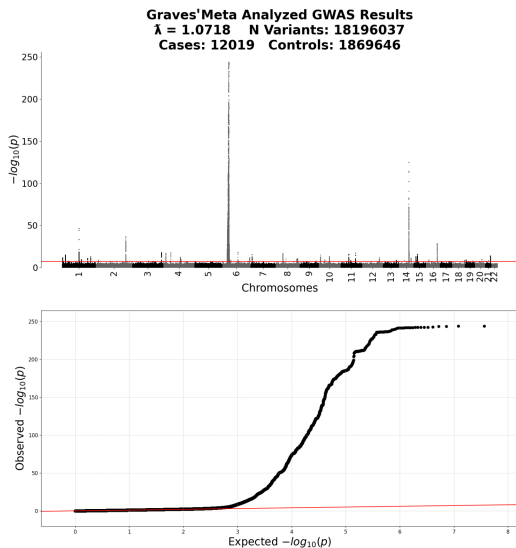


East Asian Ancestry

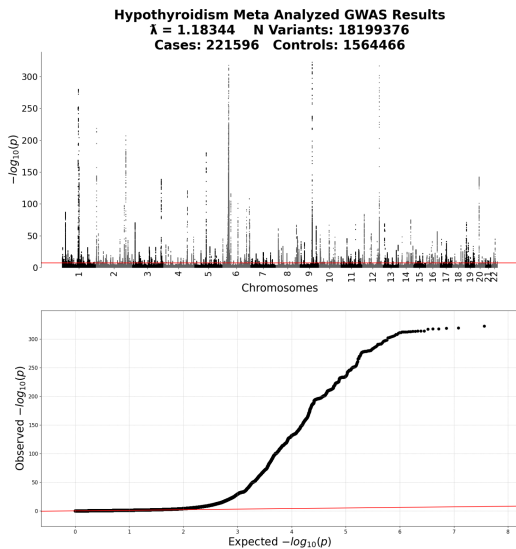
**Benign Nodular Goiter Meta Analyzed GWAS Results**  
 **$\lambda = 1.07672$  N Variants: 18196460**  
**Cases: 50603 Controls: 1756950**



European Ancestry



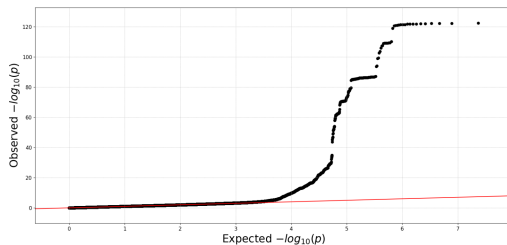
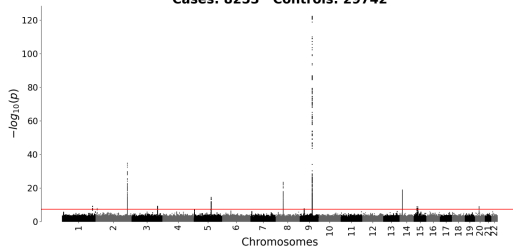
European Ancestry



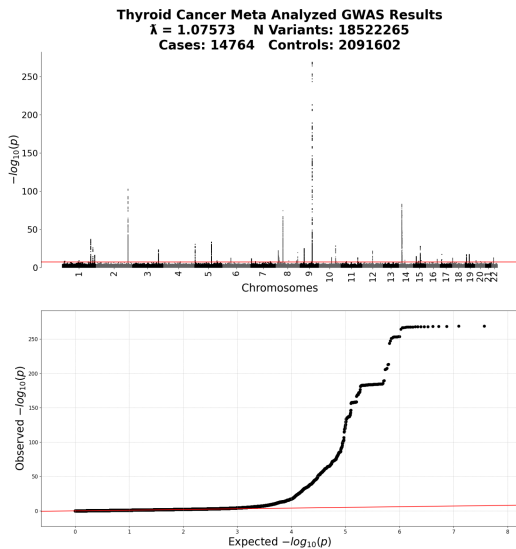
European Ancestry



**ThC vs BNG Meta Analyzed GWAS Results**  
 $\lambda = 0.99953$  N Variants: 11692853  
 Cases: 8253 Controls: 29742

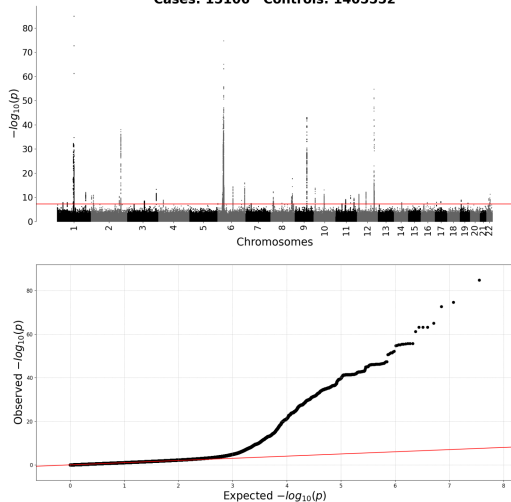


European Ancestry



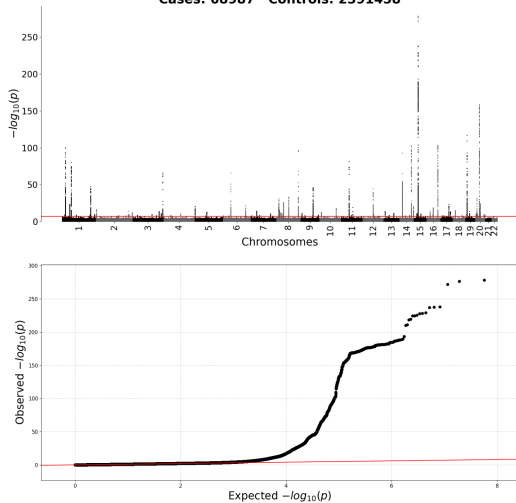
European Ancestry

**Lymphocytic Thyroiditis Meta Analyzed GWAS Results**  
 **$\lambda = 1.07131$  N Variants: 17889297**  
**Cases: 15106 Controls: 1405552**



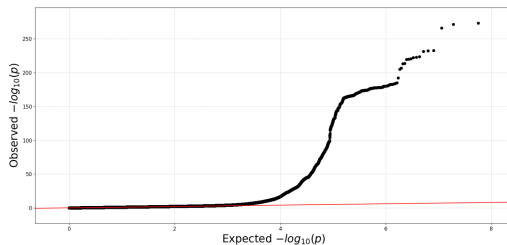
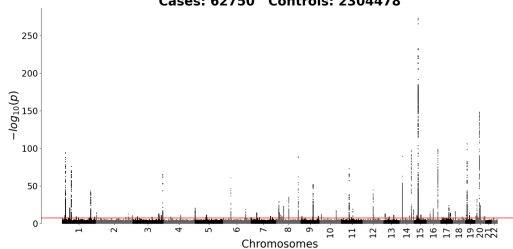
European Ancestry

**Benign Nodular Goiter Meta Analyzed GWAS Results**  
 **$\lambda = 1.04505$  N Variants: 28605347**  
**Cases: 68987 Controls: 2391458**



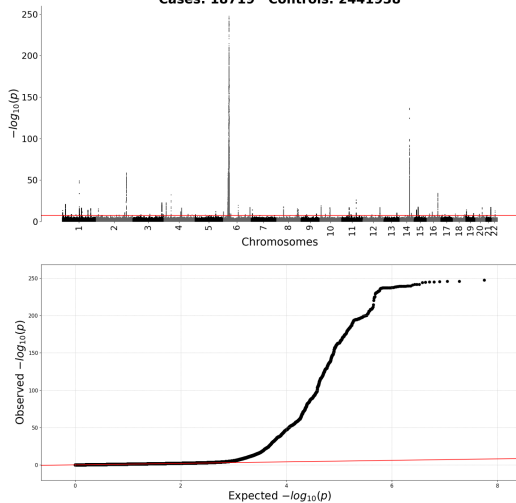
Mixed Ancestry

**Benign Nodular Goiter Meta Analyzed GWAS Results**  
 **$\lambda = 1.04216$  N Variants: 28331338**  
**Cases: 62750 Controls: 2304478**



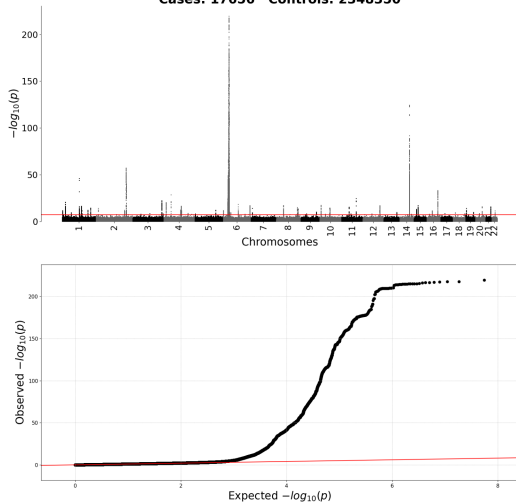
Mixed Ancestry (Leave CCPM Out)

**Graves' Meta Analyzed GWAS Results**  
 **$\lambda = 1.04939$  N Variants: 28162992**  
**Cases: 18719 Controls: 2441938**



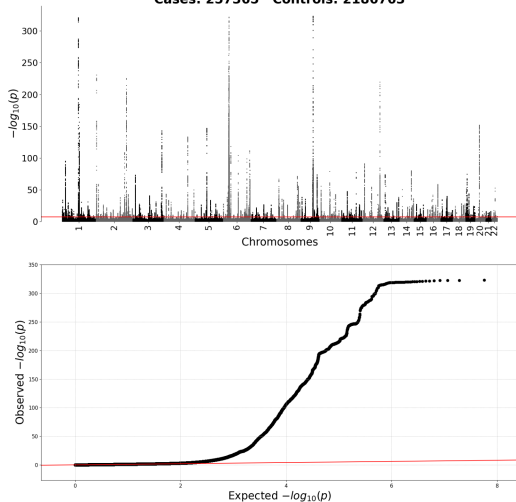
**Mixed Ancestry**

**Graves' Meta Analyzed GWAS Results**  
 **$\lambda = 1.04601$  N Variants: 27795313**  
**Cases: 17656 Controls: 2348350**



**Mixed Ancestry (Leave CCPM Out)**

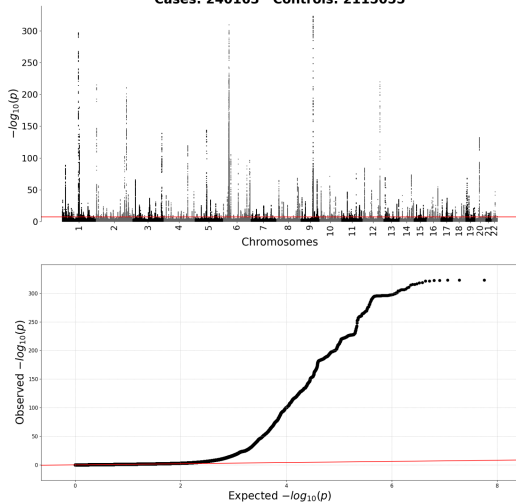
**Hypothyroidism Meta Analyzed GWAS Results**  
 **$\lambda = 1.10608$  N Variants: 28645100**  
**Cases: 257365 Controls: 2186763**



Mixed Ancestry

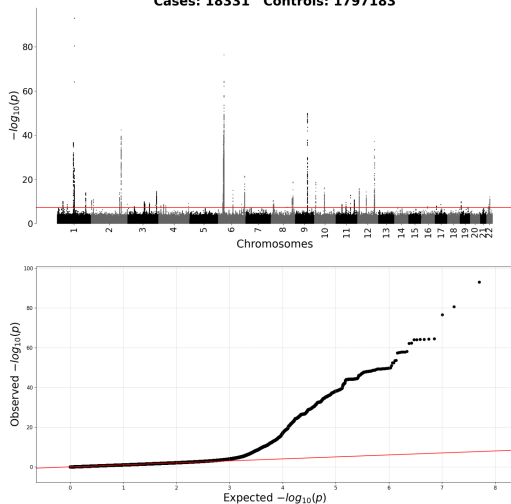


**Hypothyroidism Meta Analyzed GWAS Results**  
 $\lambda = 1.09906$  N Variants: 28379316  
 Cases: 240163 Controls: 2115055



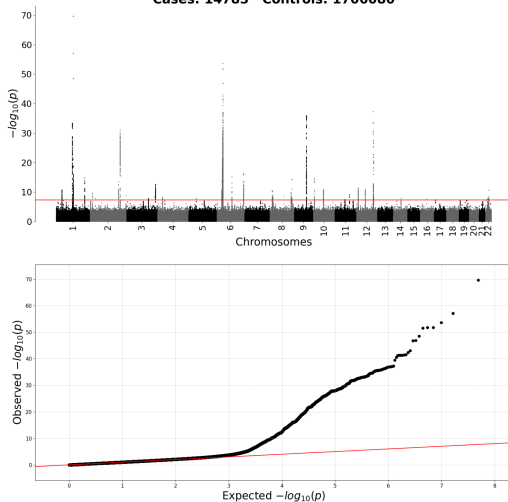
Mixed Ancestry (Leave CCPM Out)

**Lymphocytic Thyroiditis Meta Analyzed GWAS Results**  
 **$\lambda = 1.03401$  N Variants: 25145081**  
**Cases: 18331 Controls: 1797183**



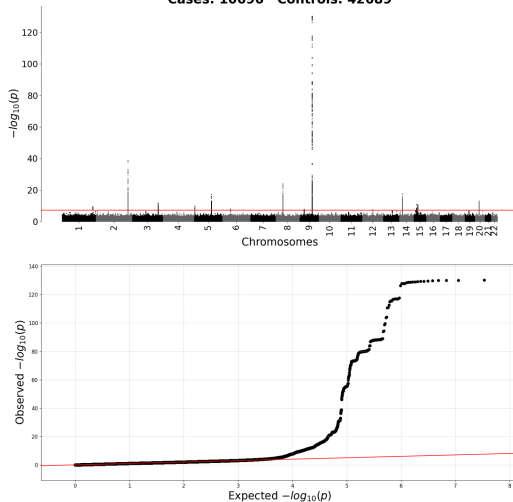
Mixed Ancestry

**Lymphocytic Thyroiditis Meta Analyzed GWAS Results**  
 **$\lambda = 1.03019$  N Variants: 24547600**  
**Cases: 14783 Controls: 1706080**



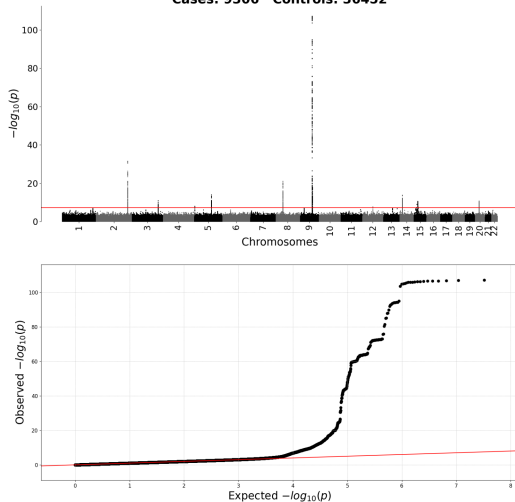
Mixed Ancestry (Leave CCPM Out)

**ThC vs BNG Meta Analyzed GWAS Results**  
 **$\lambda = 1.00093$  N Variants: 17045841**  
**Cases: 10696 Controls: 42689**

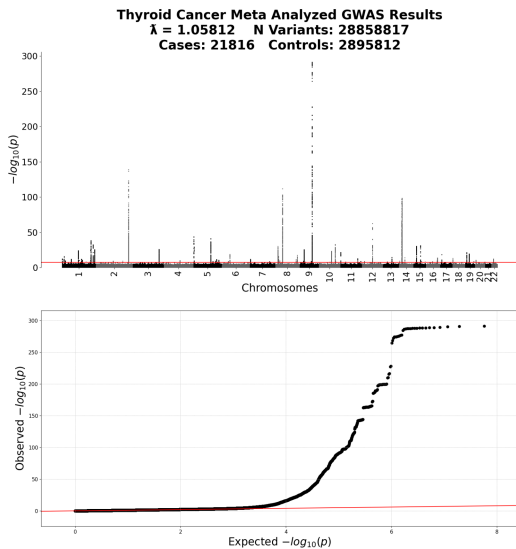


**Mixed Ancestry**

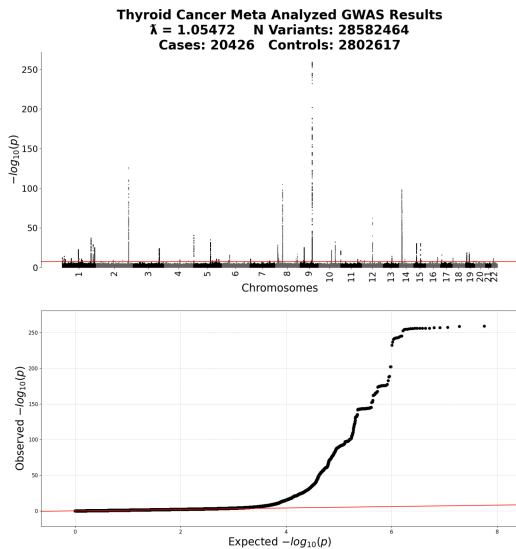
**ThC vs BNG Meta Analyzed GWAS Results**  
 $\lambda = 0.99674$  N Variants: 16341933  
 Cases: 9306 Controls: 36452



Mixed Ancestry (Leave CCPM Out)



Mixed Ancestry

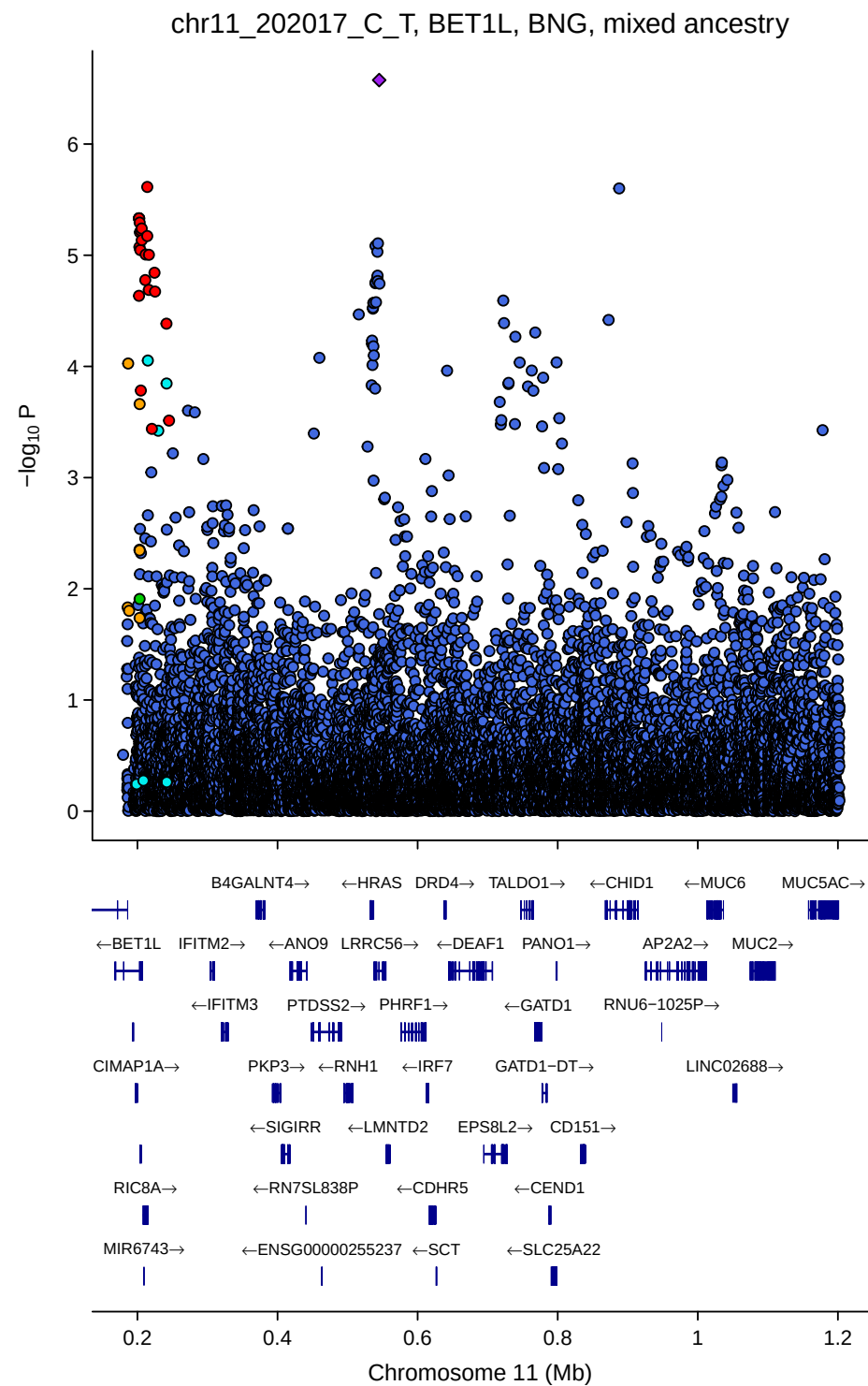
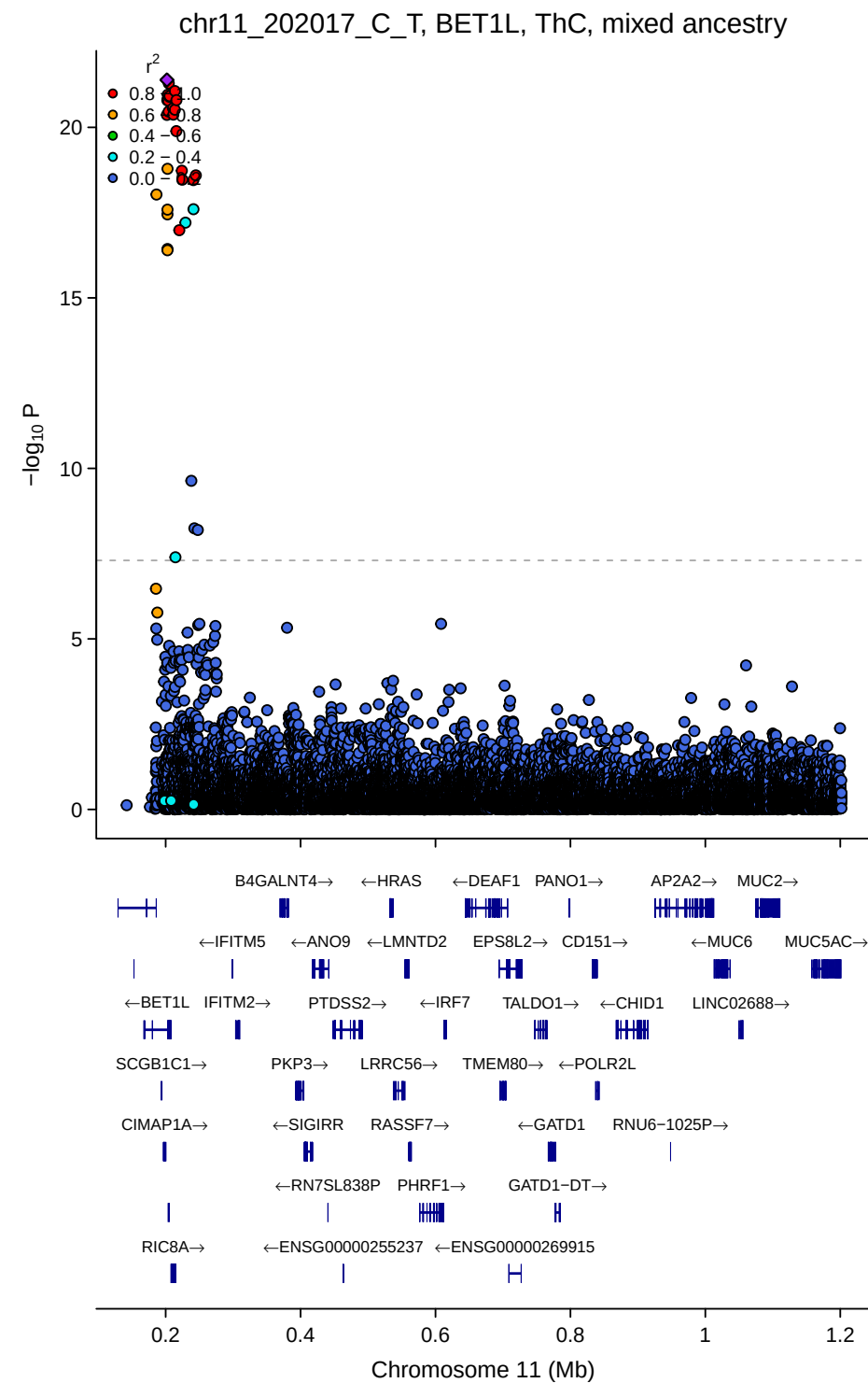


Mixed Ancestry (Leave CCPM Out)

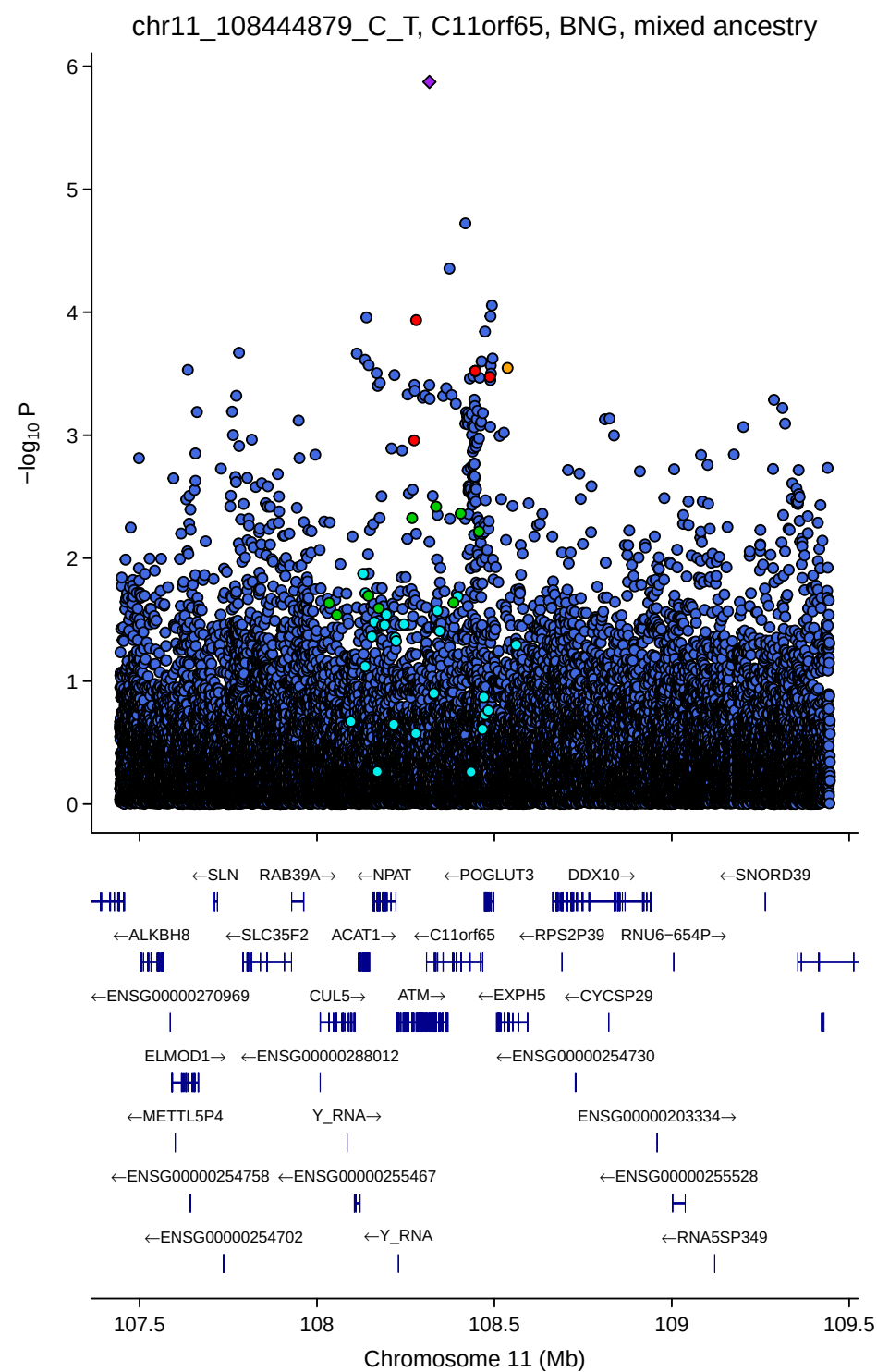
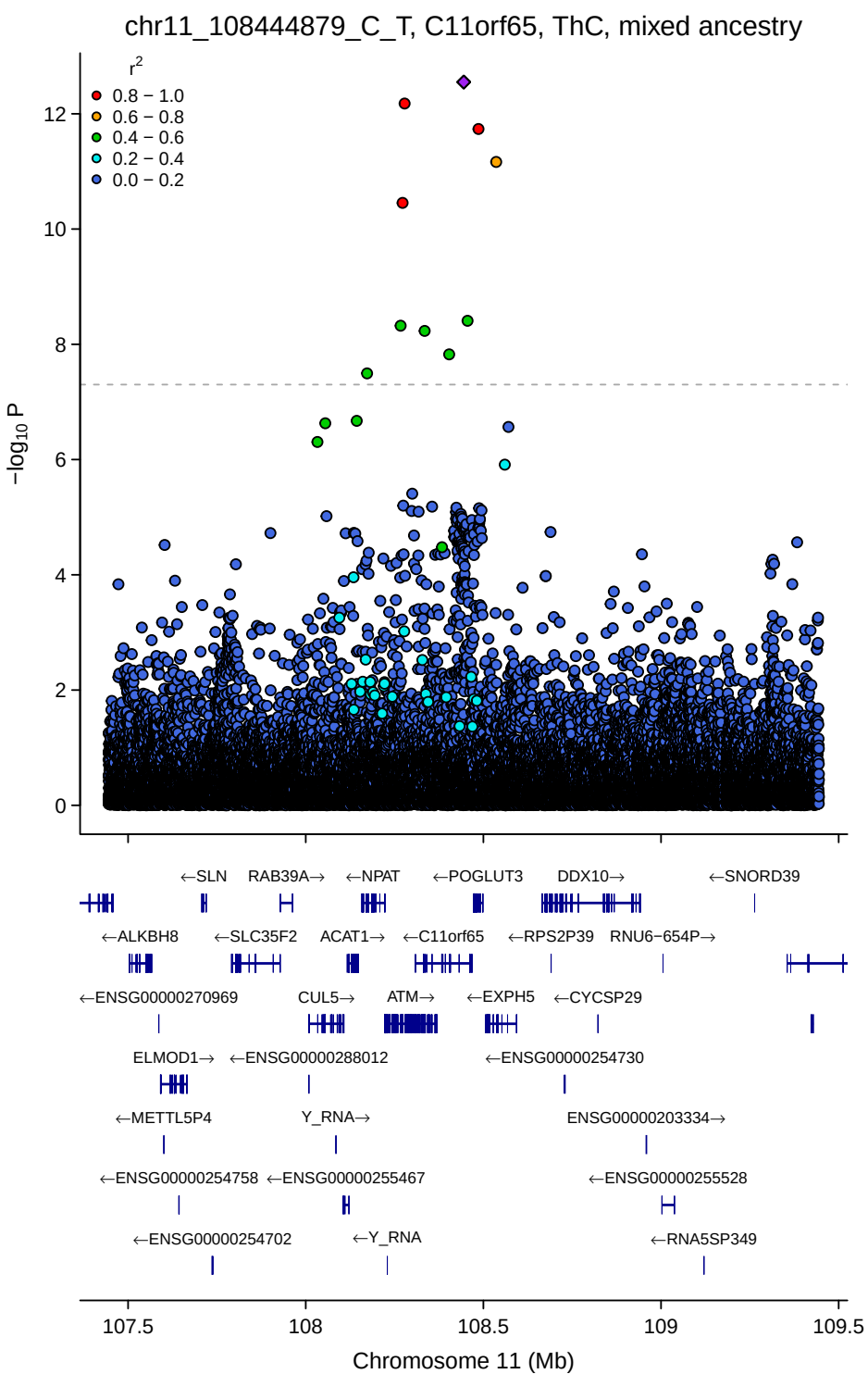
Supplementary Figure 2.1. Locus plots for loci significantly associated with thyroid cancer but not benign nodular goiter. The left plot displays  $-\log_{10}(\text{p-values})$  for variants from thyroid cancer meta-analysis, the right plot displays  $-\log_{10}(\text{p-values})$  for variants within the same genomic region from the benign nodular goiter meta-analysis. The lead variant is shown with a purple diamond. Genome wide significance is indicated by the dashed horizontal line at  $-\log_{10}(5\text{e-}8)$ .



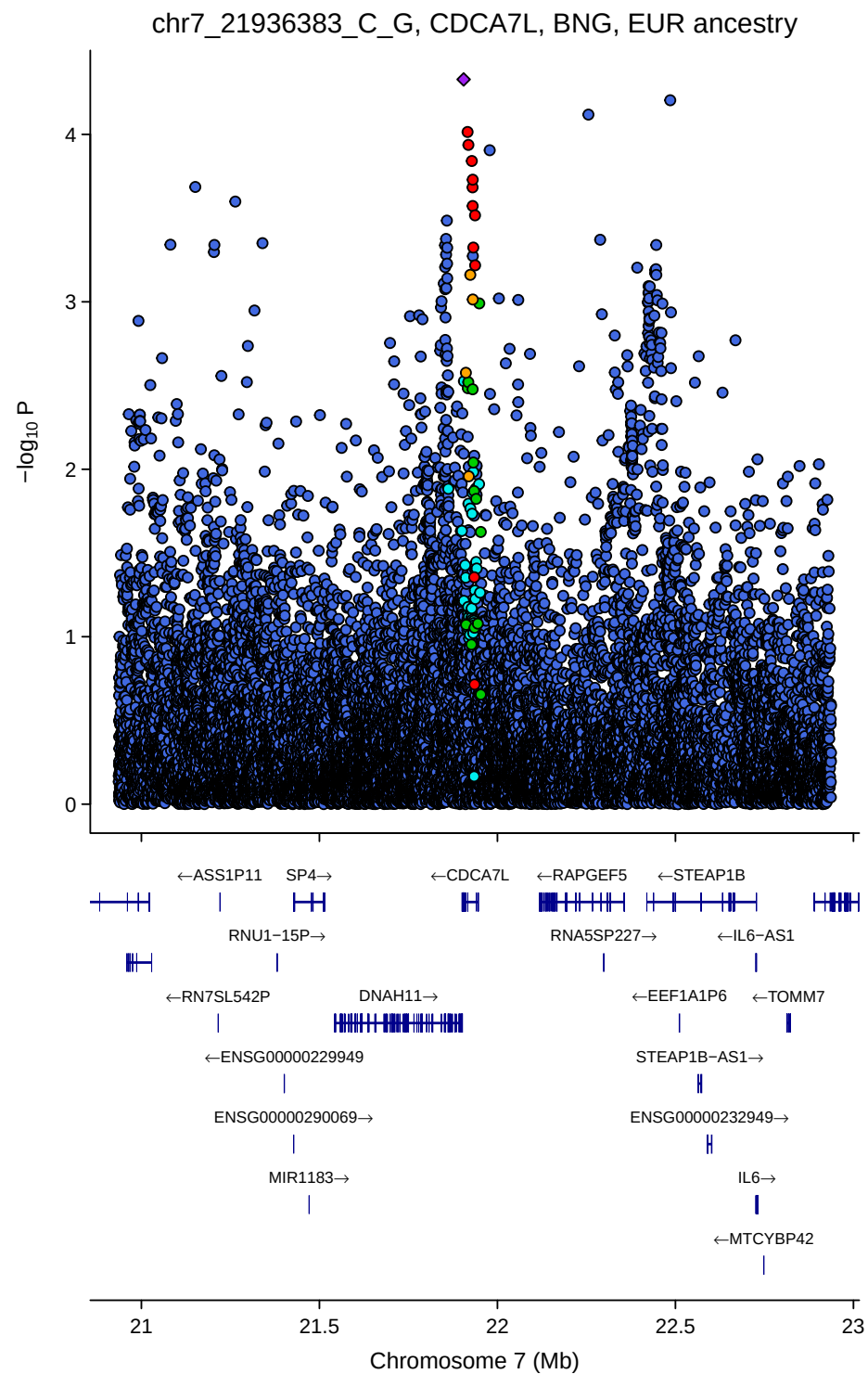
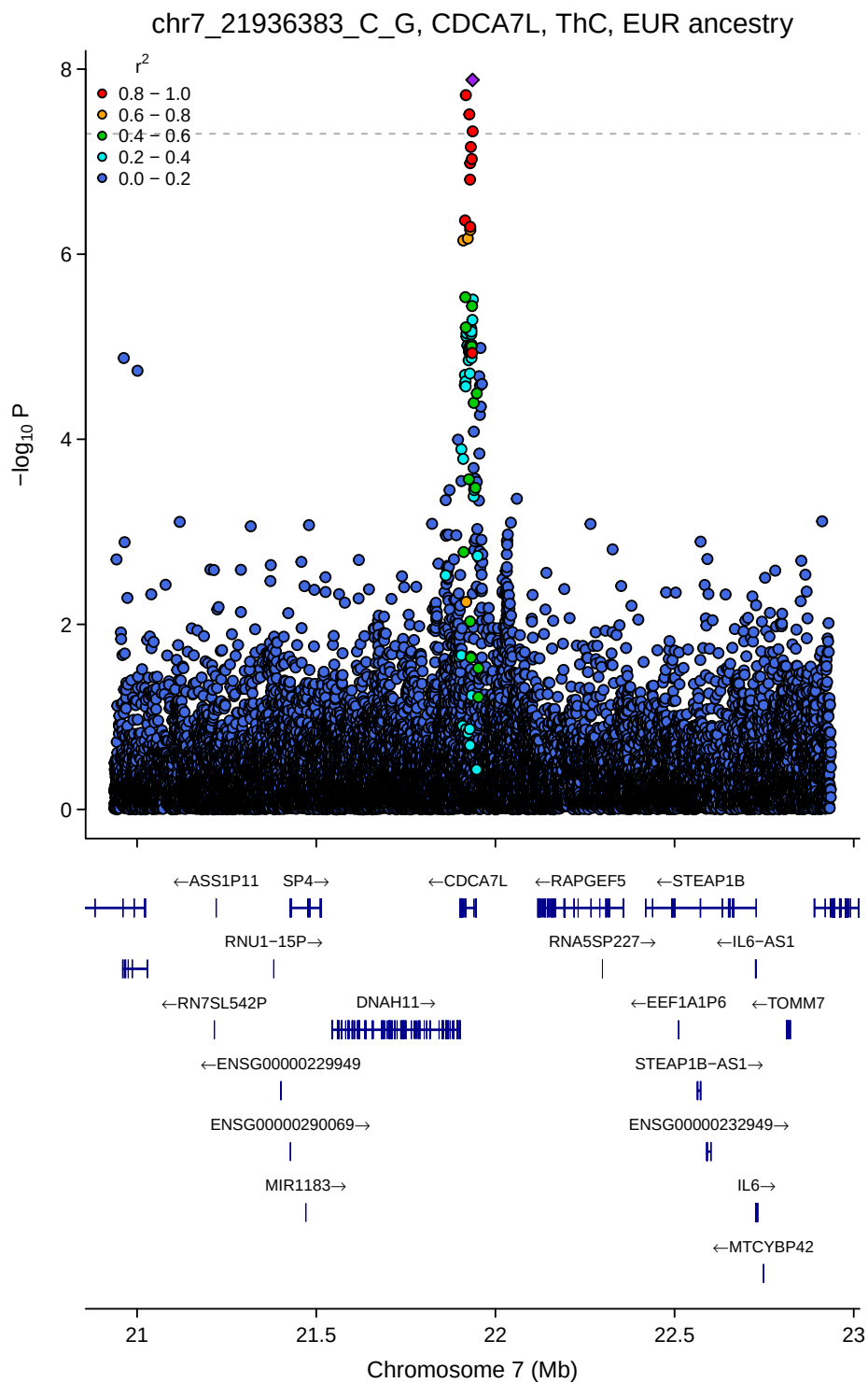
Supplementary Figure 2.1



Supplementary Figure 2.1

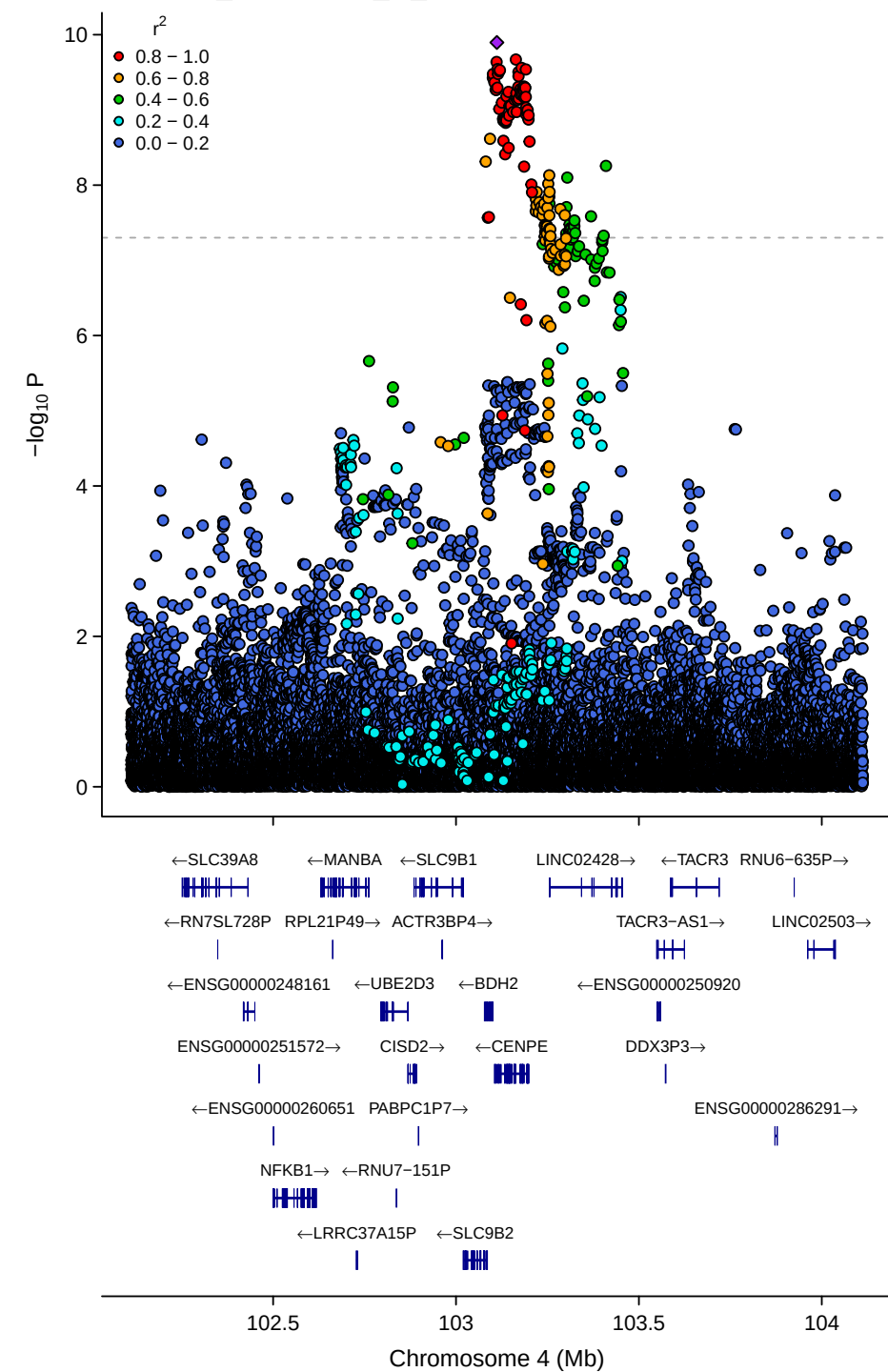


Supplementary Figure 2.1

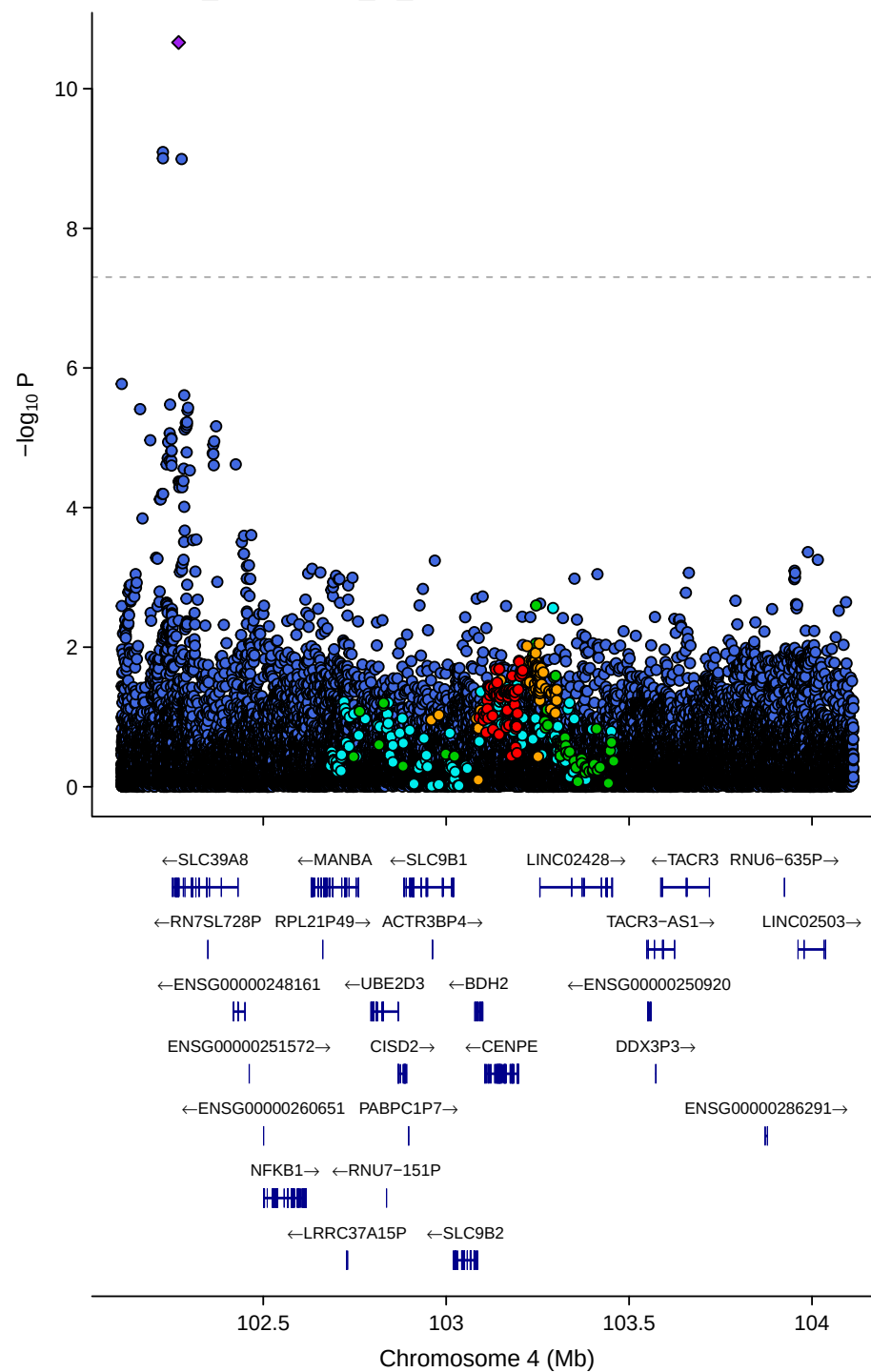


Supplementary Figure 2.1

chr4\_103111955\_G\_A, CENPE, ThC, mixed ancestry



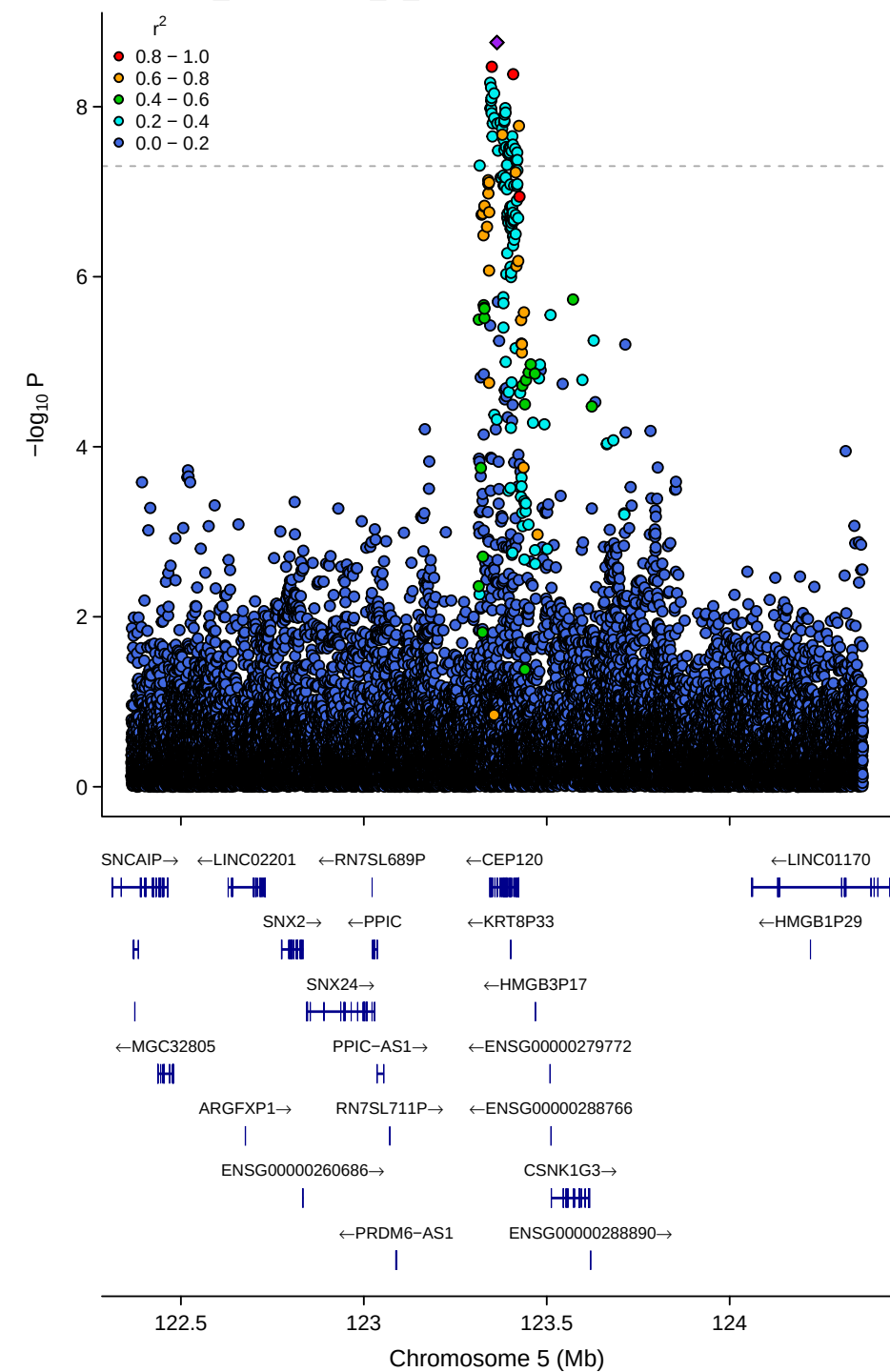
chr4\_103111955\_G\_A, CENPE, BNG, mixed ancestry



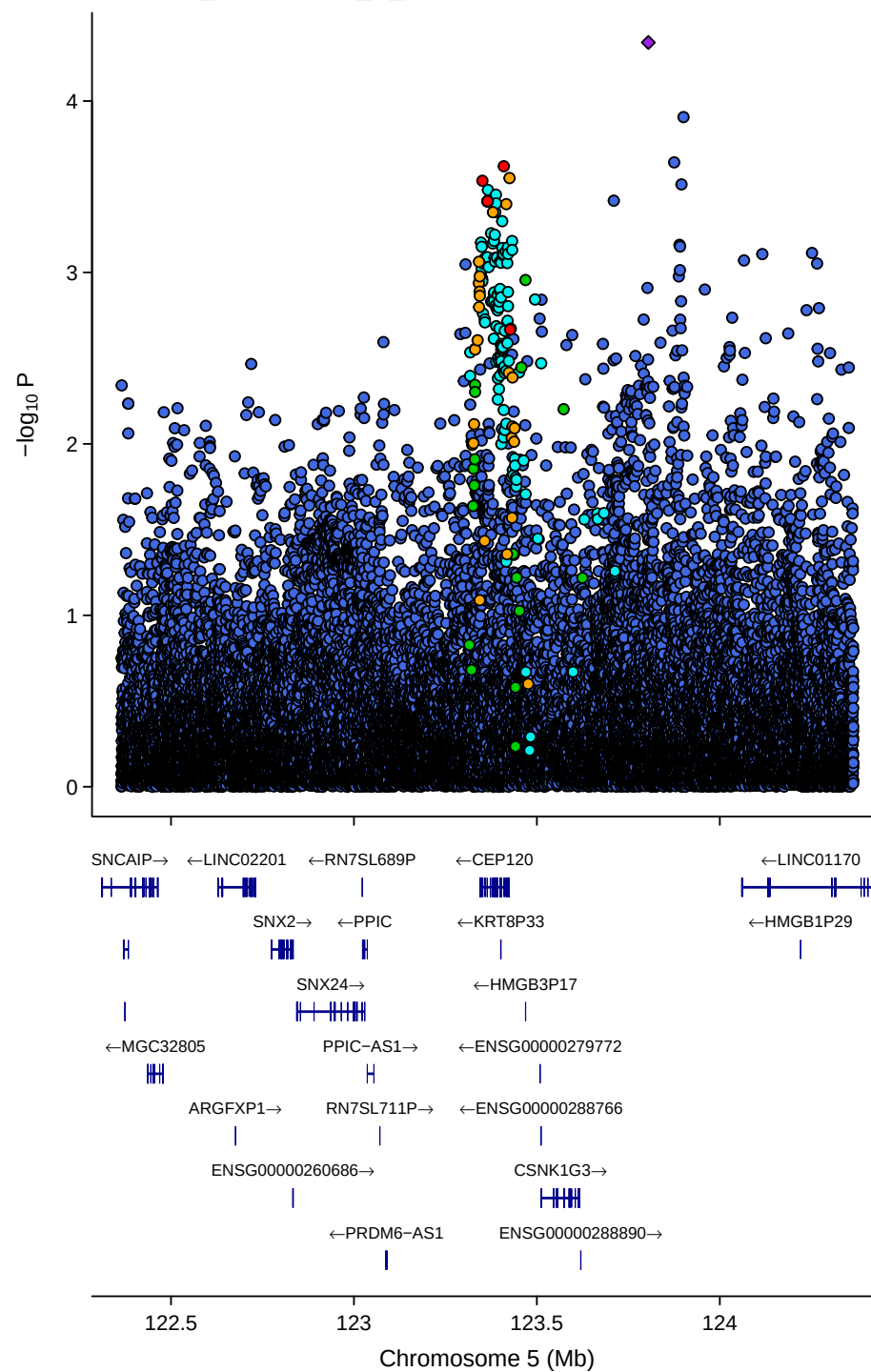


Supplementary Figure 2.1

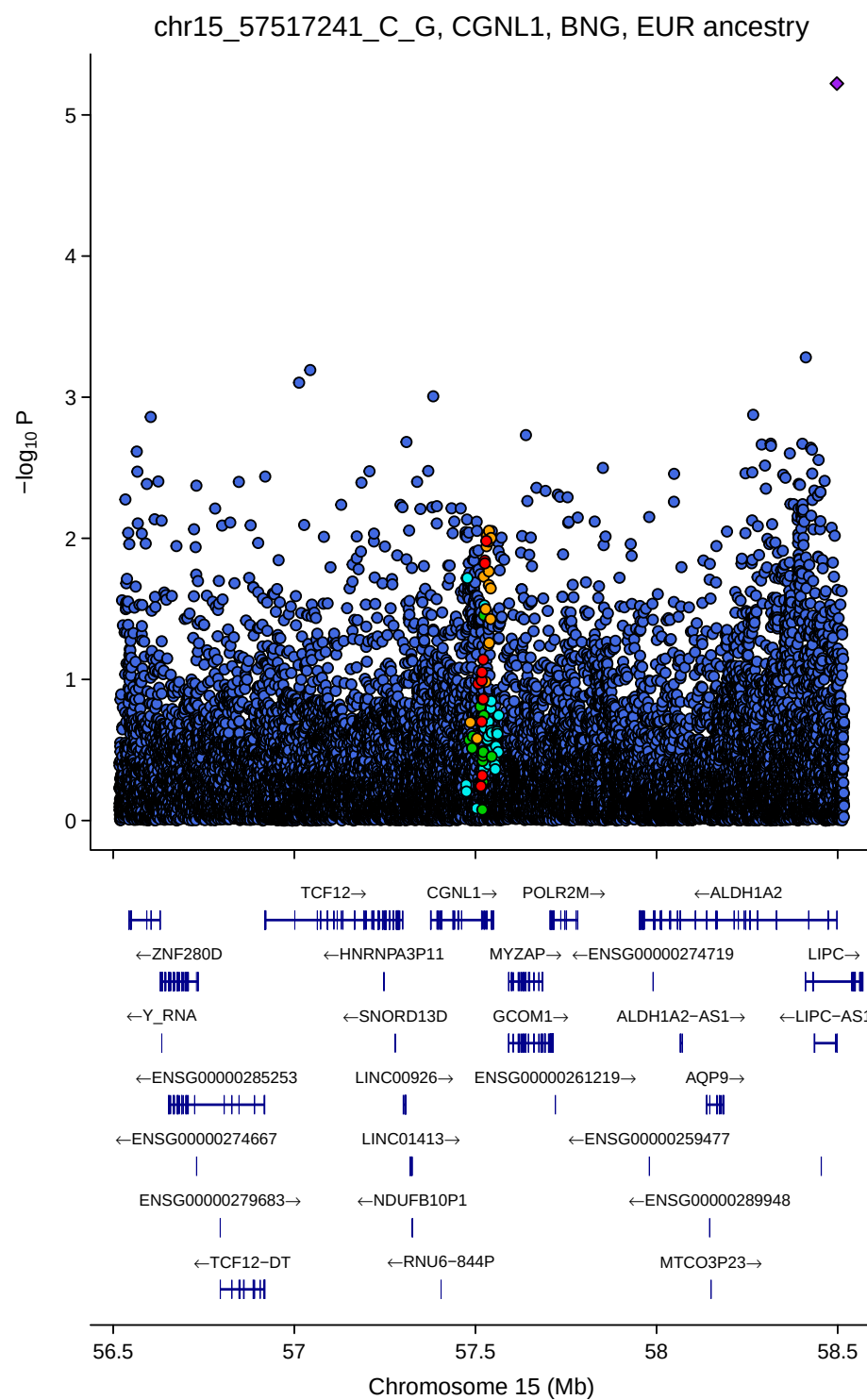
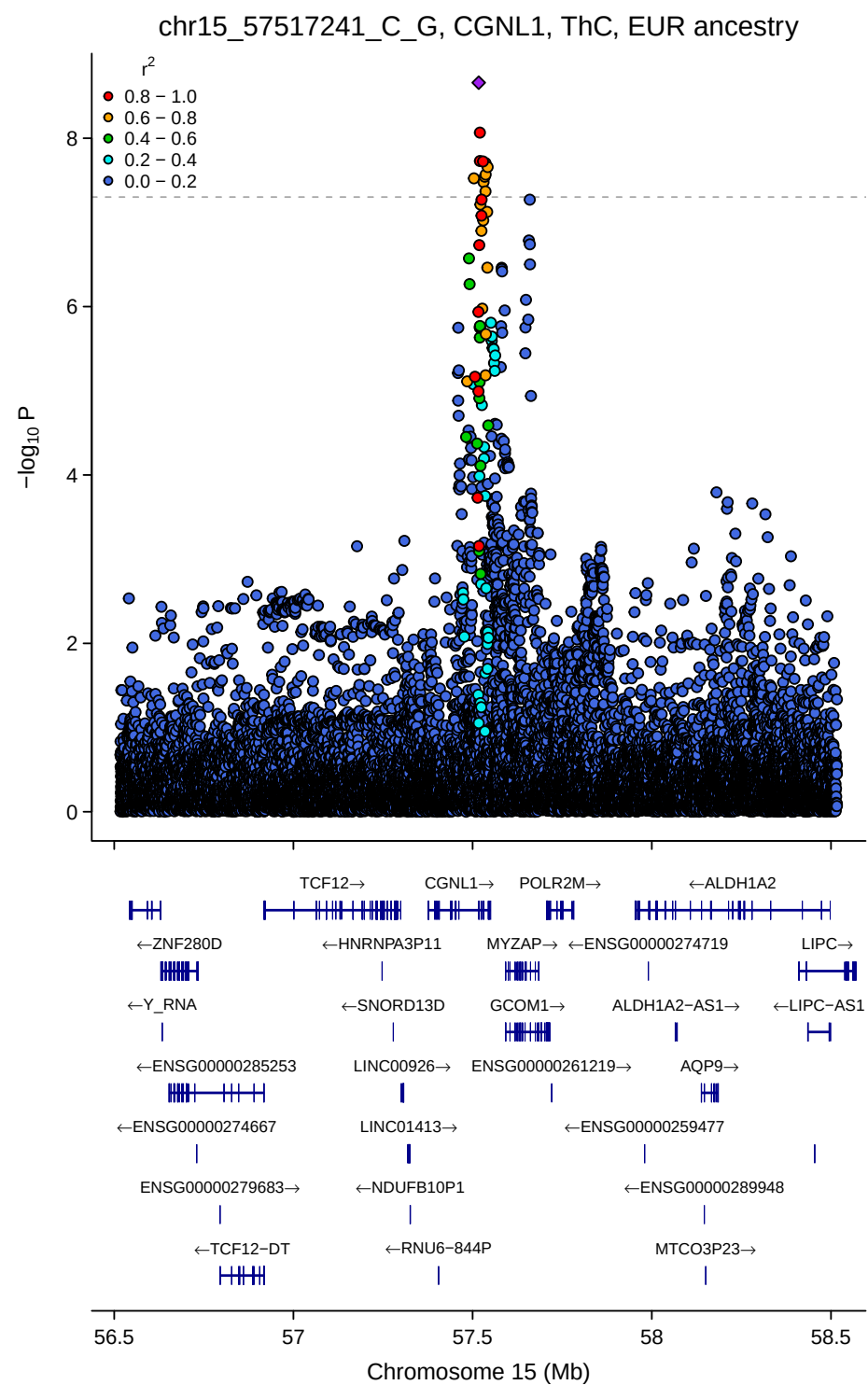
chr5\_123364118\_T\_G, CEP120, ThC, mixed ancestry



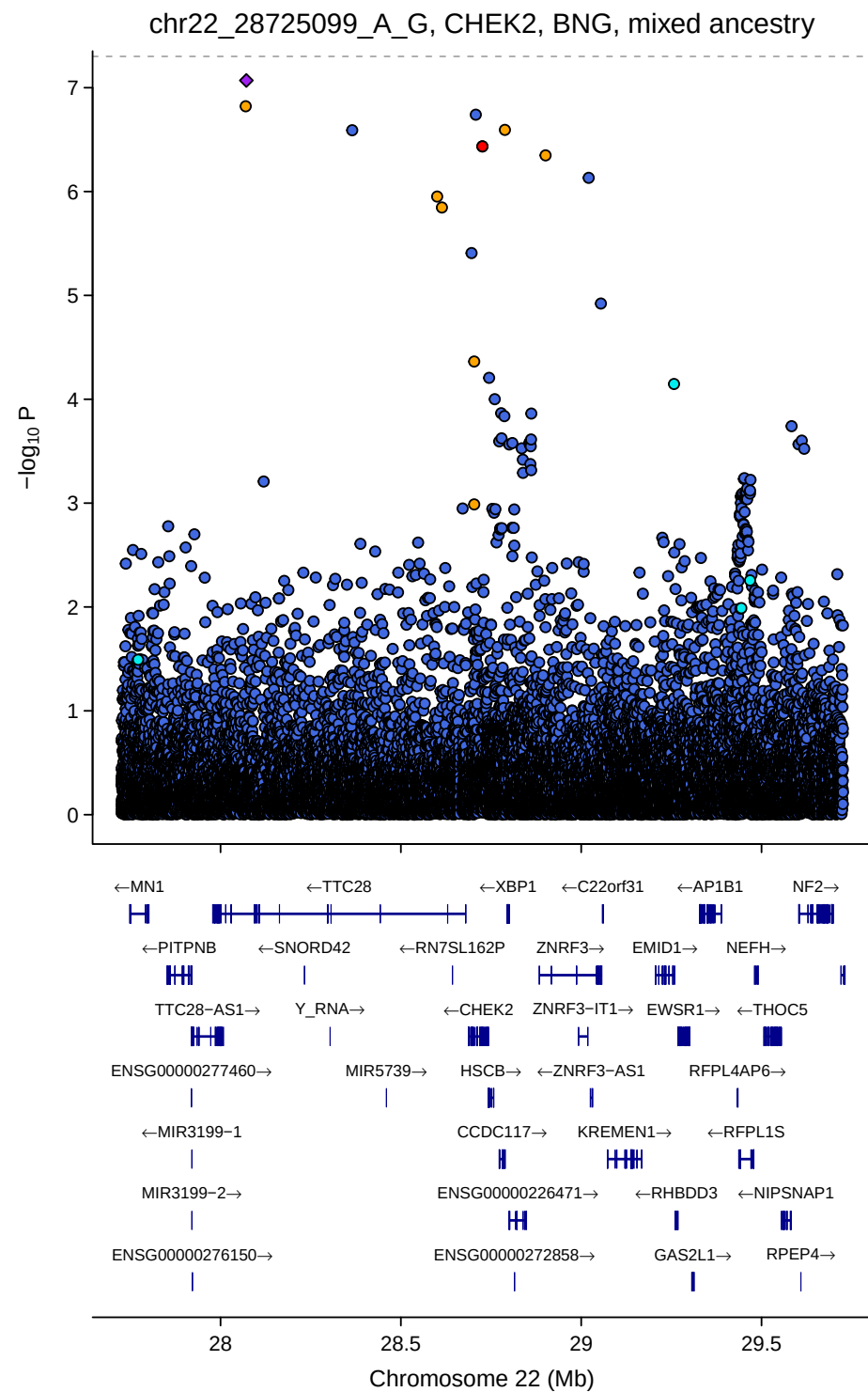
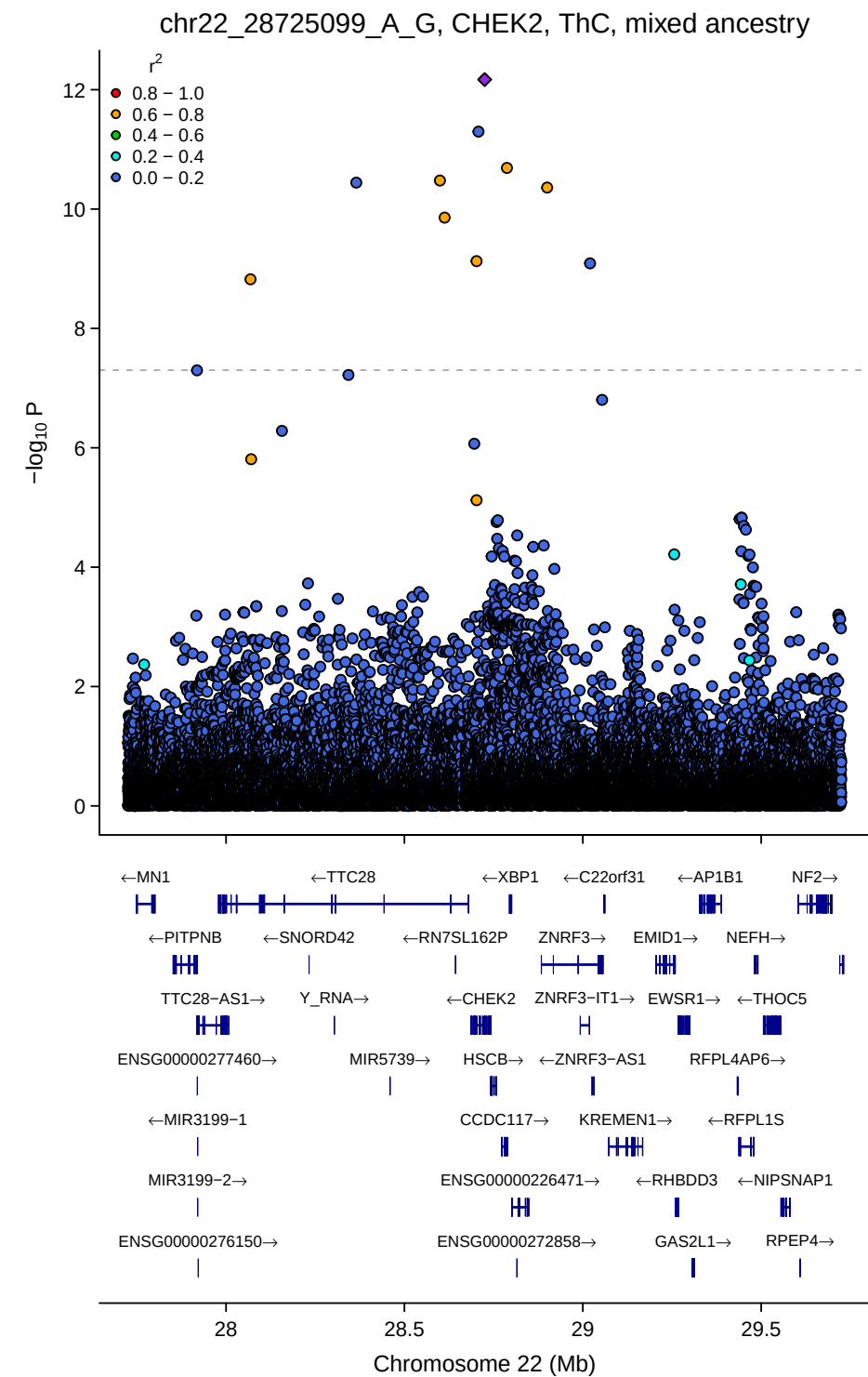
chr5\_123364118\_T\_G, CEP120, BNG, mixed ancestry



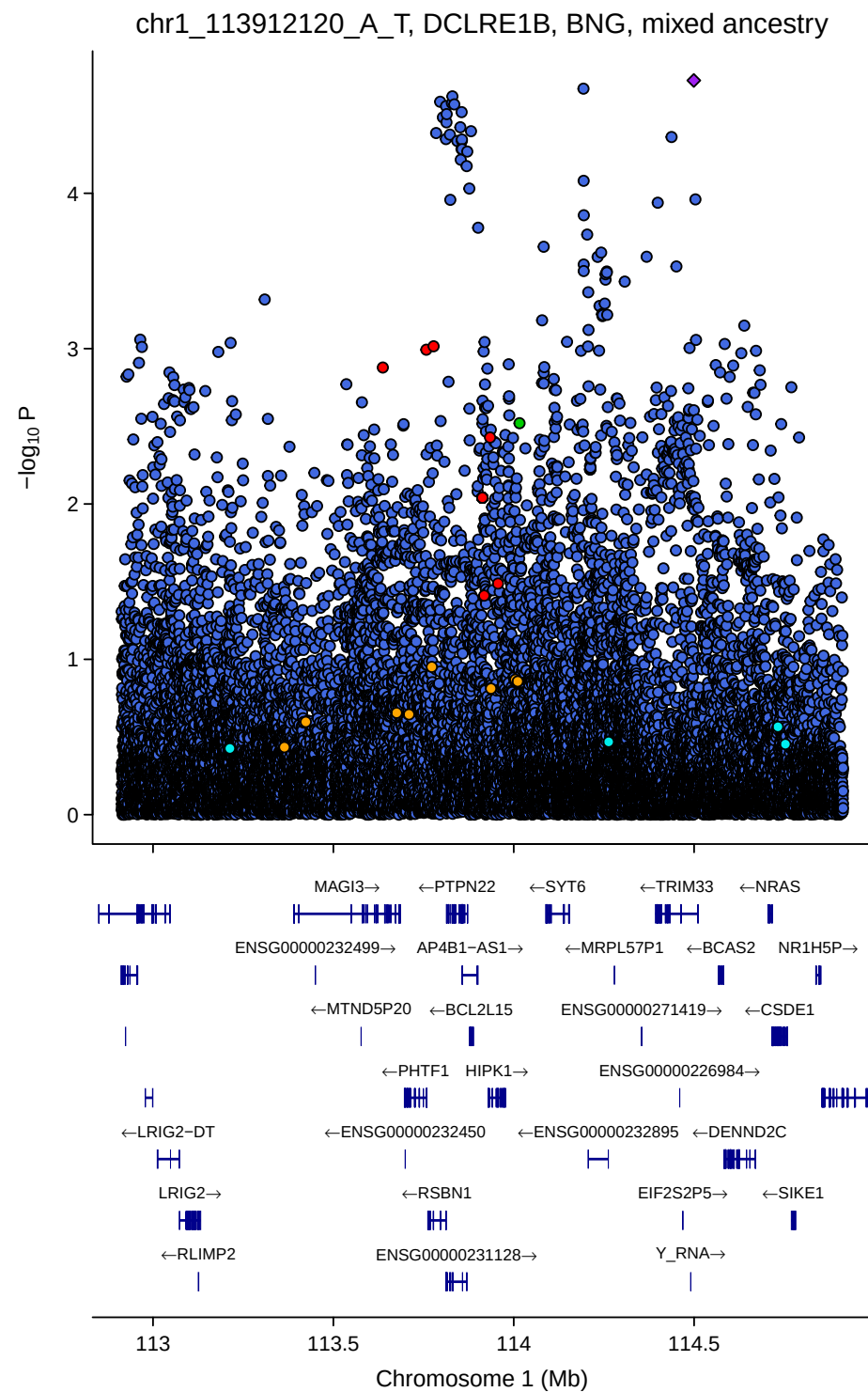
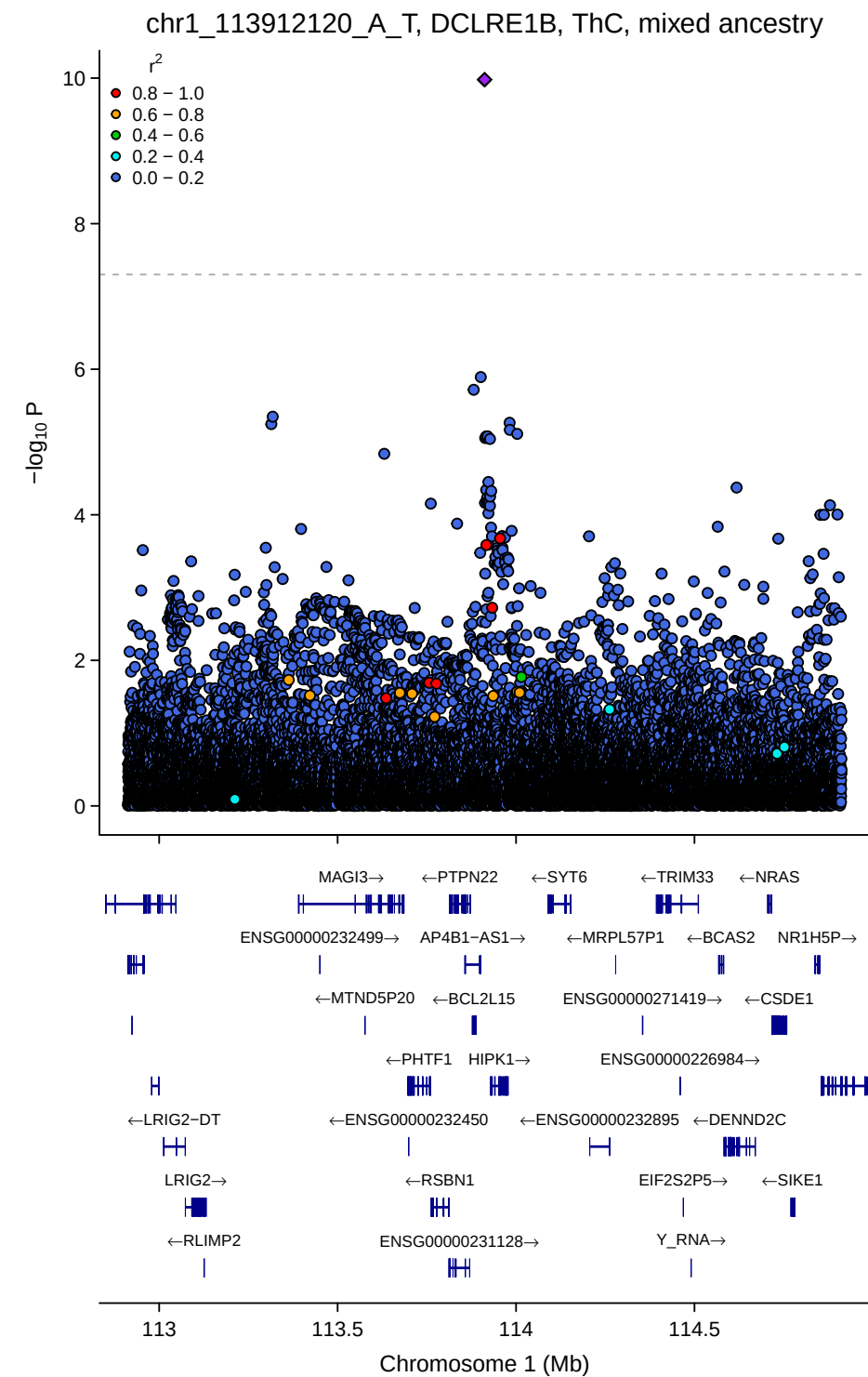
Supplementary Figure 2.1



Supplementary Figure 2.1

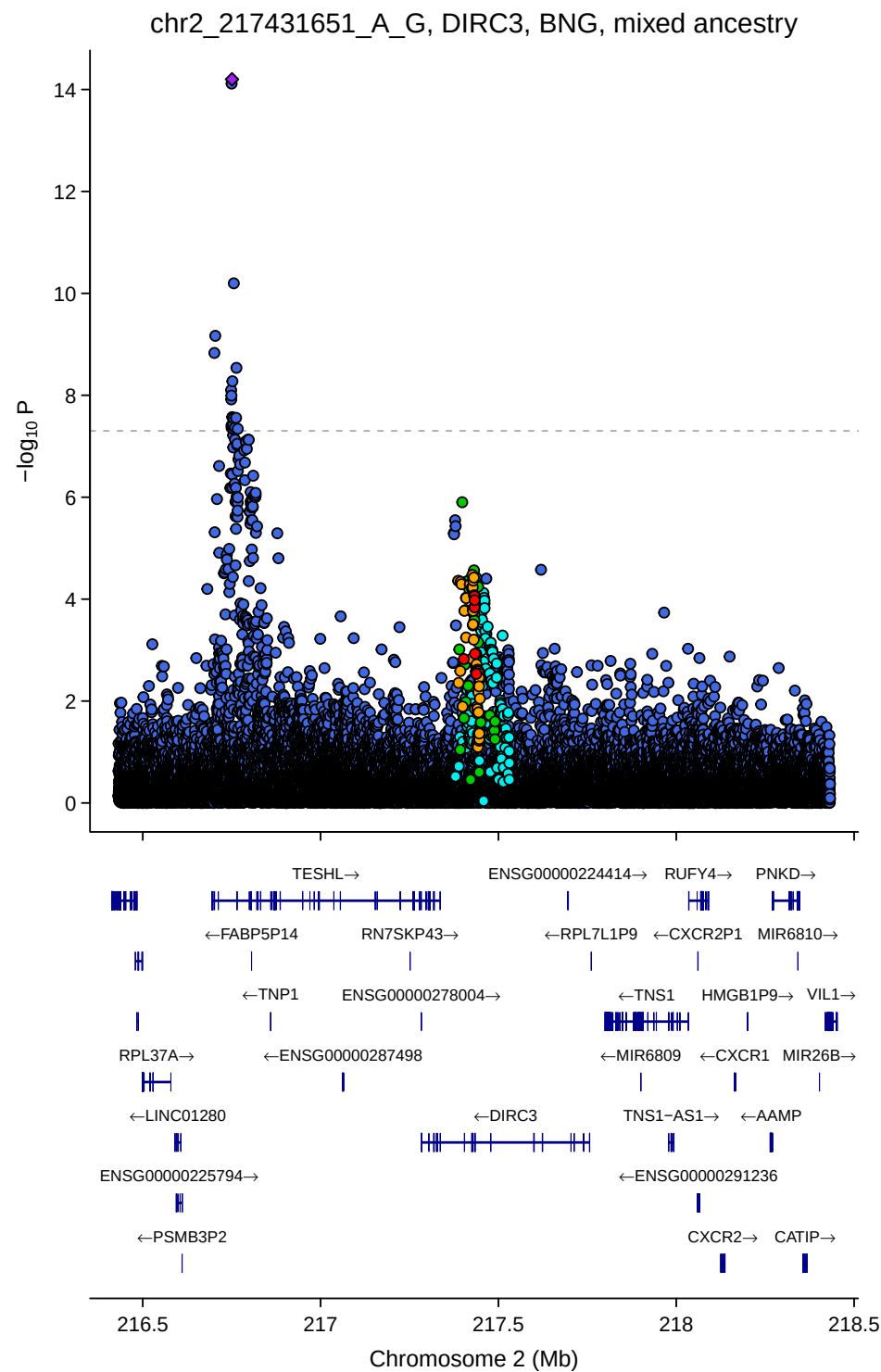
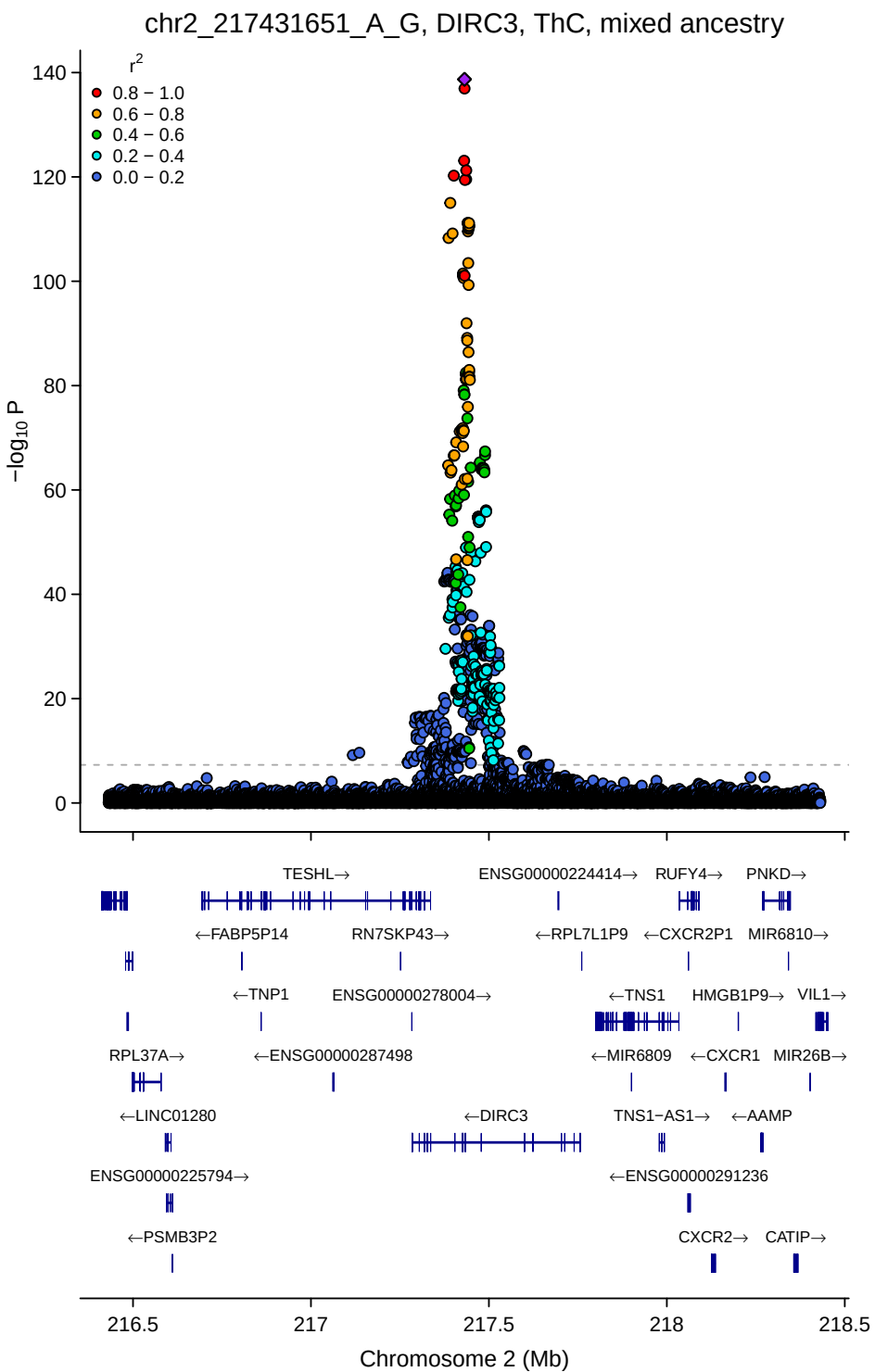


Supplementary Figure 2.1

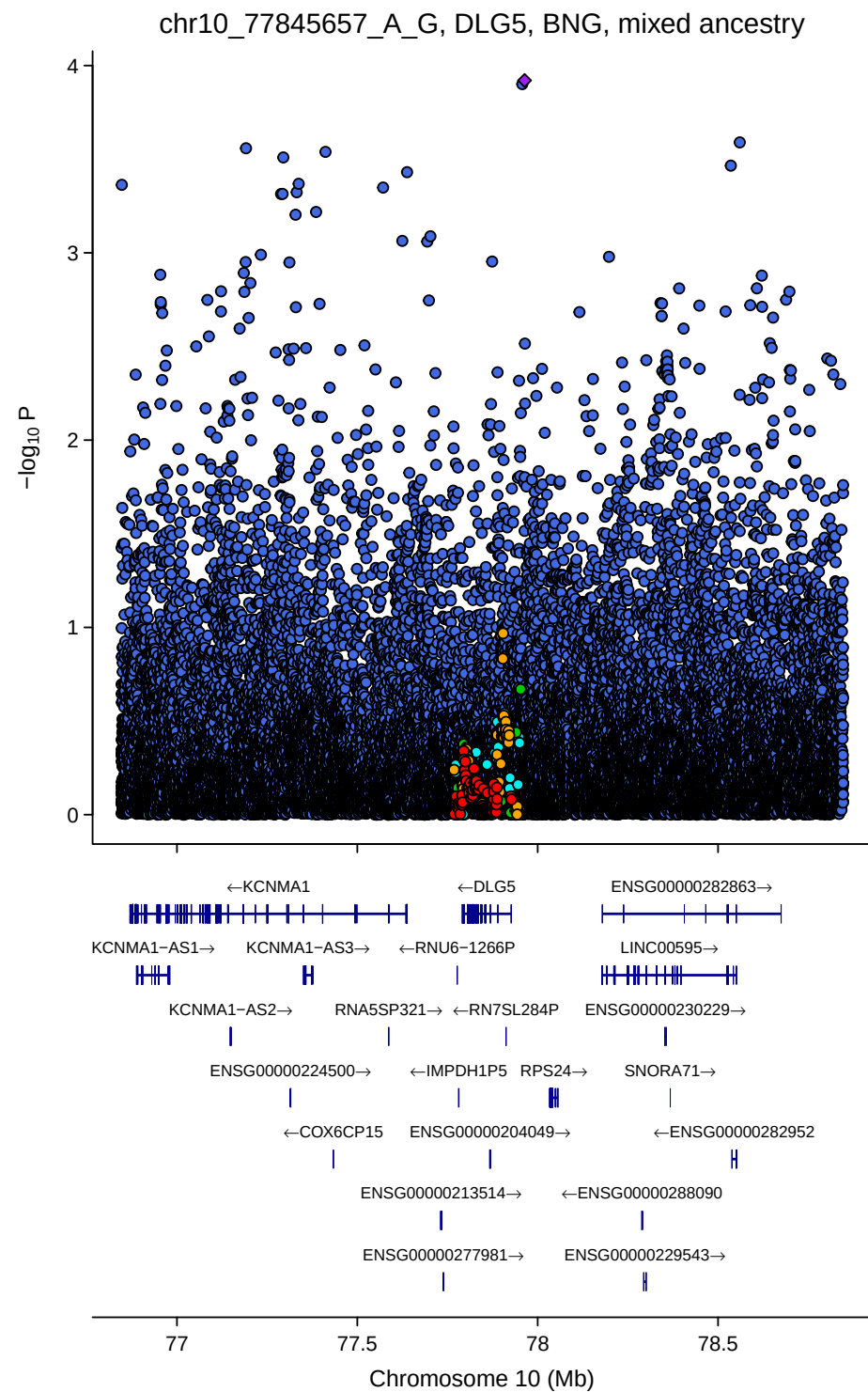
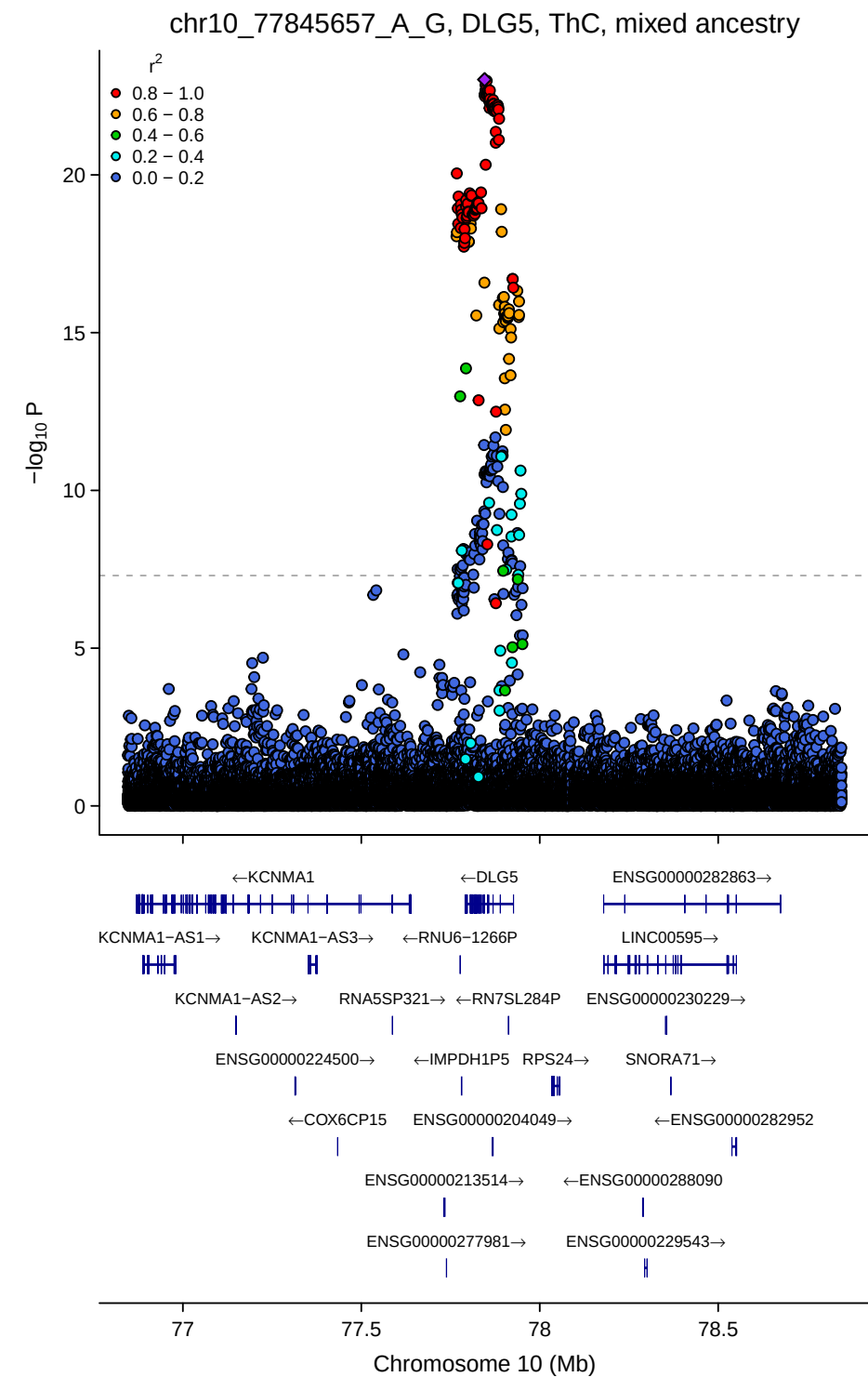




Supplementary Figure 2.1

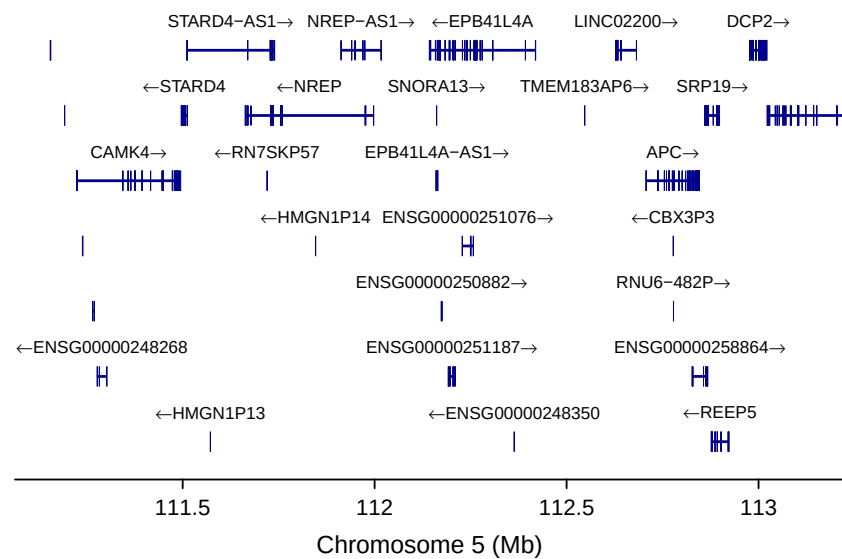
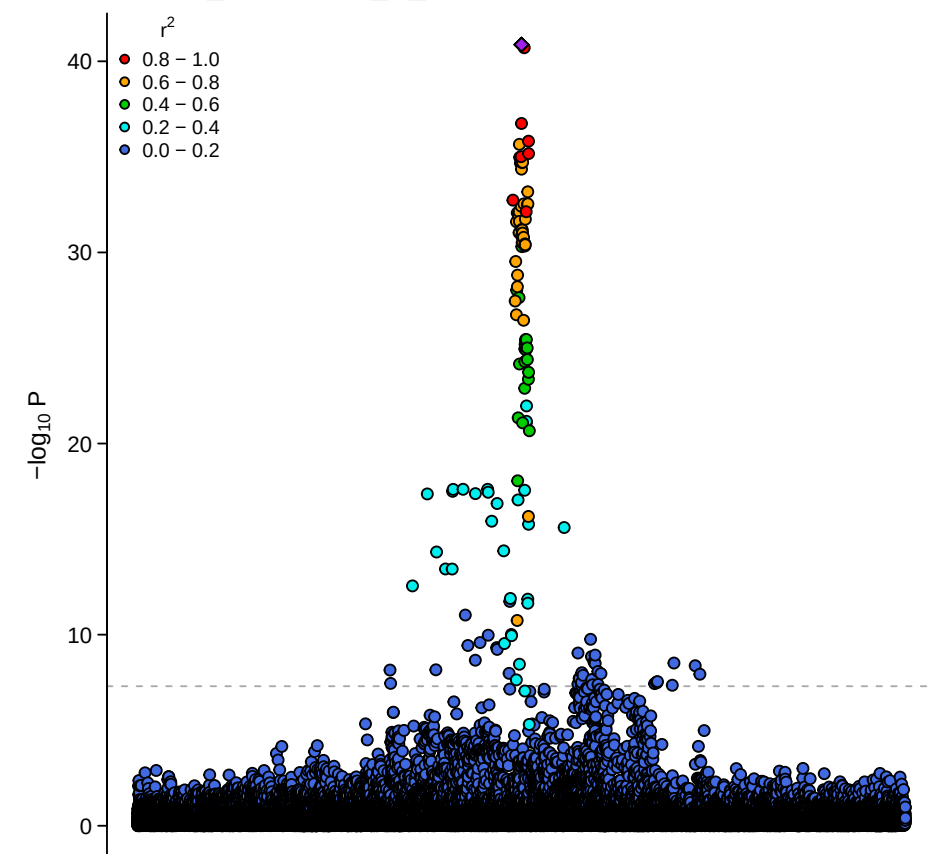


Supplementary Figure 2.1

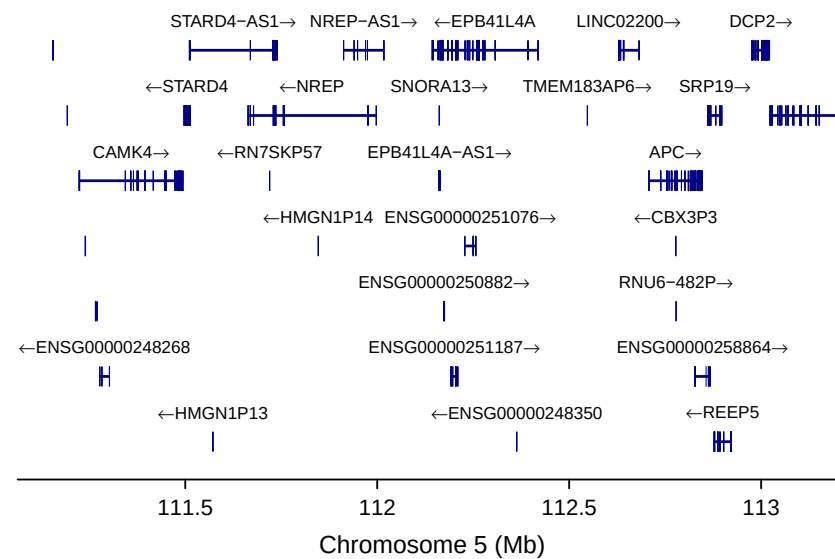
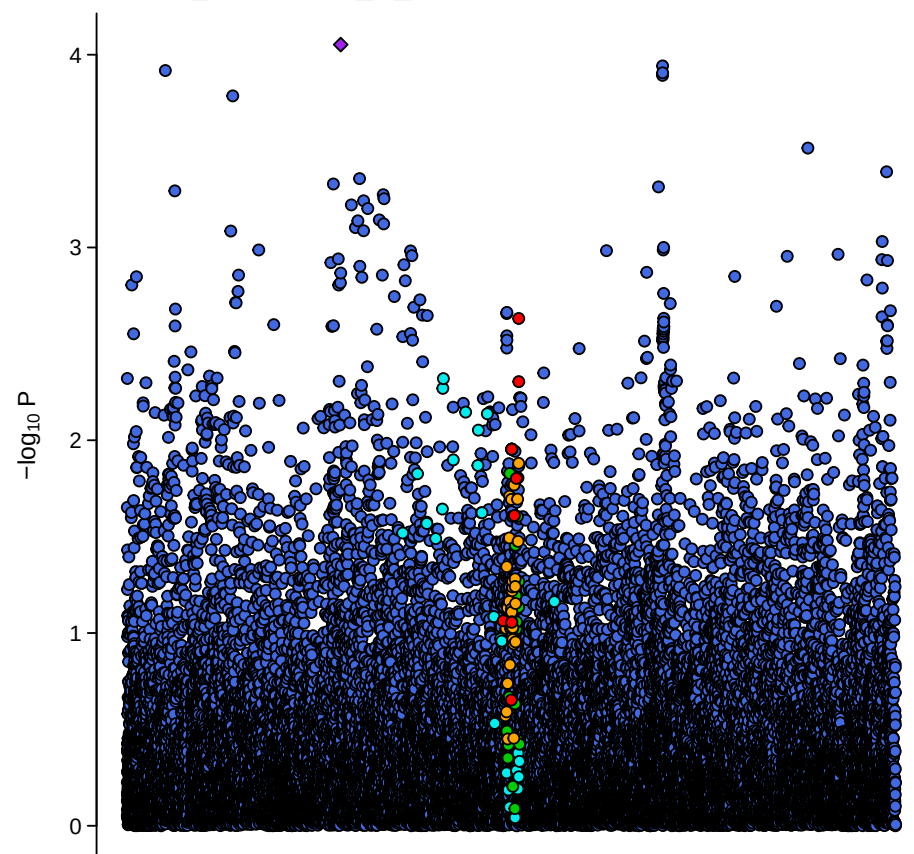


Supplementary Figure 2.1

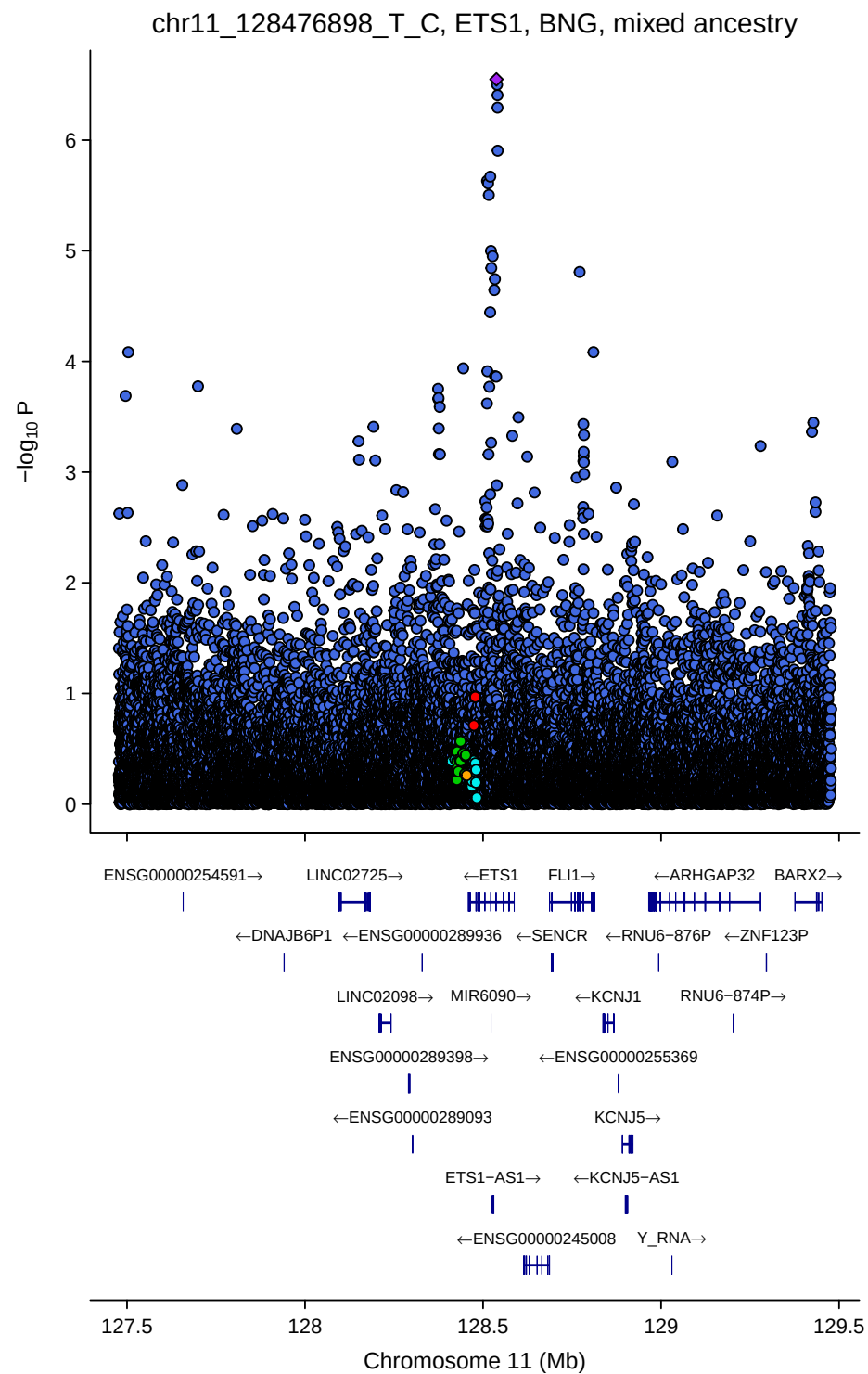
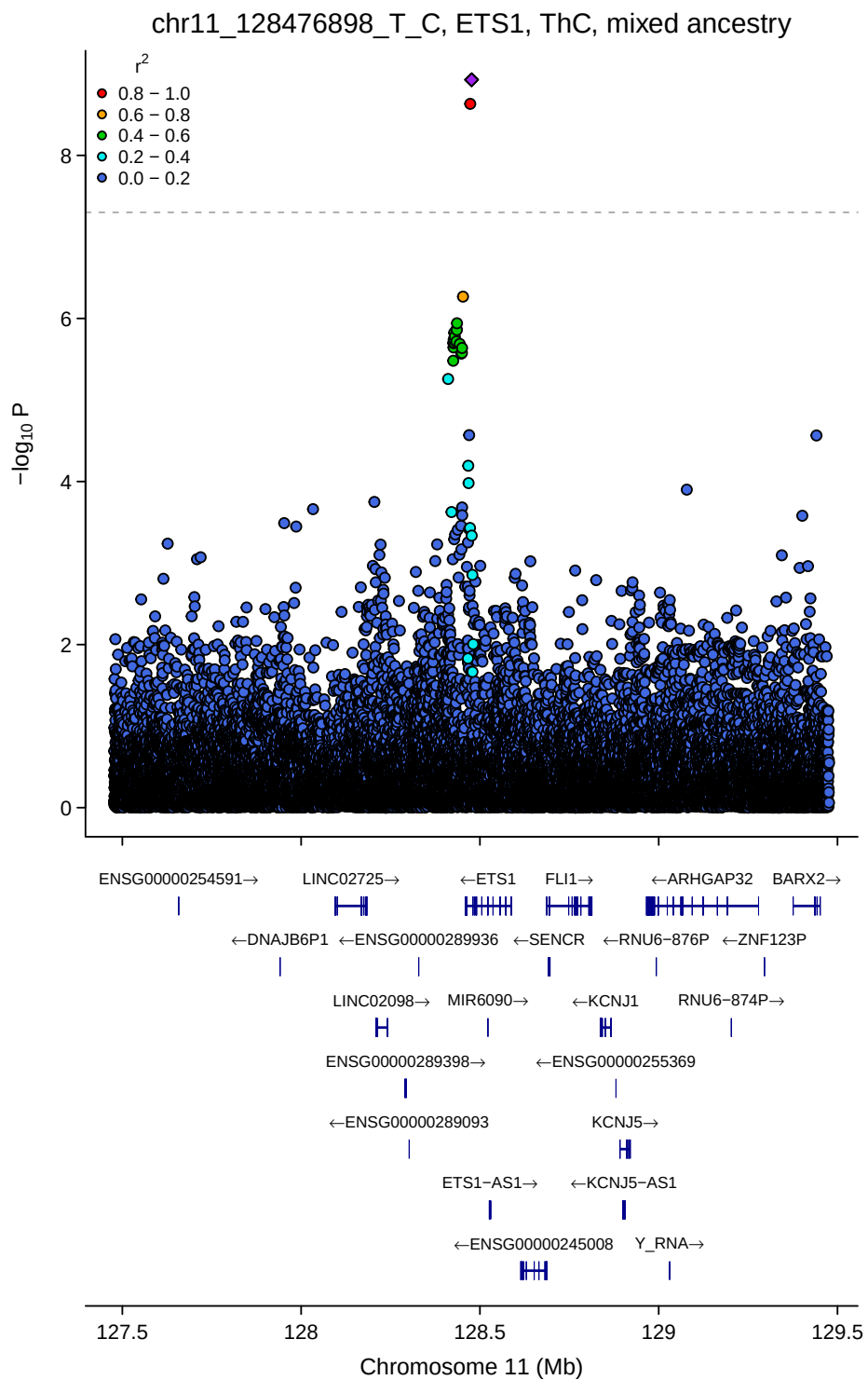
chr5\_112143173\_C\_A, EPB41L4A, ThC, mixed ancestry



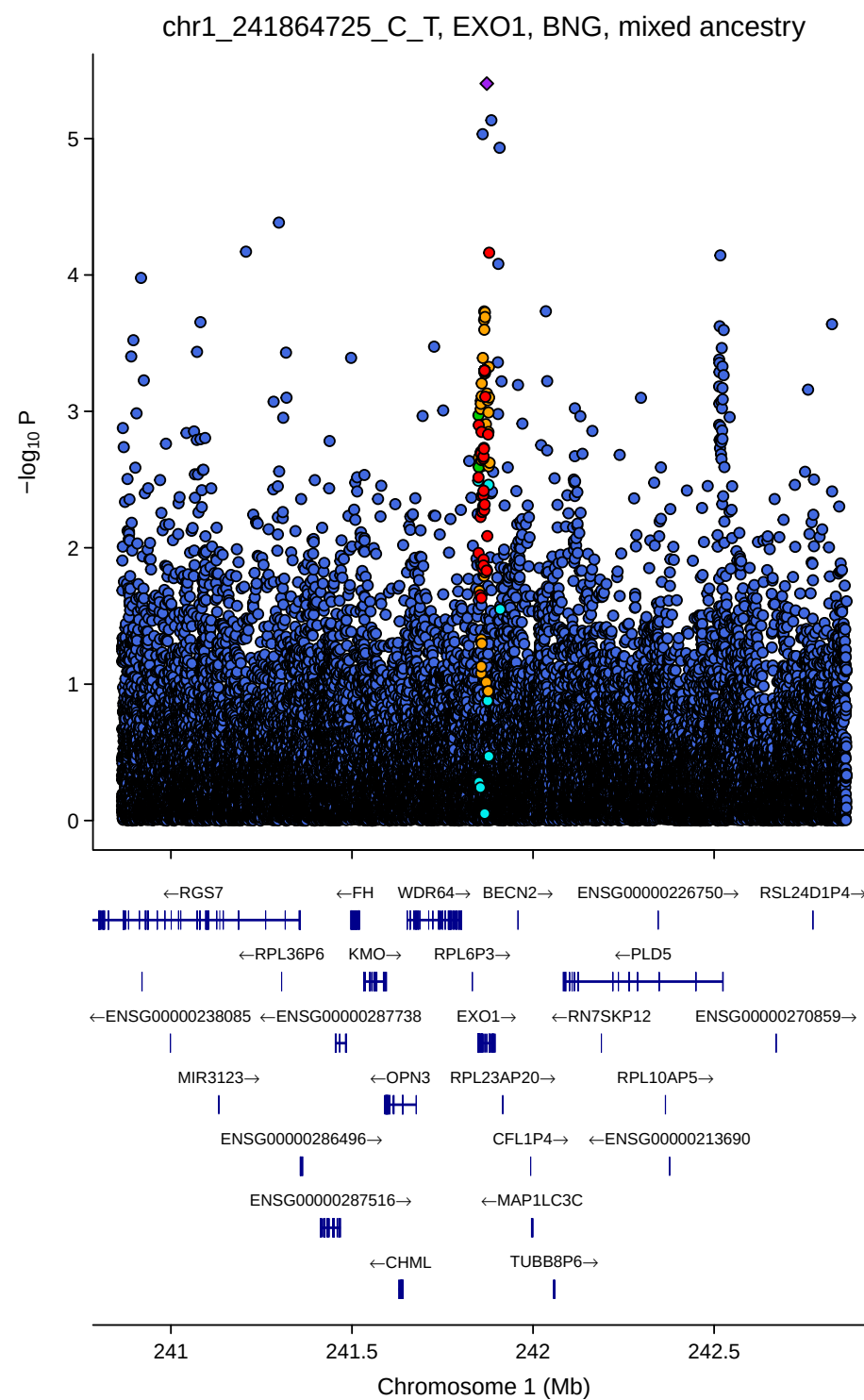
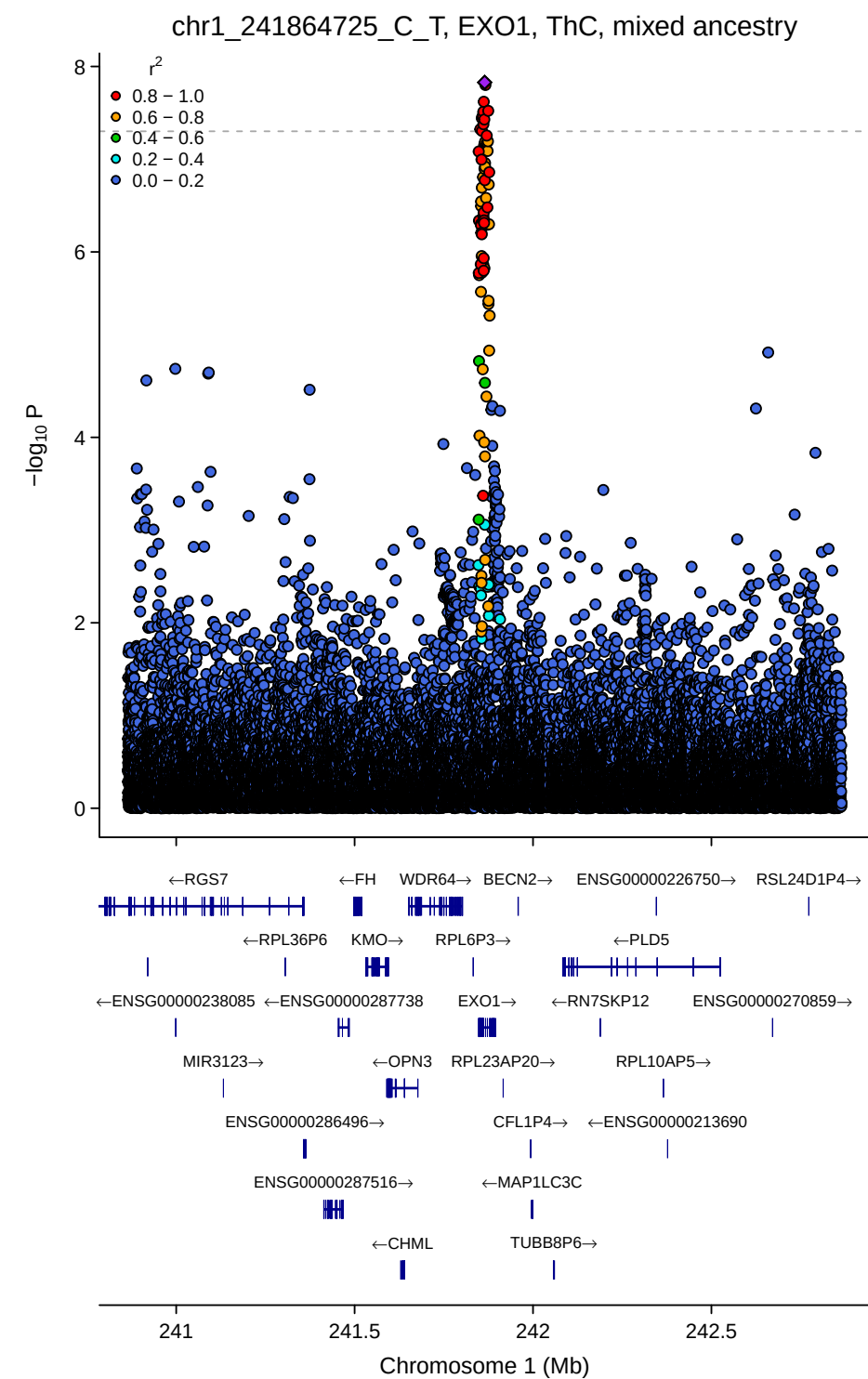
chr5\_112143173\_C\_A, EPB41L4A, BNG, mixed ancestry



Supplementary Figure 2.1

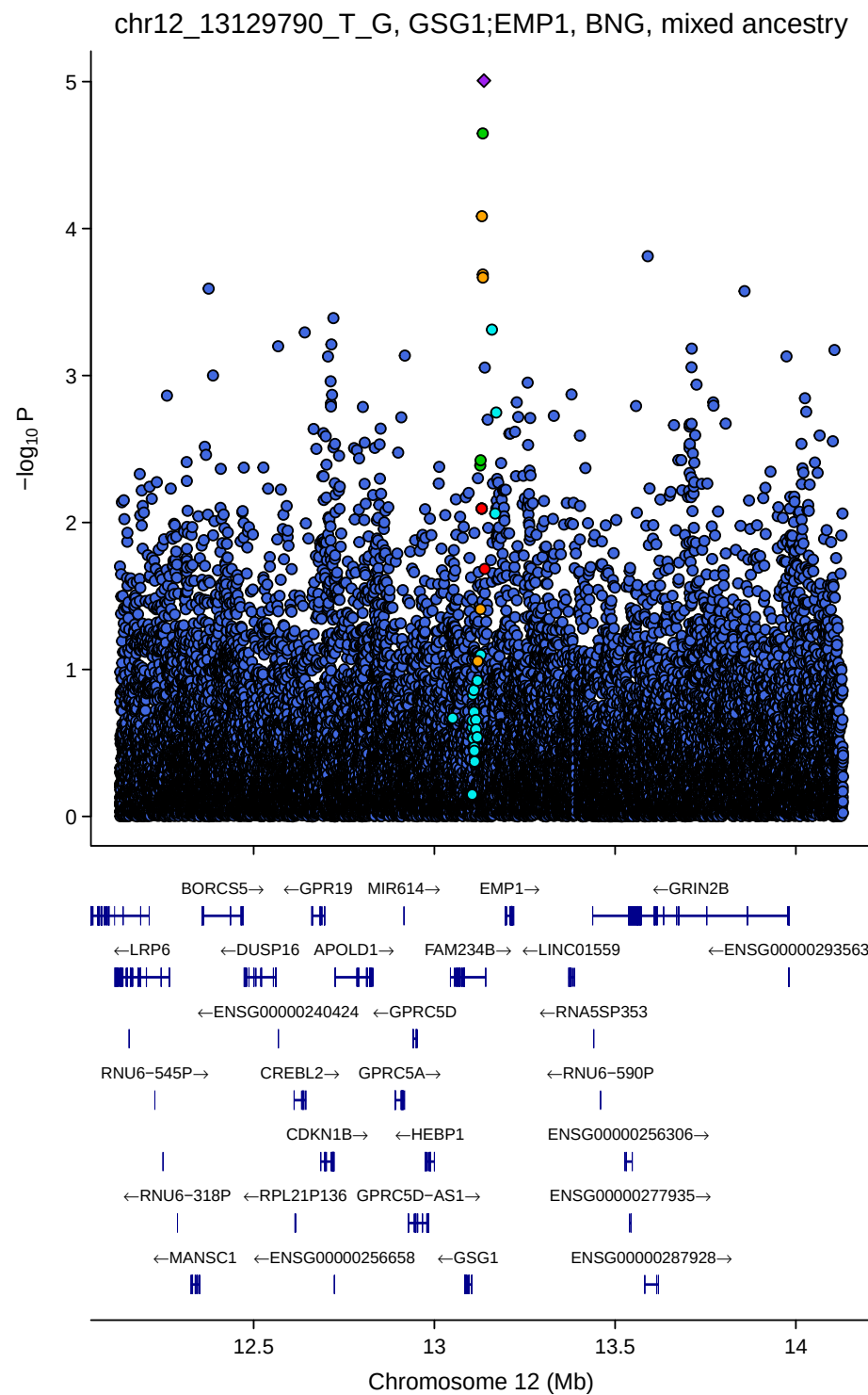
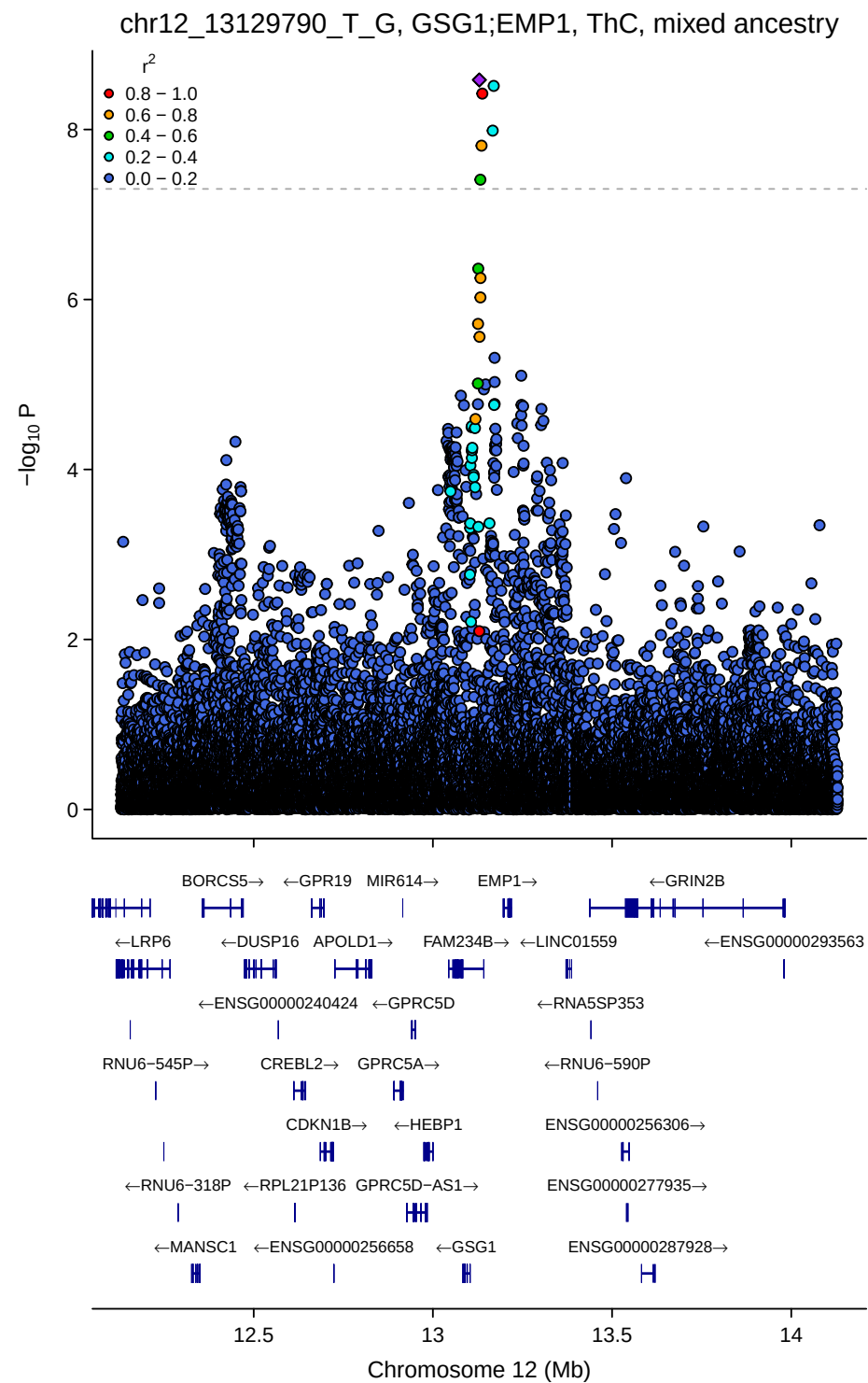


Supplementary Figure 2.1

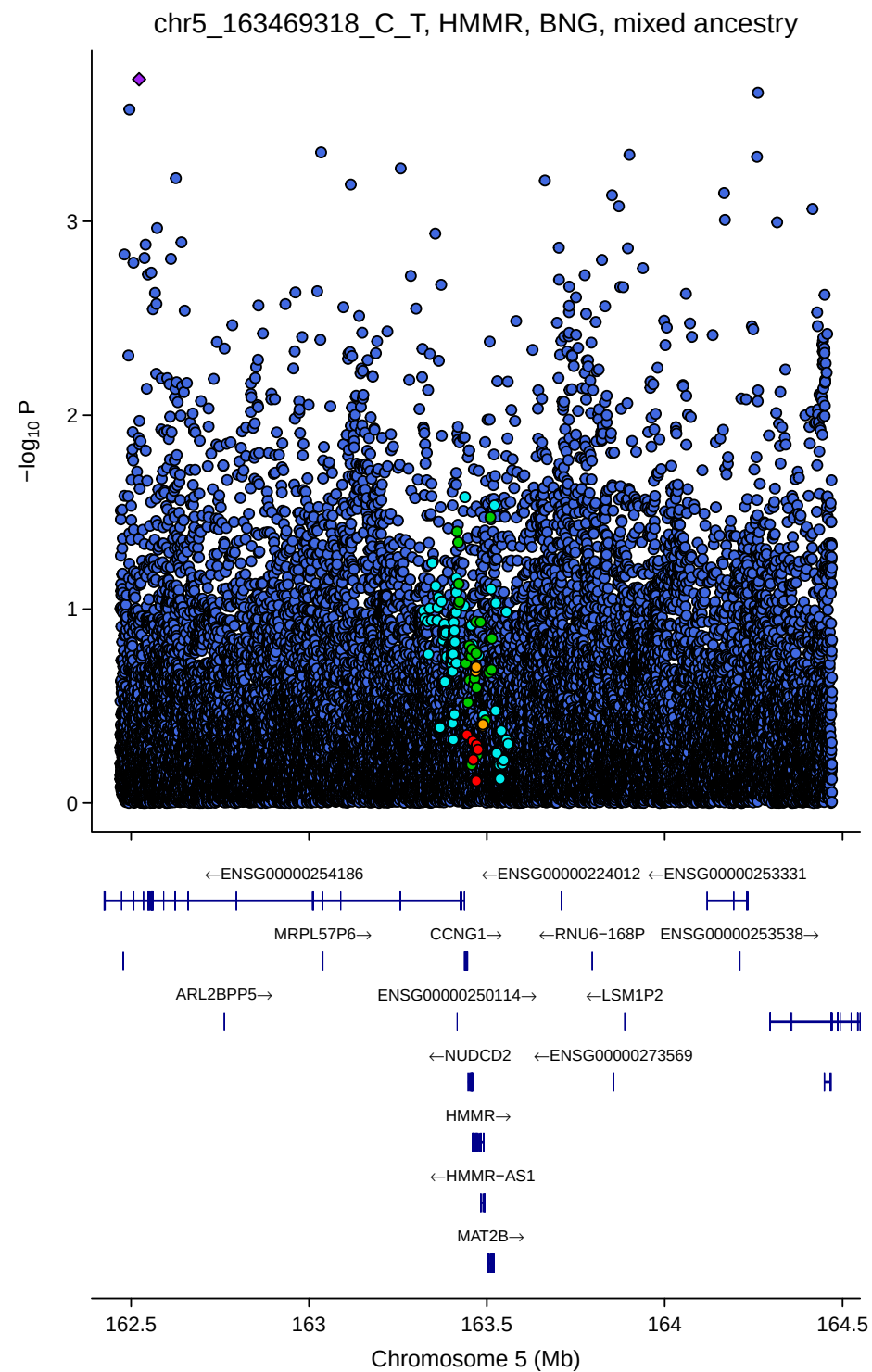
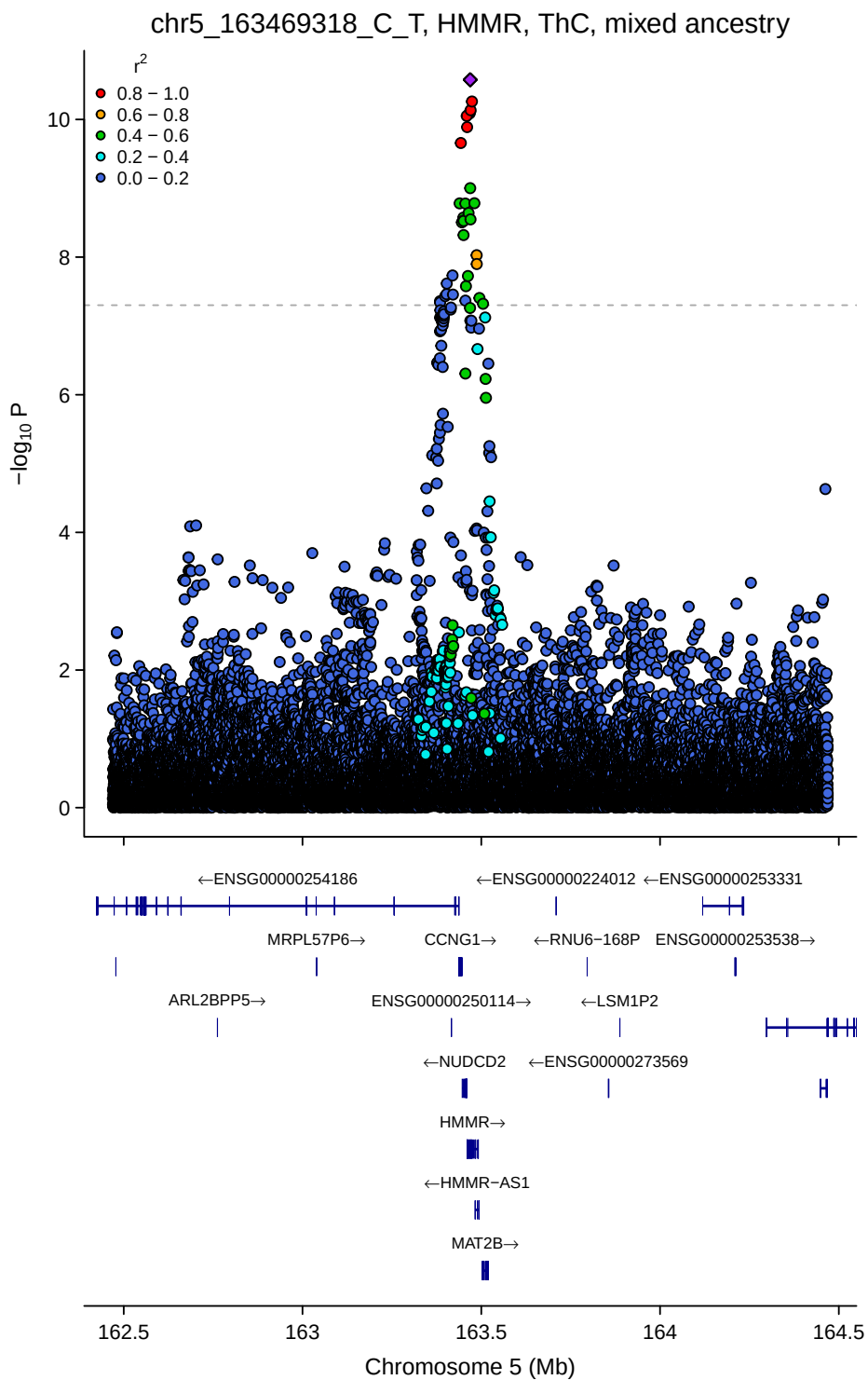




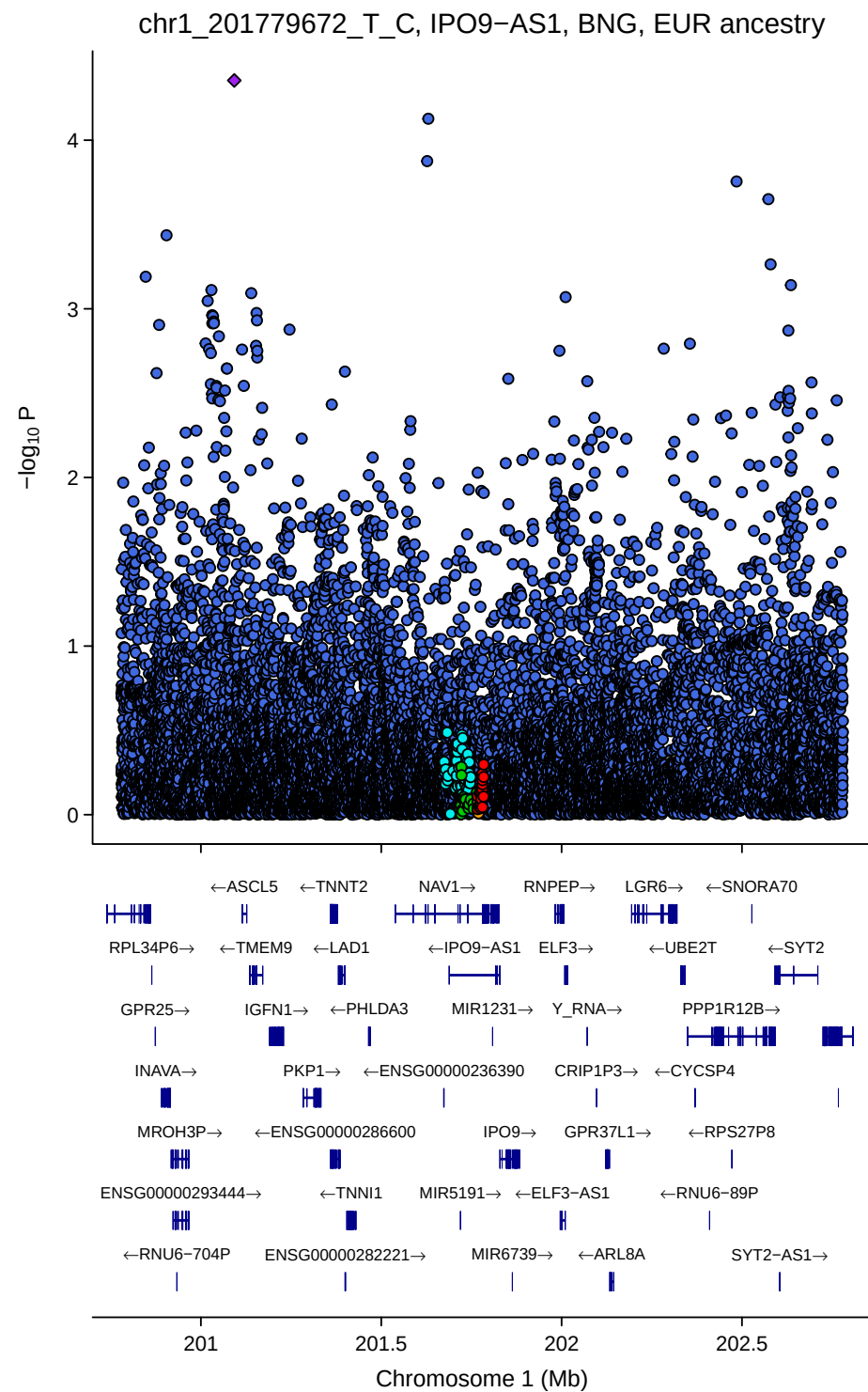
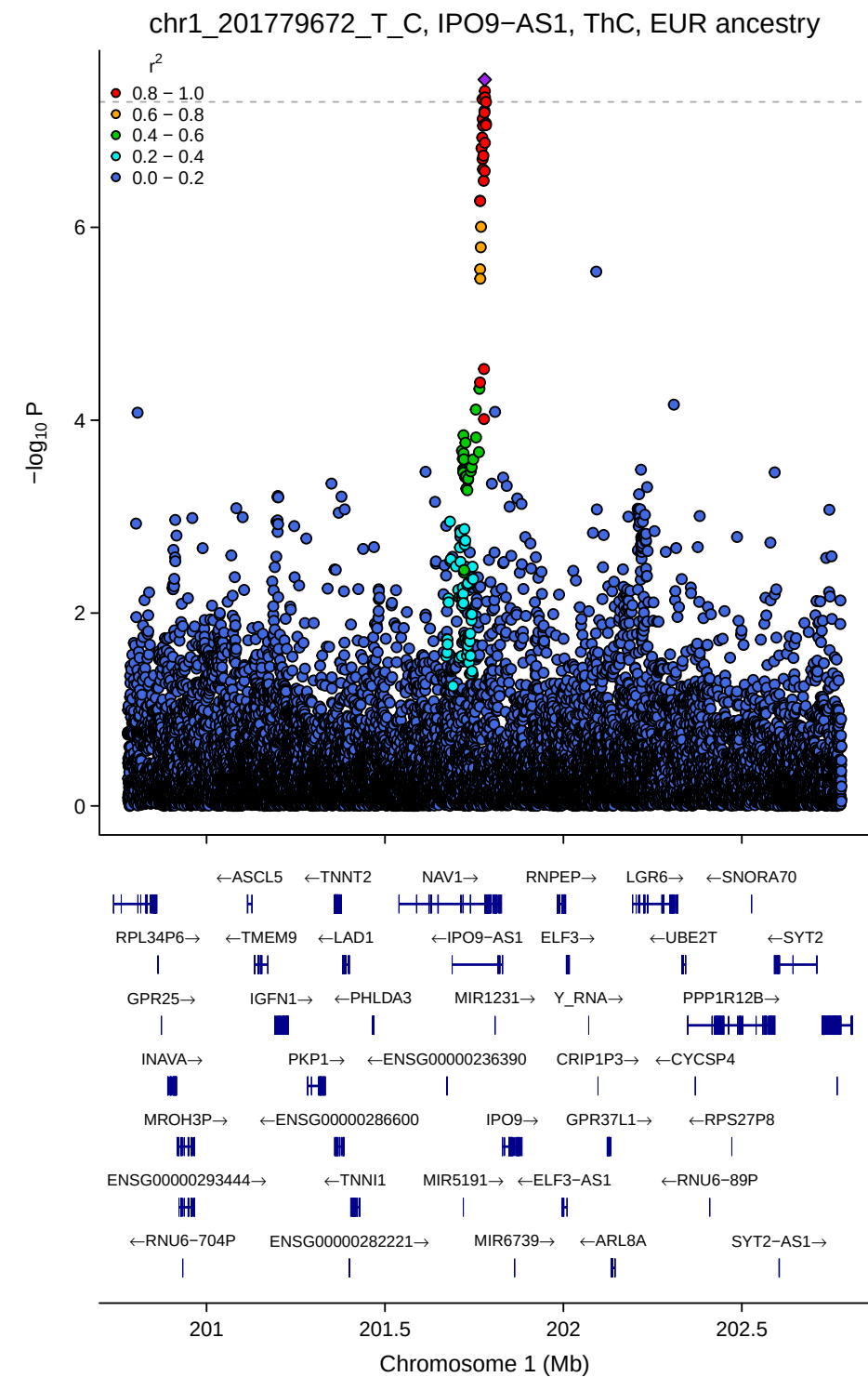
Supplementary Figure 2.1



Supplementary Figure 2.1

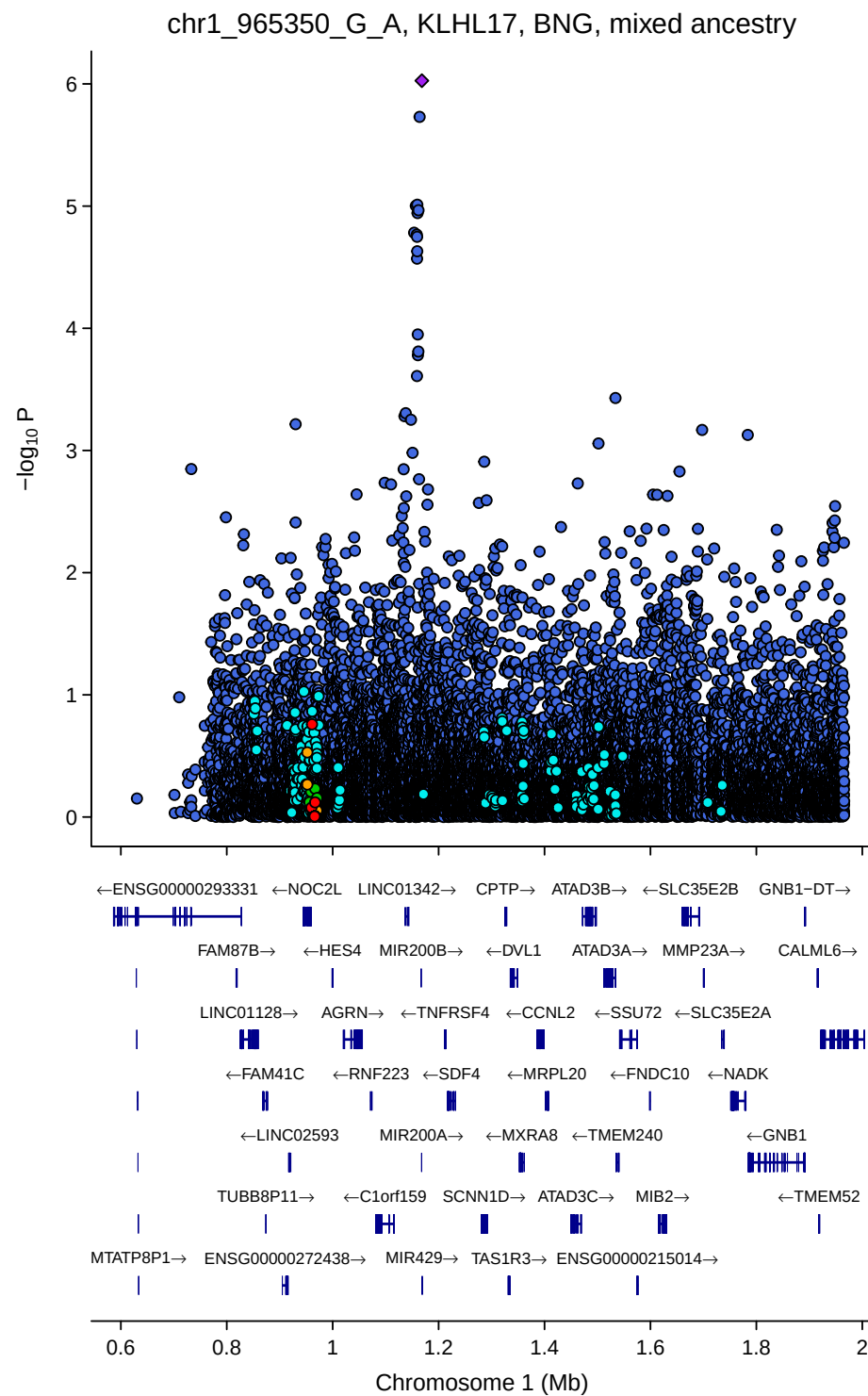
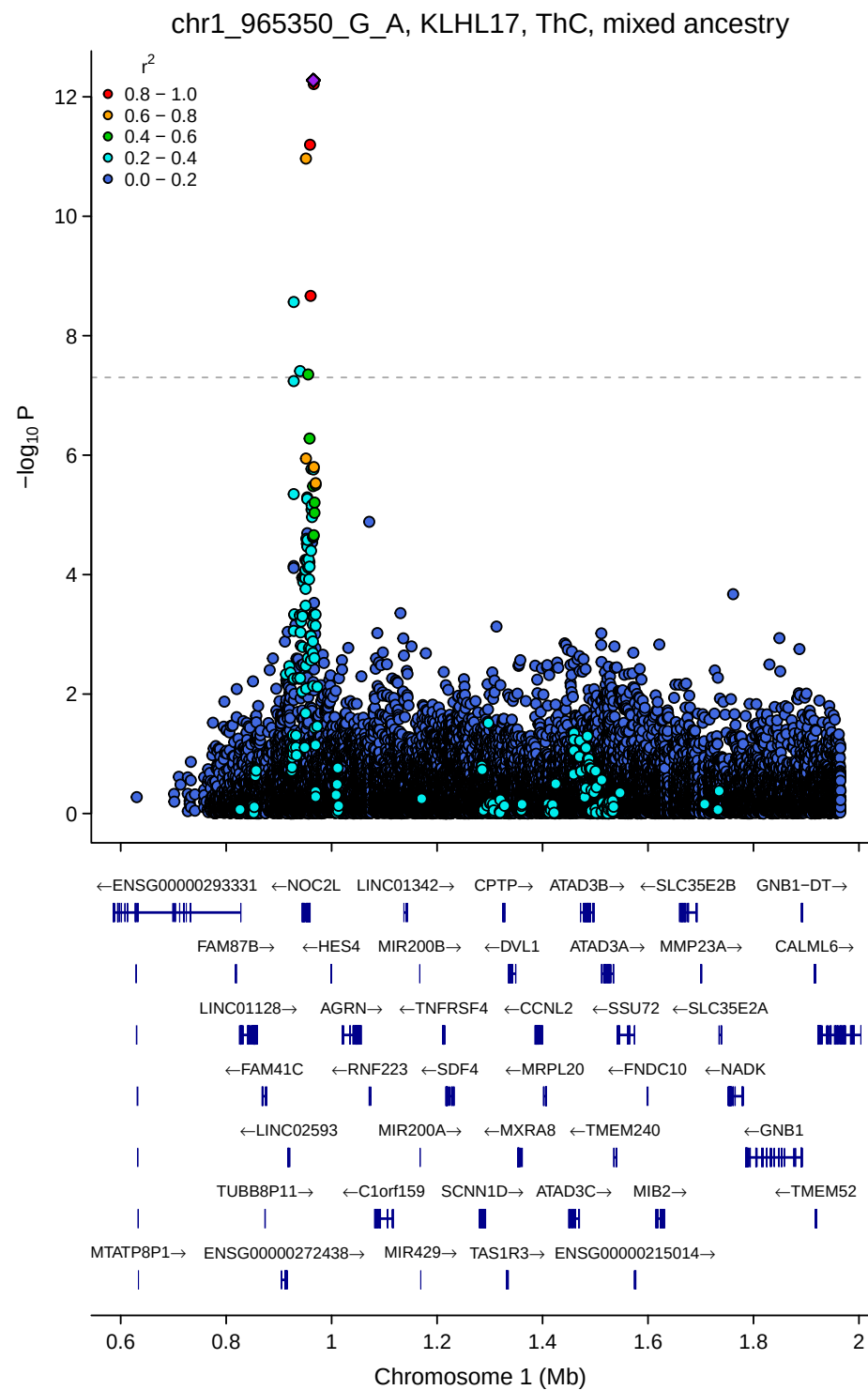


Supplementary Figure 2.1

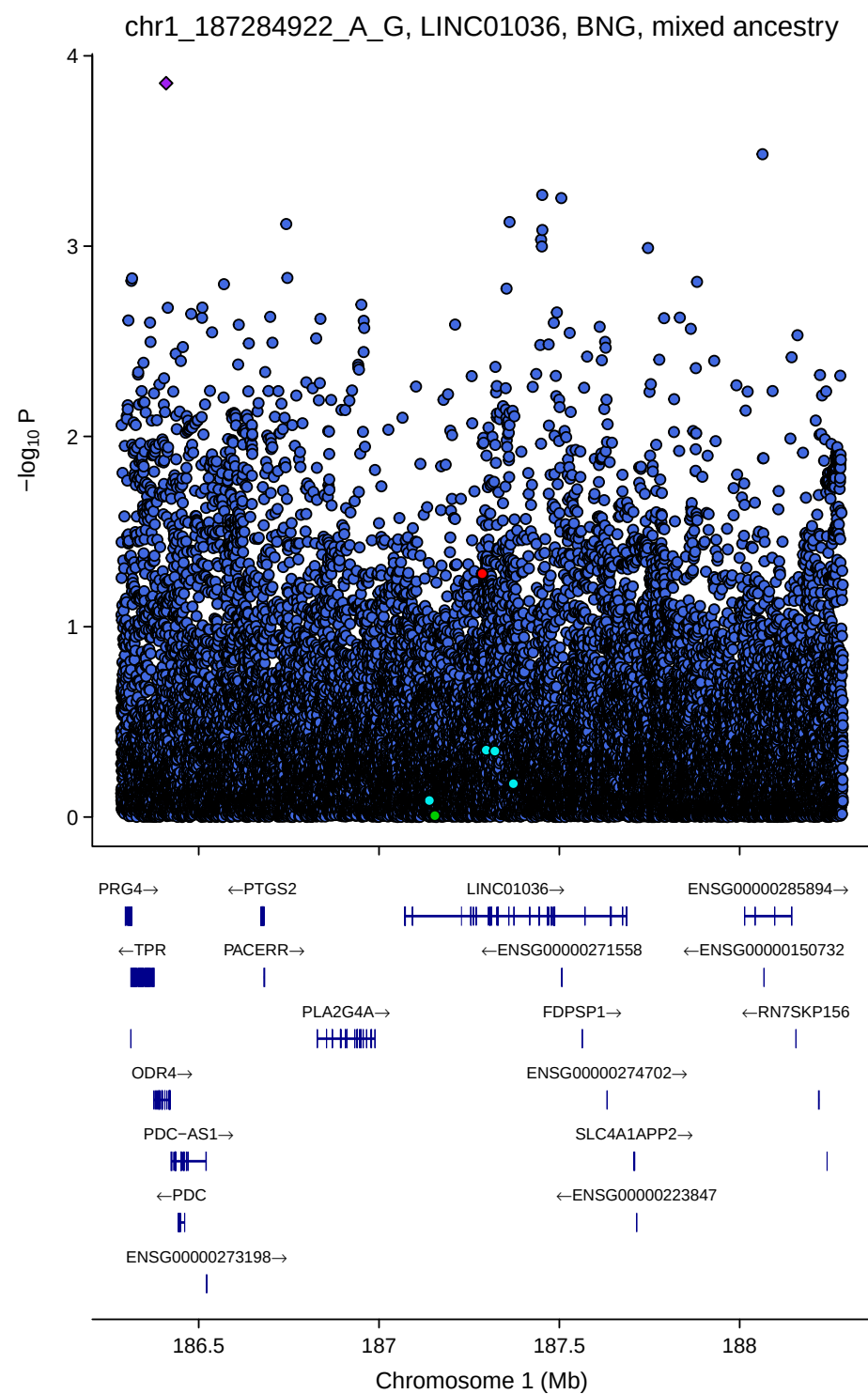
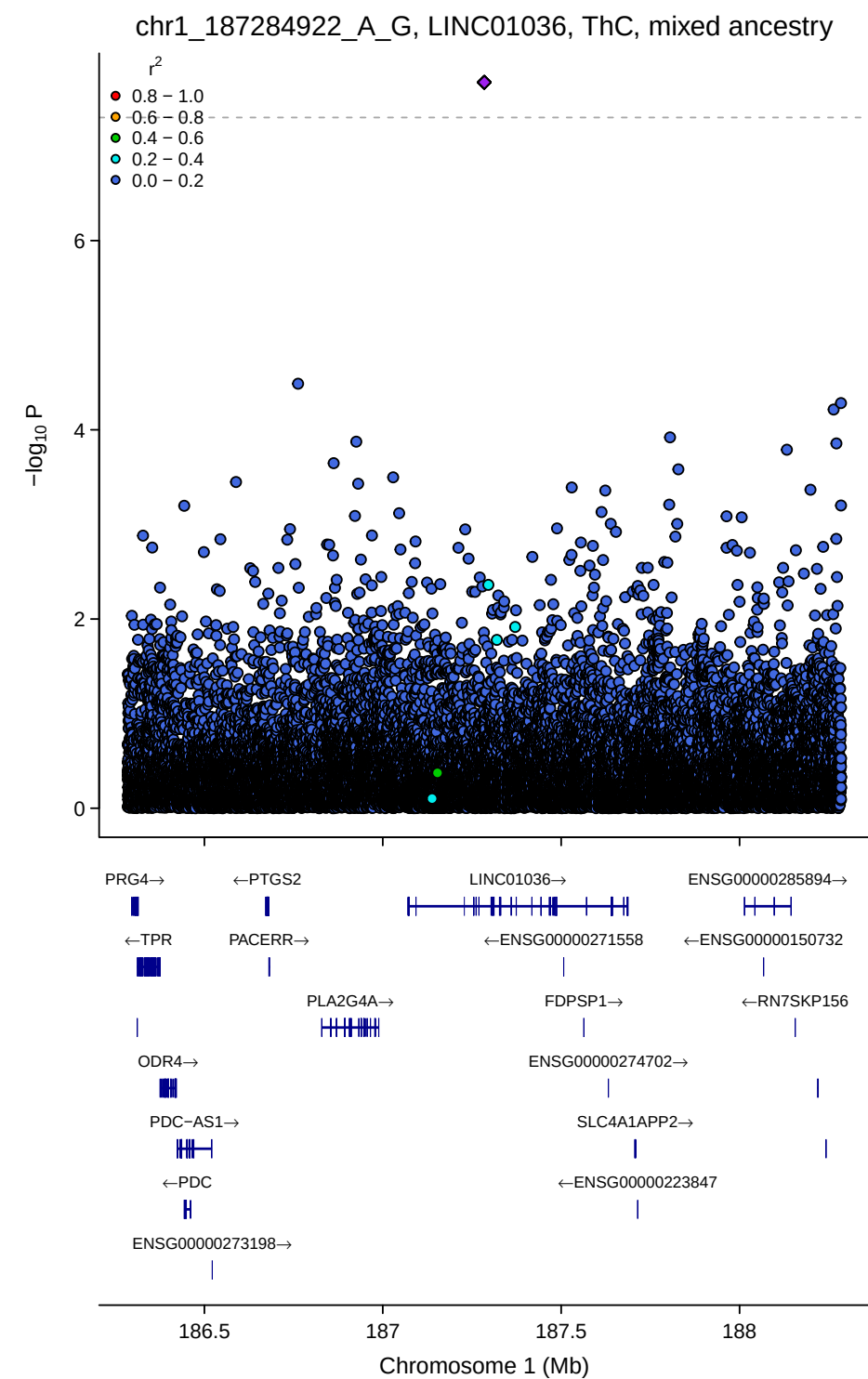




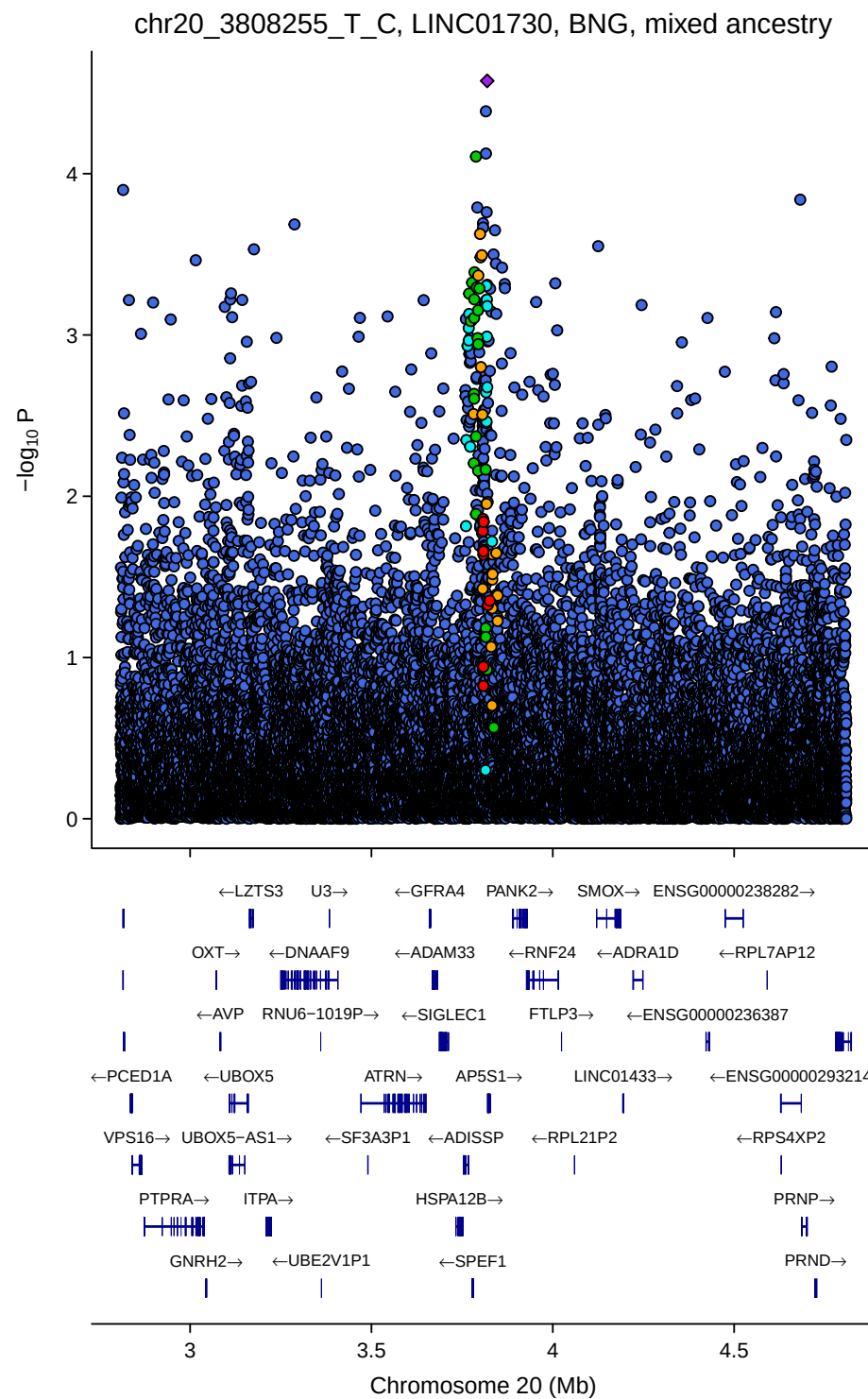
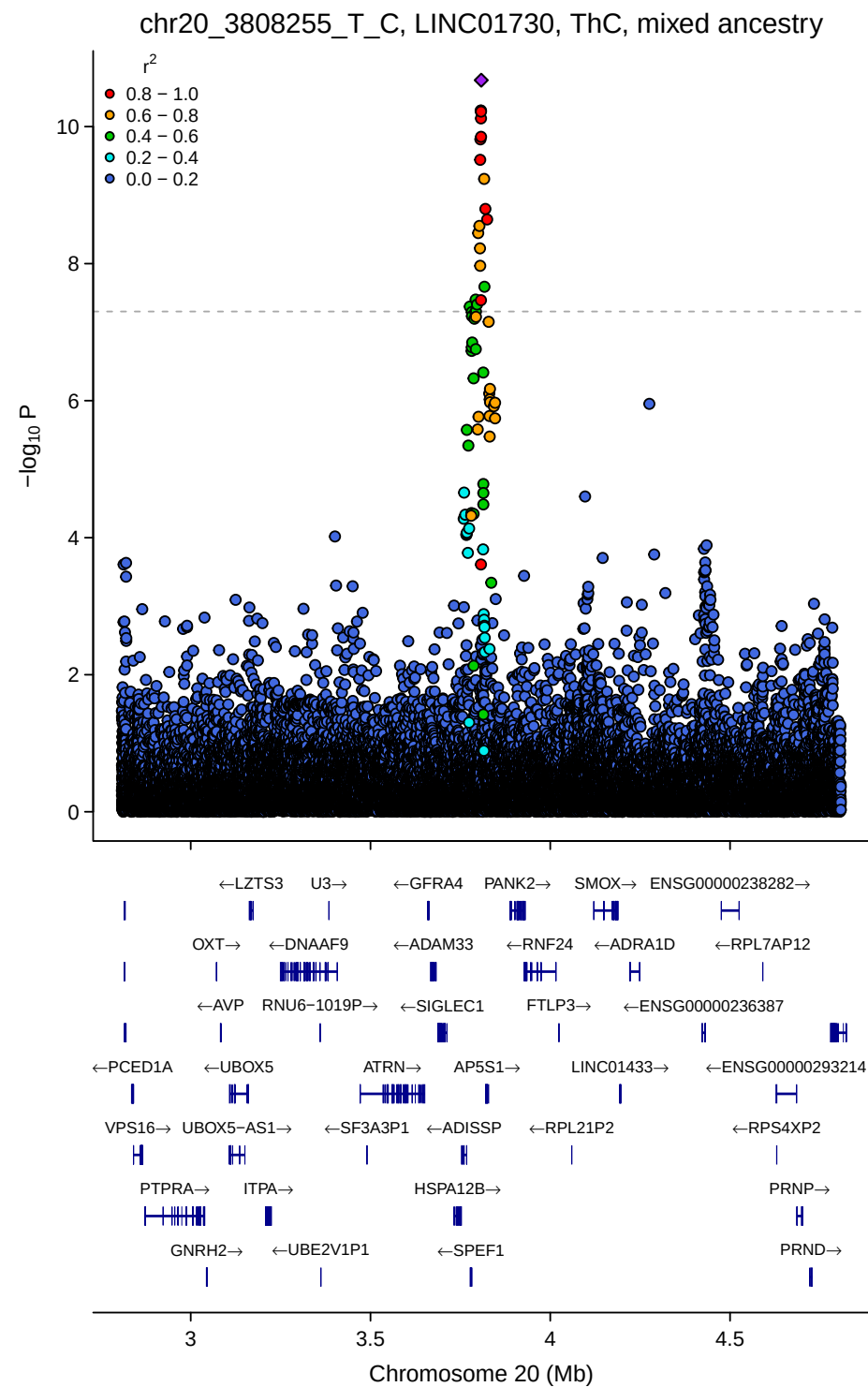
Supplementary Figure 2.1



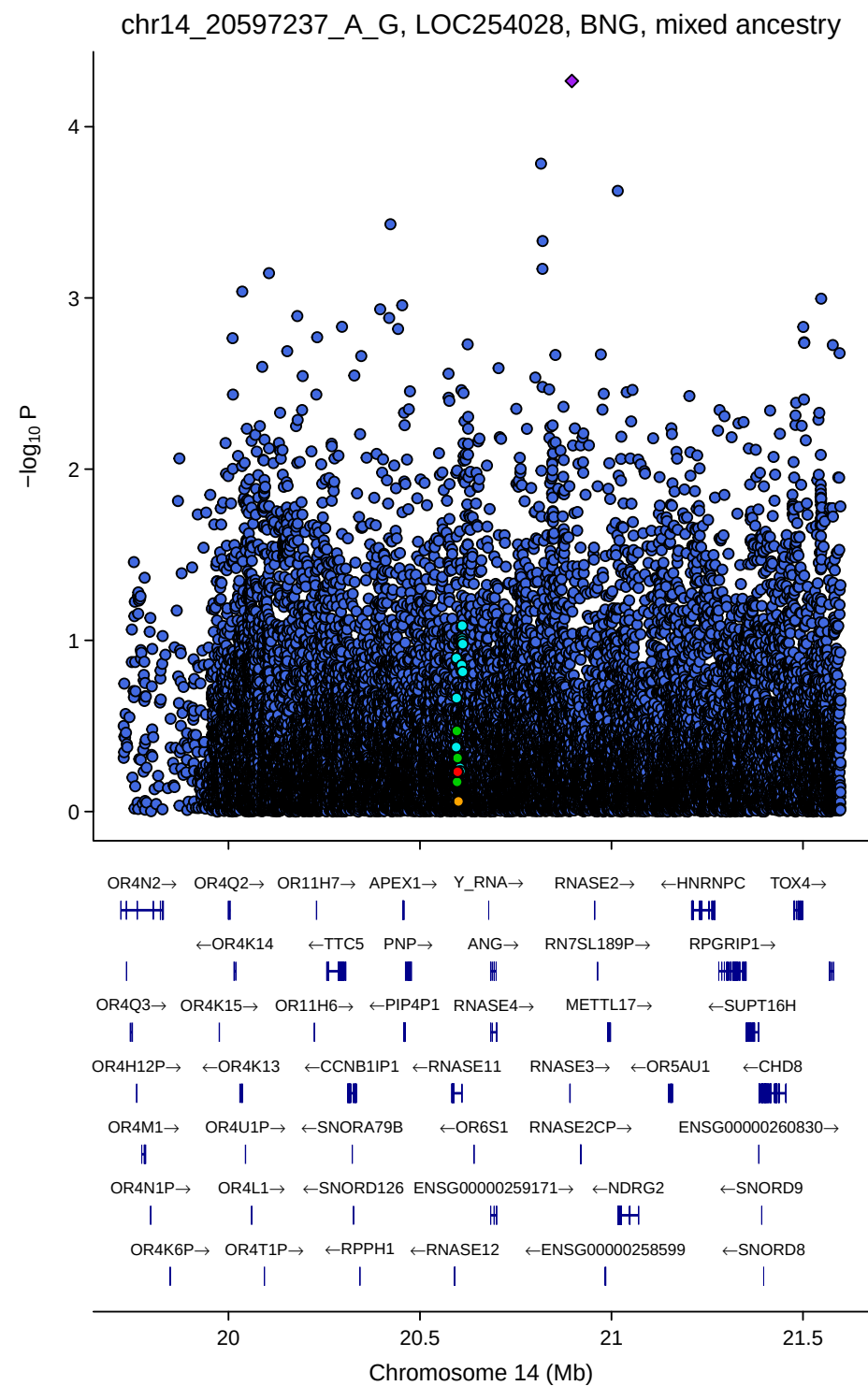
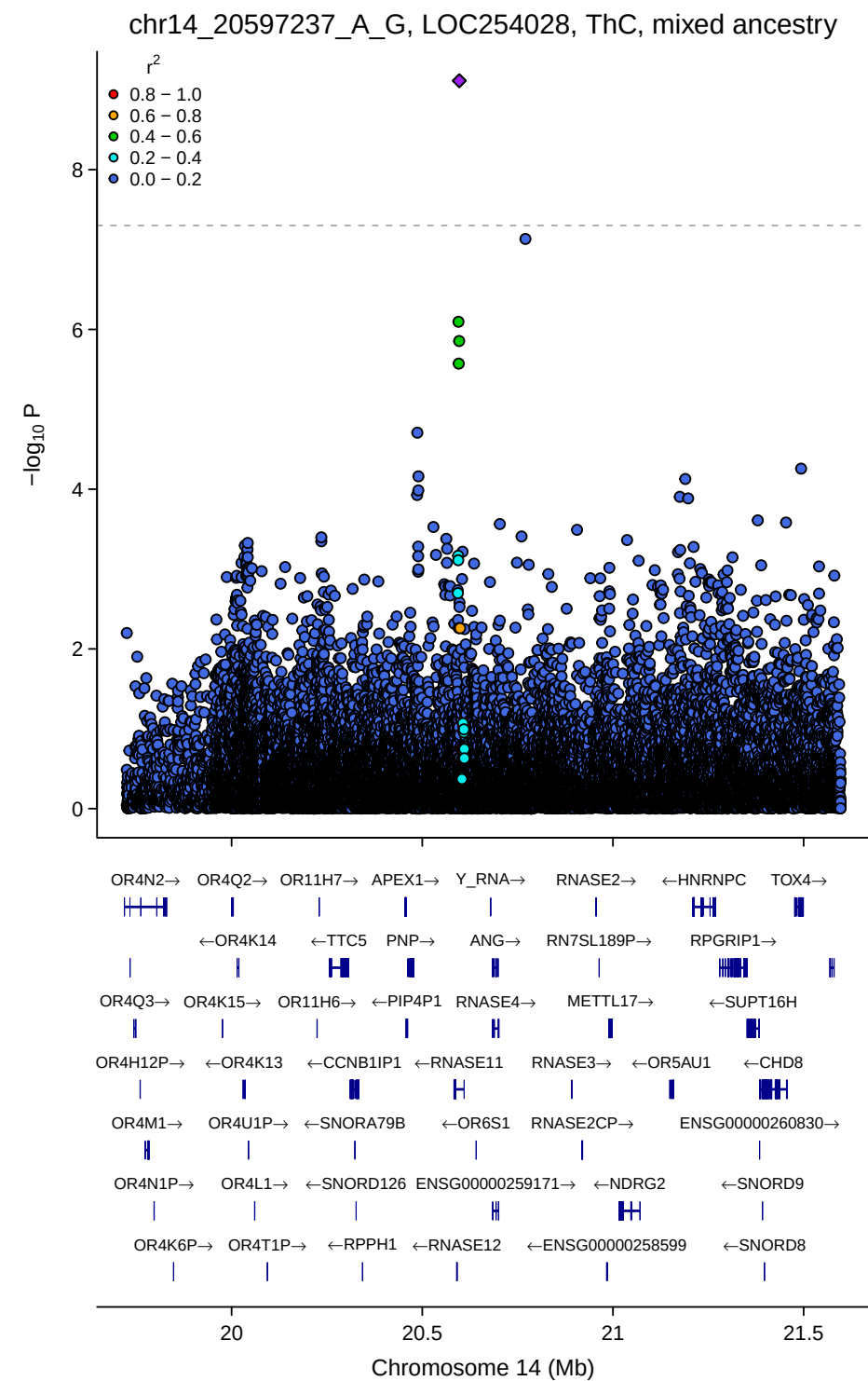
Supplementary Figure 2.1



Supplementary Figure 2.1

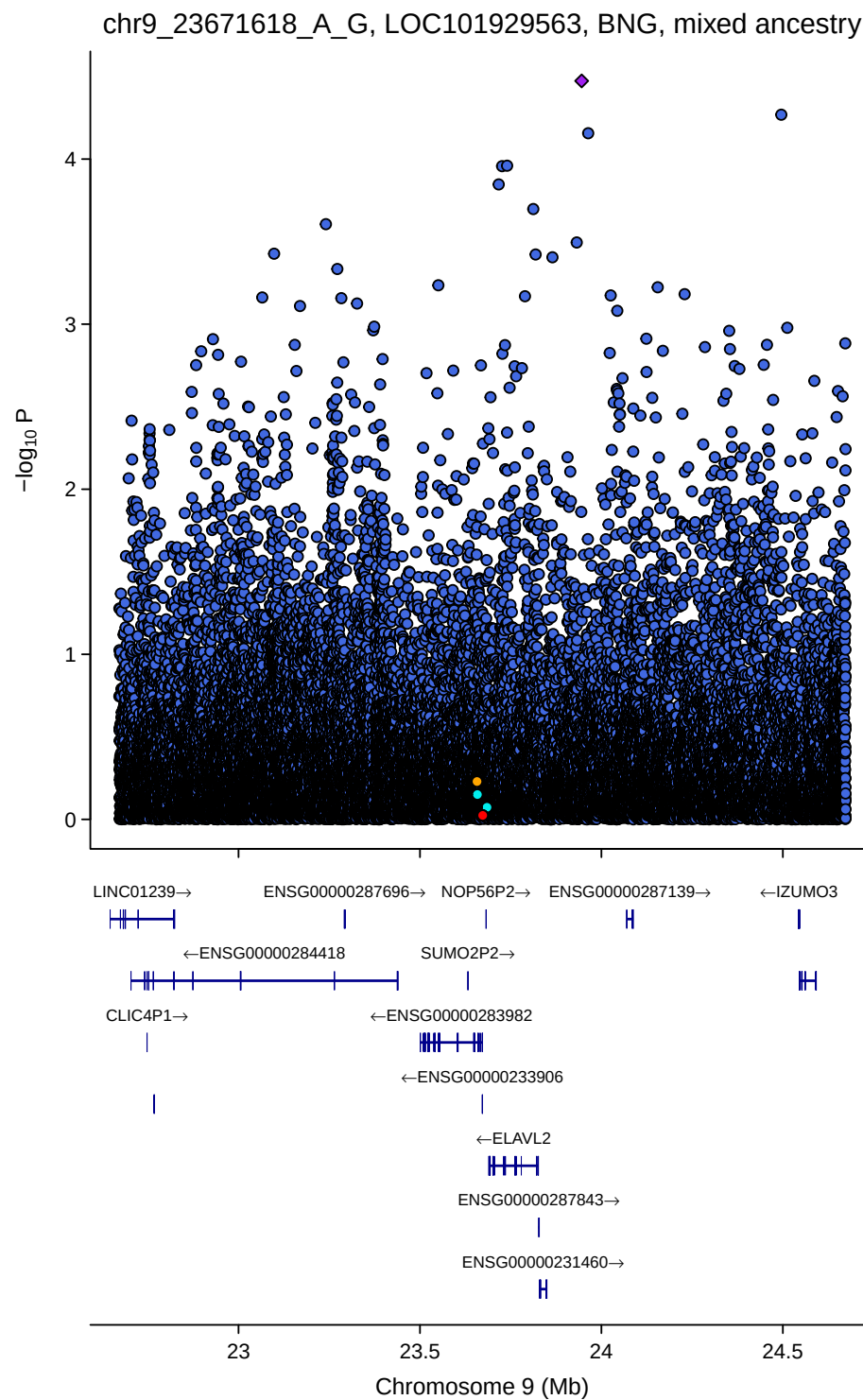
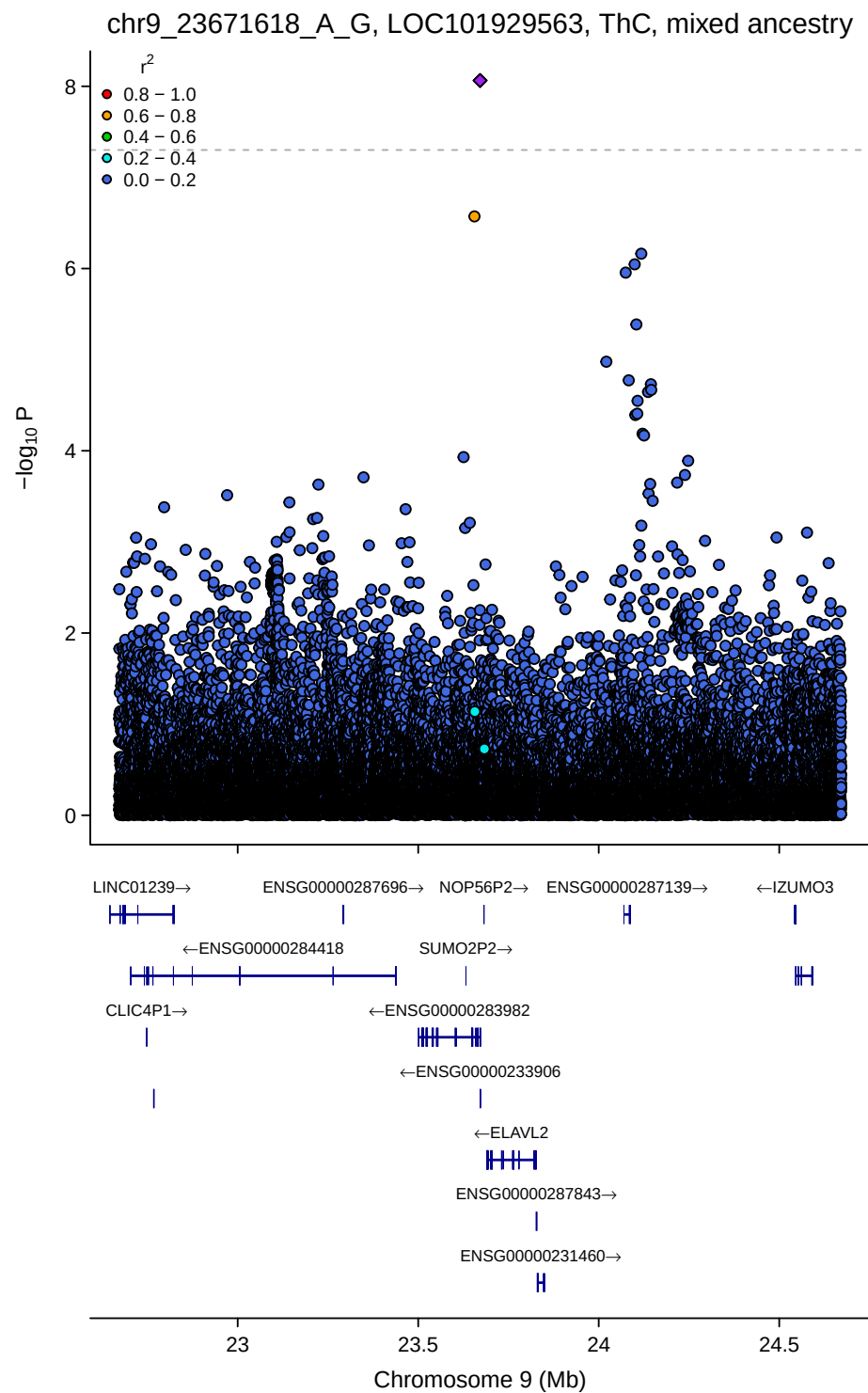


Supplementary Figure 2.1

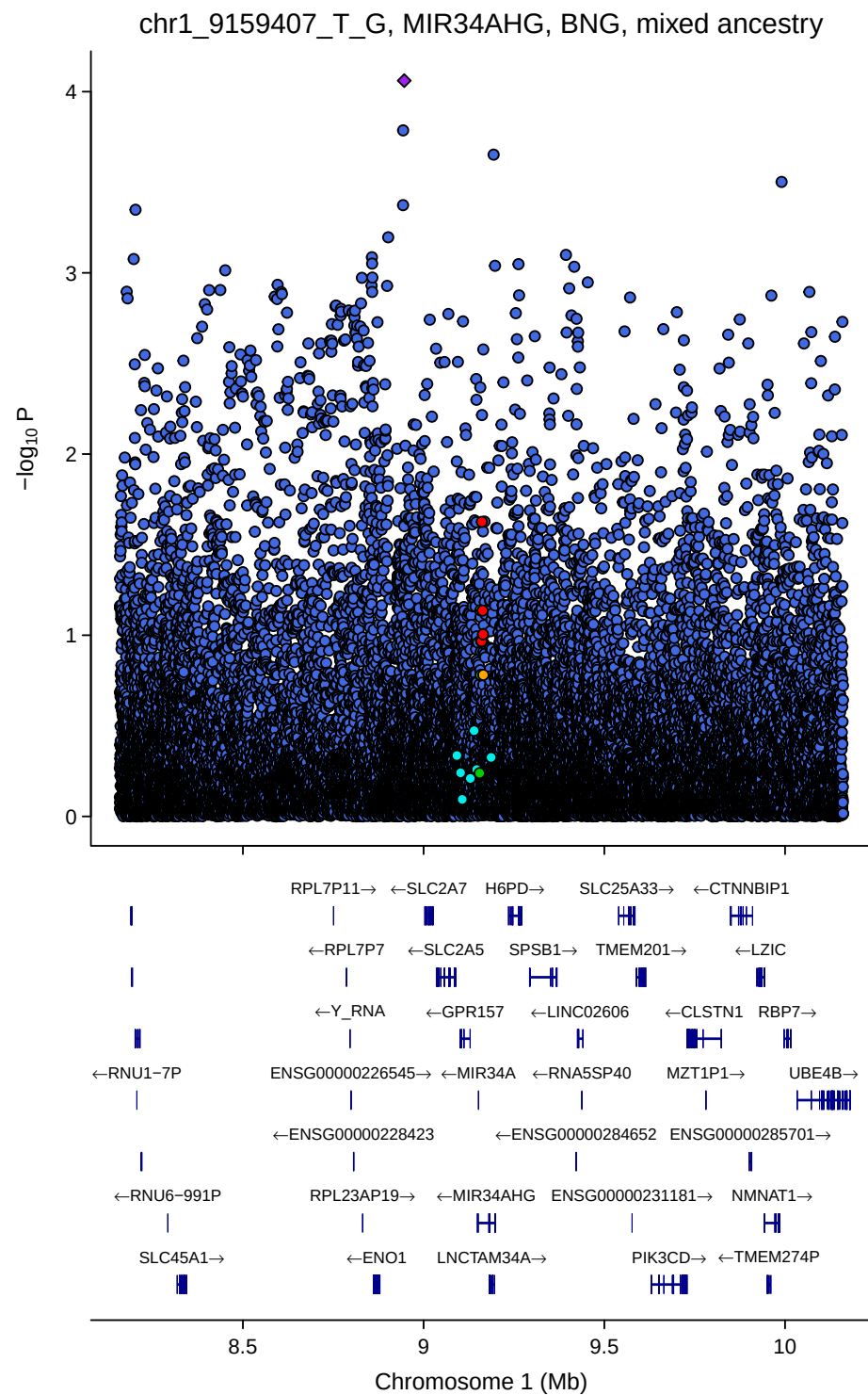
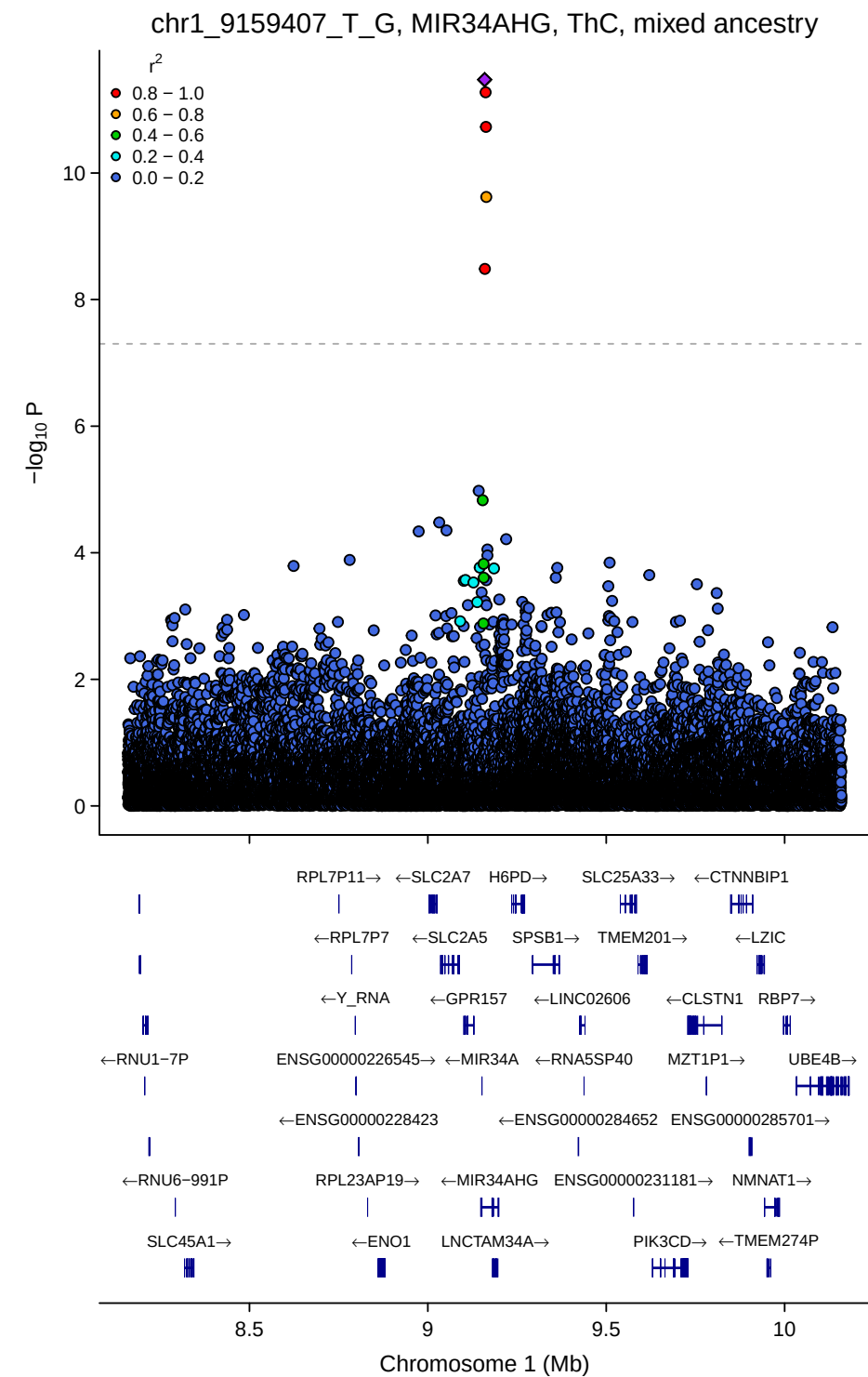




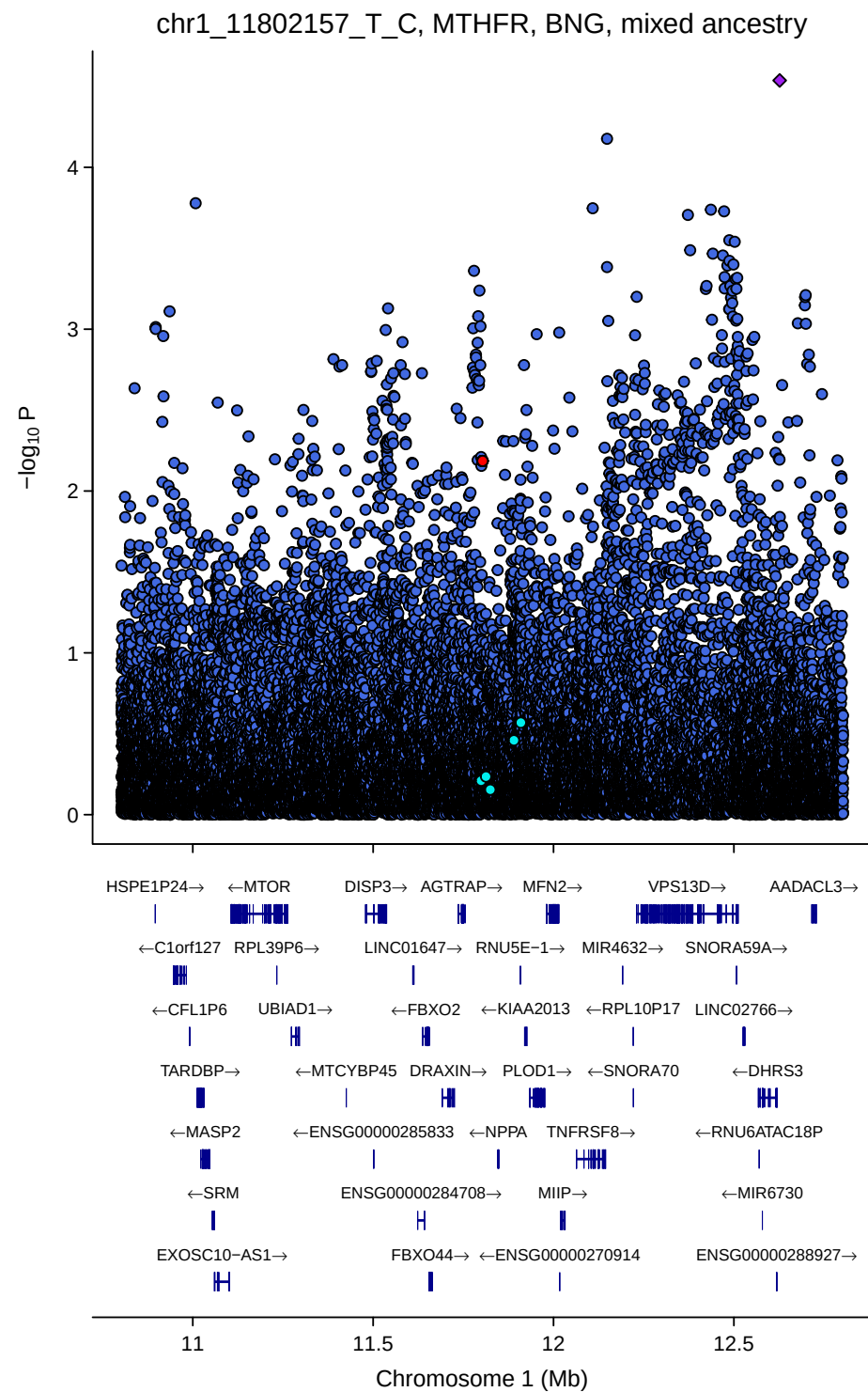
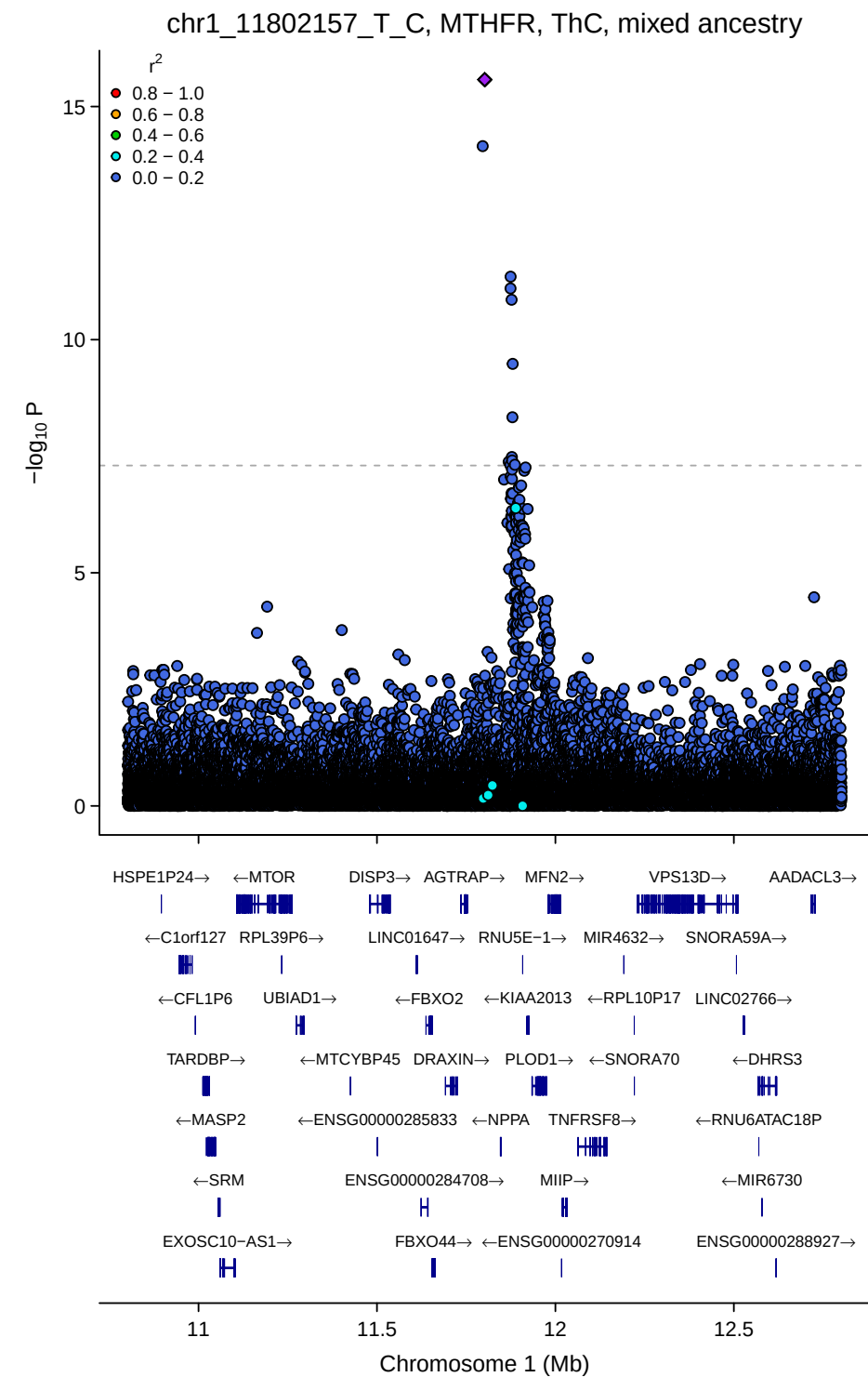
Supplementary Figure 2.1



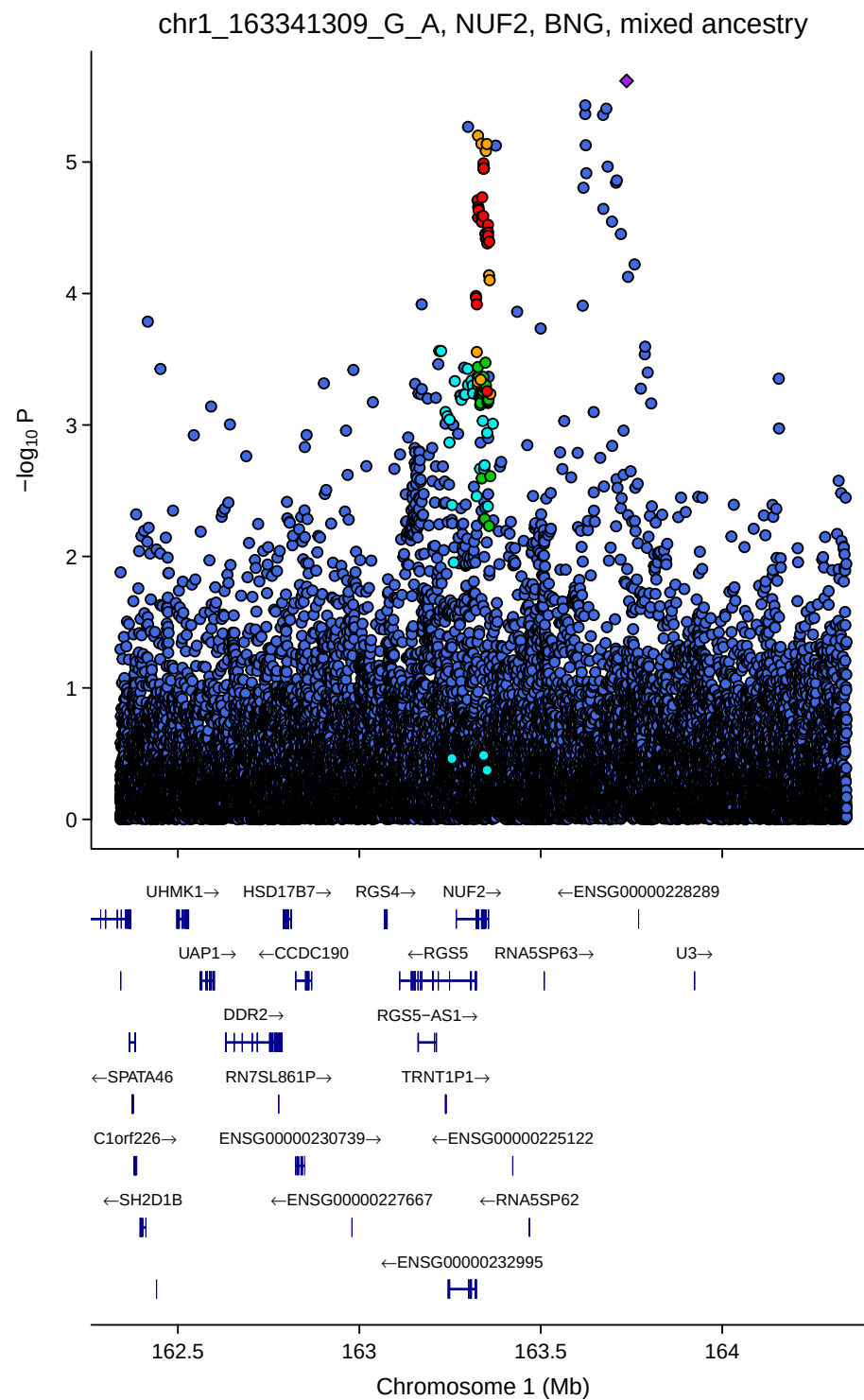
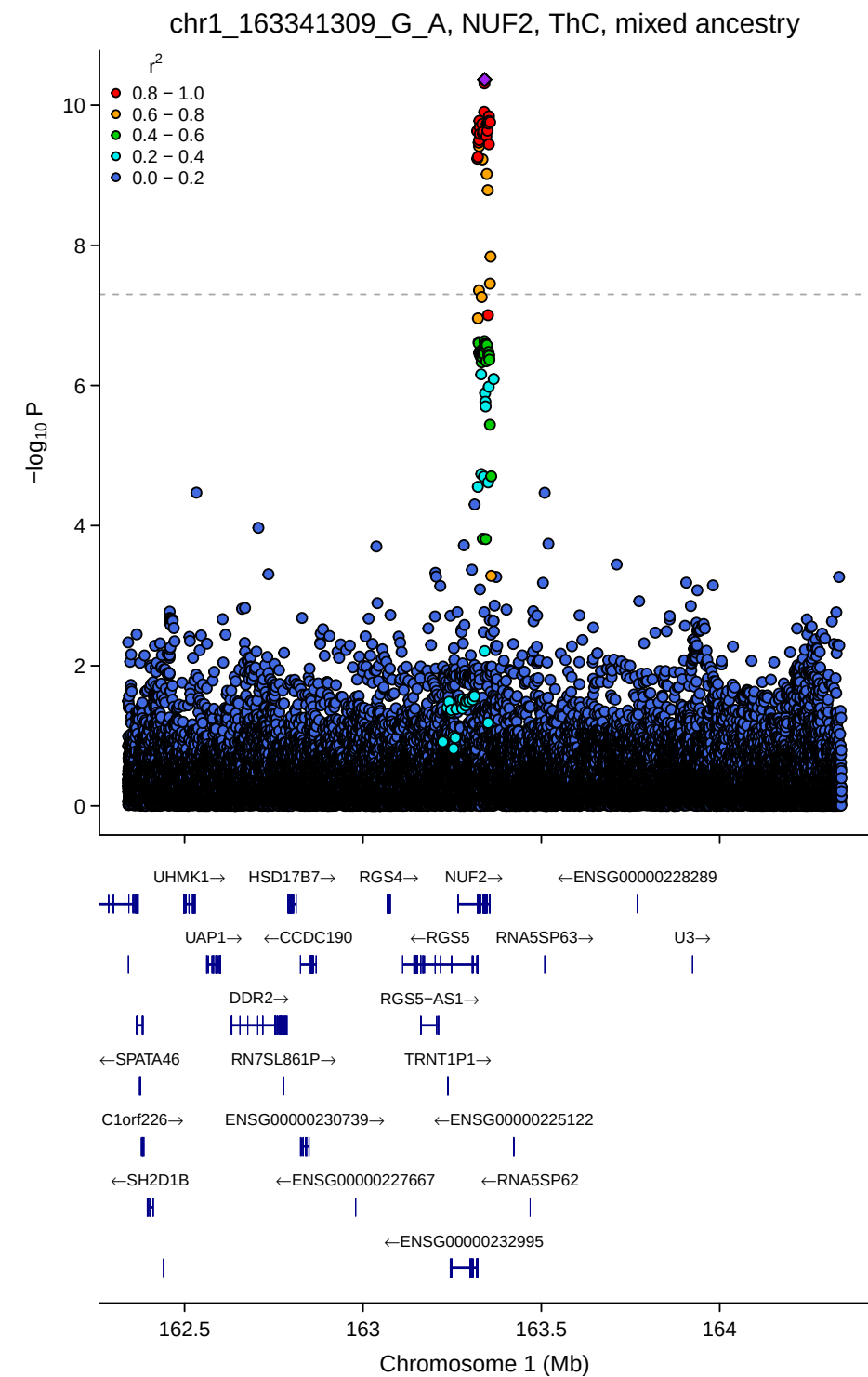
Supplementary Figure 2.1



Supplementary Figure 2.1

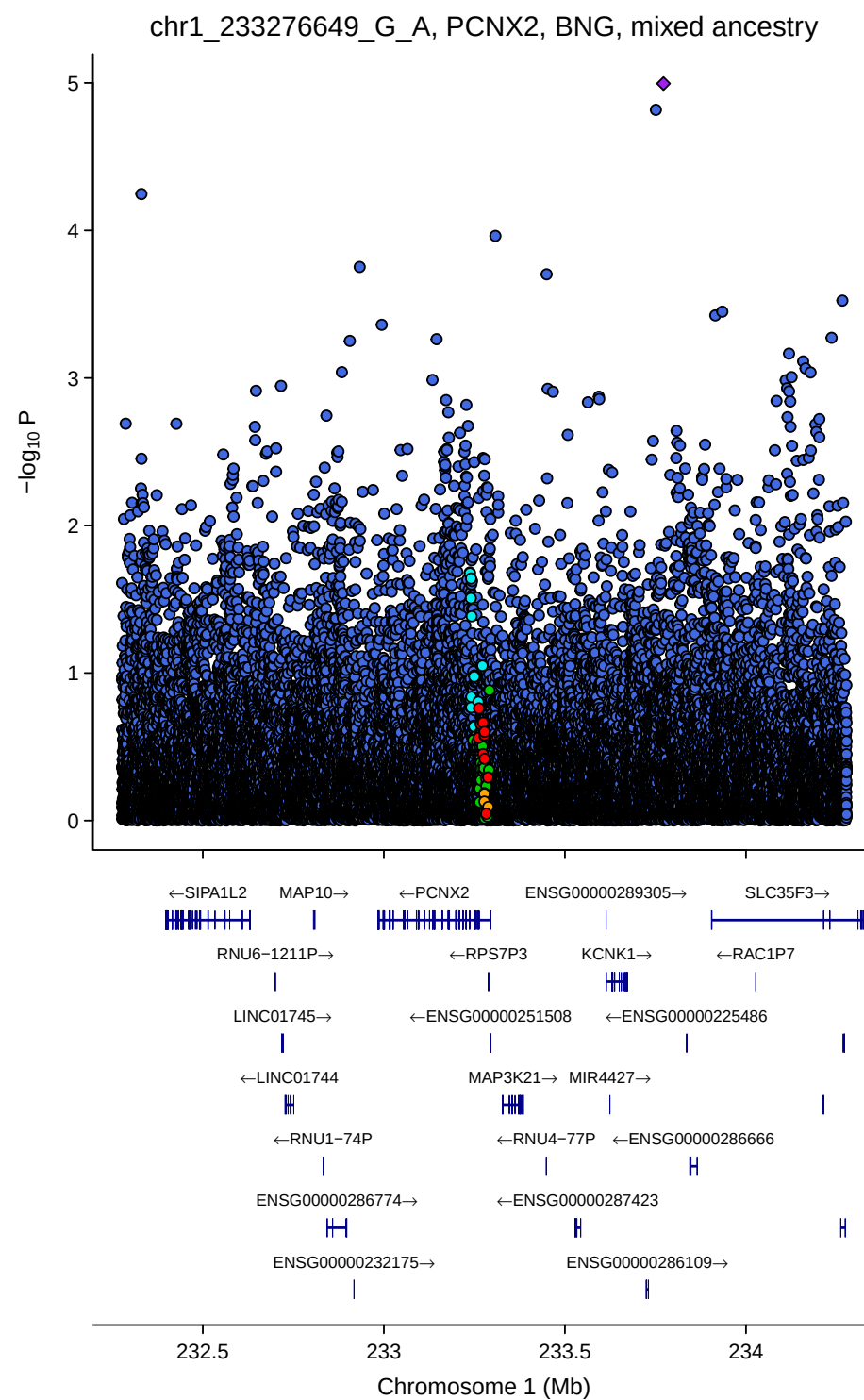
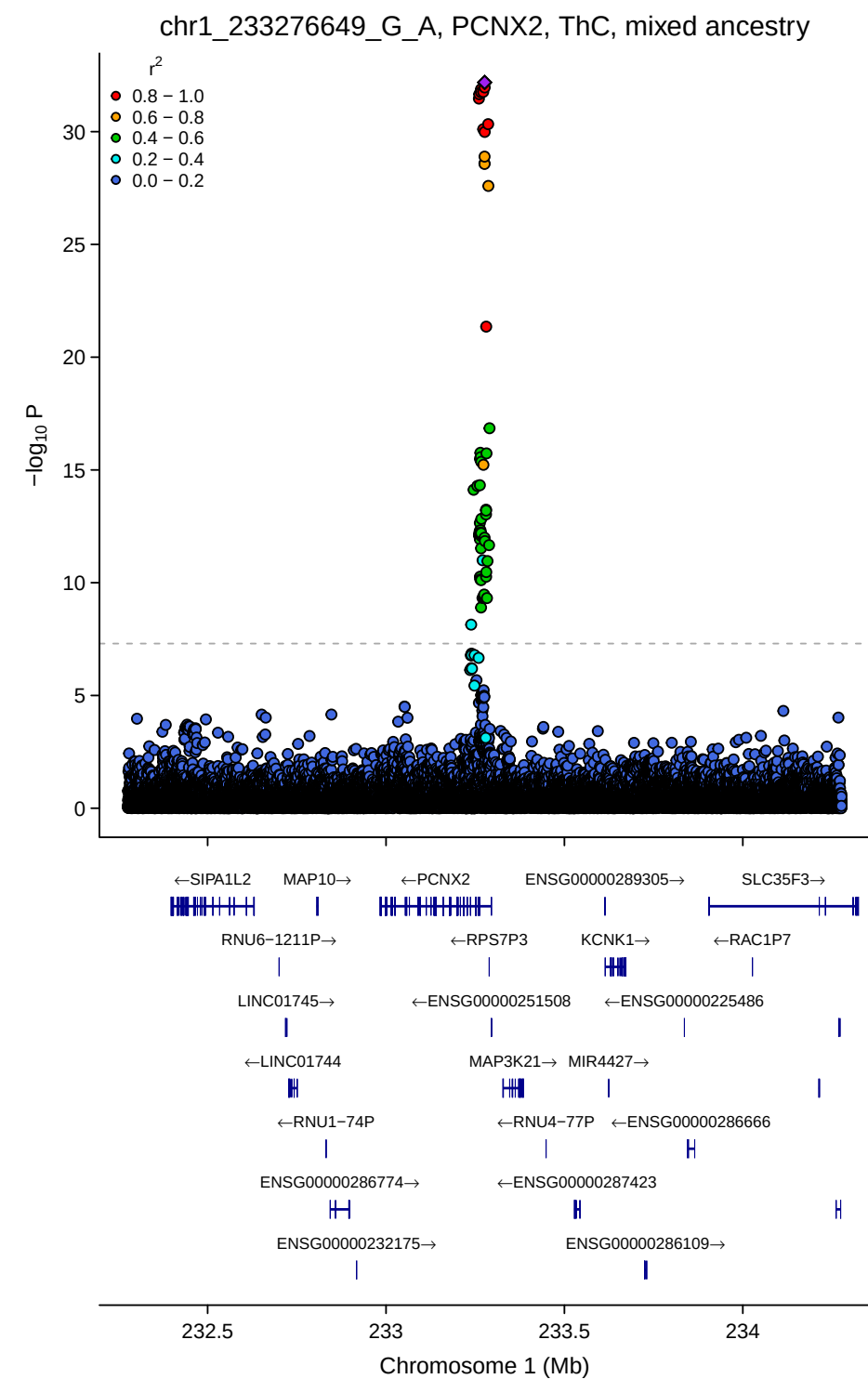


Supplementary Figure 2.1

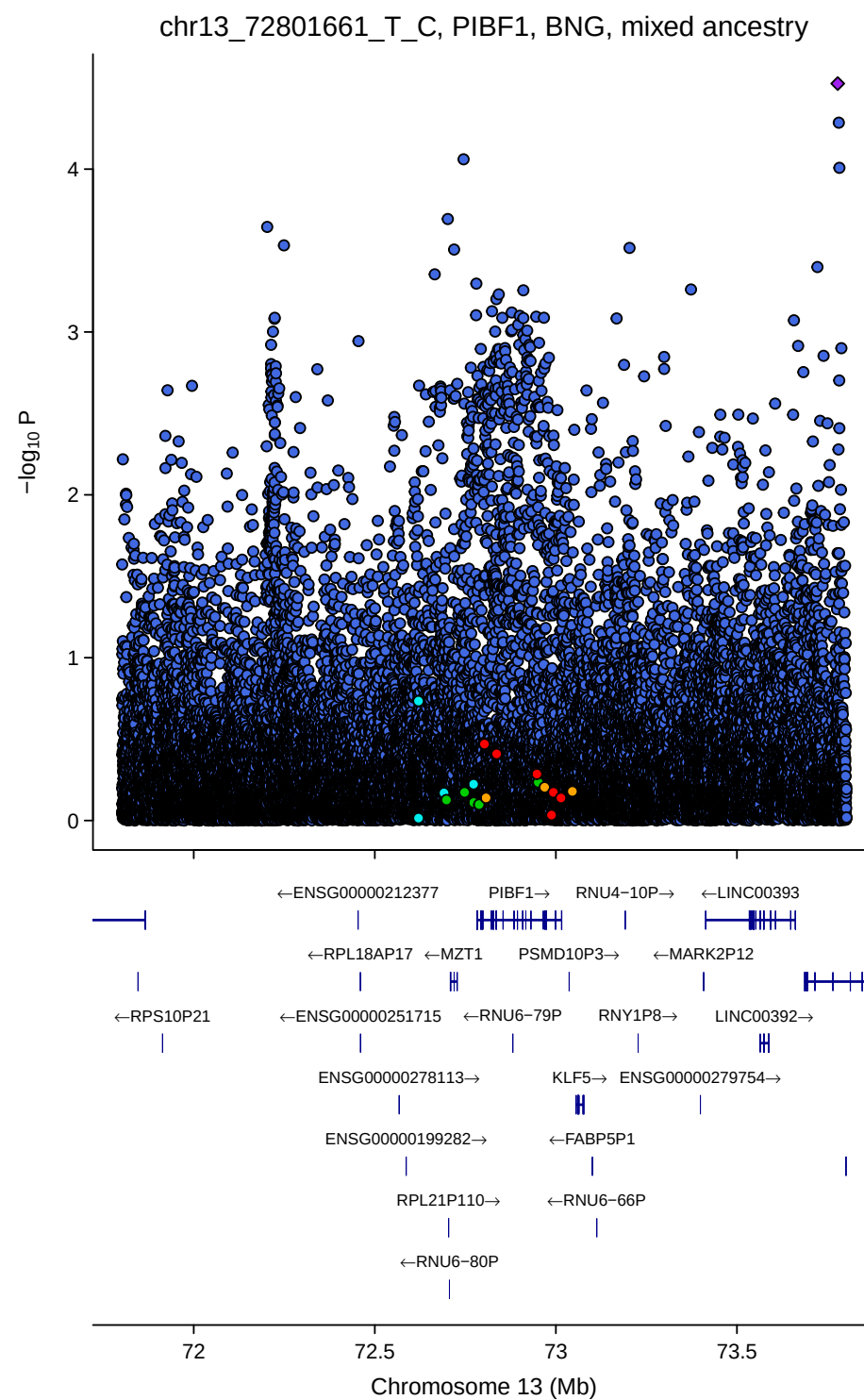
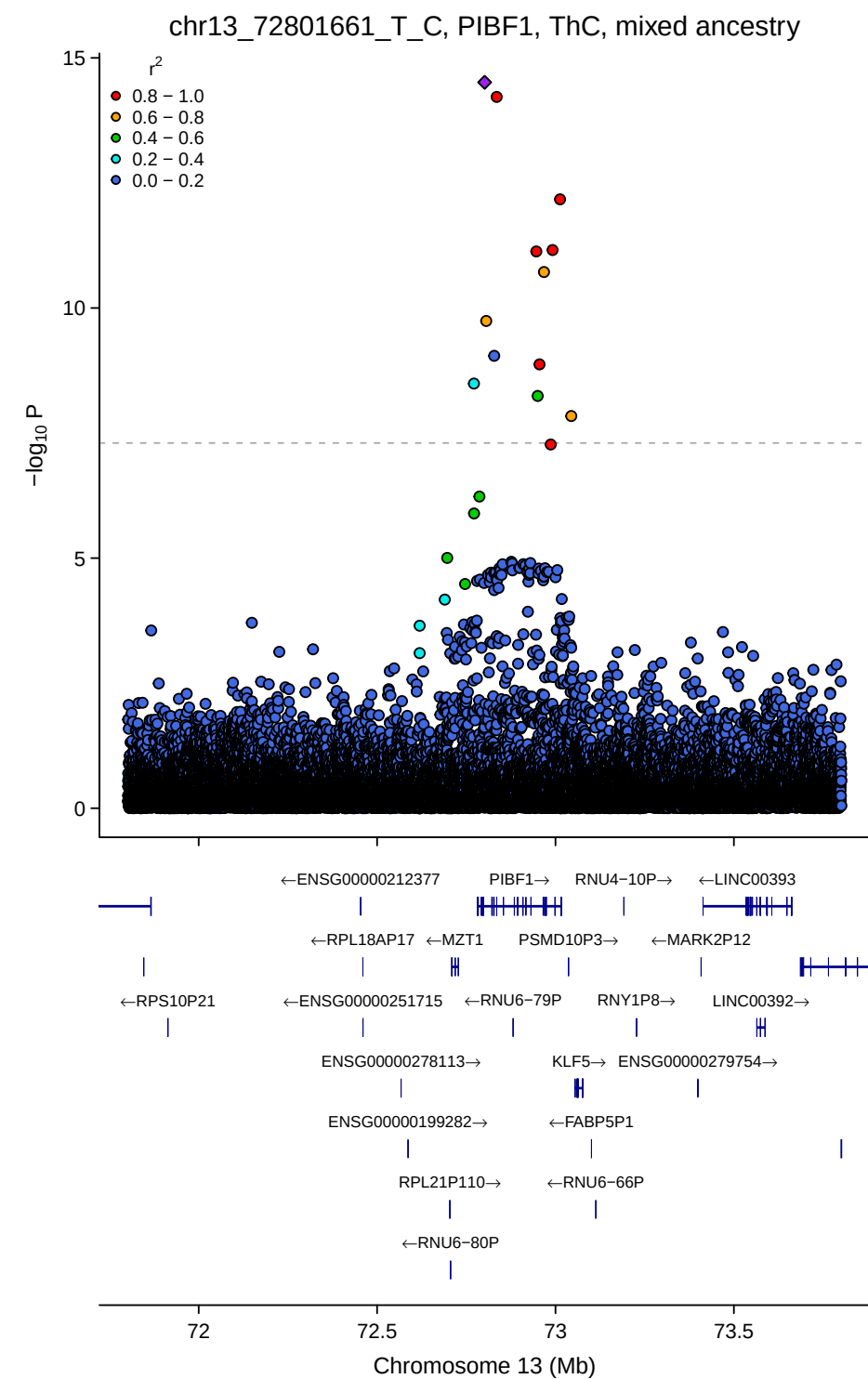




Supplementary Figure 2.1

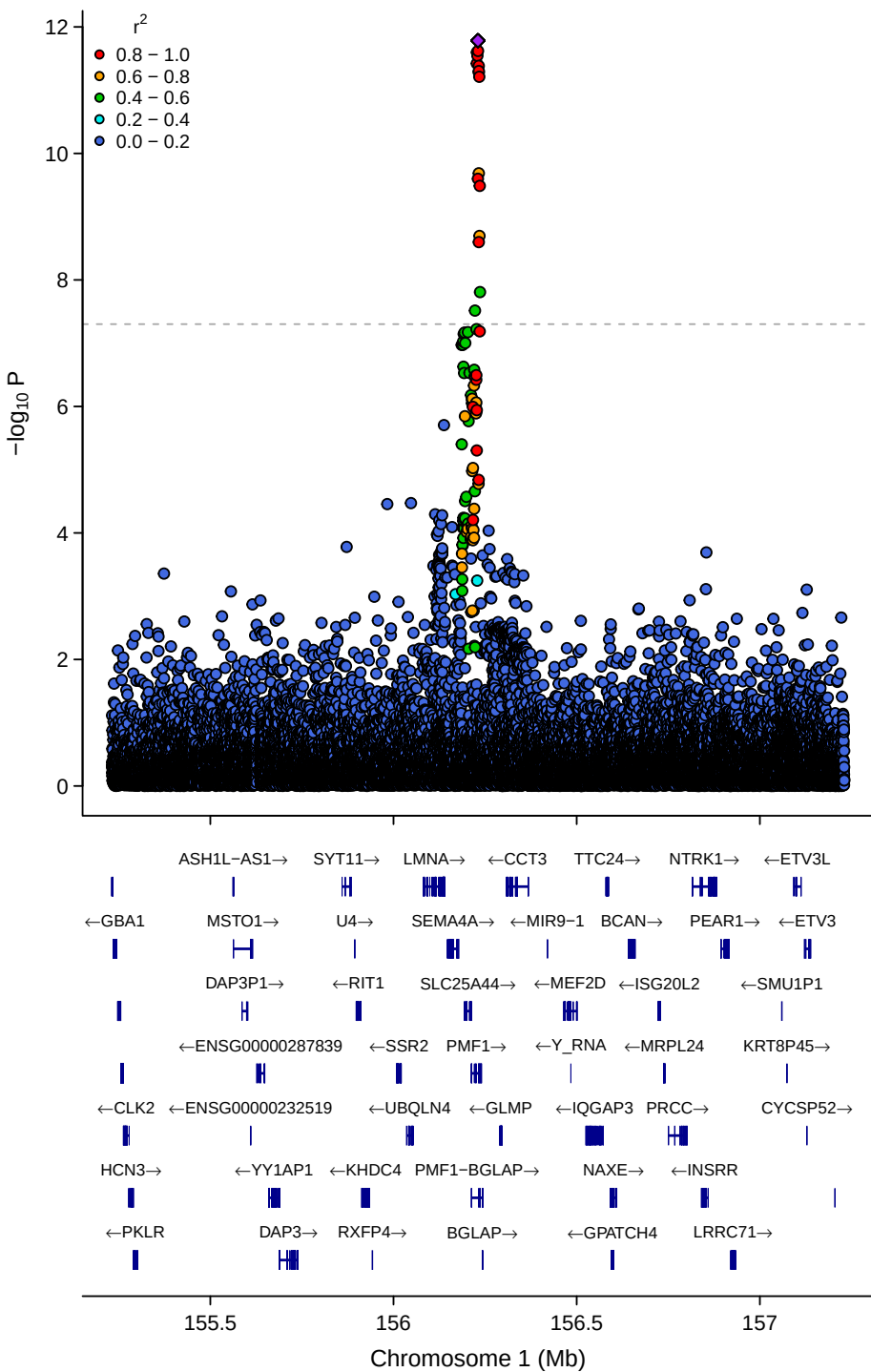


Supplementary Figure 2.1

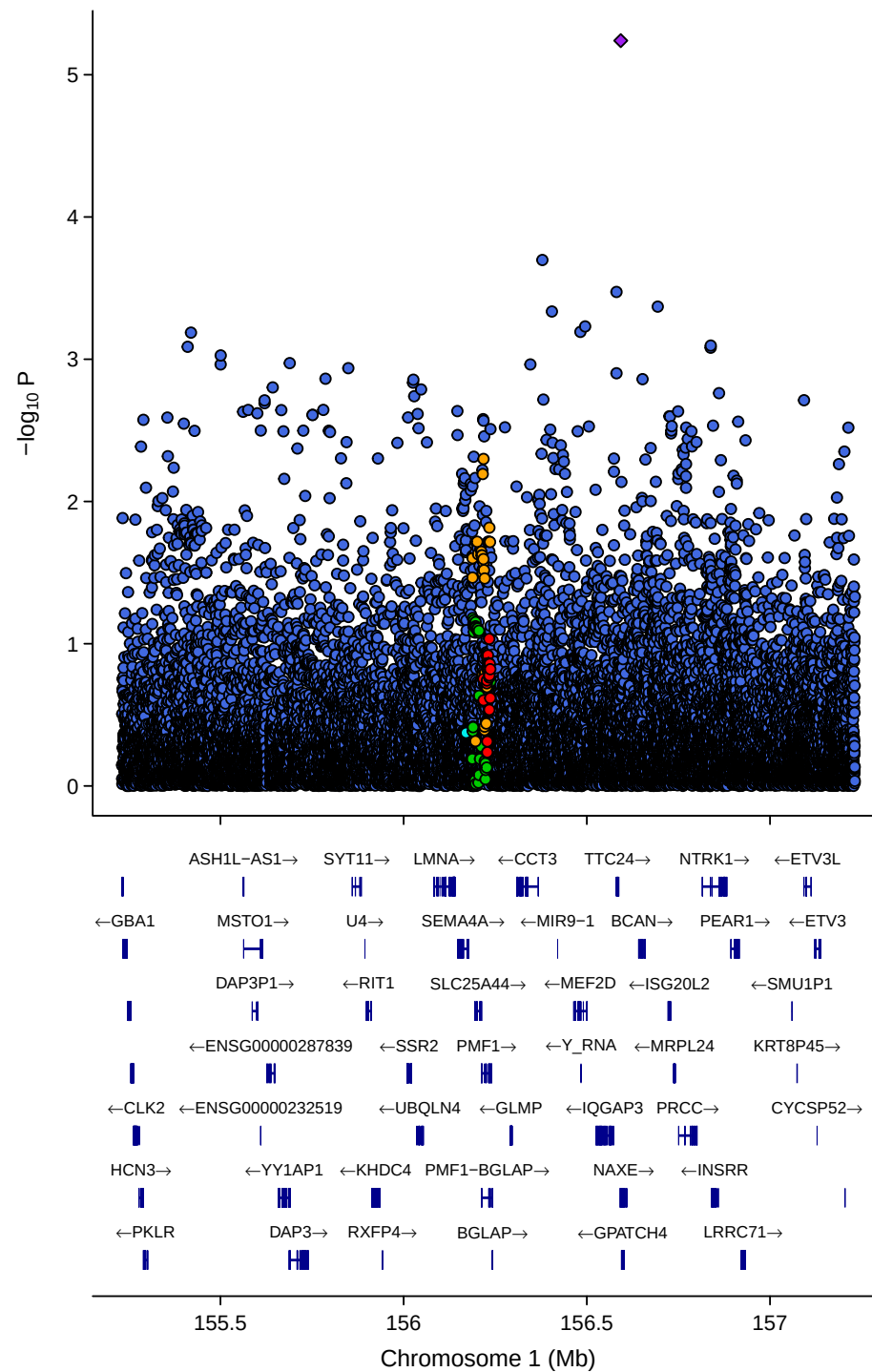


Supplementary Figure 2.1

chr1\_156230654\_G\_C, PMF1;PMF1-BGLAP, ThC, mixed ancestry

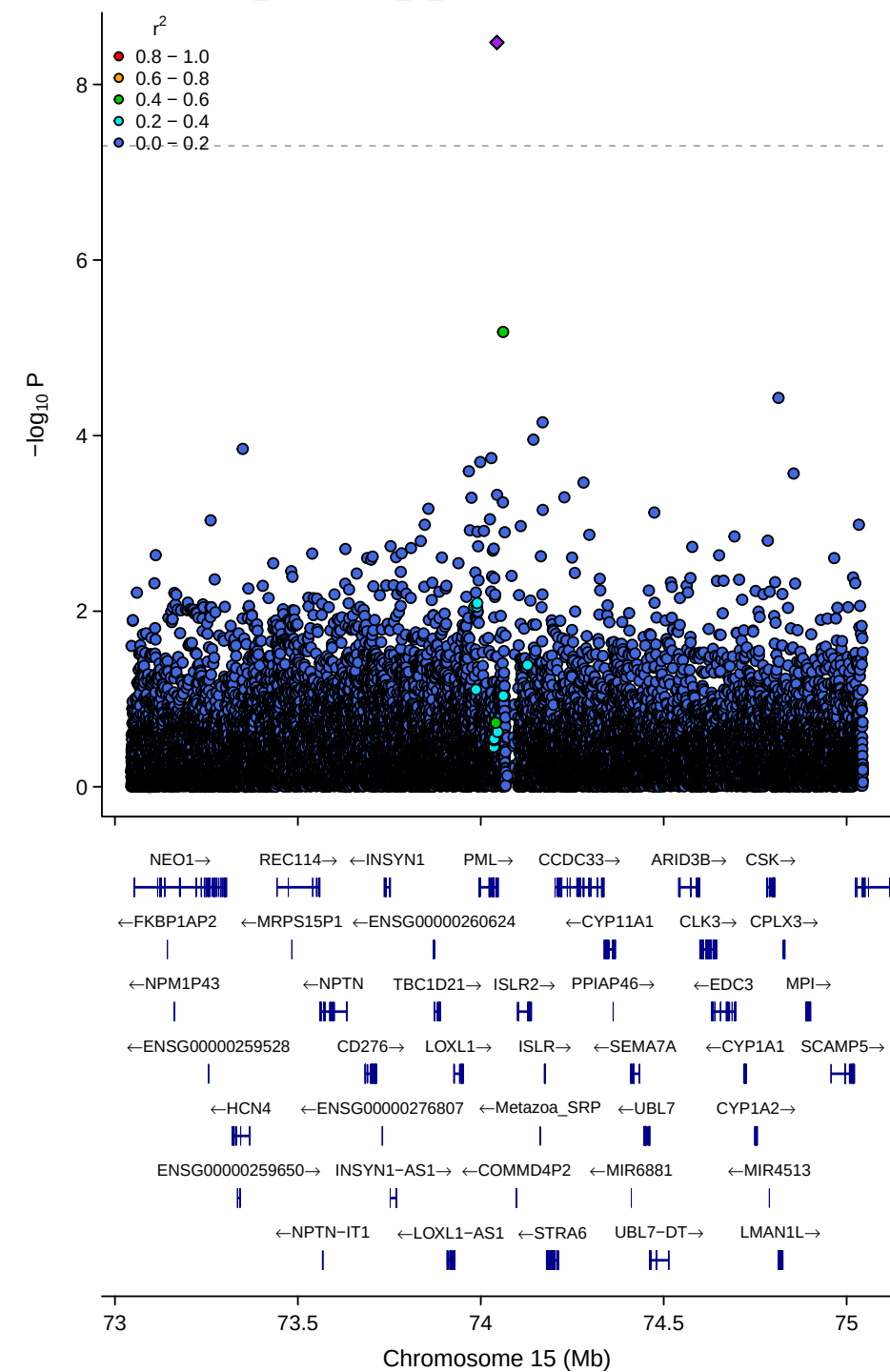


chr1\_156230654\_G\_C, PMF1;PMF1-BGLAP, BNG, mixed ancestry

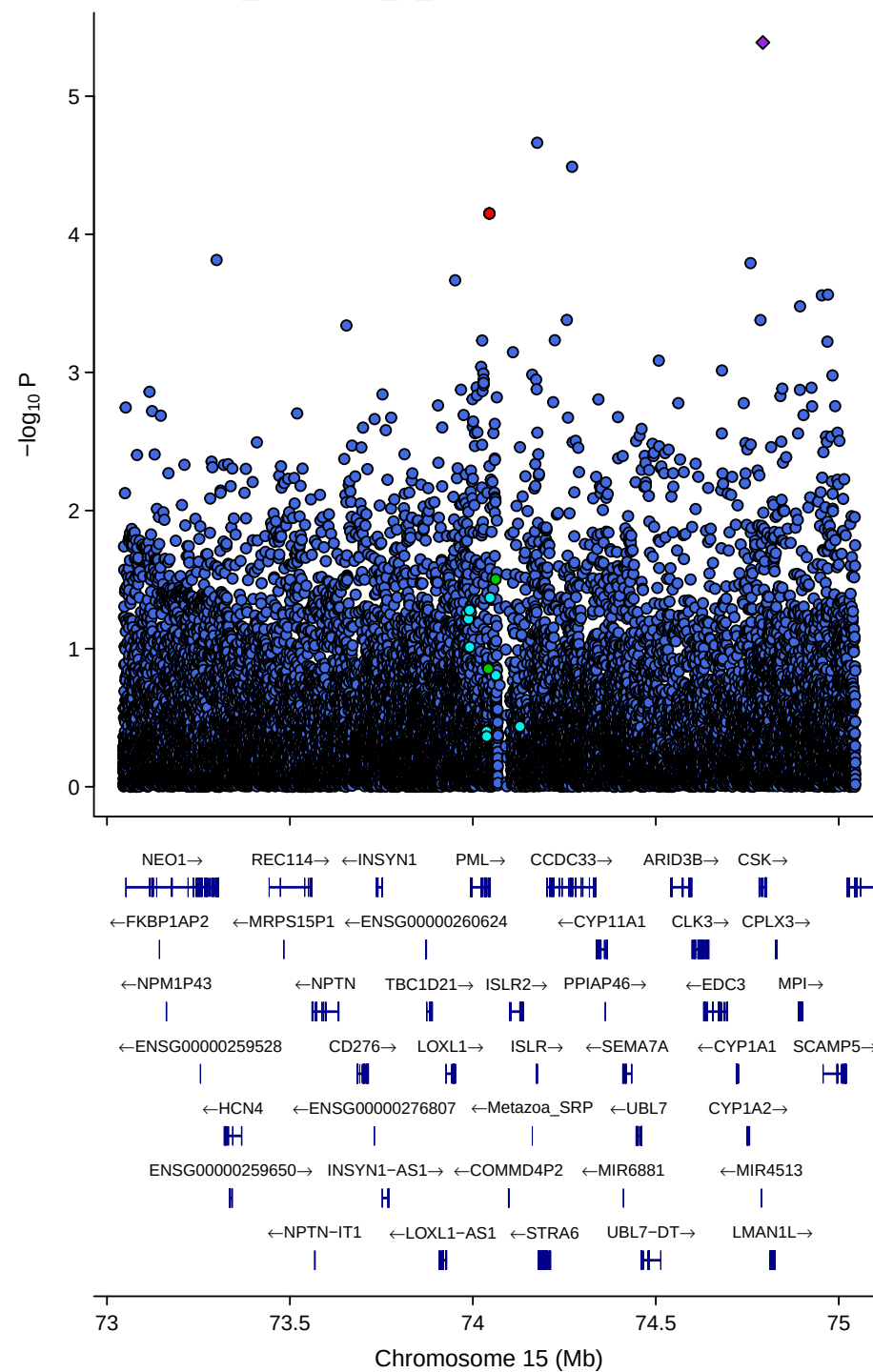


Supplementary Figure 2.1

chr15\_74044292\_T\_C, PML, ThC, mixed ancestry

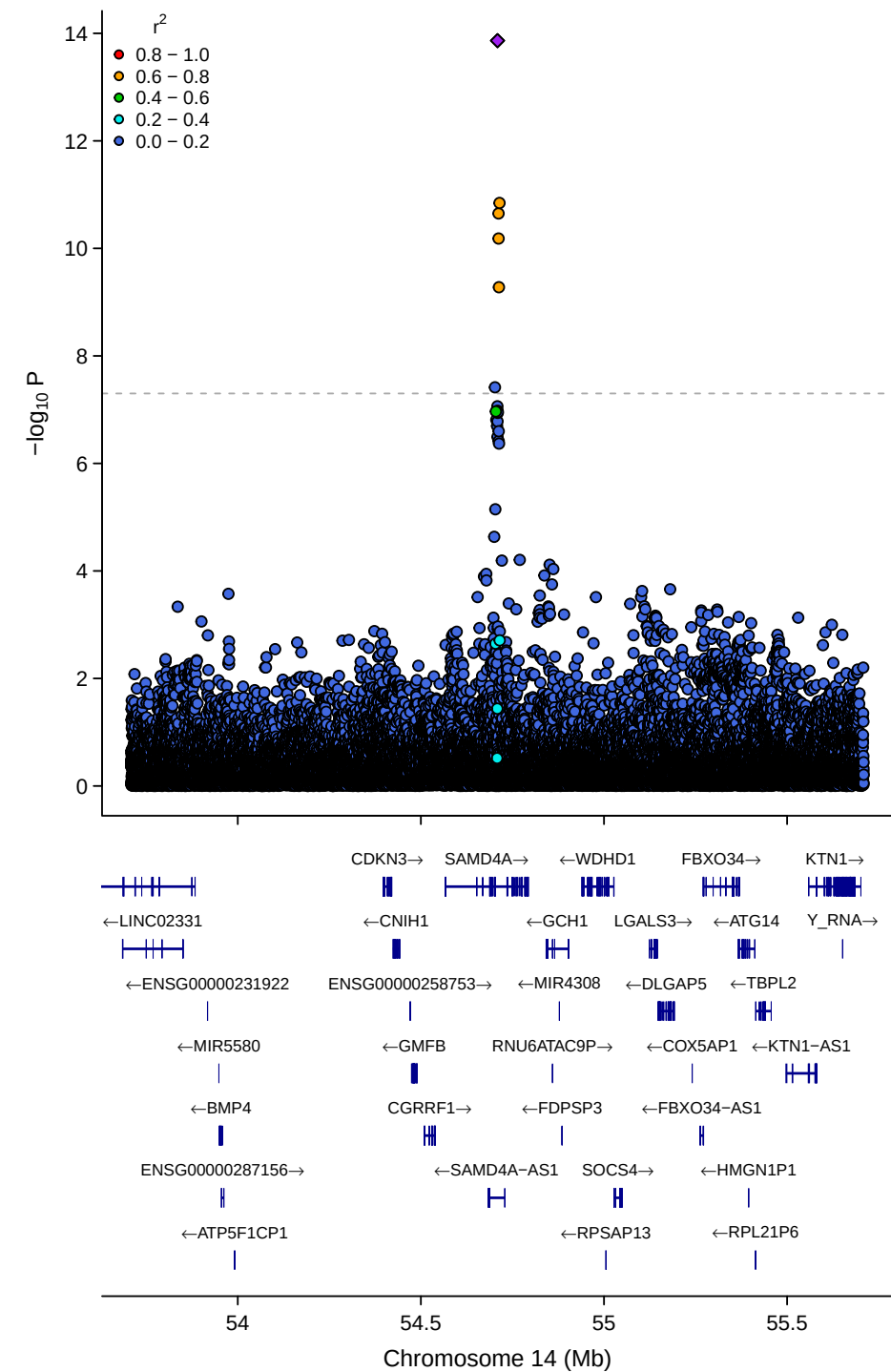


chr15\_74044292\_T\_C, PML, BNG, mixed ancestry

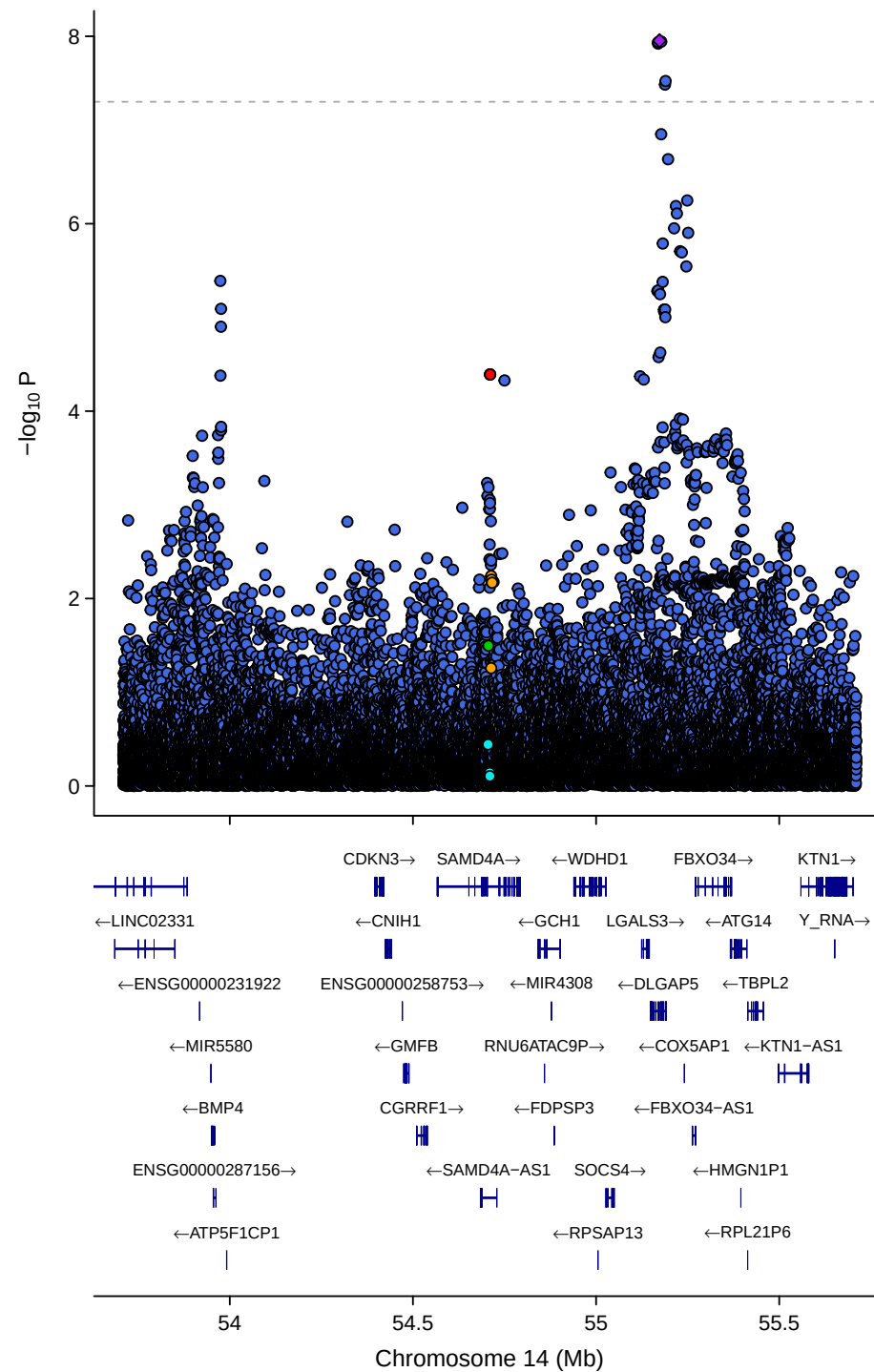


Supplementary Figure 2.1

chr14\_54709452\_T\_C, SAMD4A, ThC, mixed ancestry



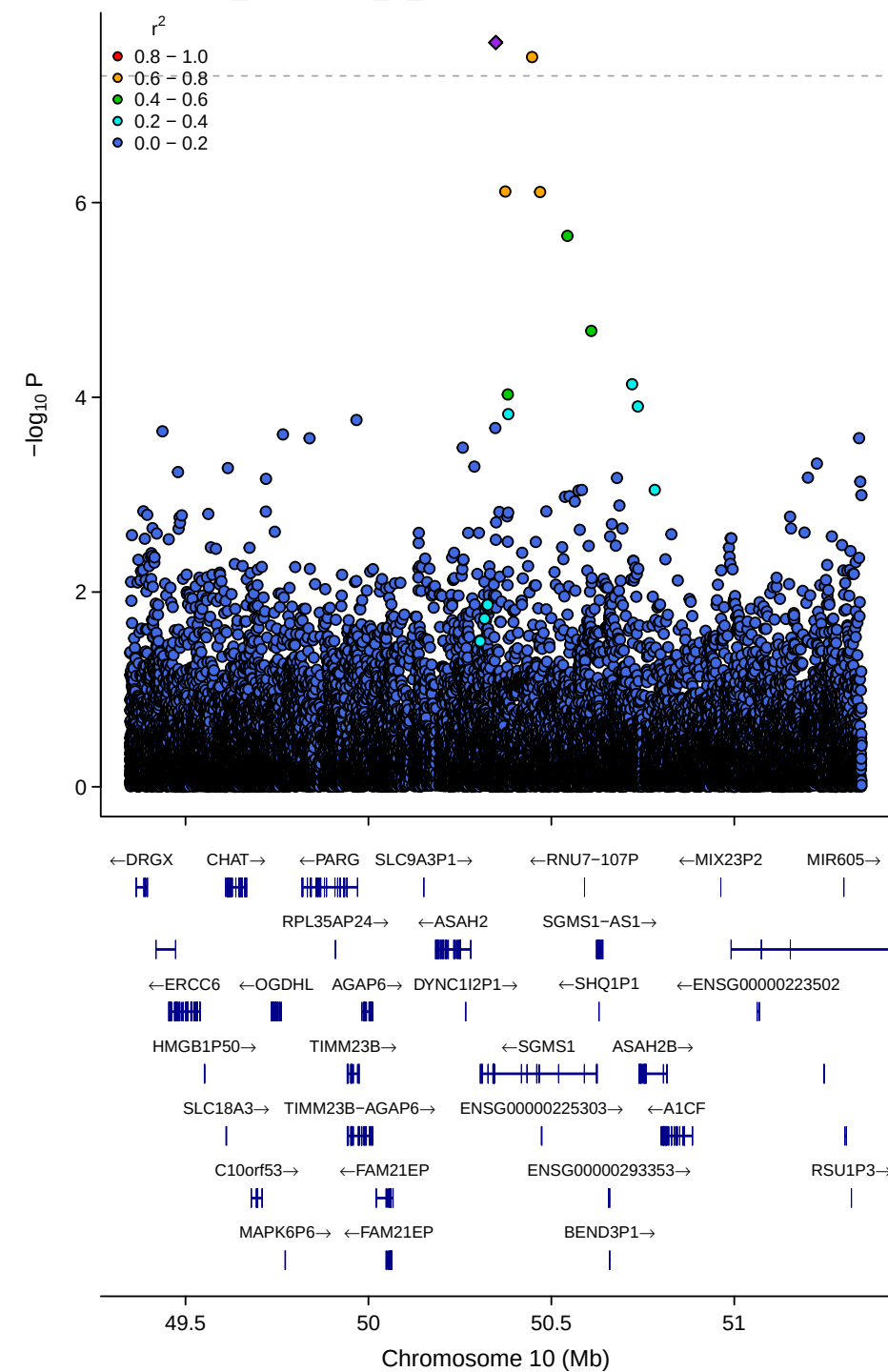
chr14\_54709452\_T\_C, SAMD4A, BNG, mixed ancestry



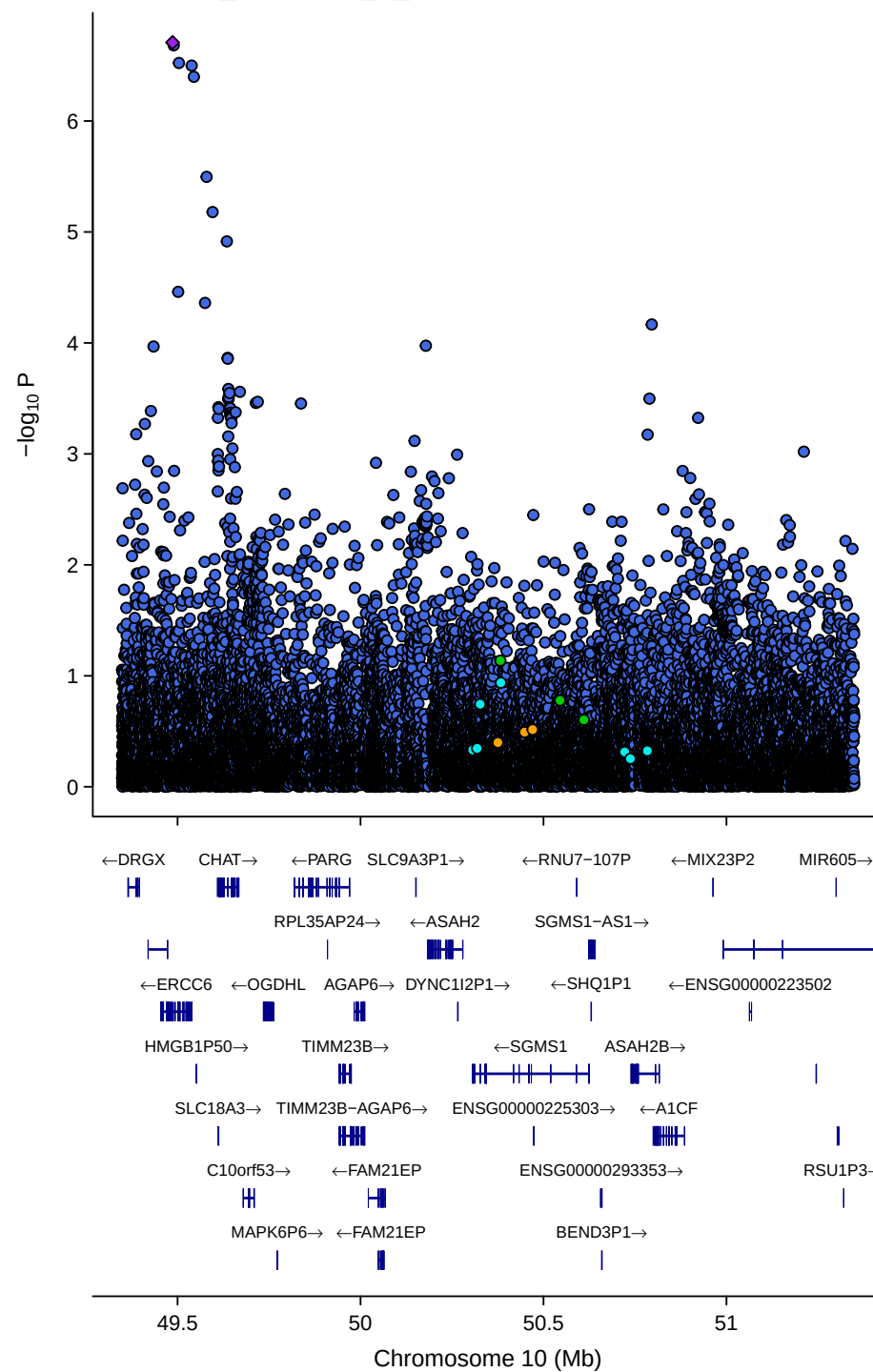


Supplementary Figure 2.1

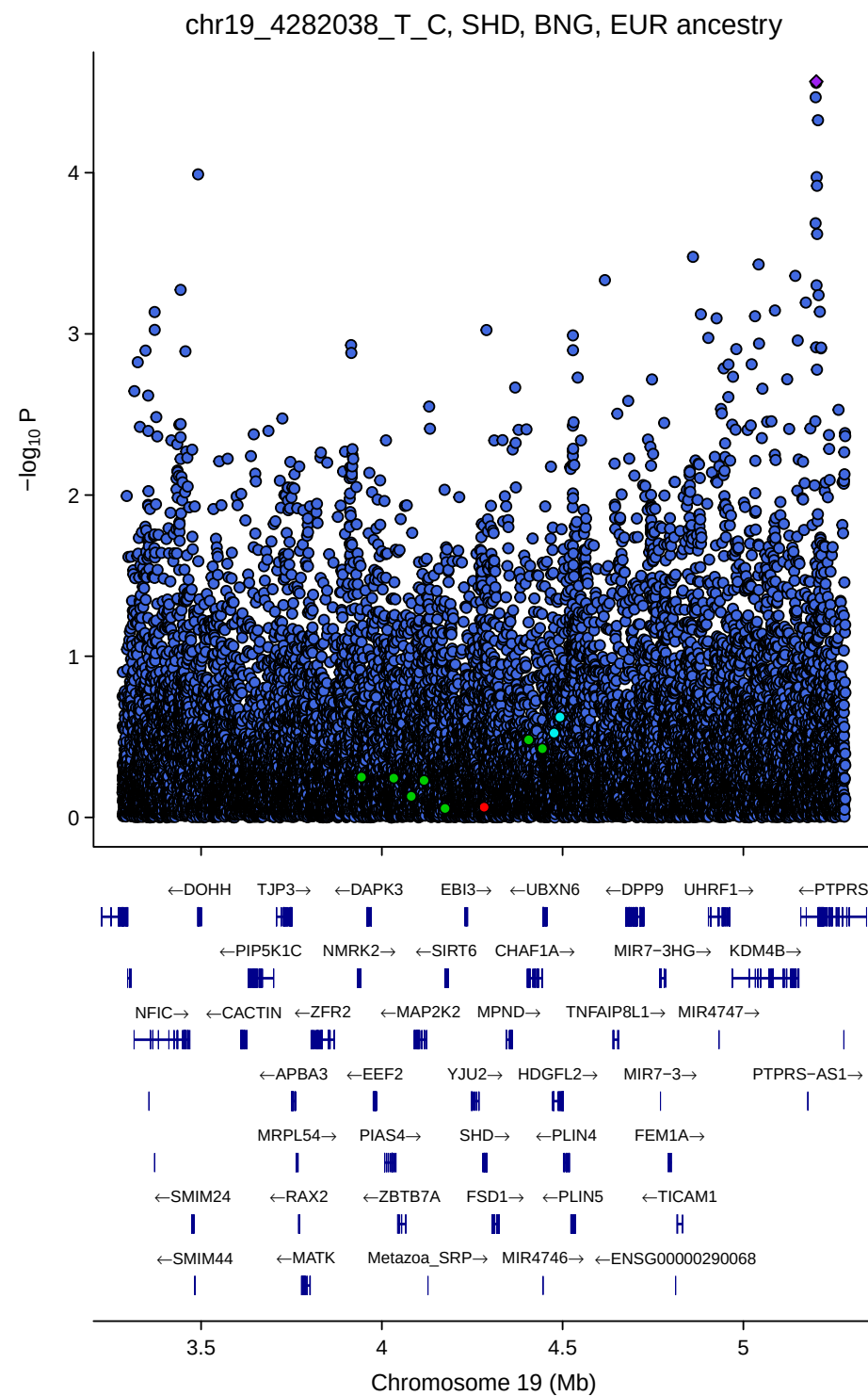
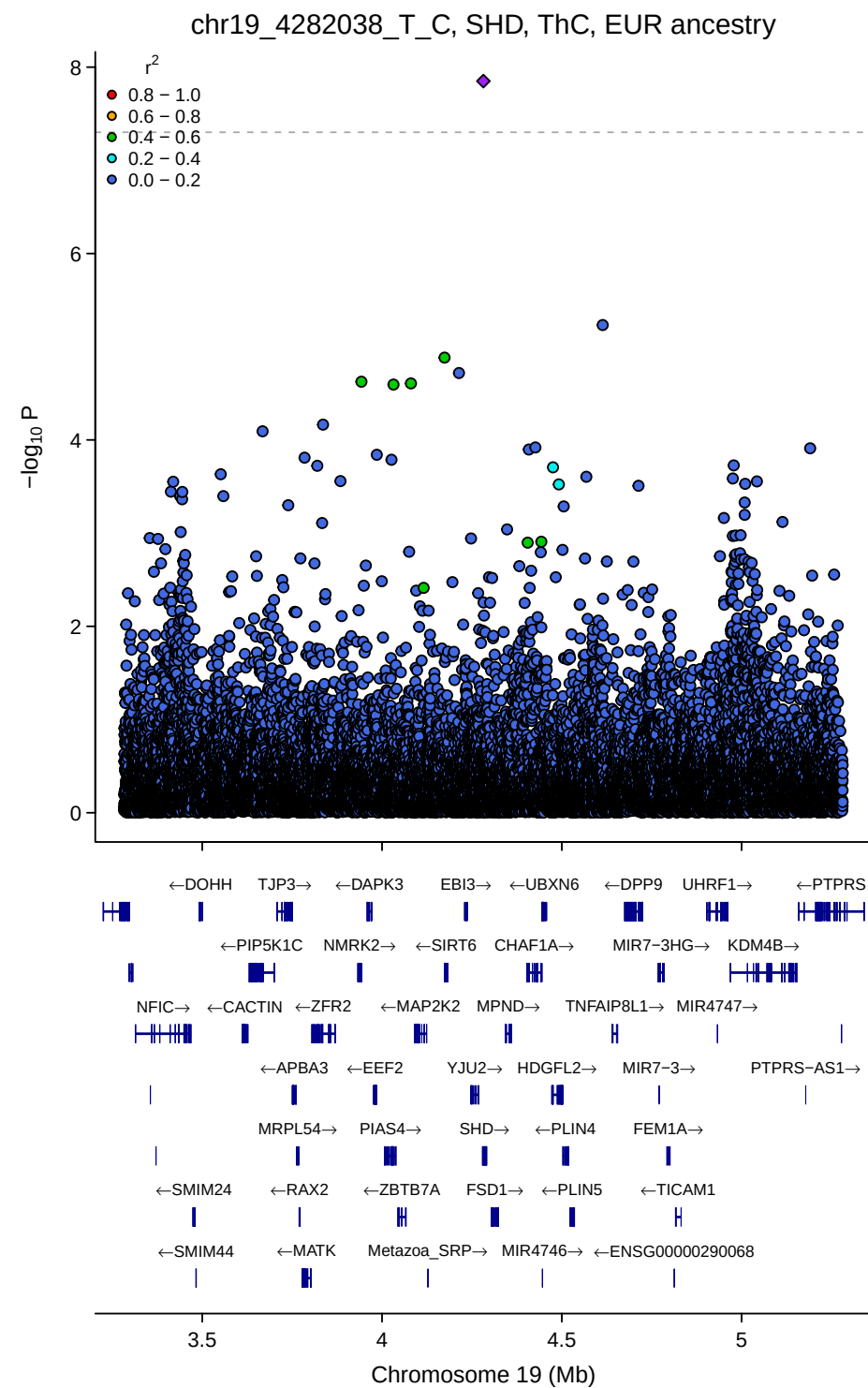
chr10\_50348247\_T\_C, SGMS1, ThC, mixed ancestry



chr10\_50348247\_T\_C, SGMS1, BNG, mixed ancestry

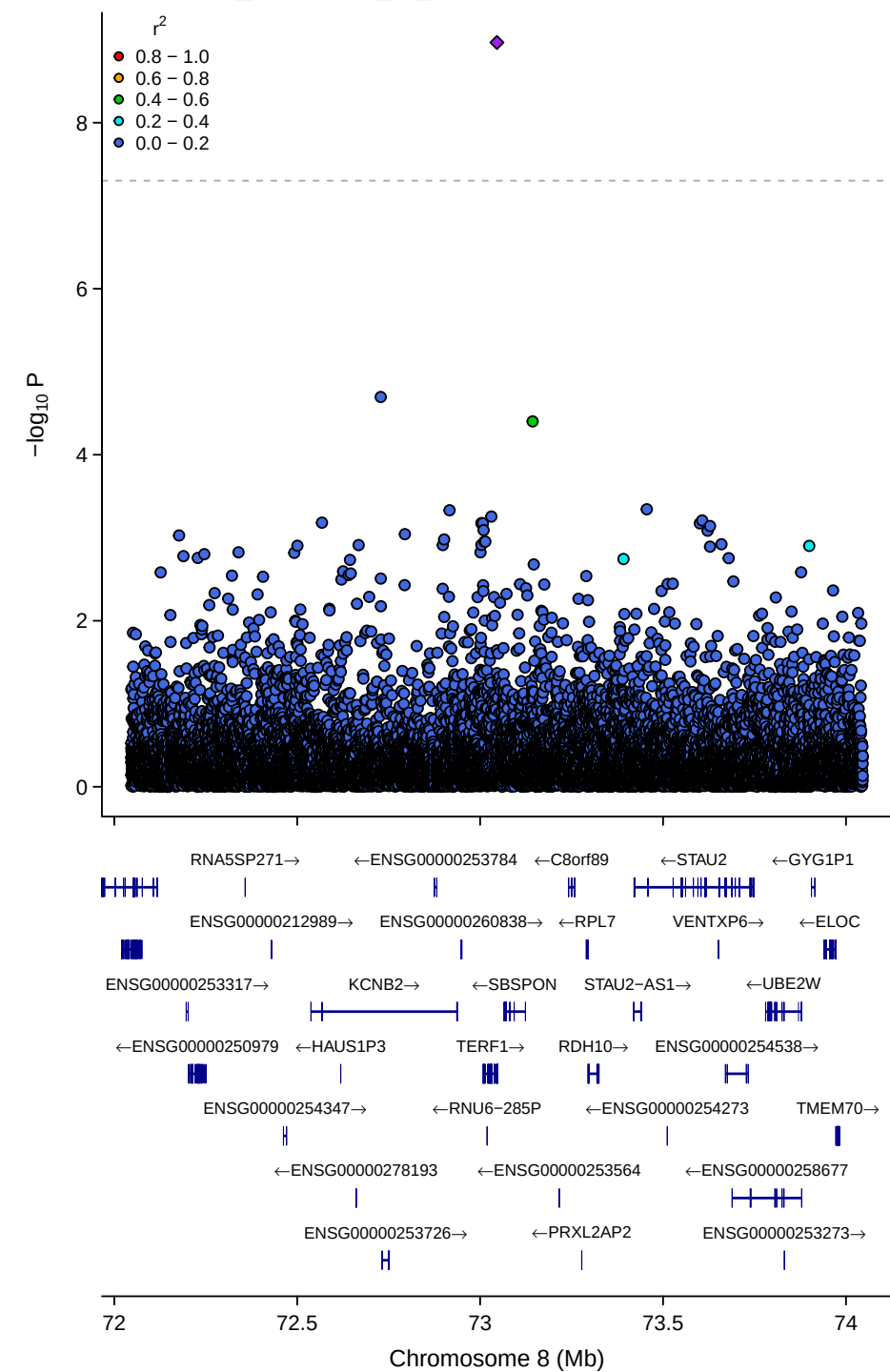


Supplementary Figure 2.1

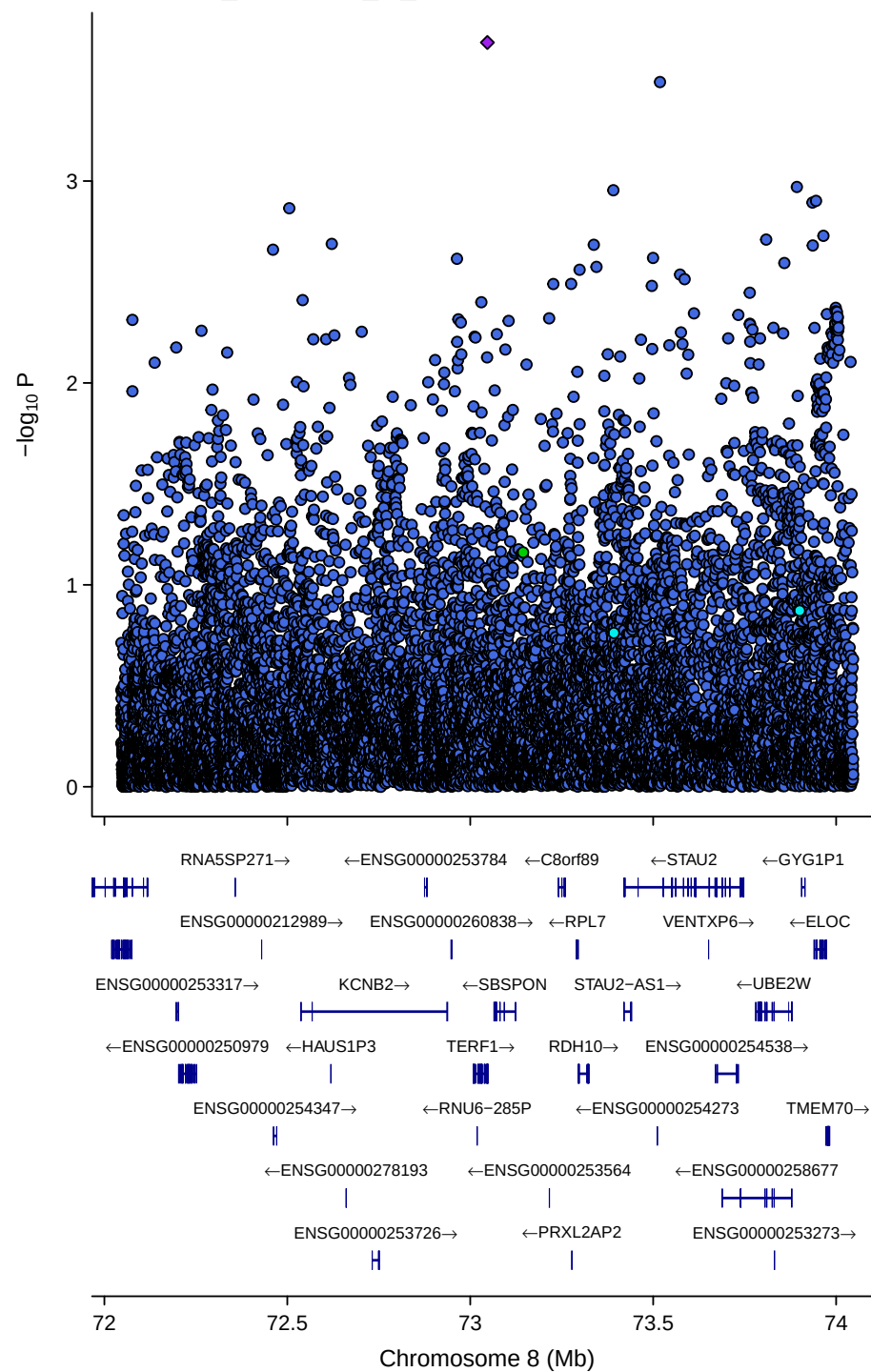


Supplementary Figure 2.1

chr8\_73046129\_G\_A, TERF1, ThC, EUR ancestry



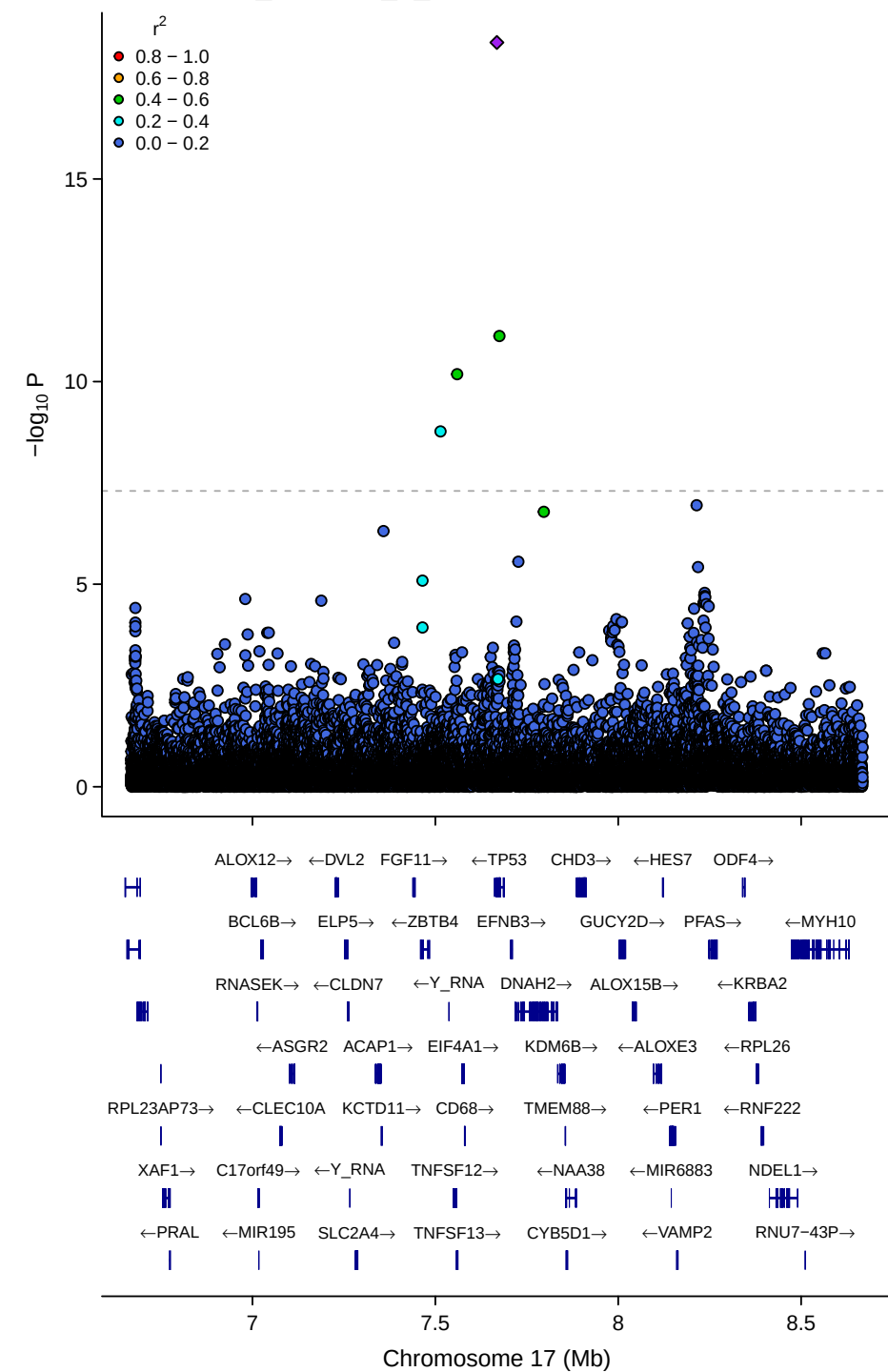
chr8\_73046129\_G\_A, TERF1, BNG, EUR ancestry



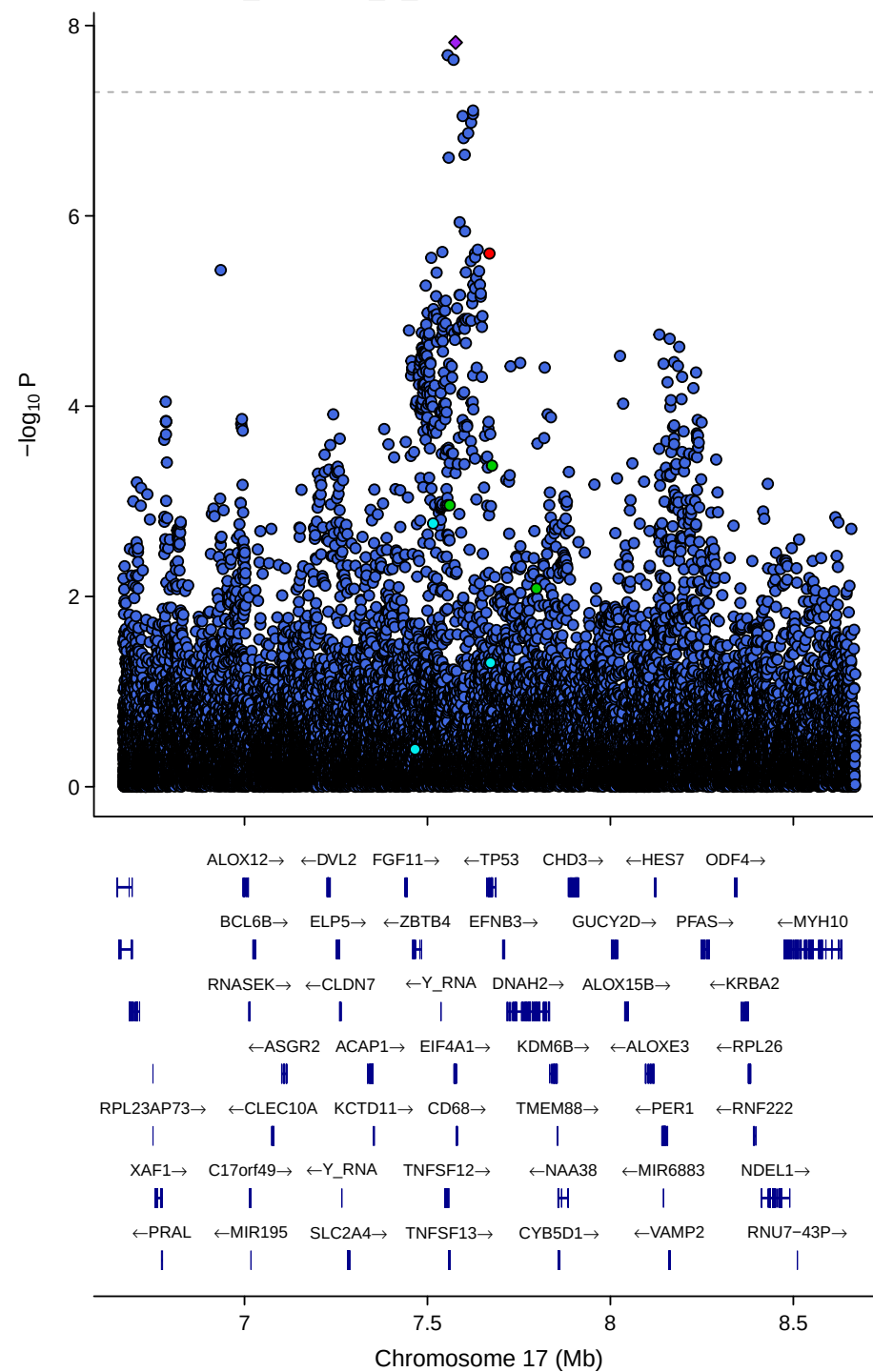


Supplementary Figure 2.1

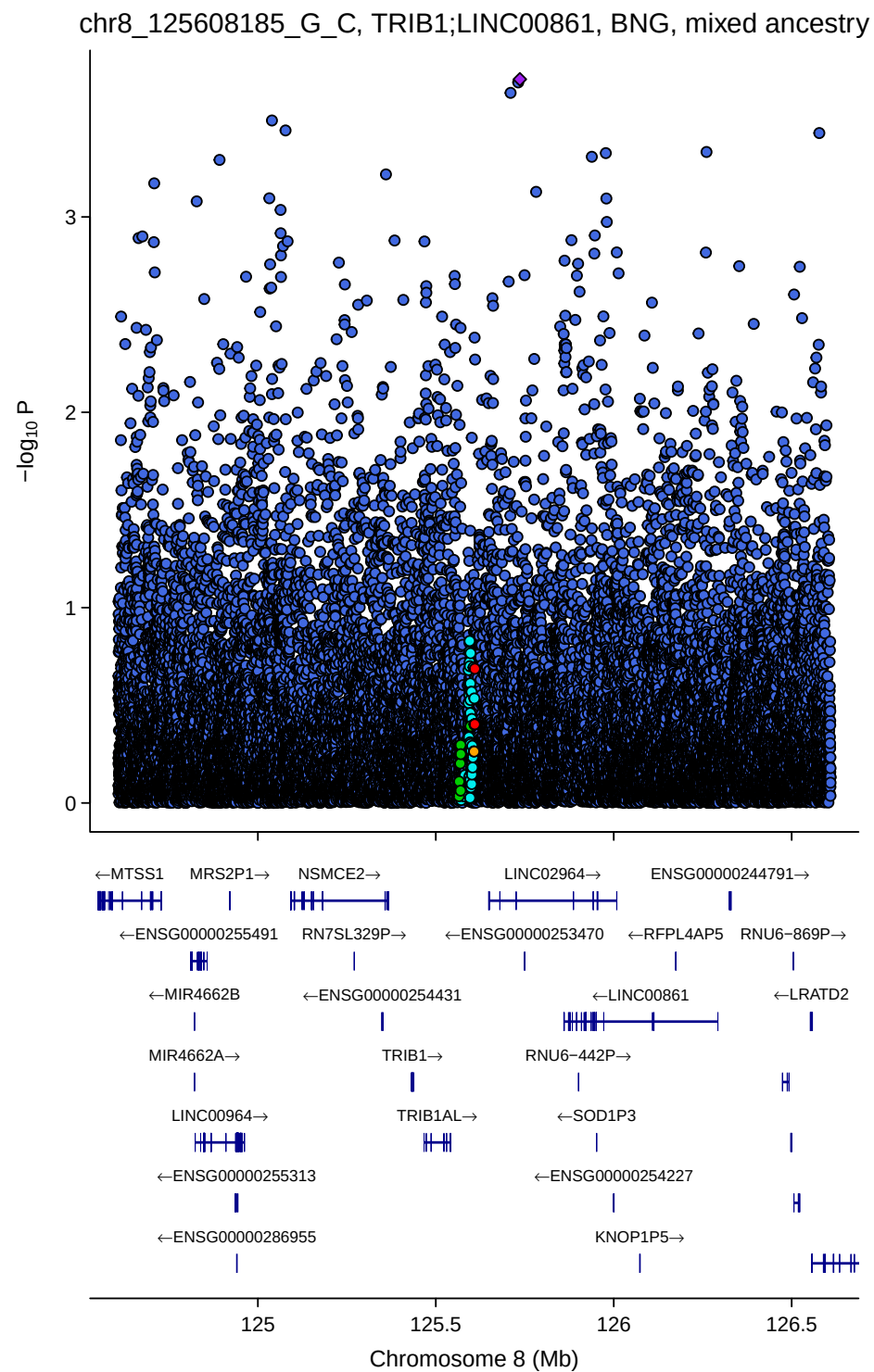
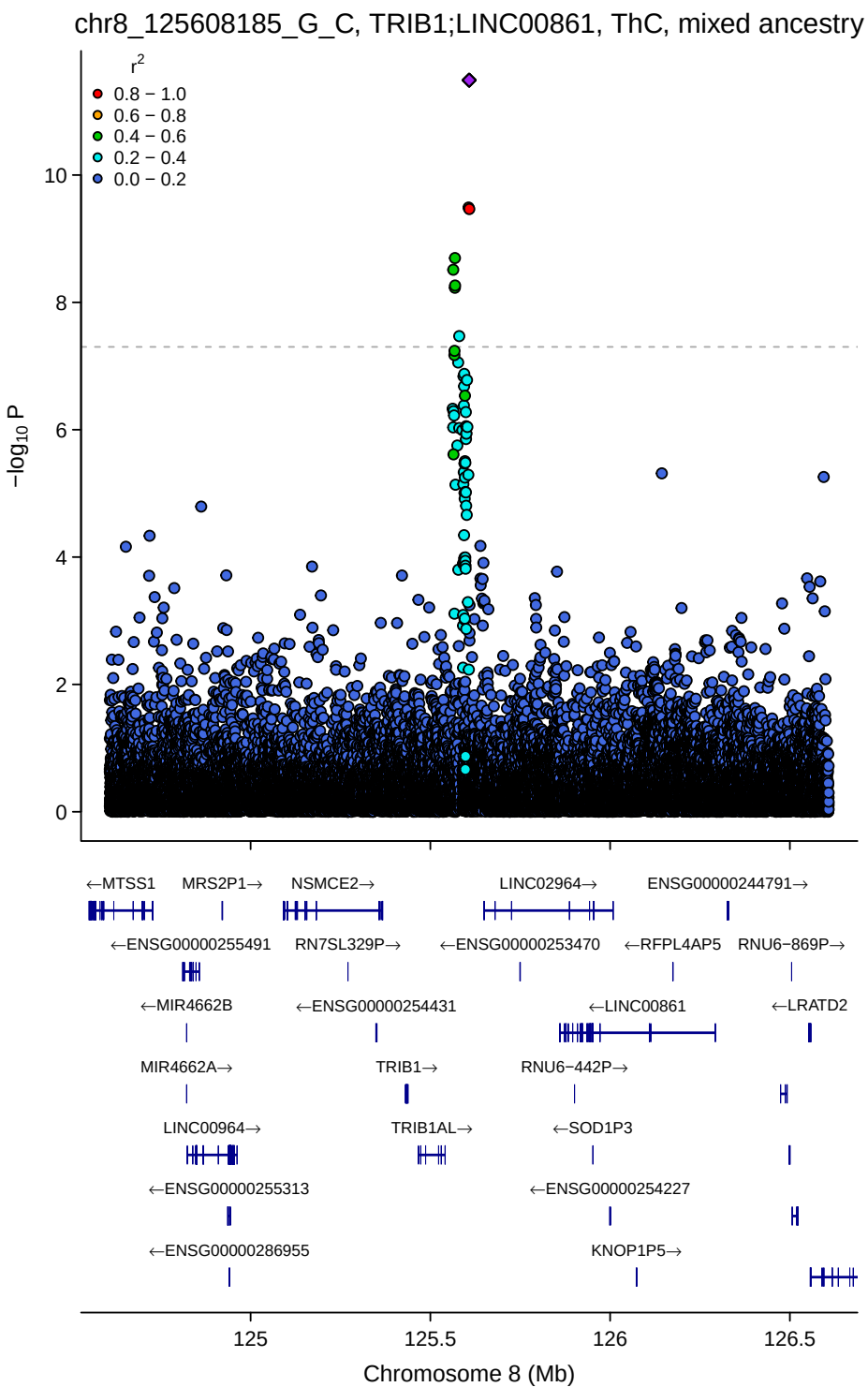
chr17\_7668434\_T\_G, TP53, ThC, mixed ancestry



chr17\_7668434\_T\_G, TP53, BNG, mixed ancestry

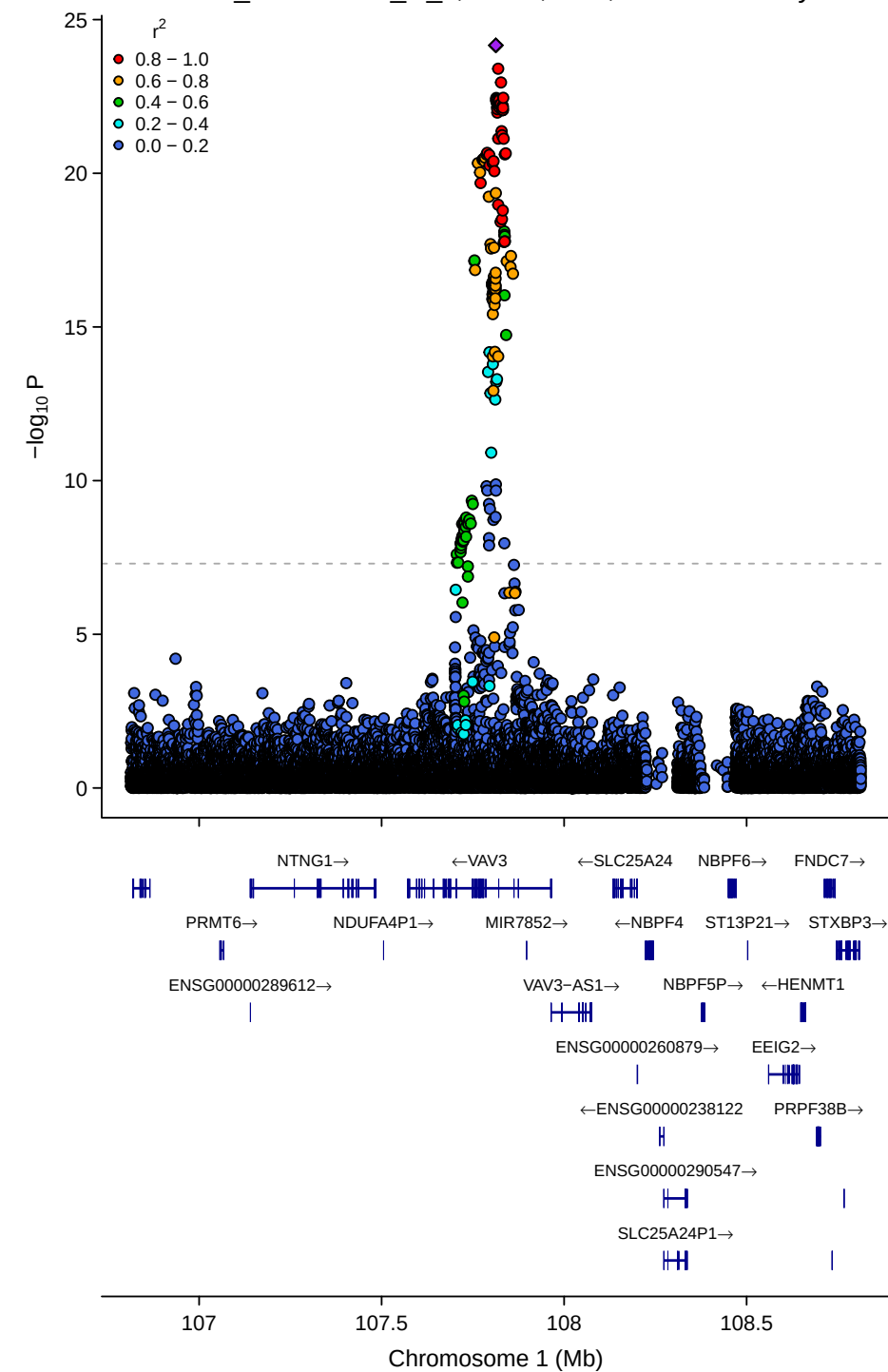


Supplementary Figure 2.1

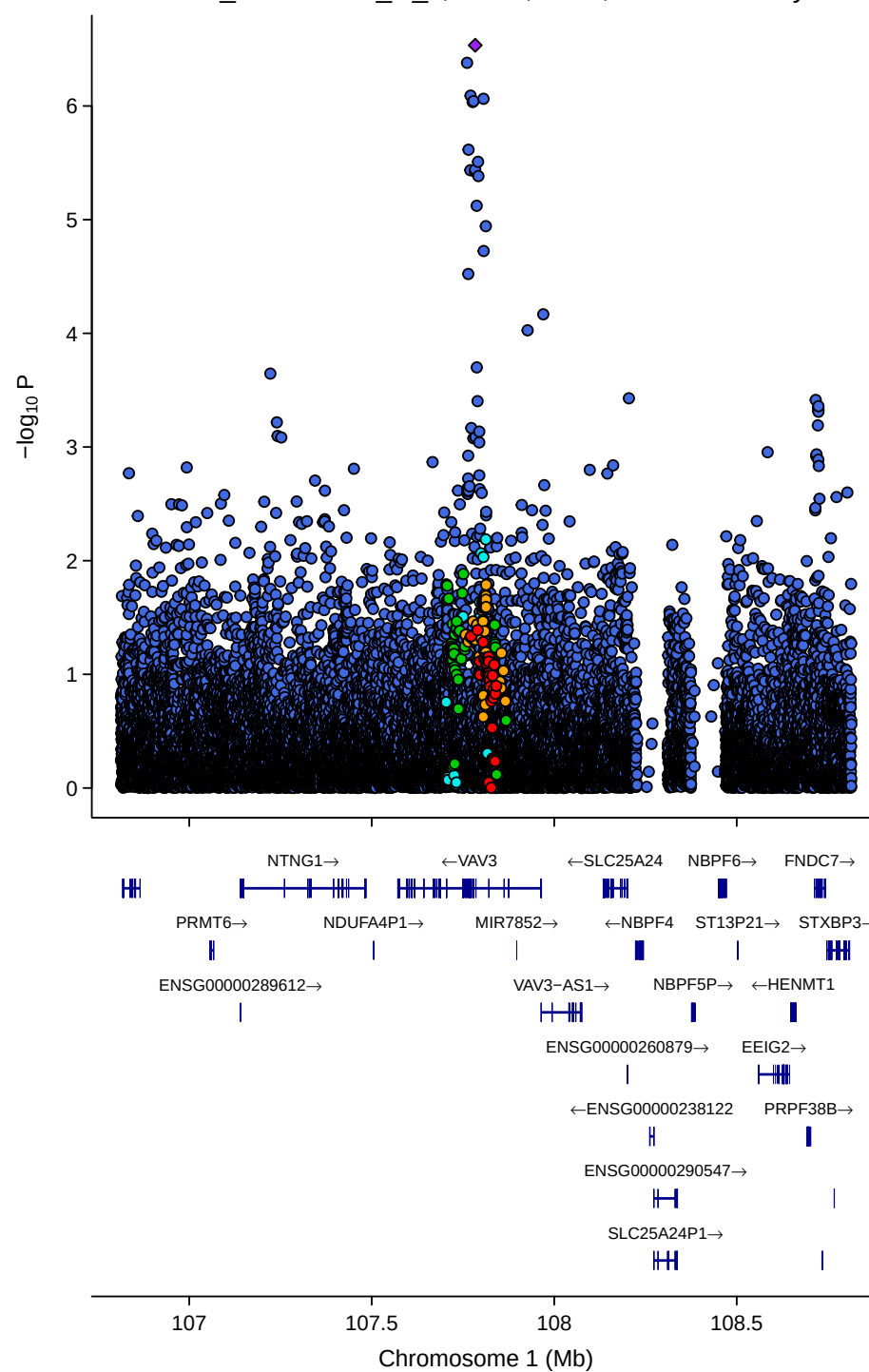


Supplementary Figure 2.1

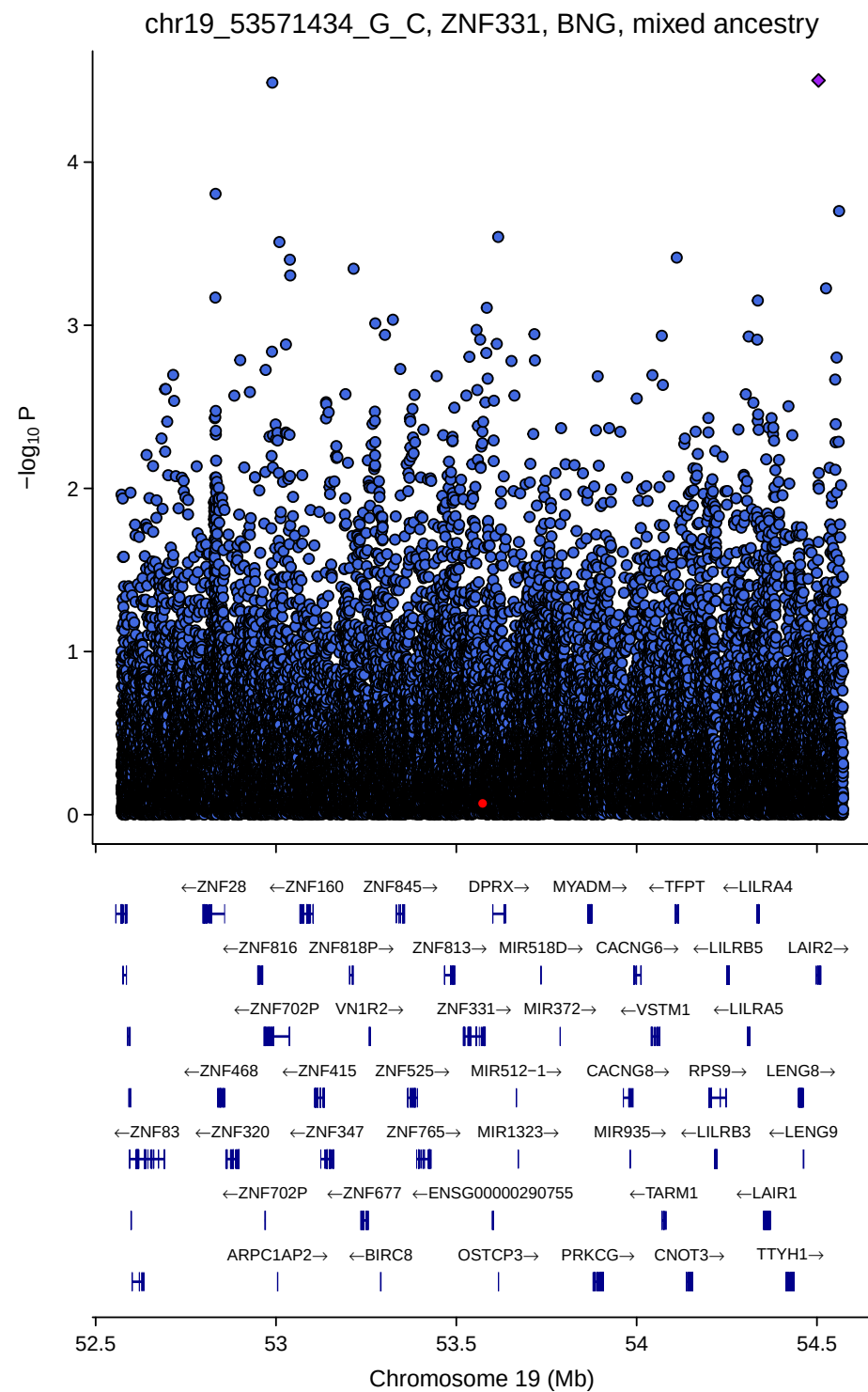
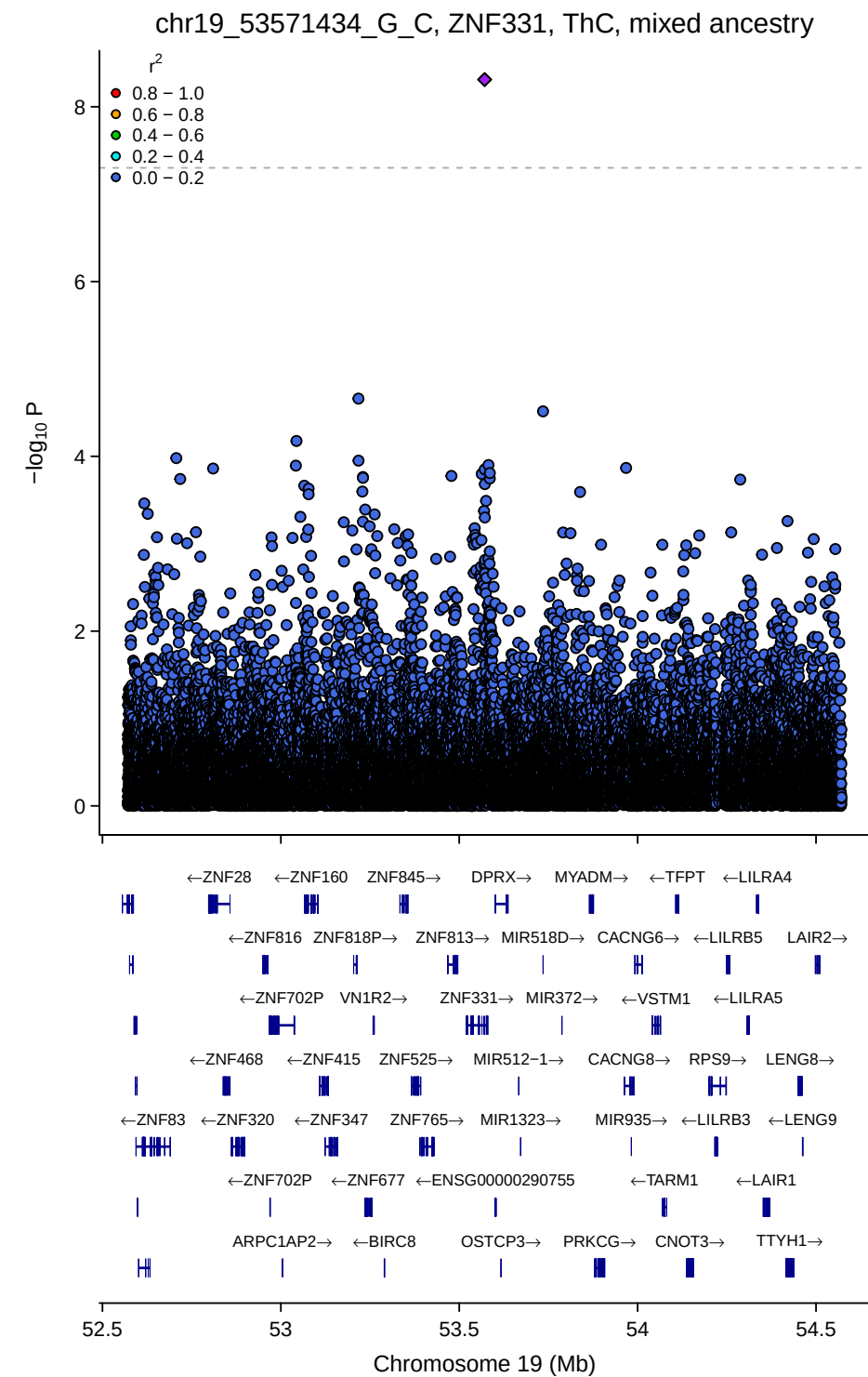
chr1\_107813097\_C\_T, VAV3, ThC, mixed ancestry



chr1\_107813097\_C\_T, VAV3, BNG, mixed ancestry



Supplementary Figure 2.1

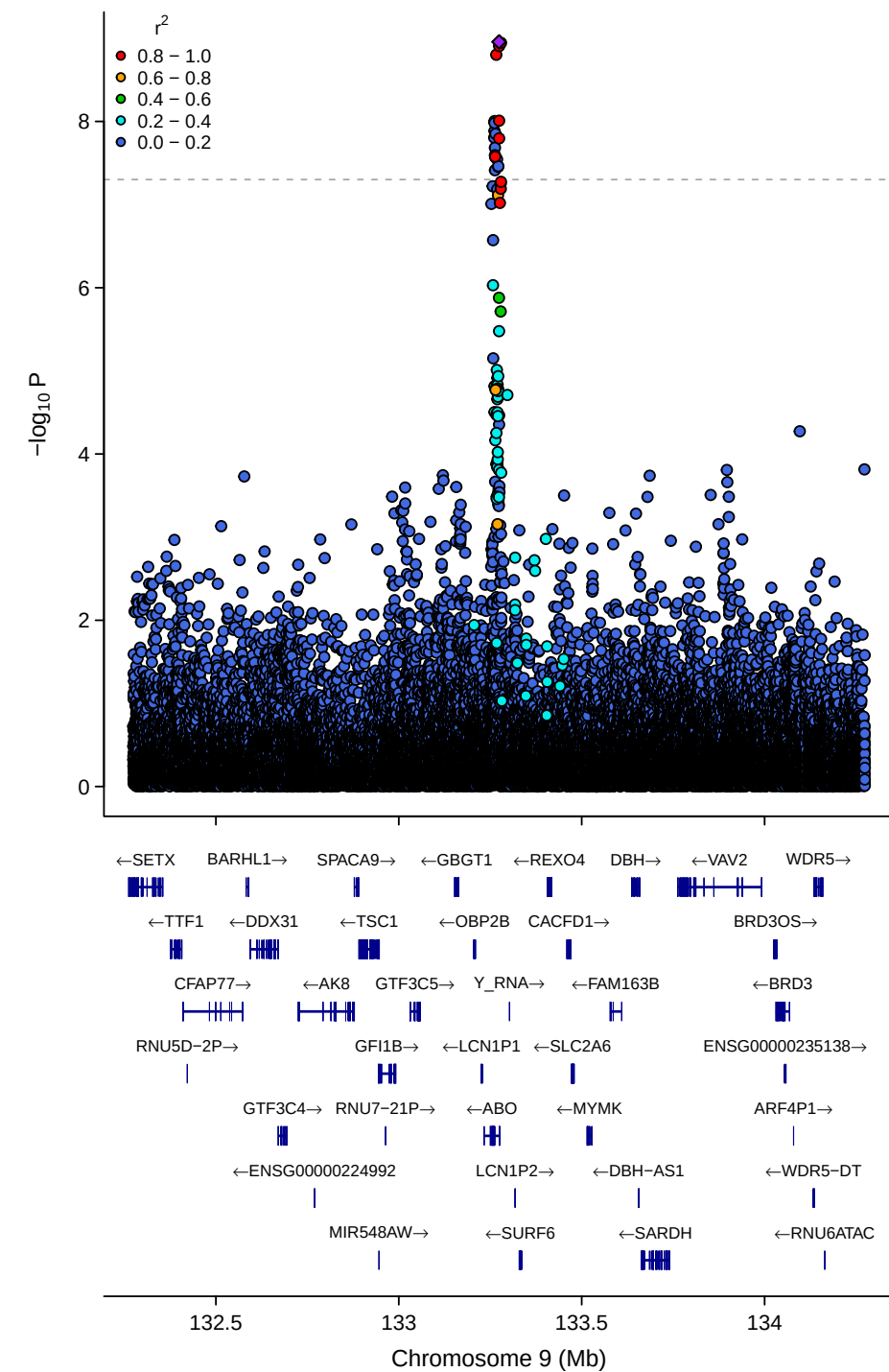


Supplementary Figure 2.2. Locus plots for loci significantly associated with benign nodular goiter but not thyroid cancer. The left plot displays  $-\log_{10}(\text{p-values})$  for variants from thyroid cancer meta-analysis, the right plot displays  $-\log_{10}(\text{p-values})$  for variants within the same genomic region from the benign nodular goiter meta-analysis. The lead variant is shown with a purple diamond. Genome wide significance is indicated by the dashed horizontal line at  $-\log_{10}(5\text{e-}8)$ .

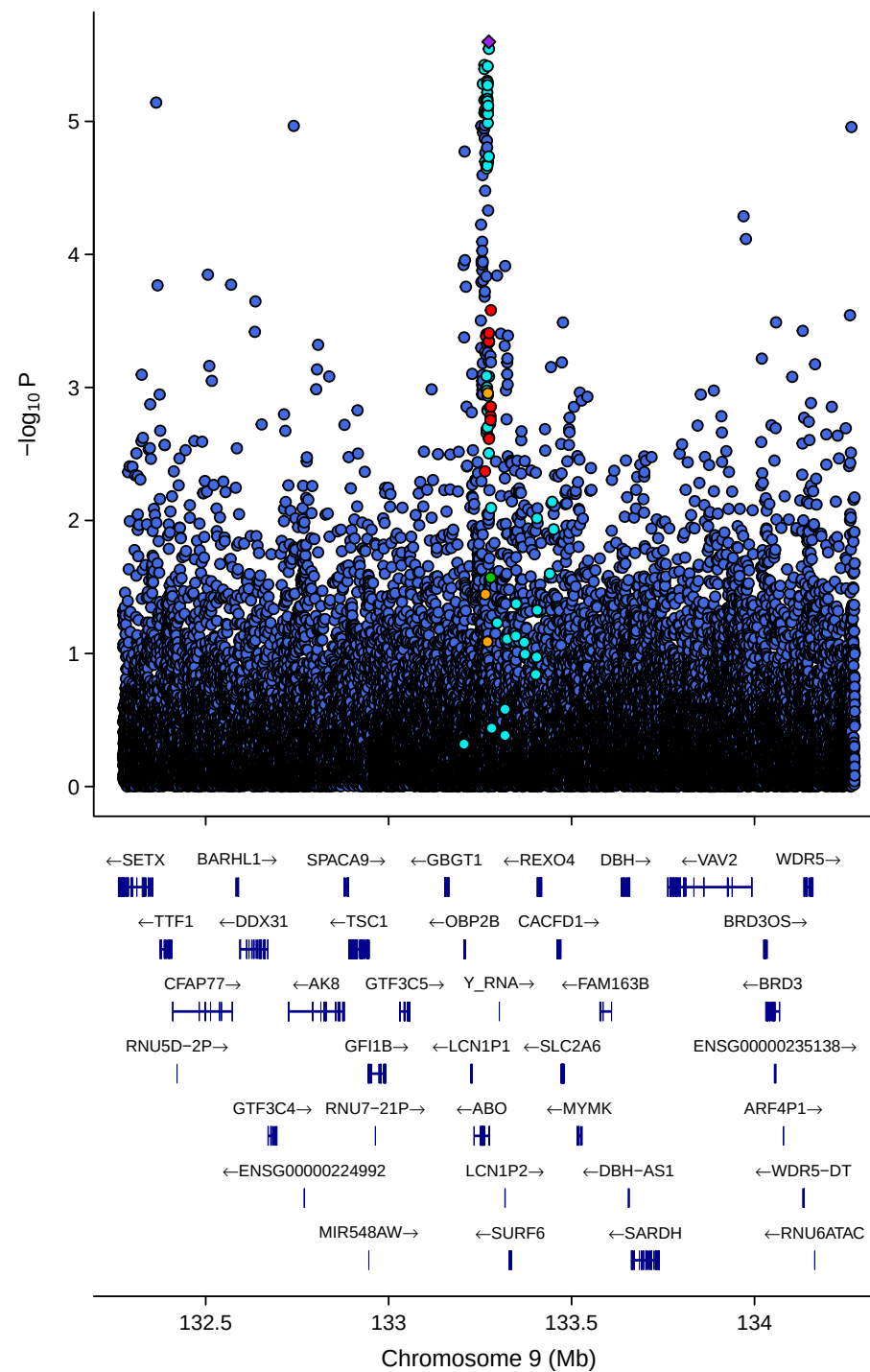


Supplementary Figure 2.2

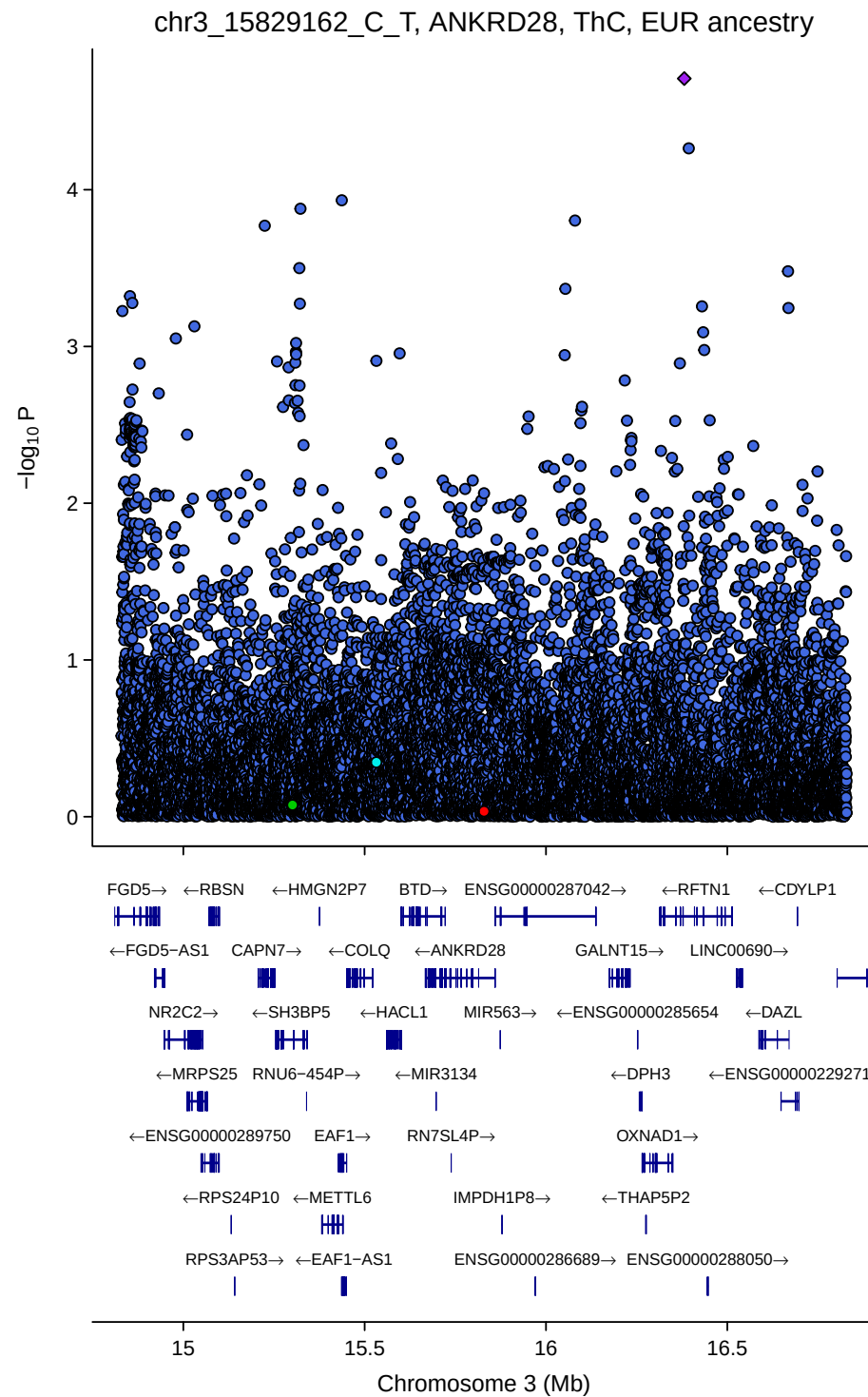
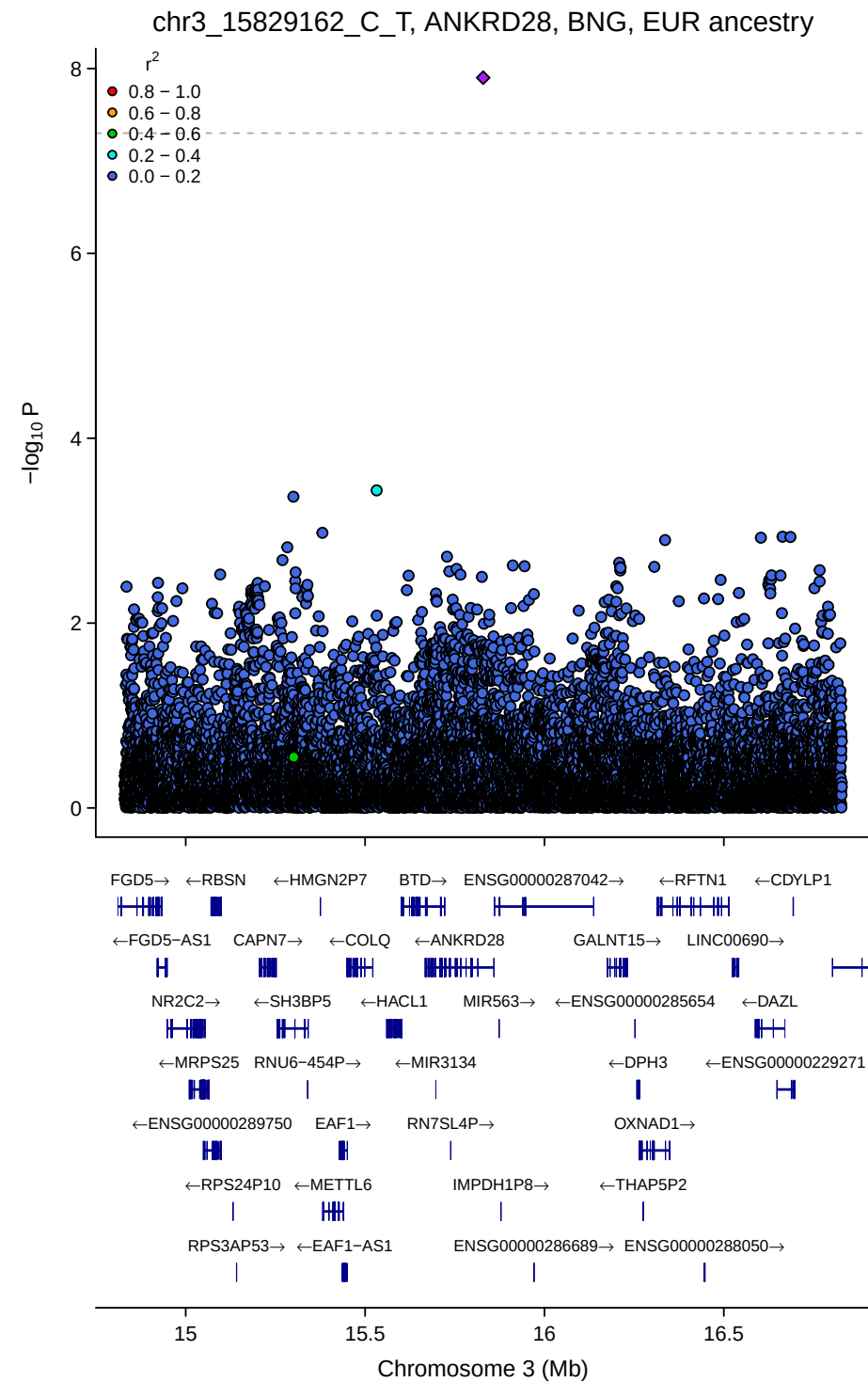
chr9\_133273983\_A\_G, ABO, BNG, mixed ancestry



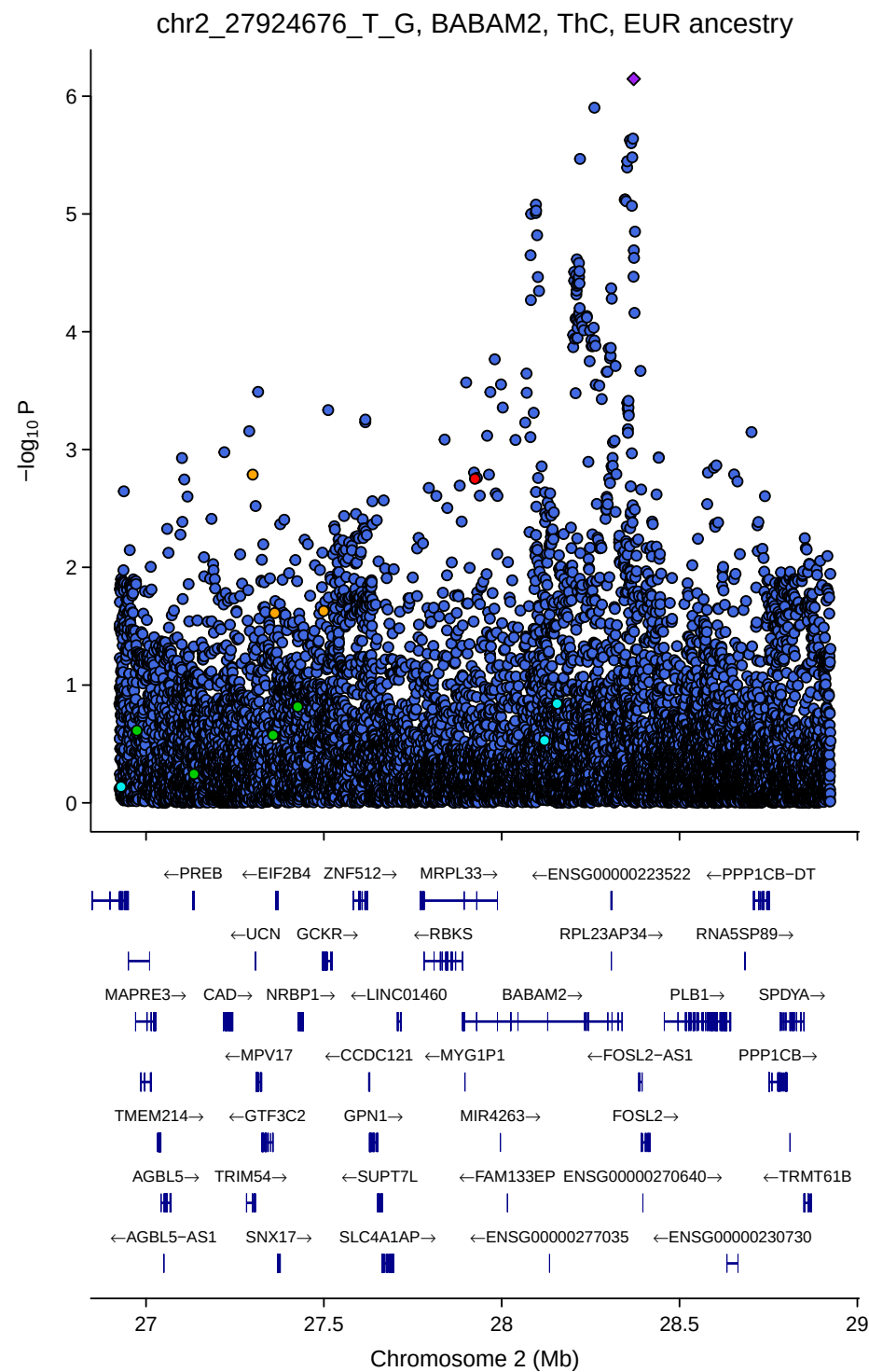
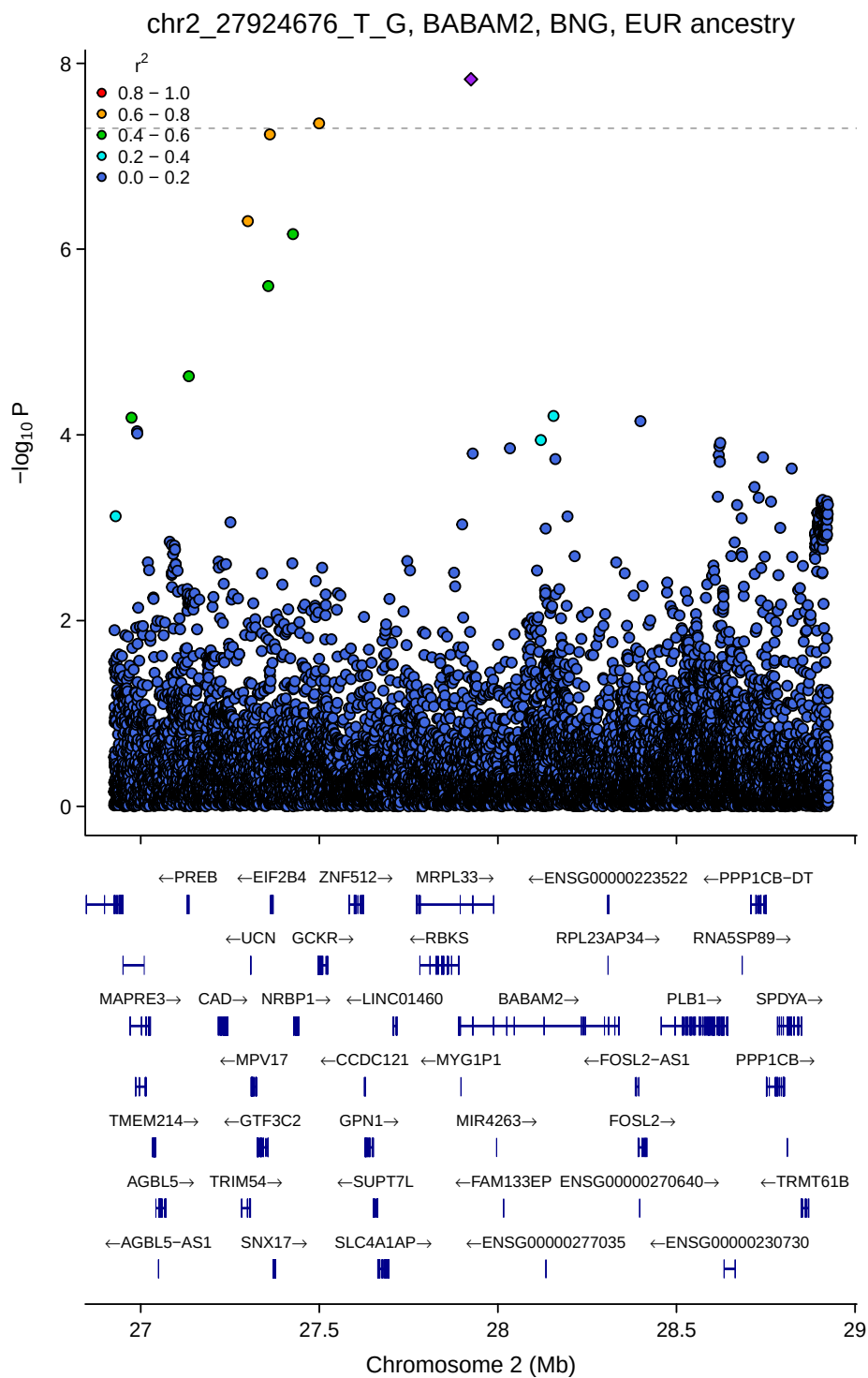
chr9\_133273983\_A\_G, ABO, ThC, mixed ancestry



# Supplementary Figure 2.2



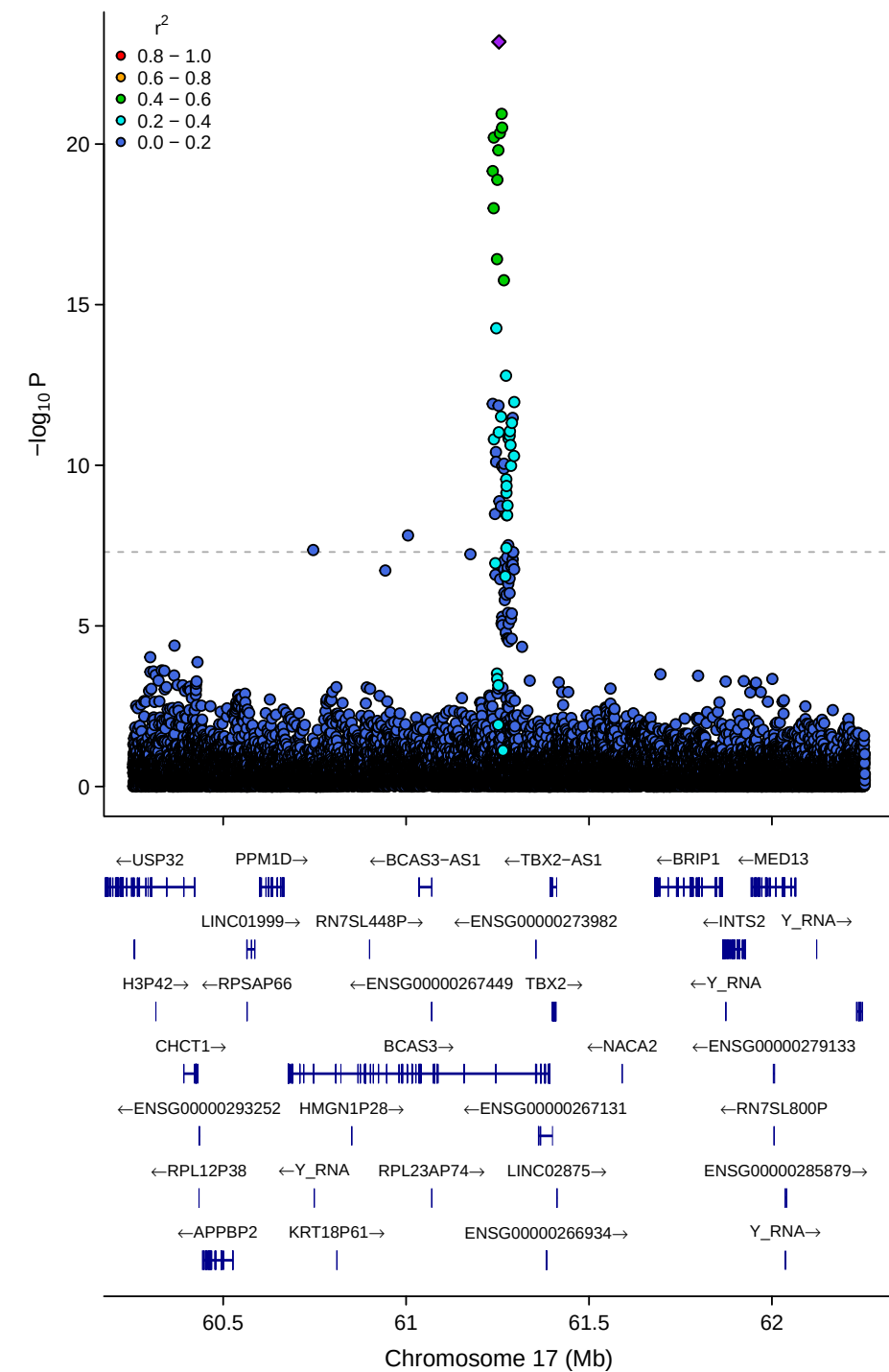
# Supplementary Figure 2.2



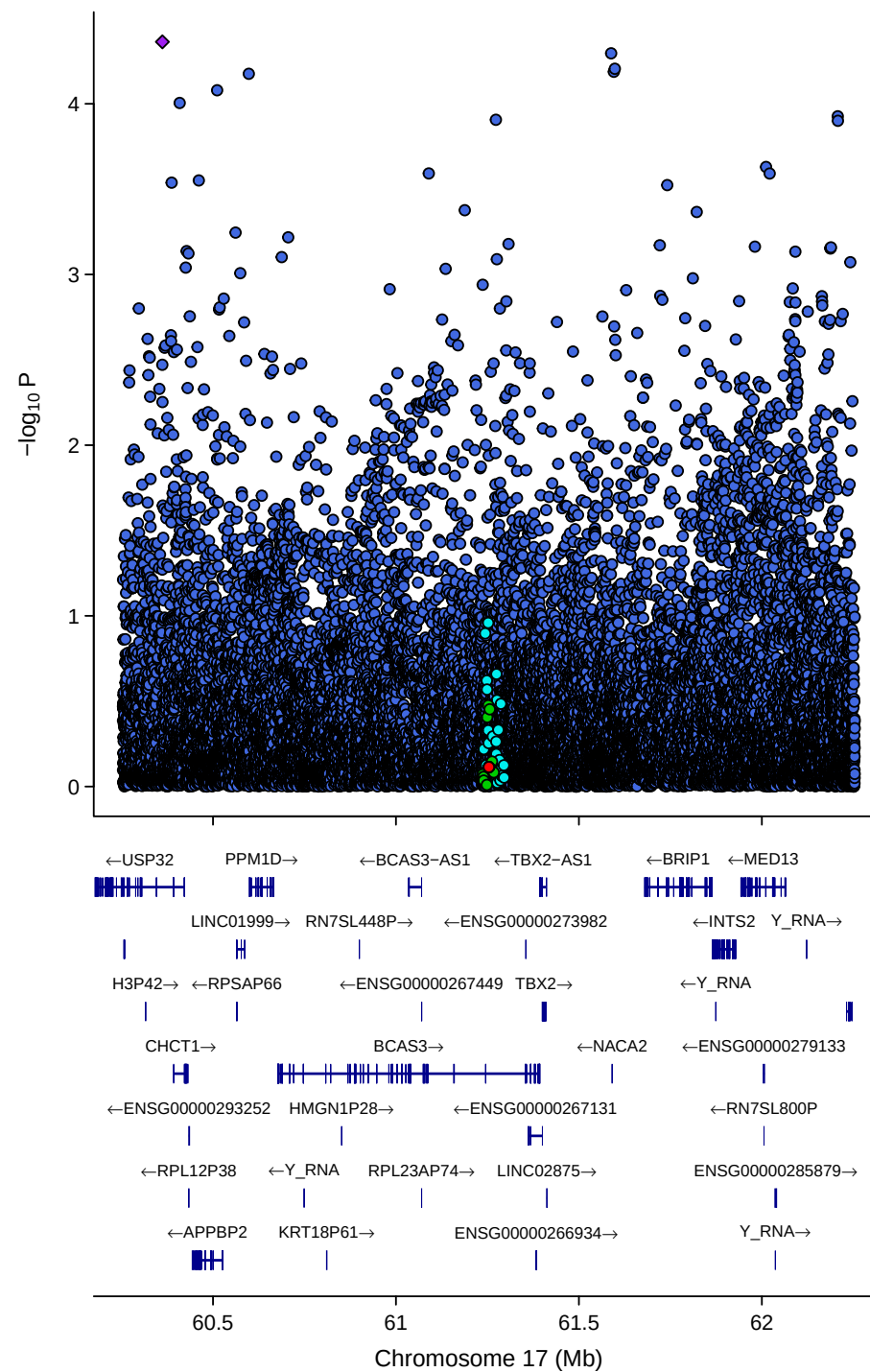


Supplementary Figure 2.2

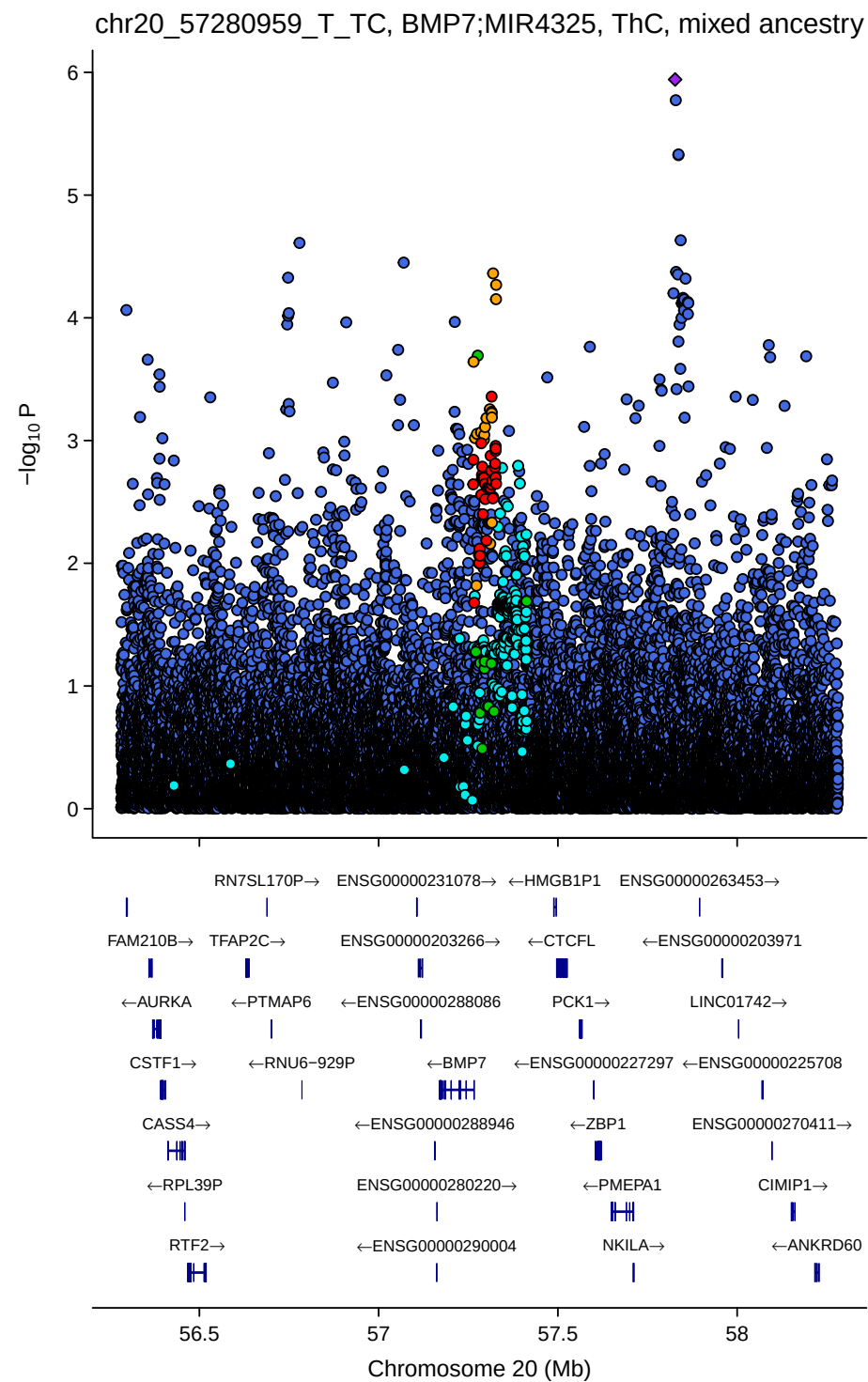
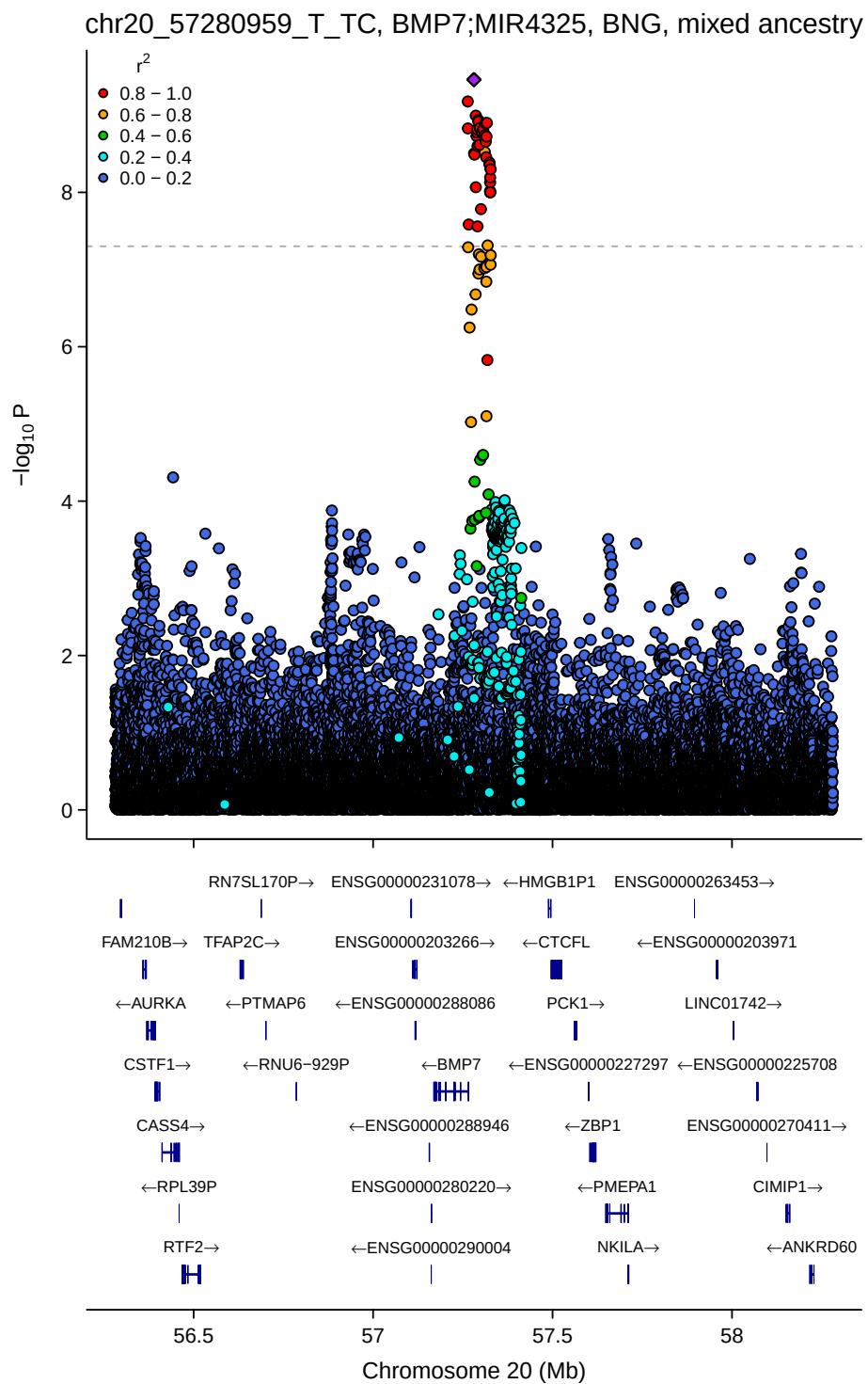
chr17\_61253946\_A\_C, BCAS3, BNG, mixed ancestry



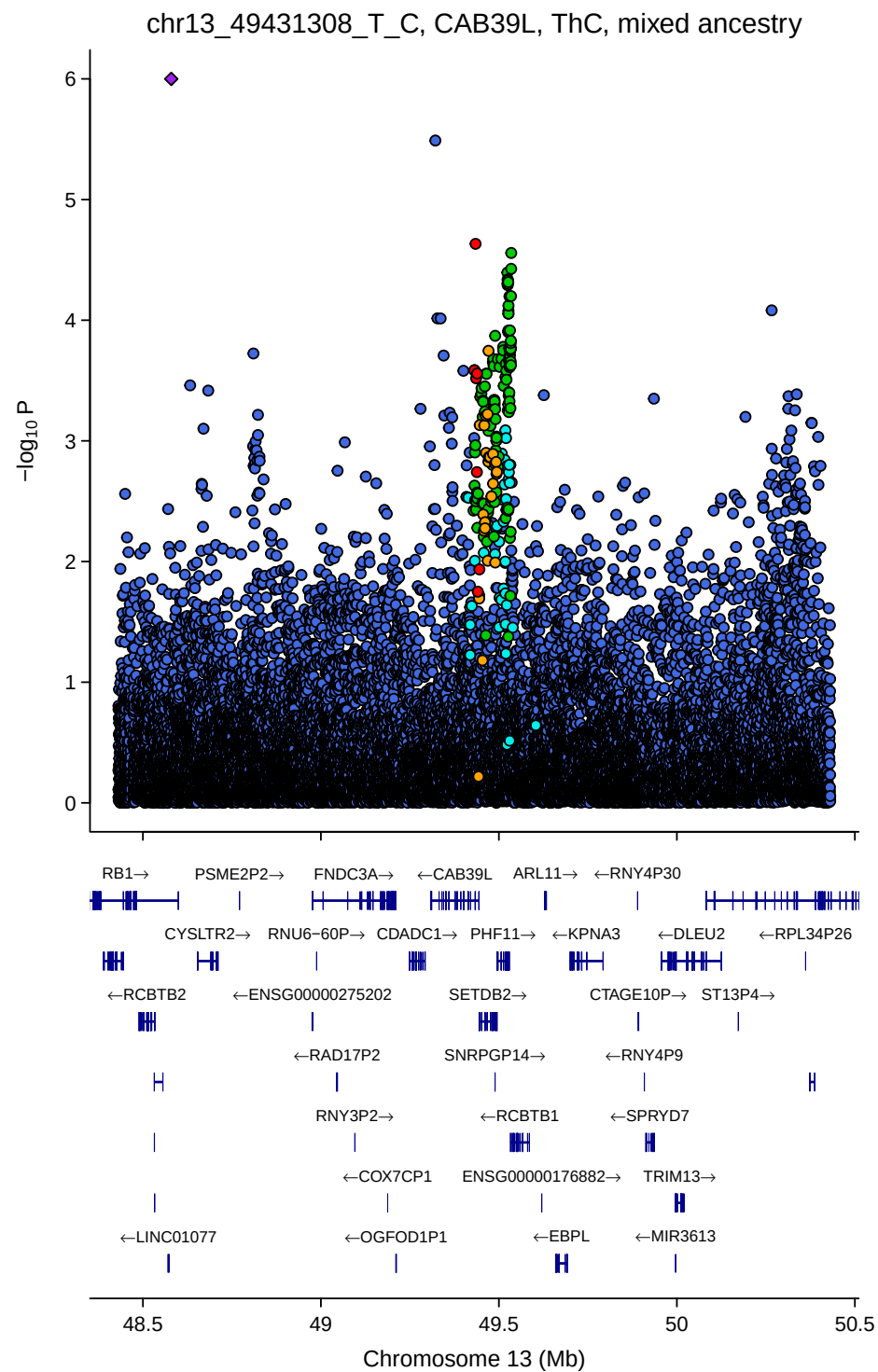
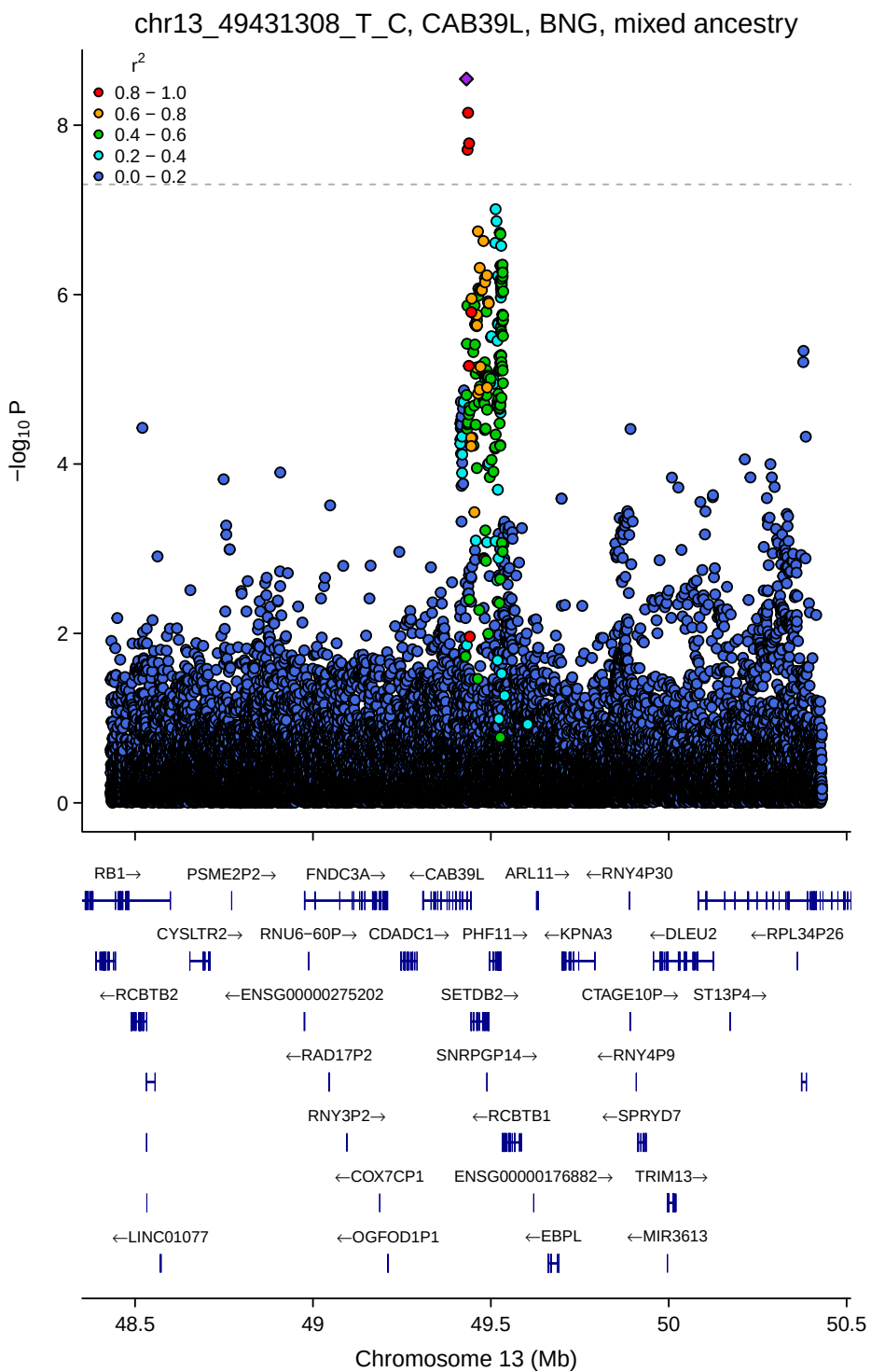
chr17\_61253946\_A\_C, BCAS3, ThC, mixed ancestry



Supplementary Figure 2.2

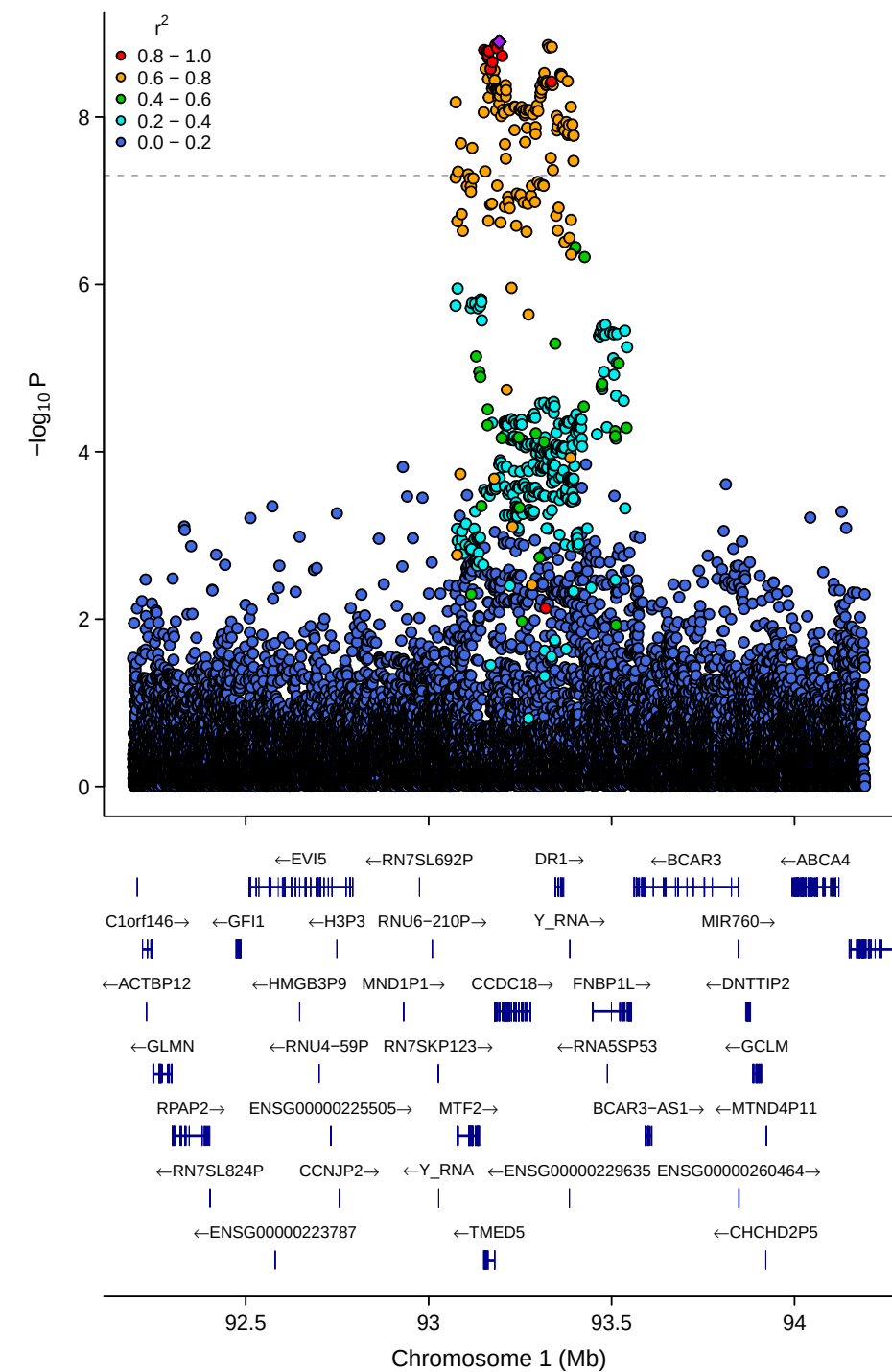


# Supplementary Figure 2.2

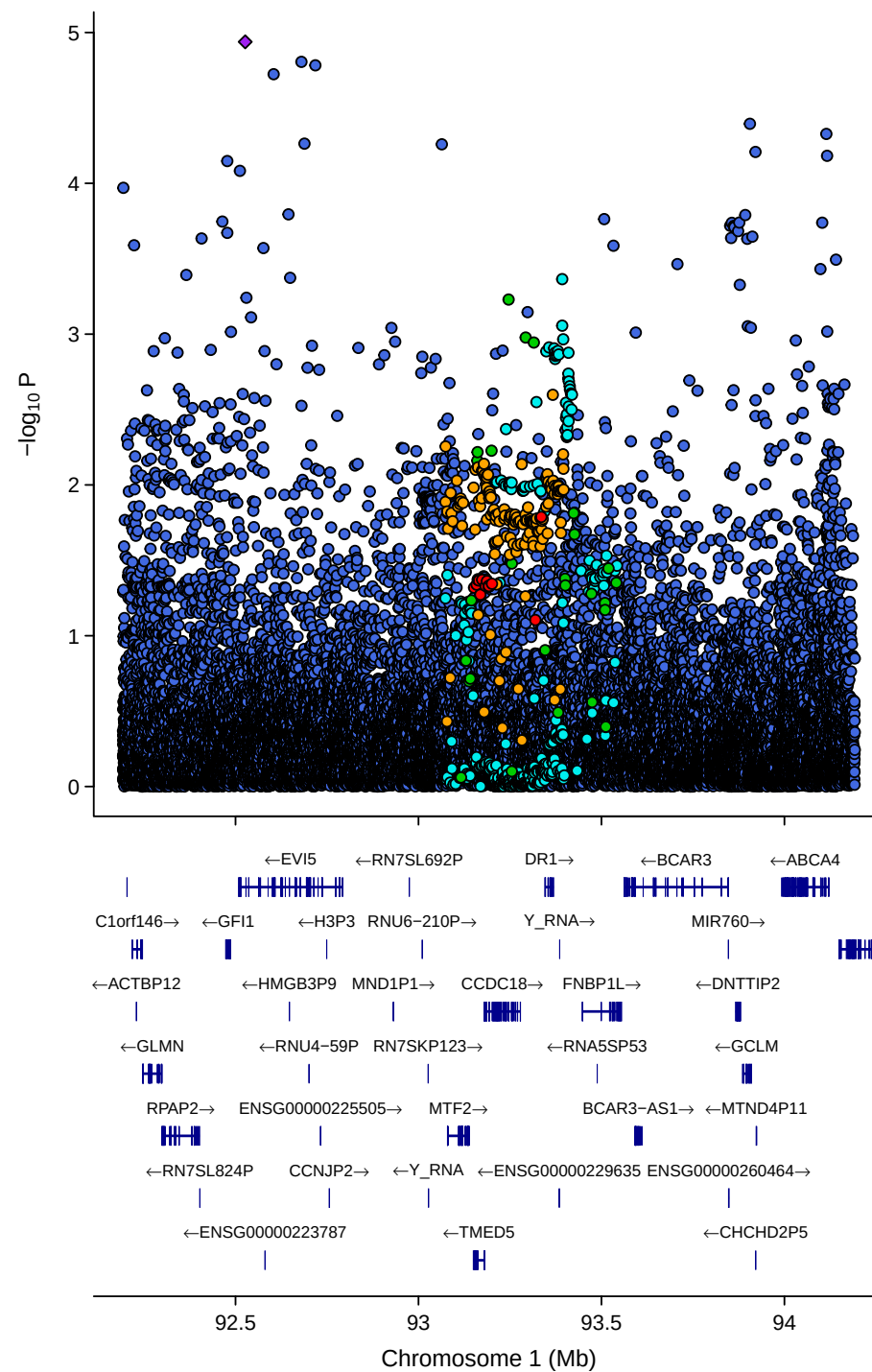


# Supplementary Figure 2.2

chr1\_93192539\_A\_C, CCDC18, BNG, mixed ancestry

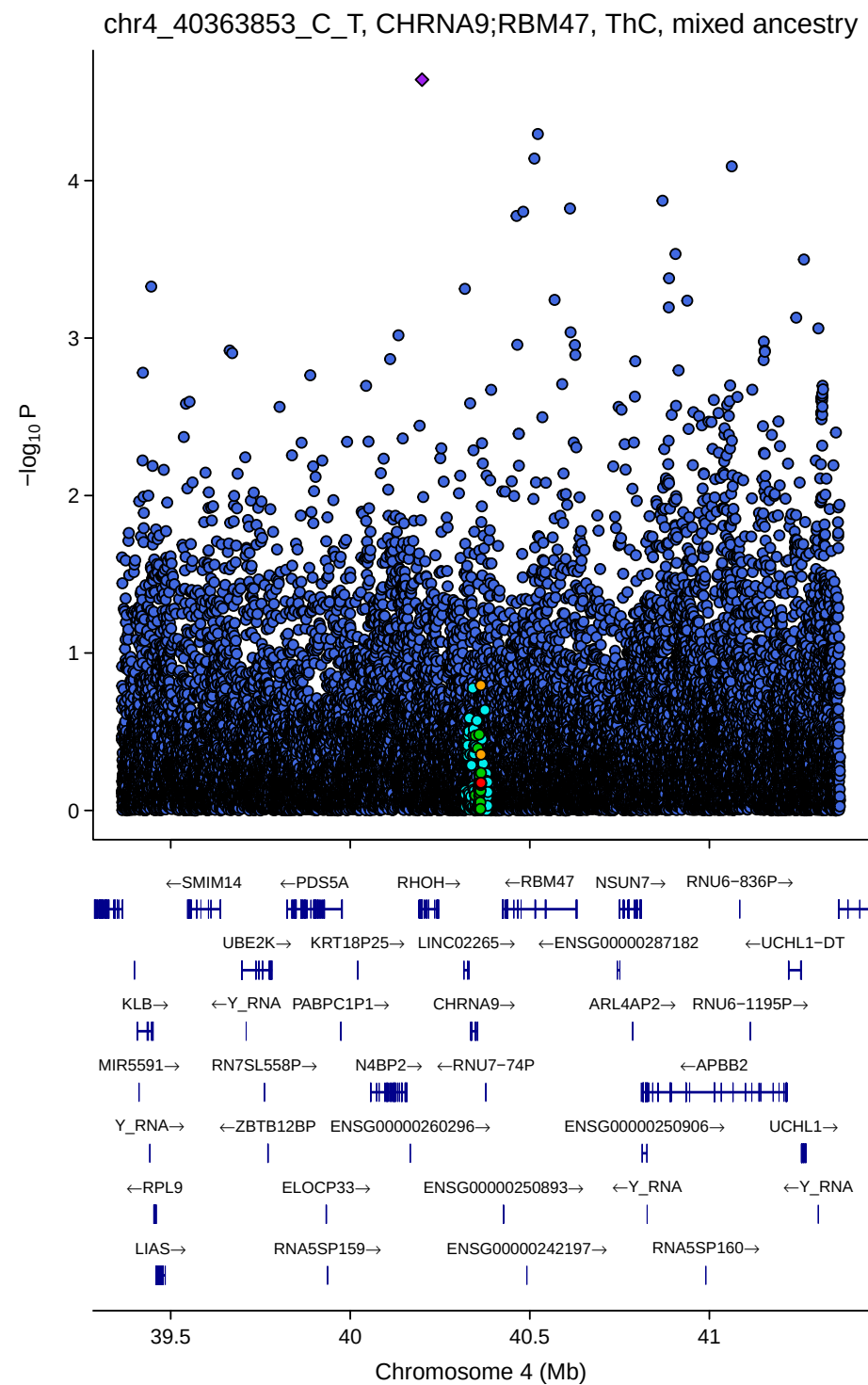
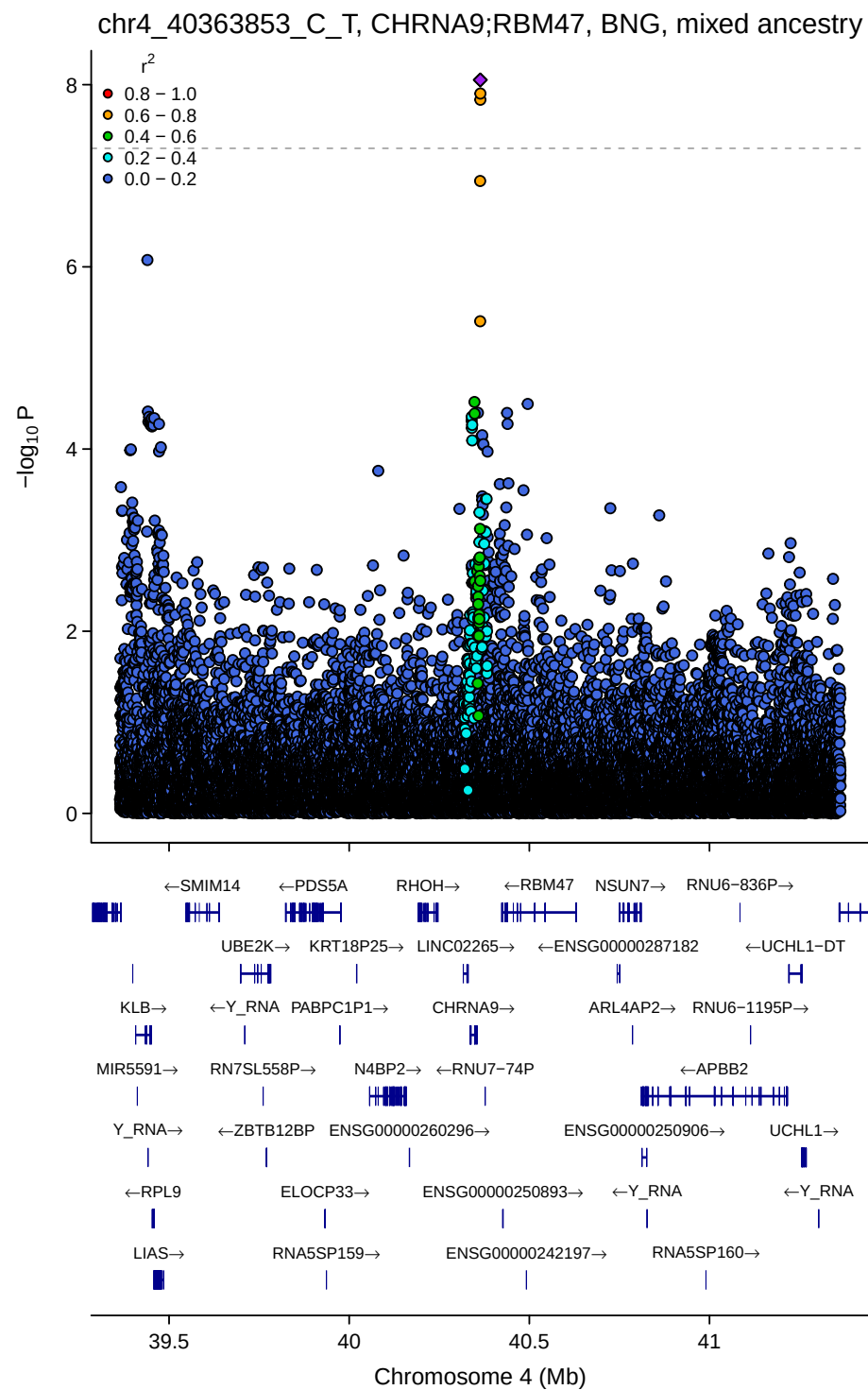


chr1\_93192539\_A\_C, CCDC18, ThC, mixed ancestry

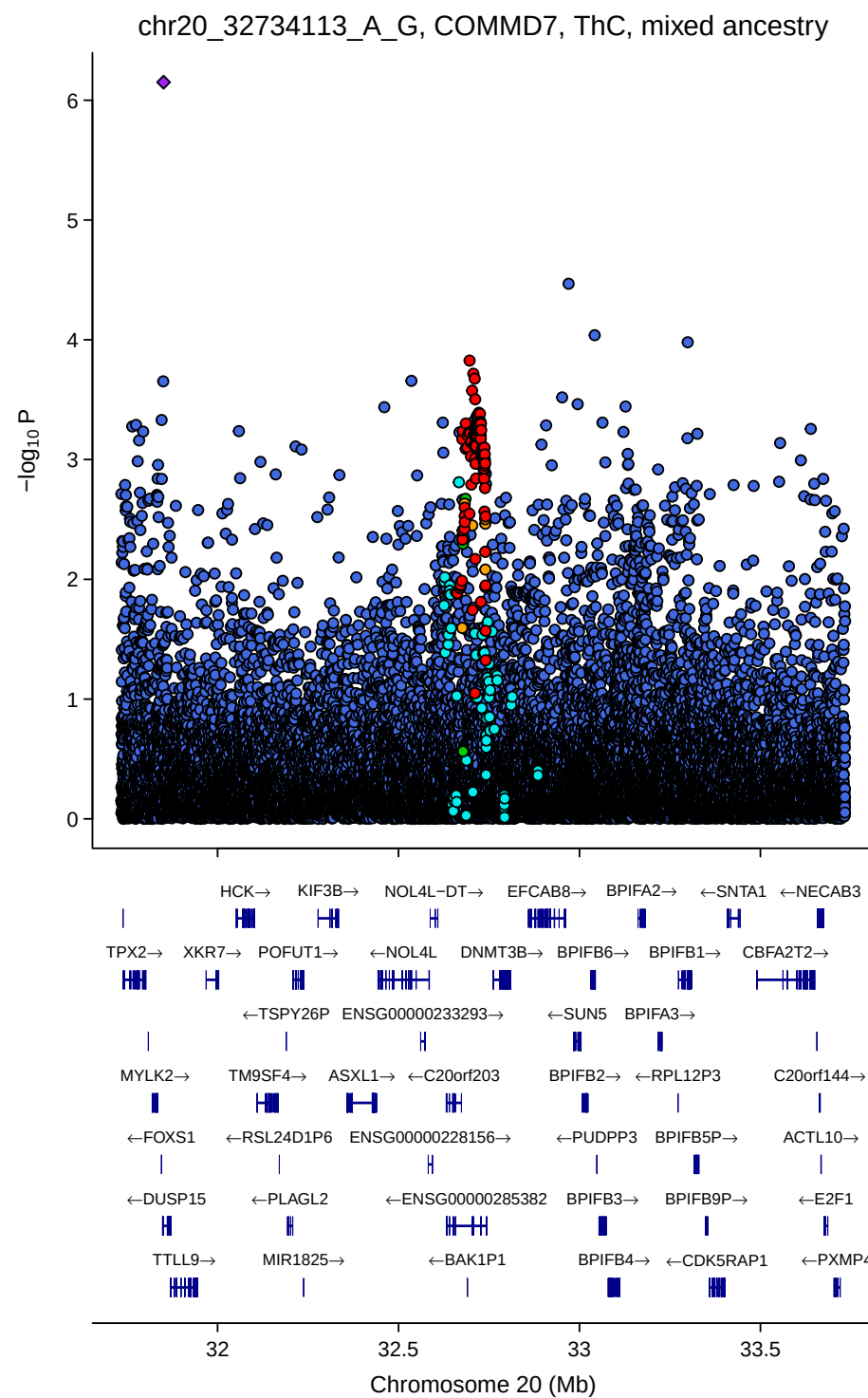
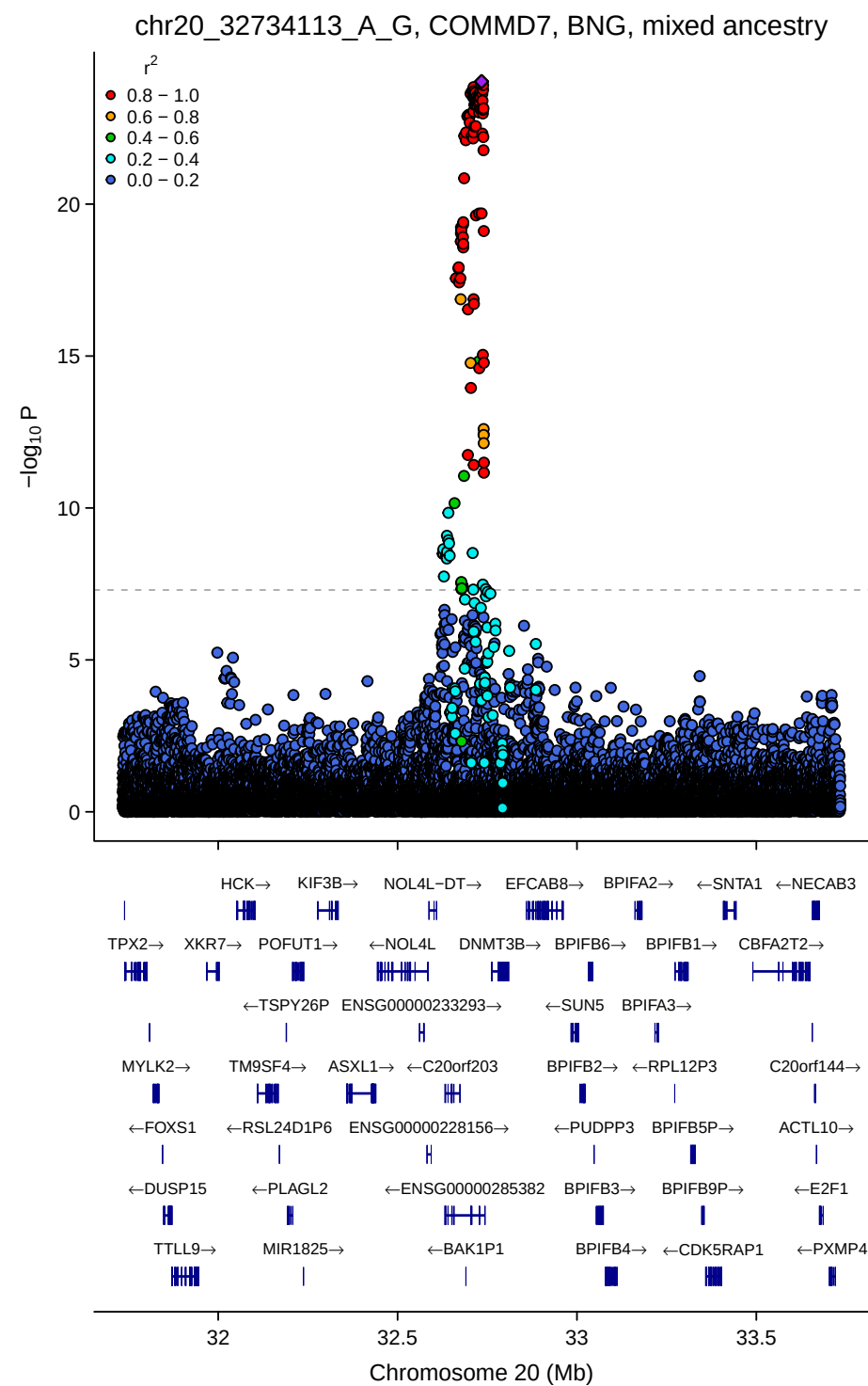




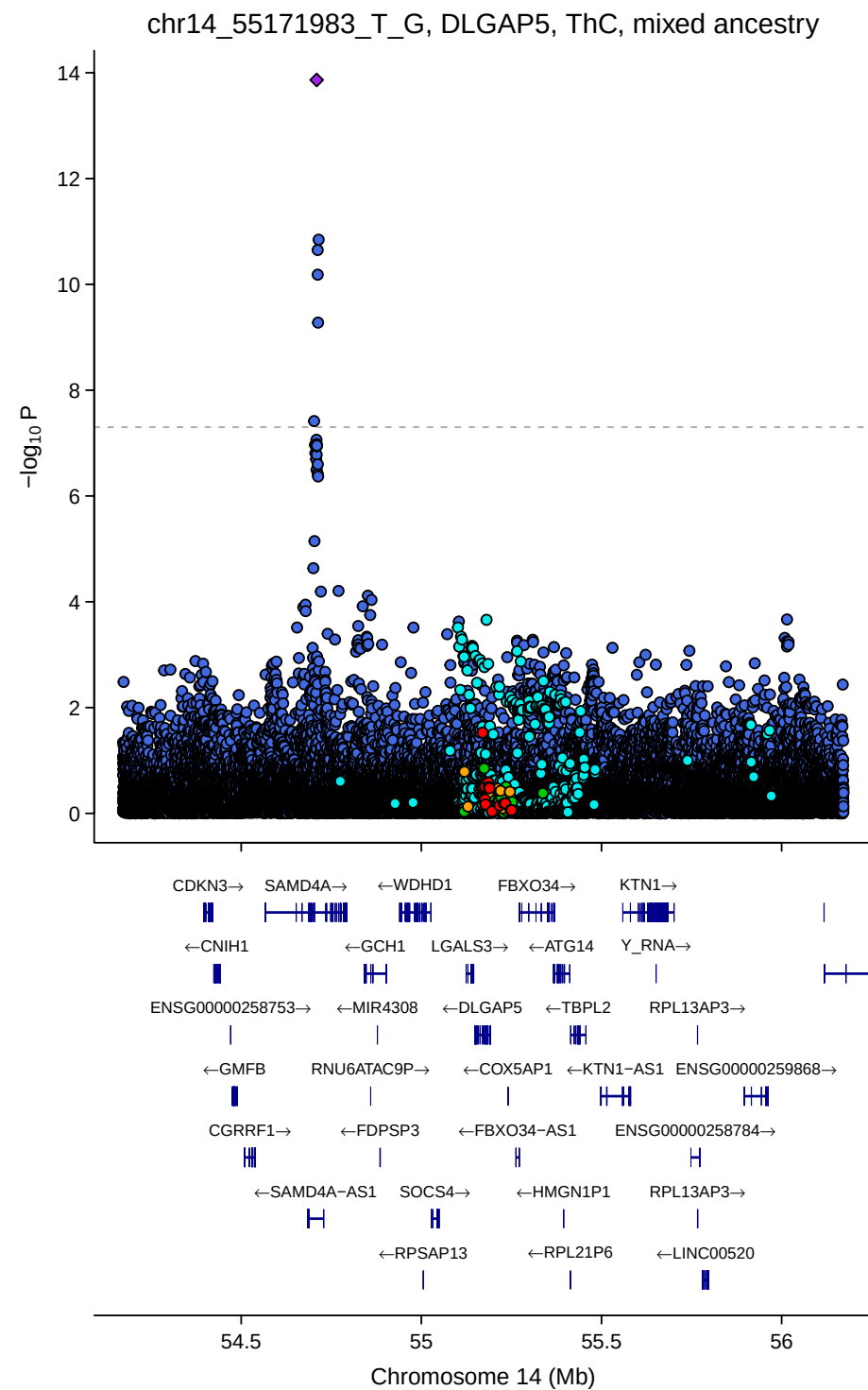
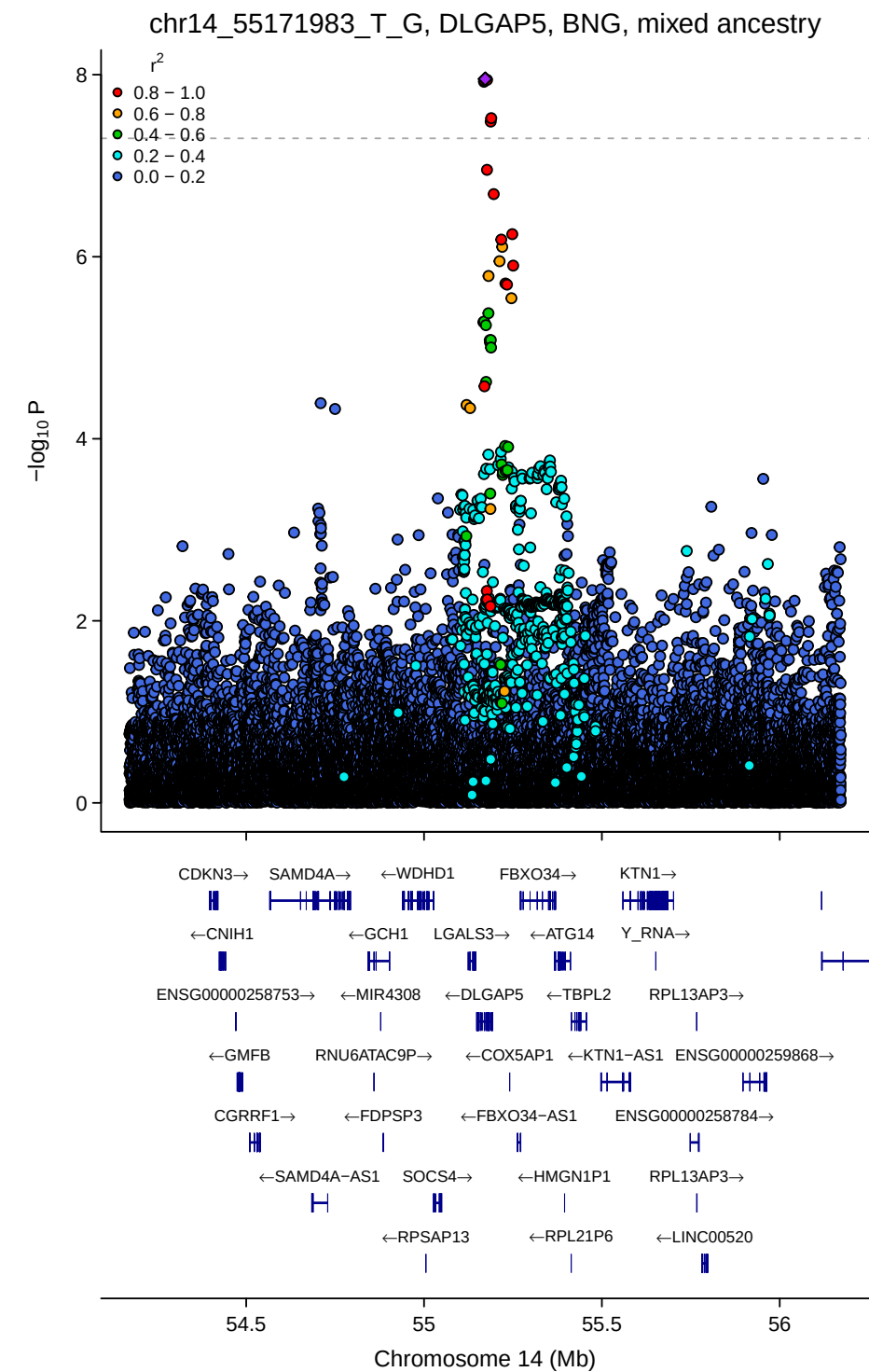
# Supplementary Figure 2.2



# Supplementary Figure 2.2

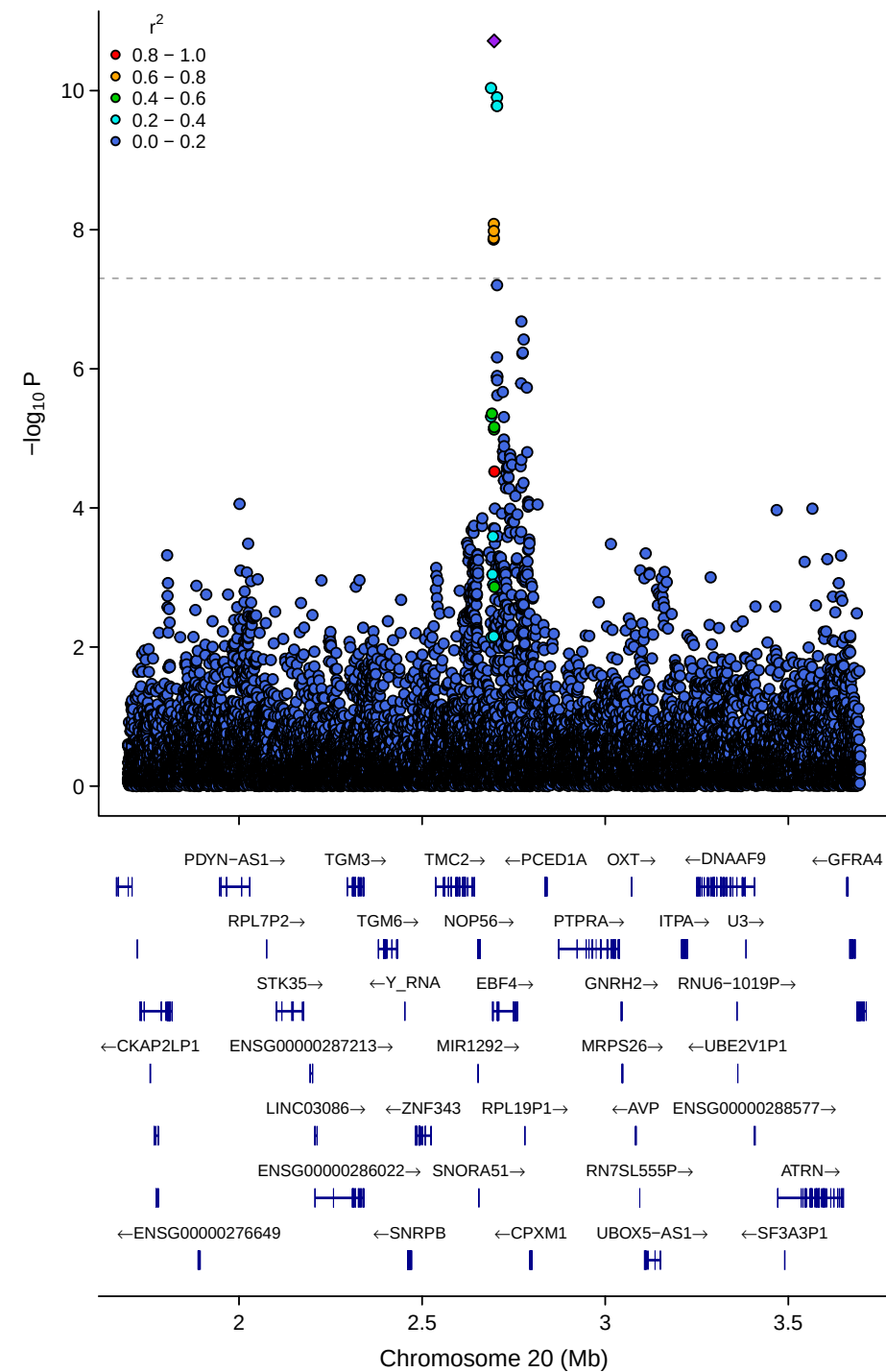


Supplementary Figure 2.2

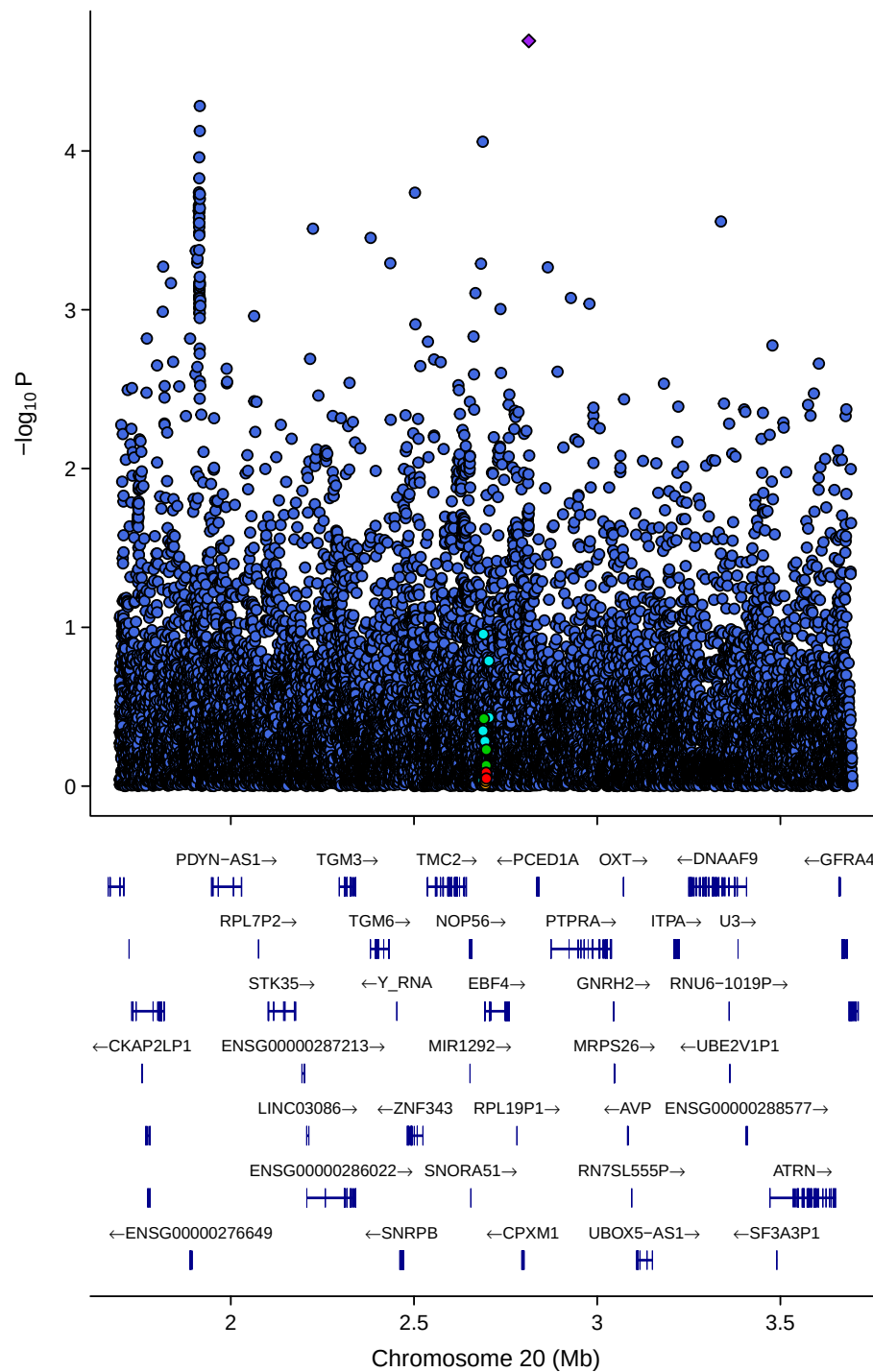


Supplementary Figure 2.2

chr20\_2696683\_A\_G, EBF4, BNG, EUR ancestry



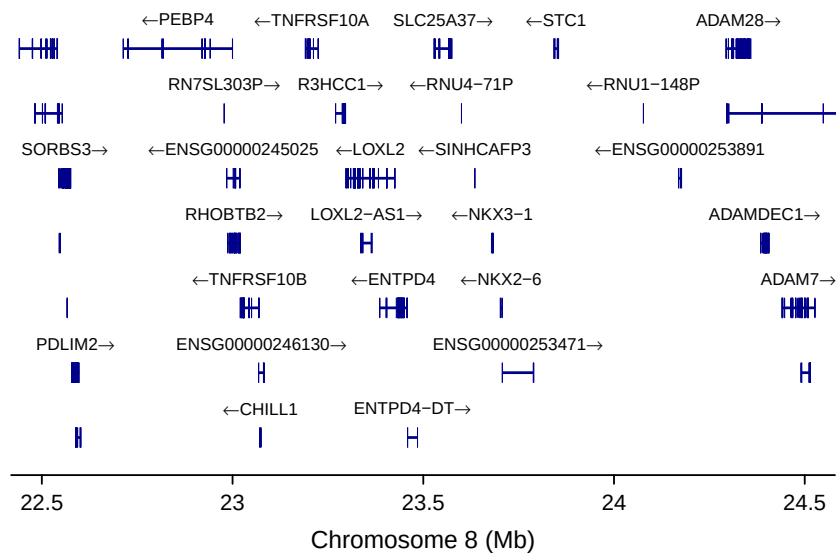
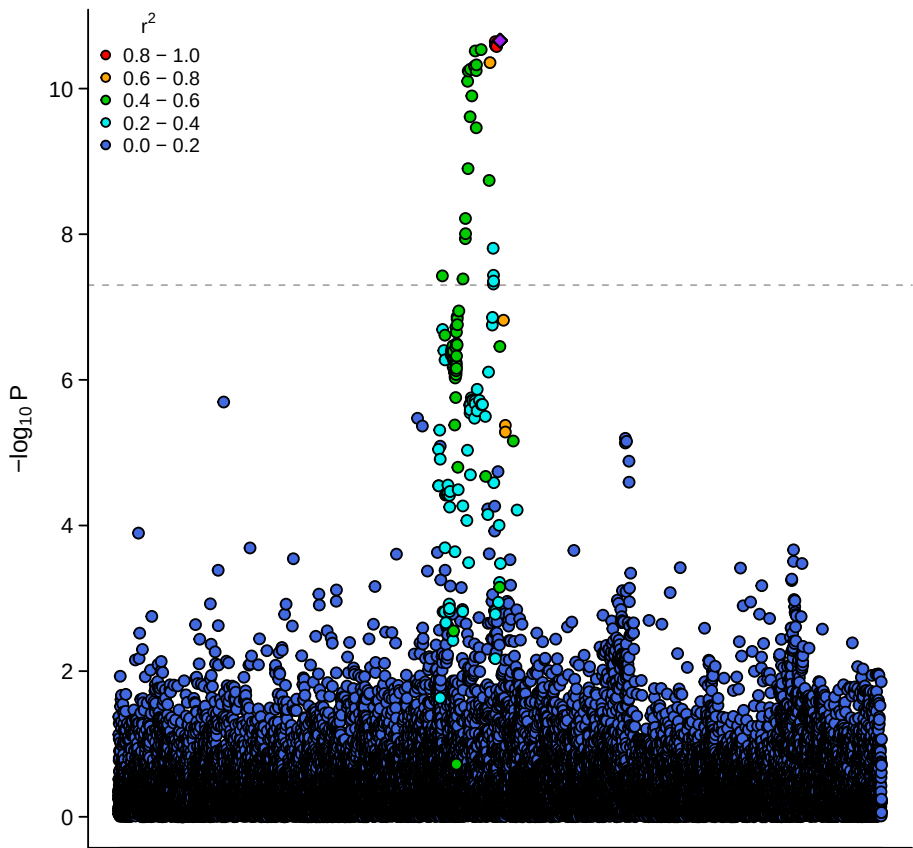
chr20\_2696683\_A\_G, EBF4, ThC, EUR ancestry



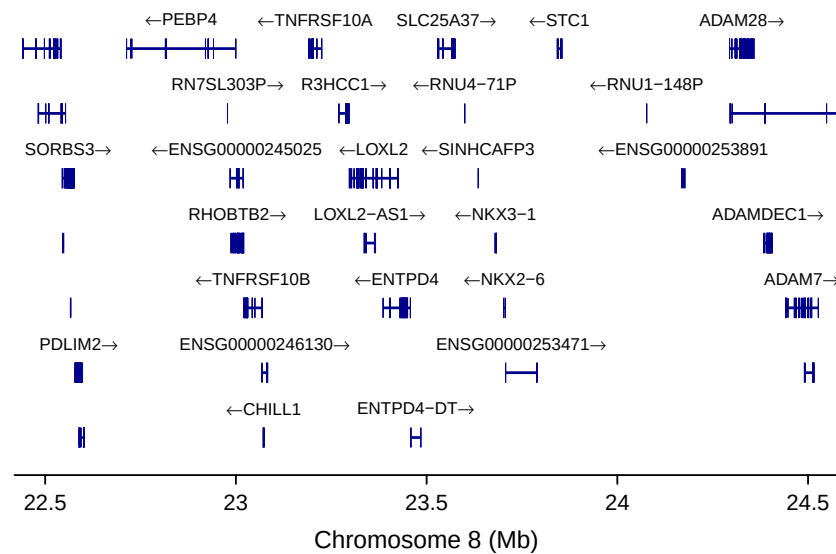
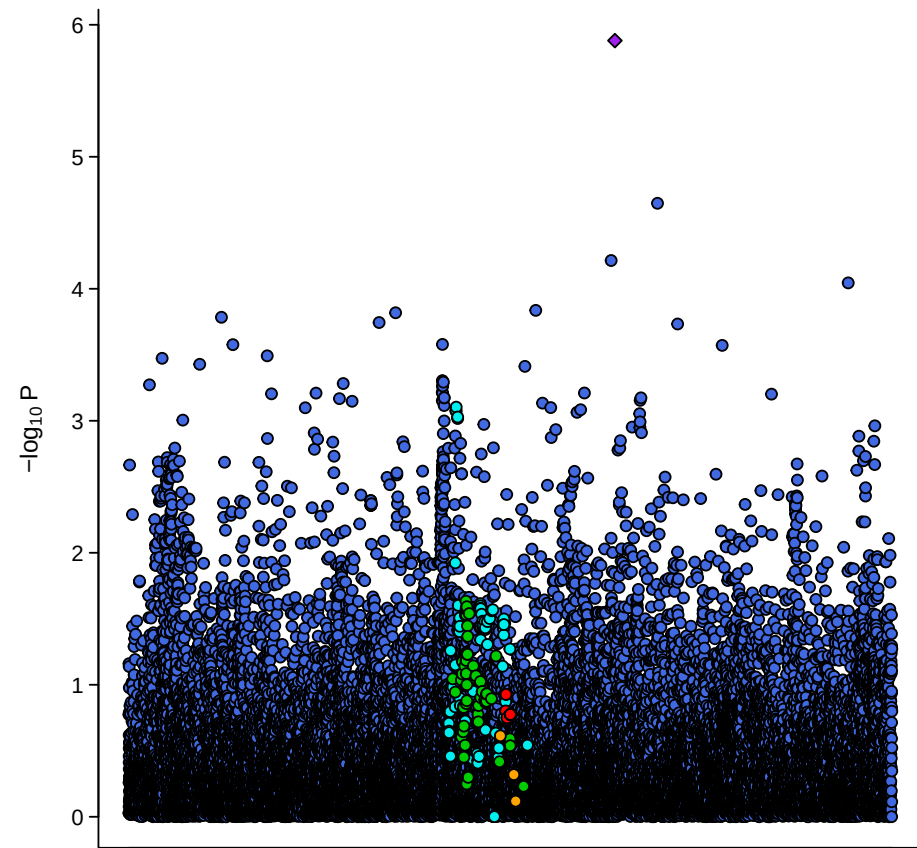


# Supplementary Figure 2.2

chr8\_23499451\_A\_G, ENTPD4;SLC25A37, BNG, mixed ancestry

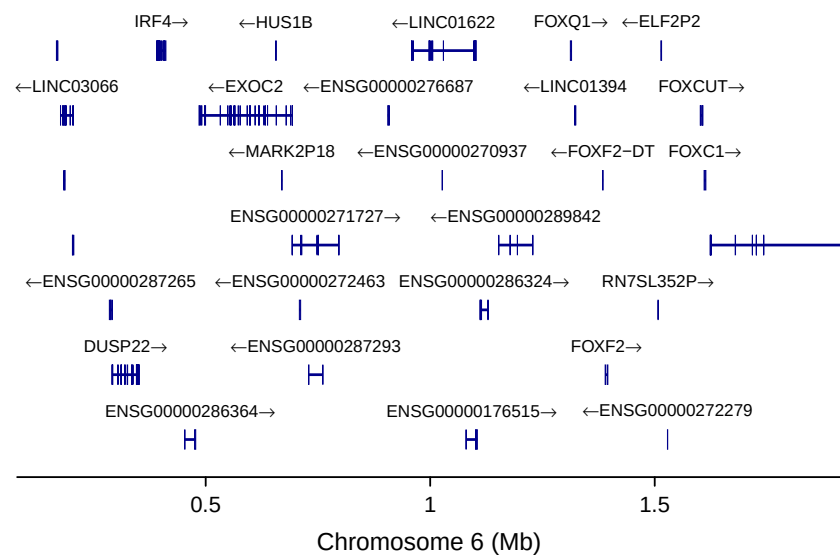
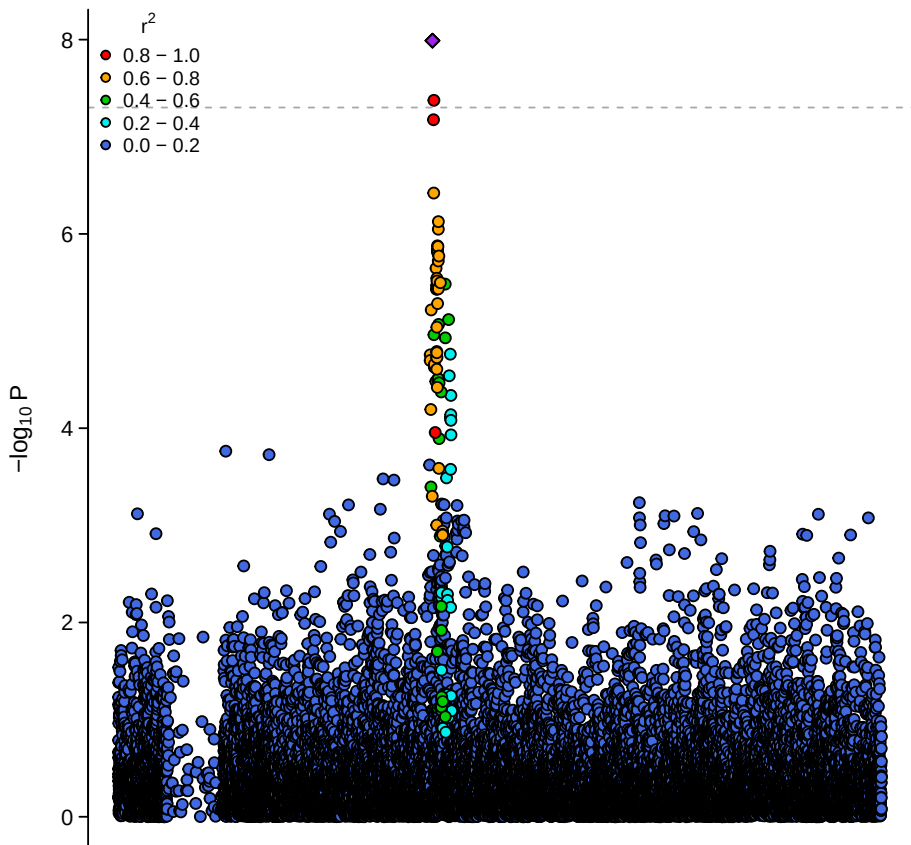


chr8\_23499451\_A\_G, ENTPD4;SLC25A37, ThC, mixed ancestry

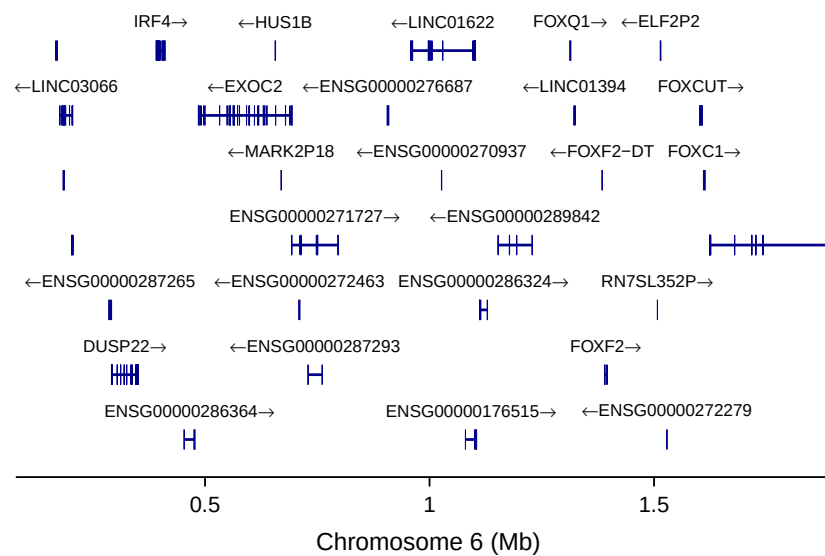
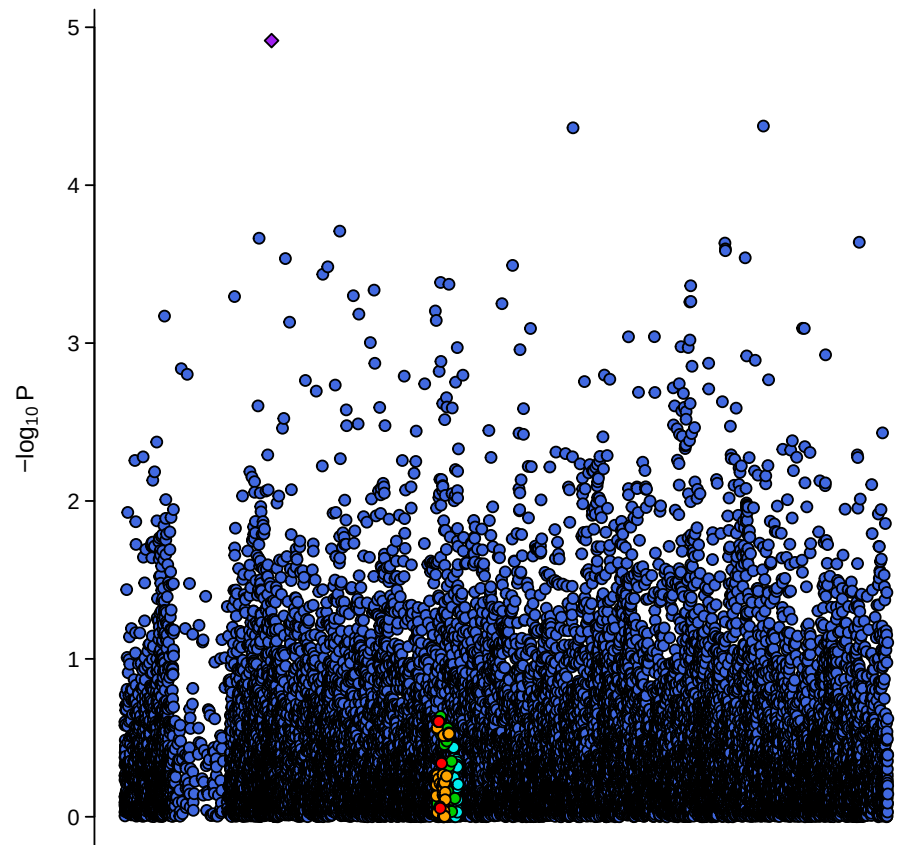


# Supplementary Figure 2.2

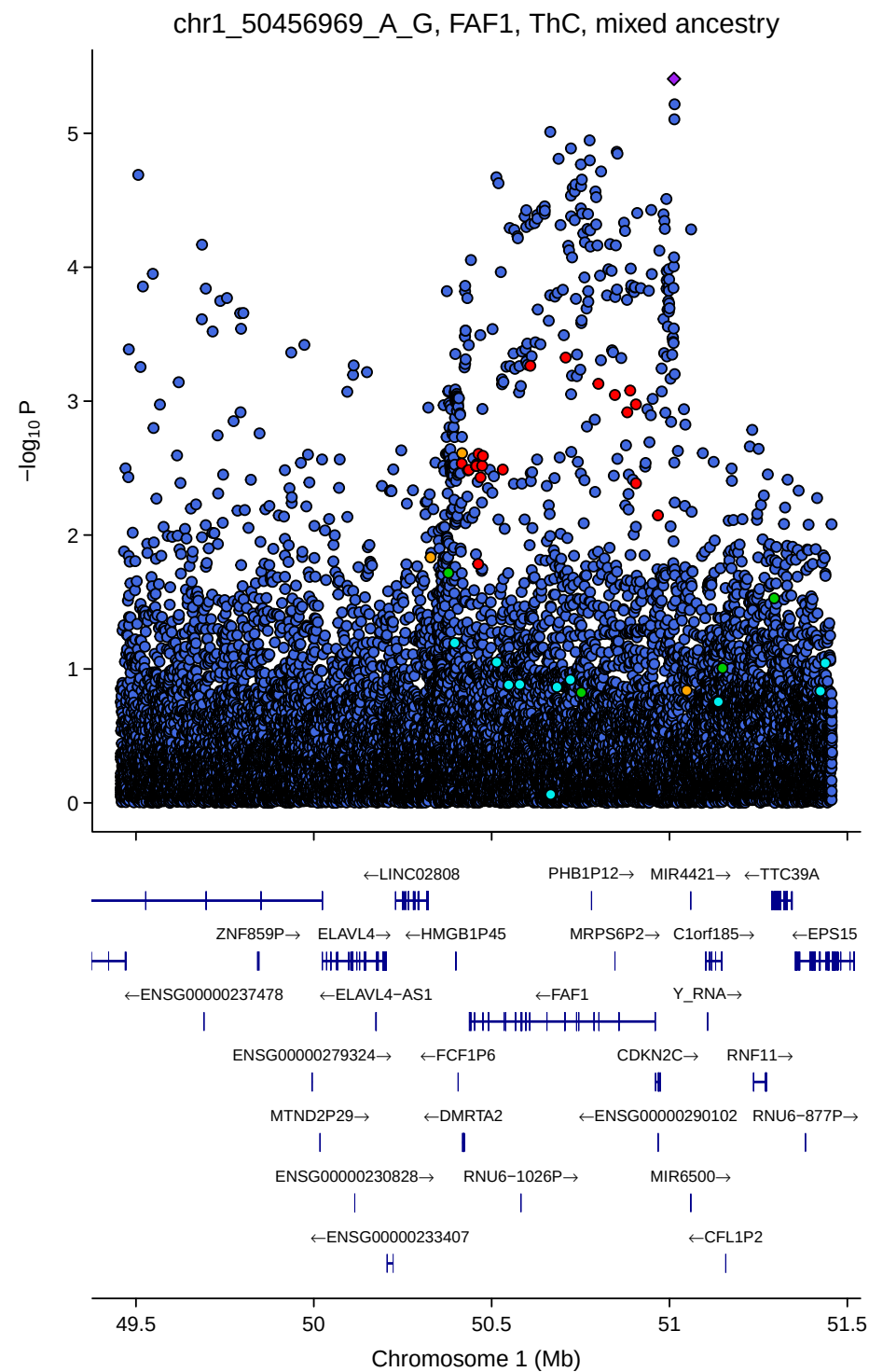
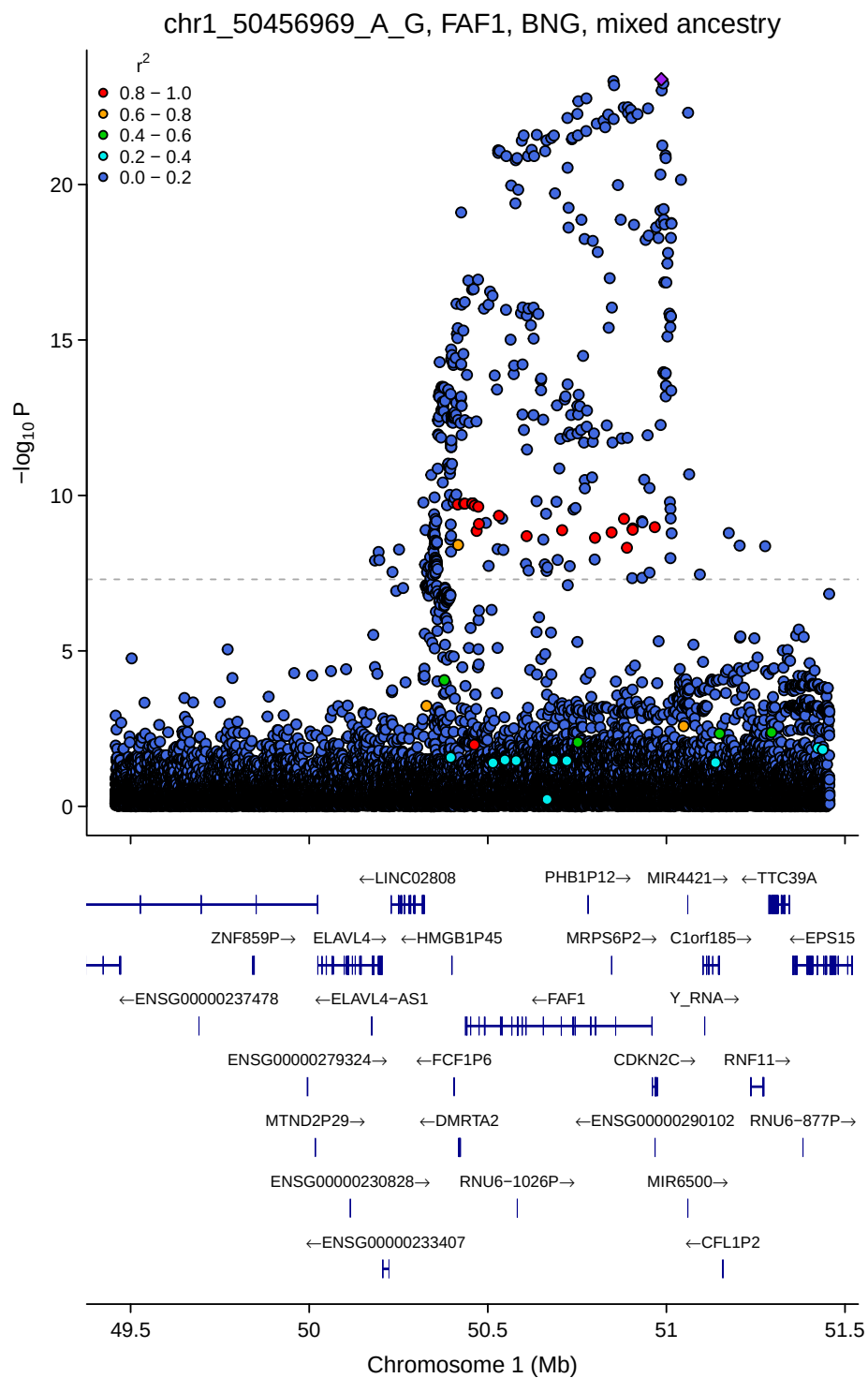
chr6\_846919\_C\_G, EXOC2;LOC101927691, BNG, mixed ancestry



chr6\_846919\_C\_G, EXOC2;LOC101927691, ThC, mixed ancestry

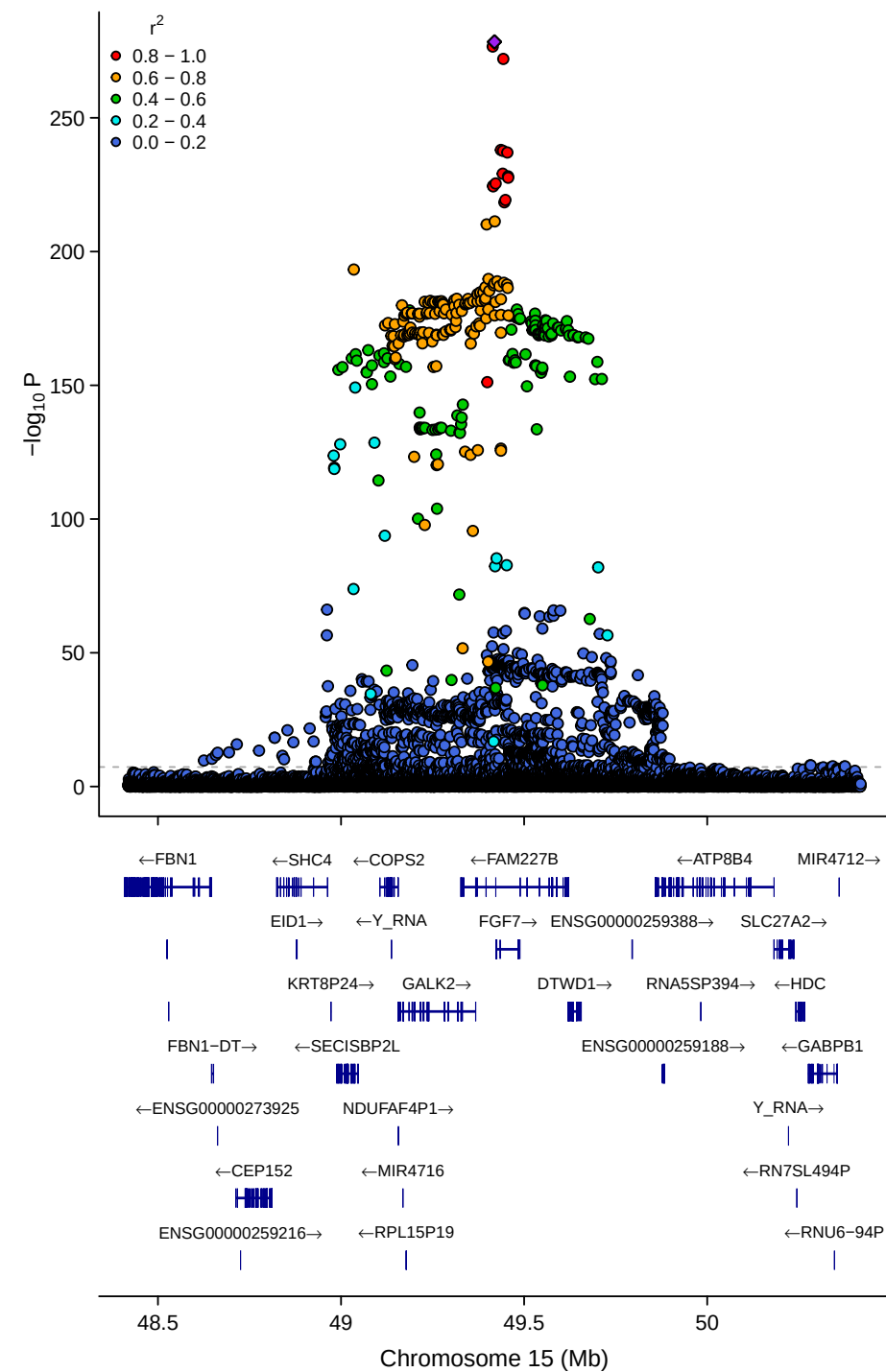


# Supplementary Figure 2.2

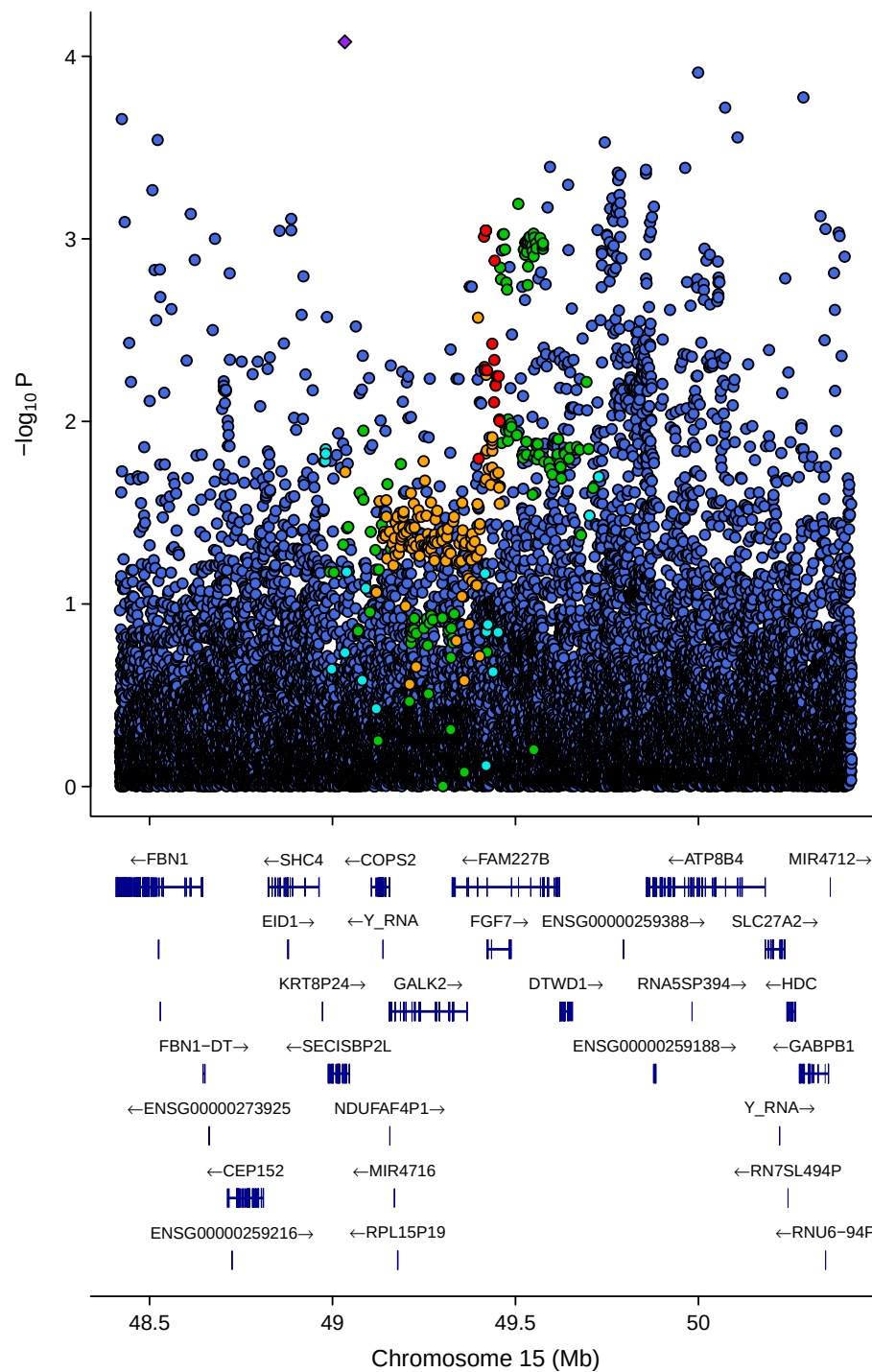


# Supplementary Figure 2.2

chr15\_49418988\_T\_C, FAM227B, BNG, mixed ancestry



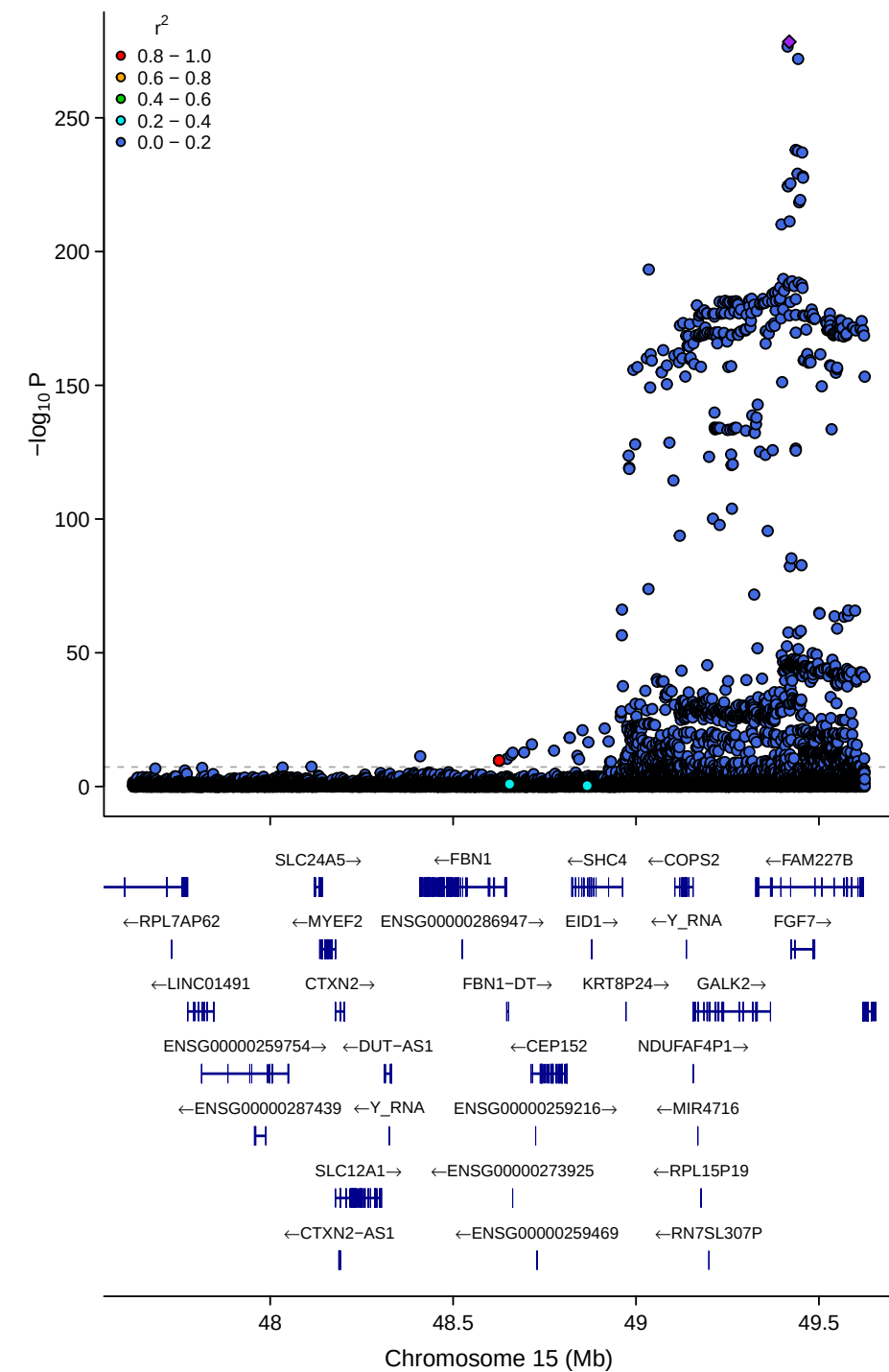
chr15\_49418988\_T\_C, FAM227B, ThC, mixed ancestry



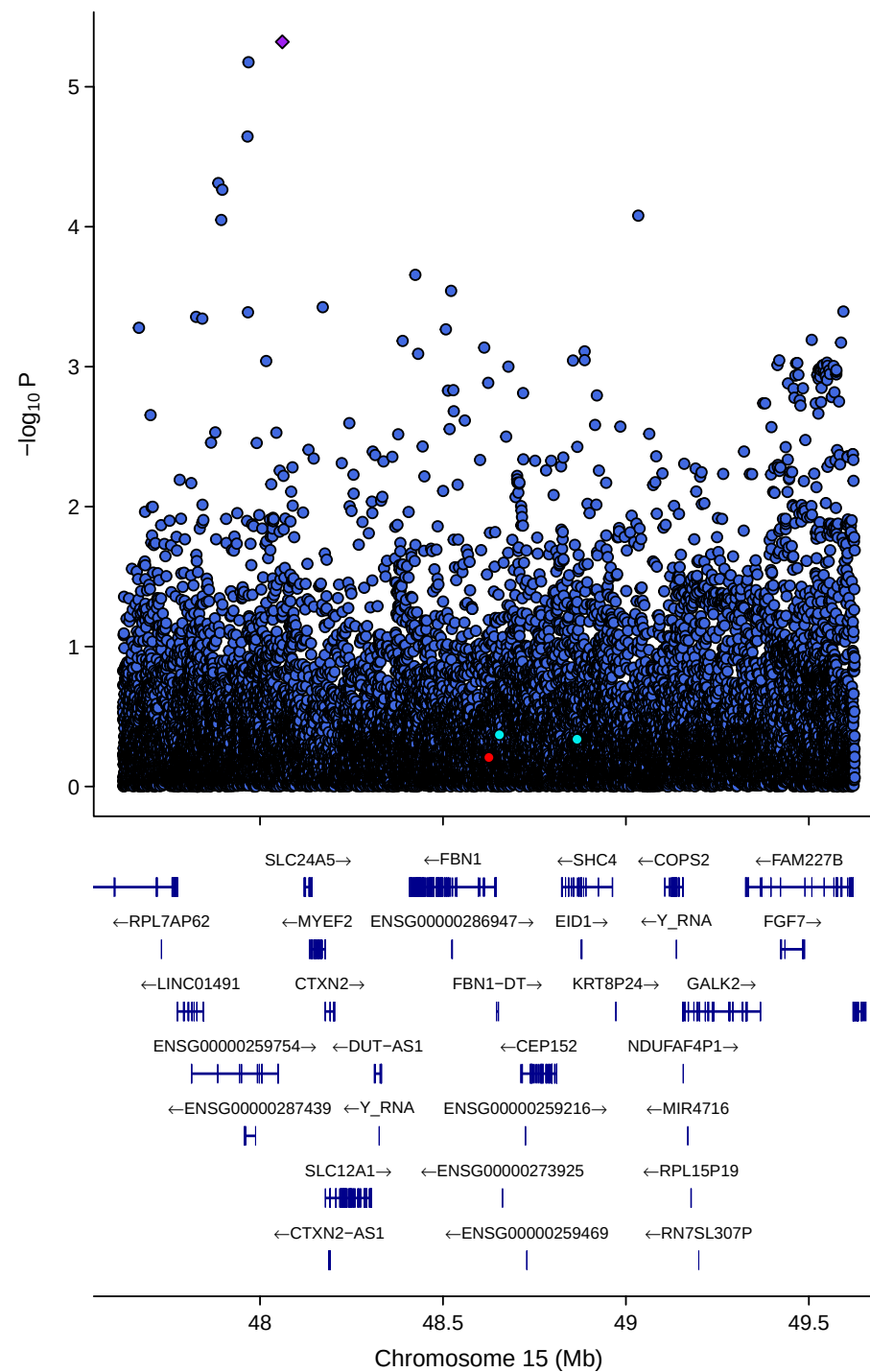


Supplementary Figure 2.2

chr15\_48625487\_G\_A, FBN1, BNG, mixed ancestry

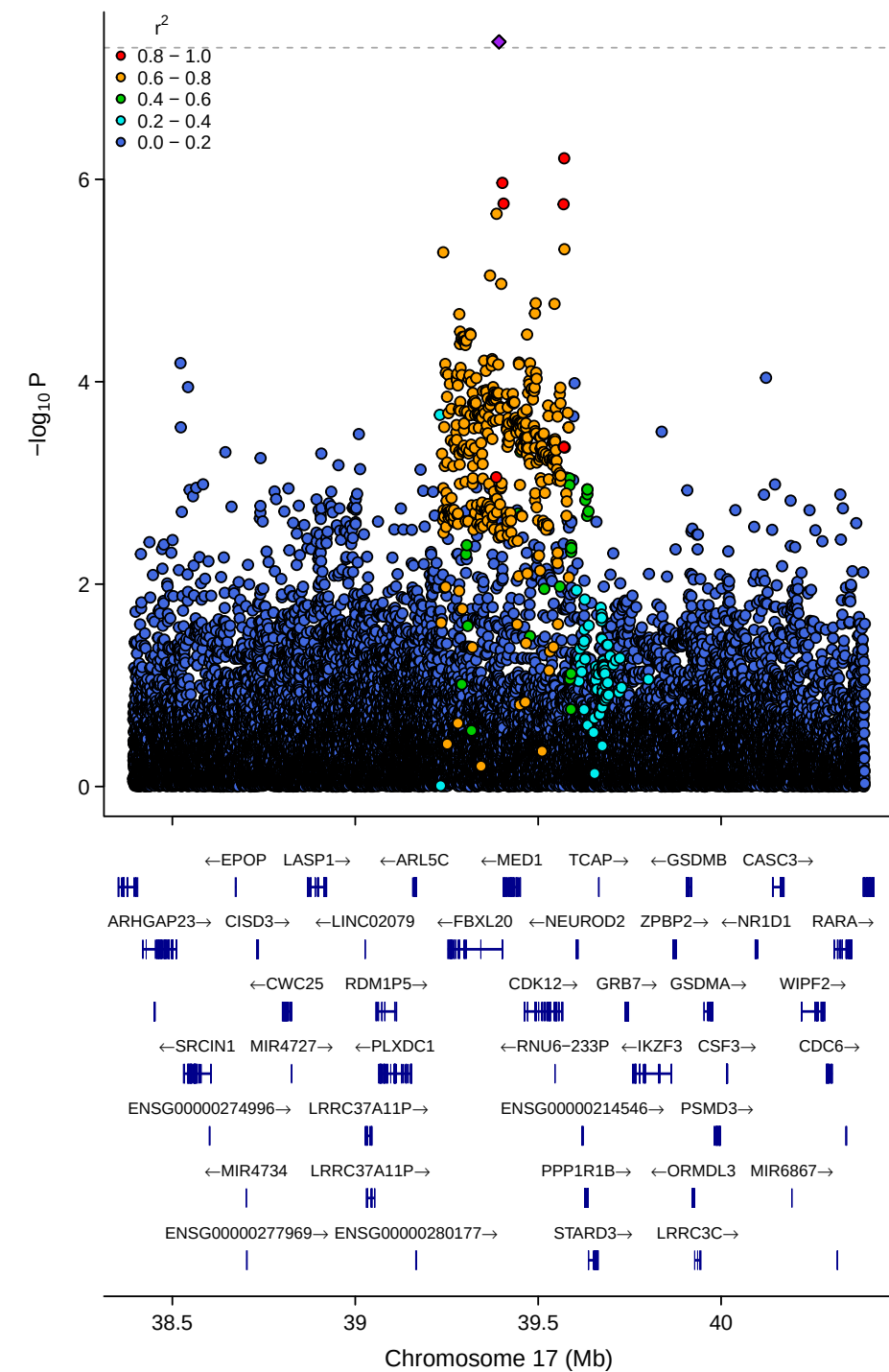


chr15\_48625487\_G\_A, FBN1, ThC, mixed ancestry

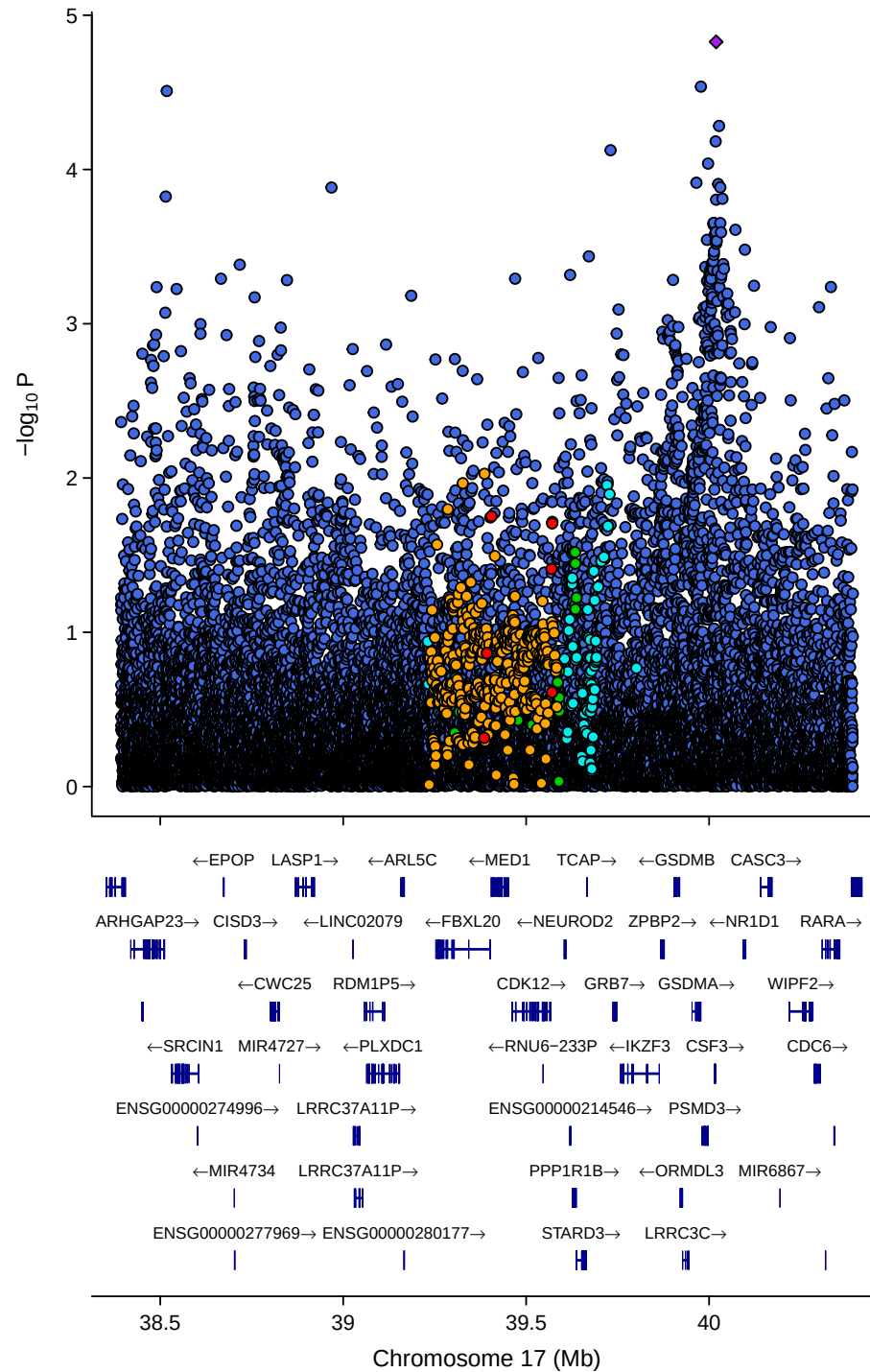


# Supplementary Figure 2.2

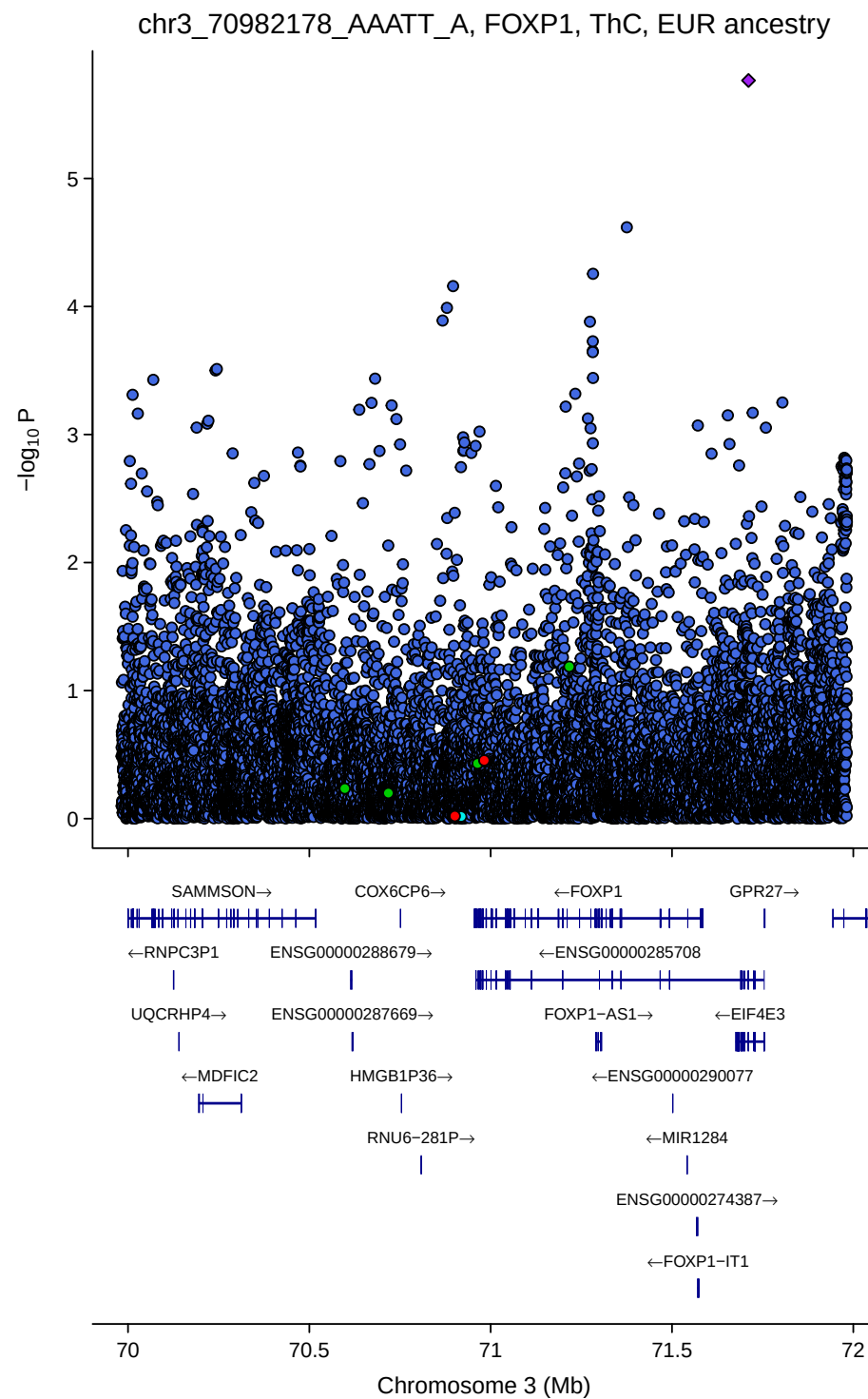
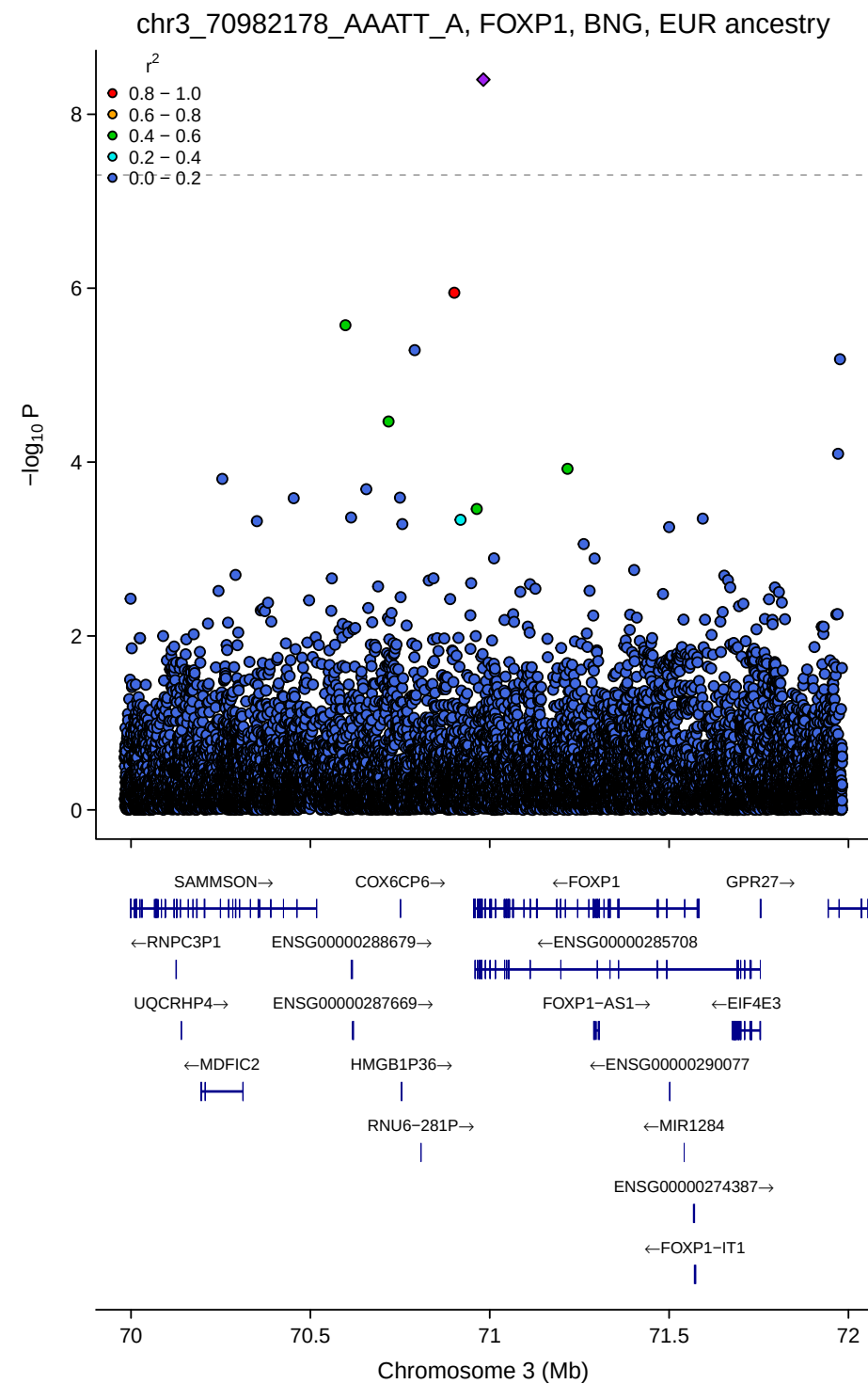
chr17\_39392947\_C\_T, FBXL20, BNG, mixed ancestry



chr17\_39392947\_C\_T, FBXL20, ThC, mixed ancestry

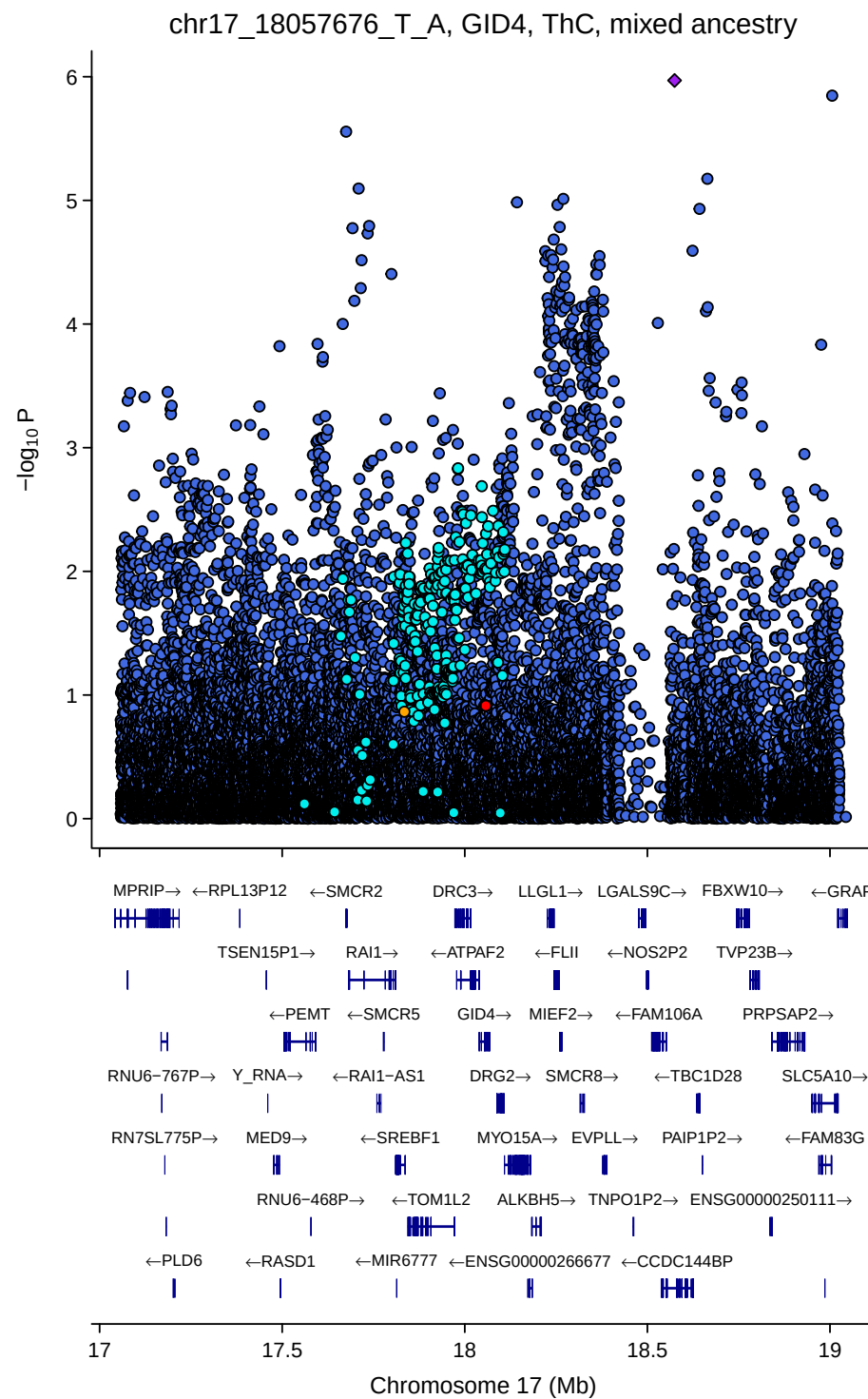
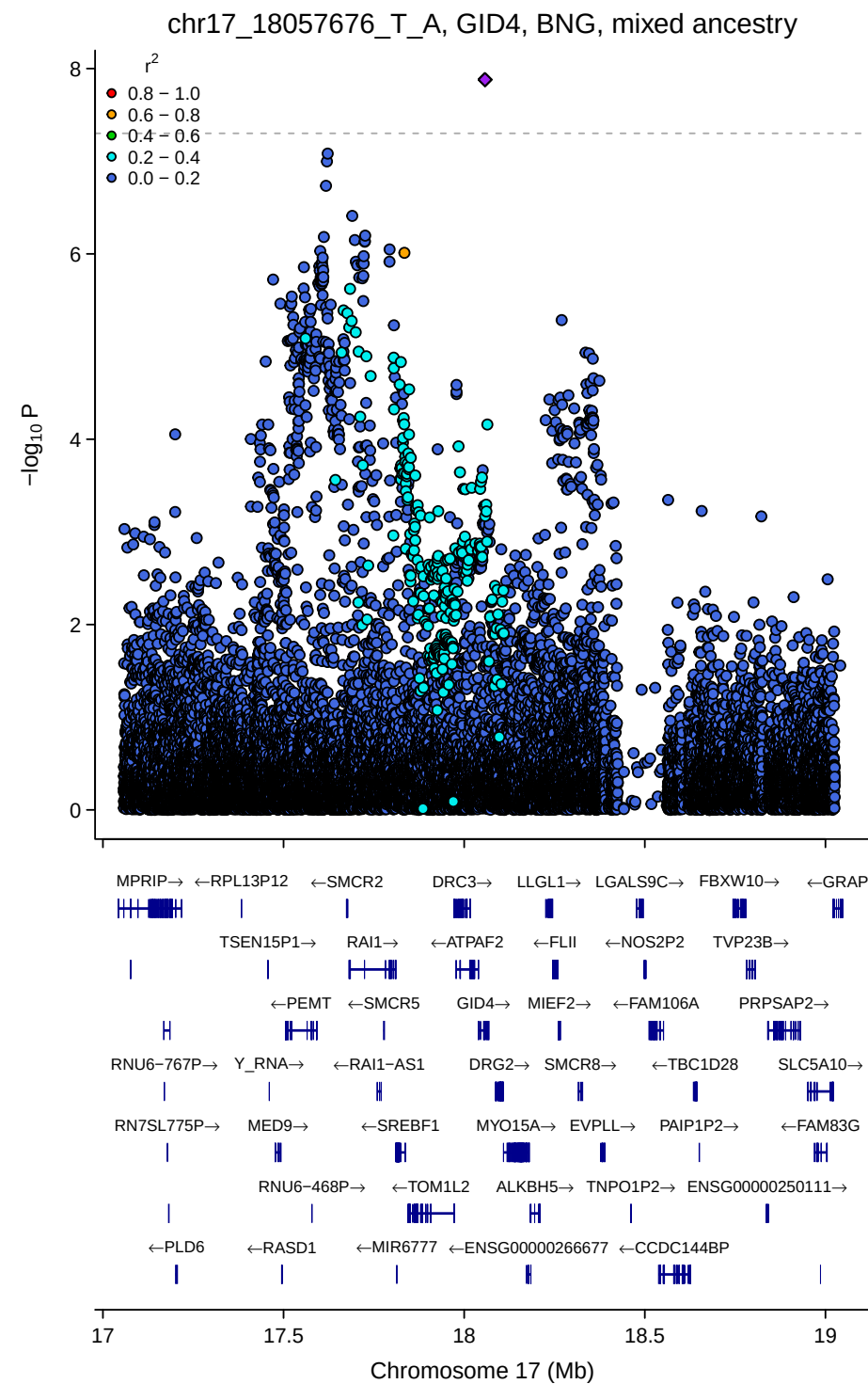


Supplementary Figure 2.2



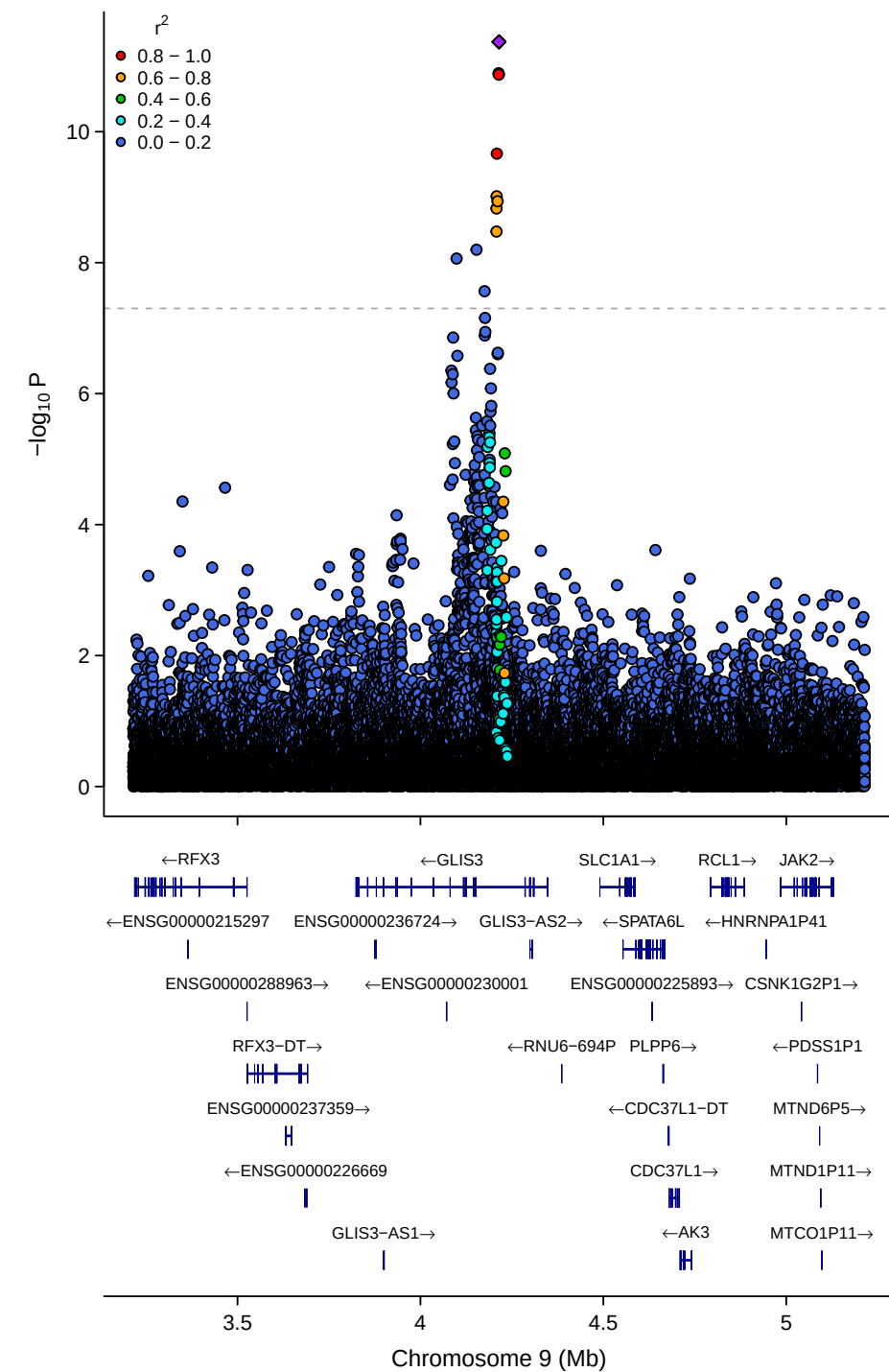


# Supplementary Figure 2.2

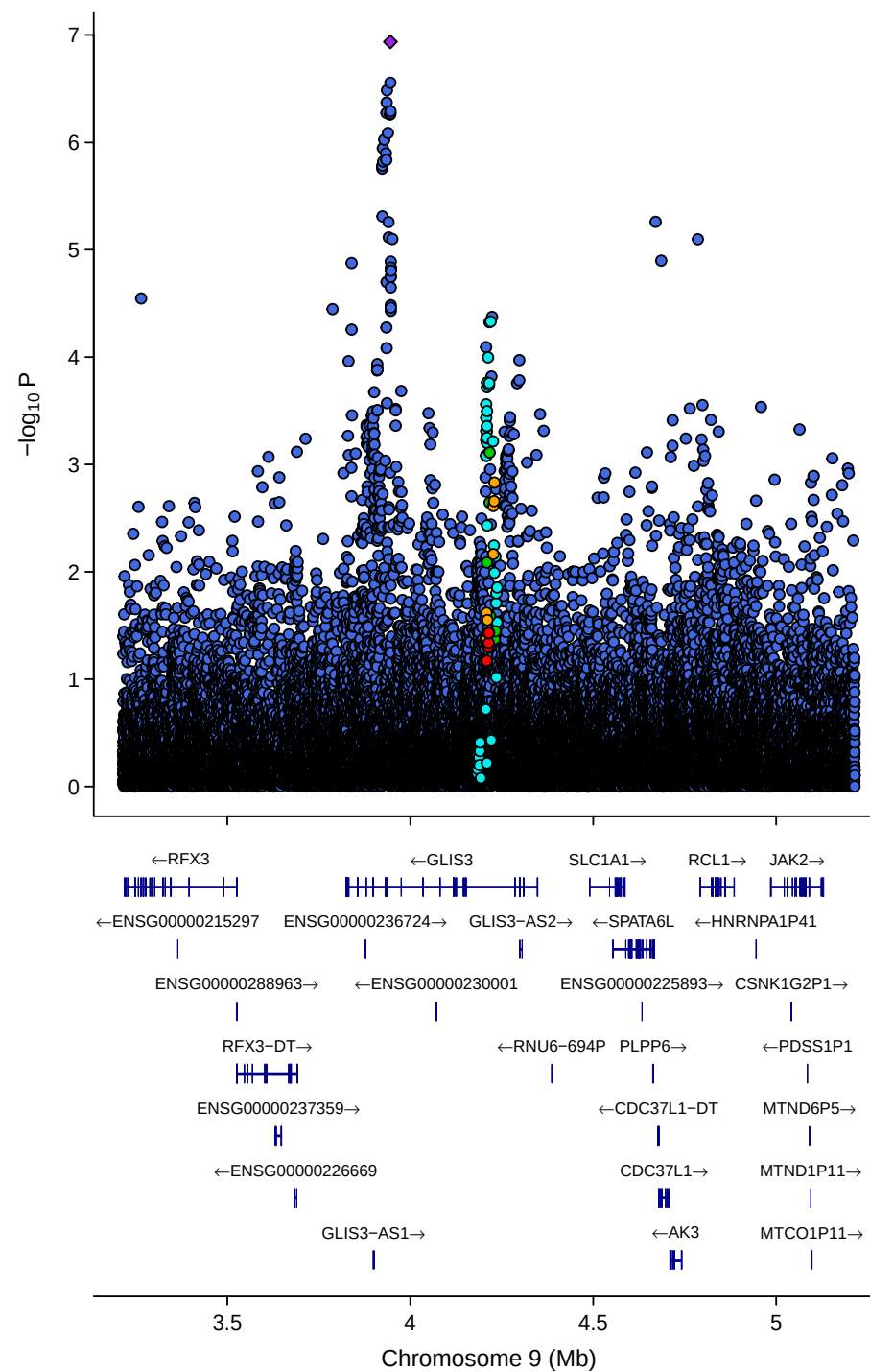


Supplementary Figure 2.2

chr9\_4214847\_T\_C, GLIS3, BNG, mixed ancestry

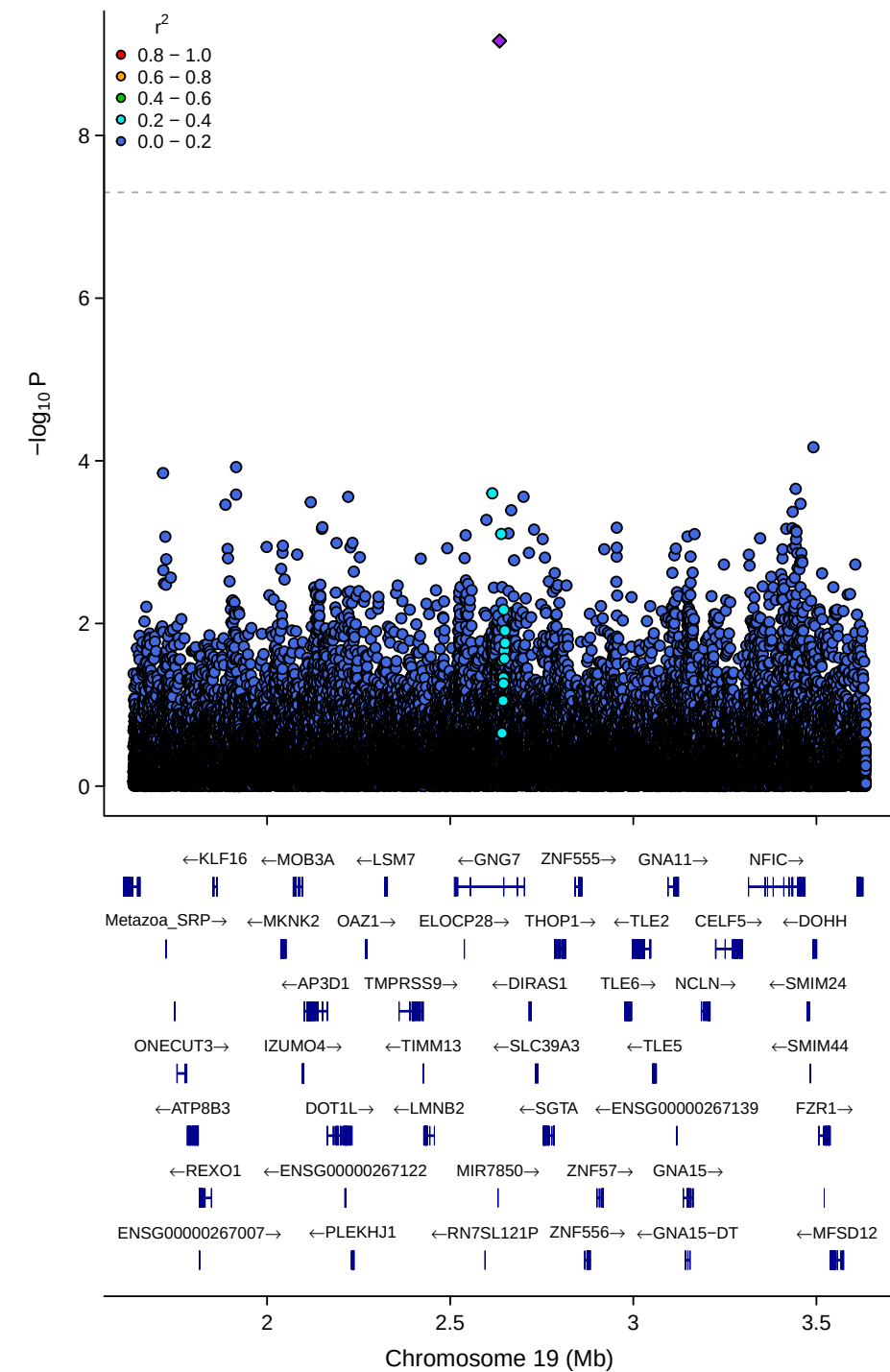


chr9\_4214847\_T\_C, GLIS3, ThC, mixed ancestry

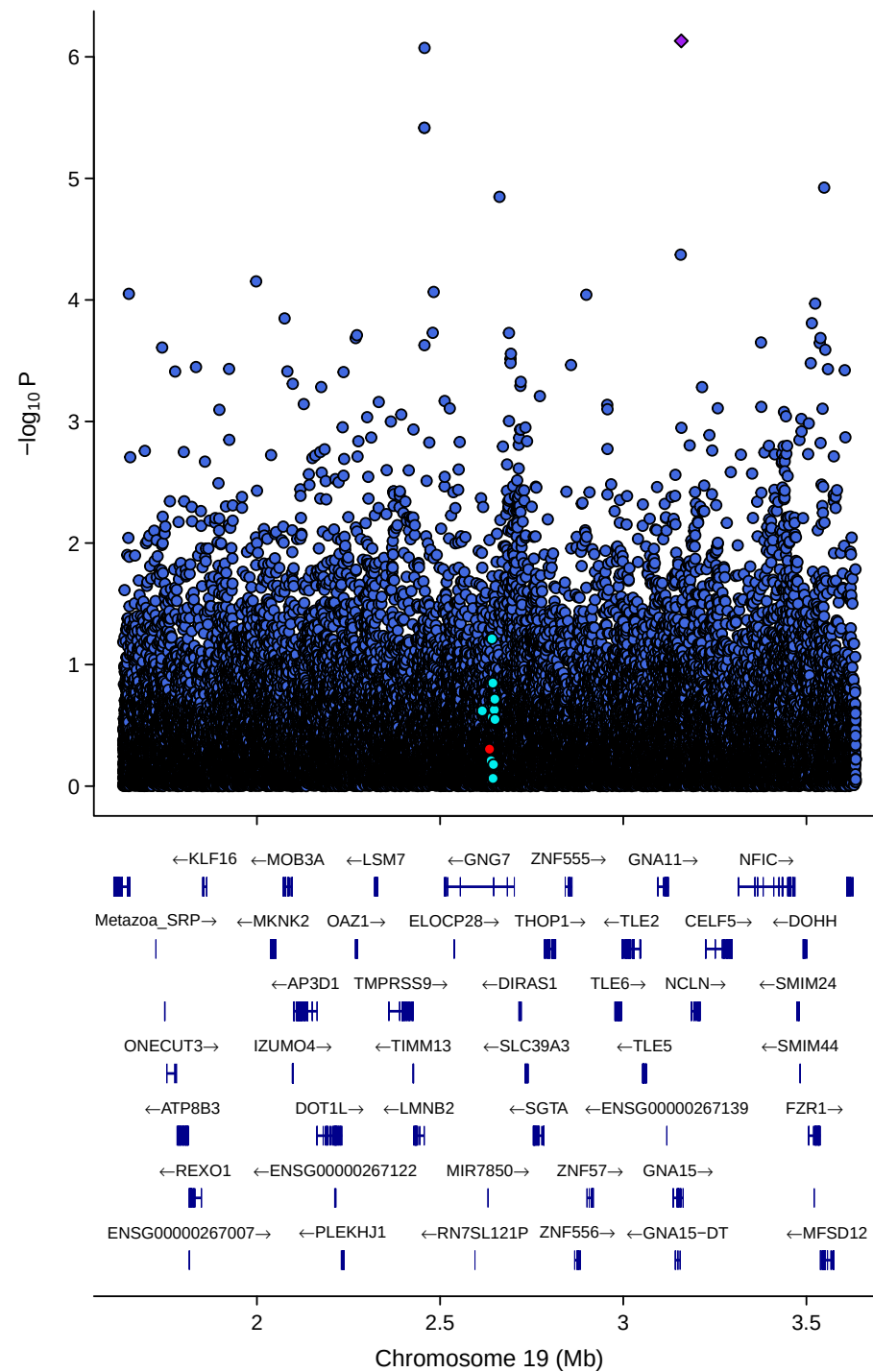


# Supplementary Figure 2.2

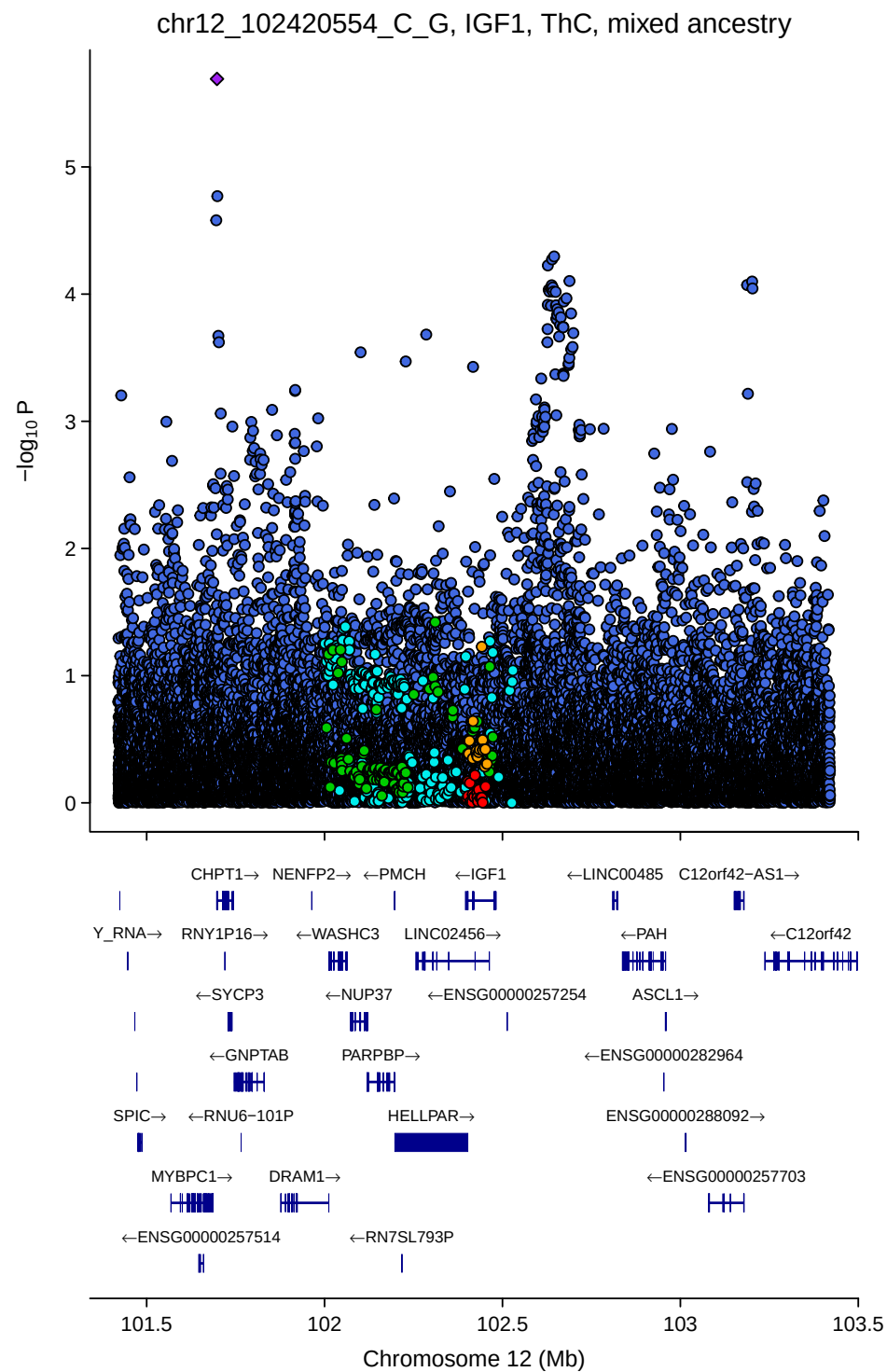
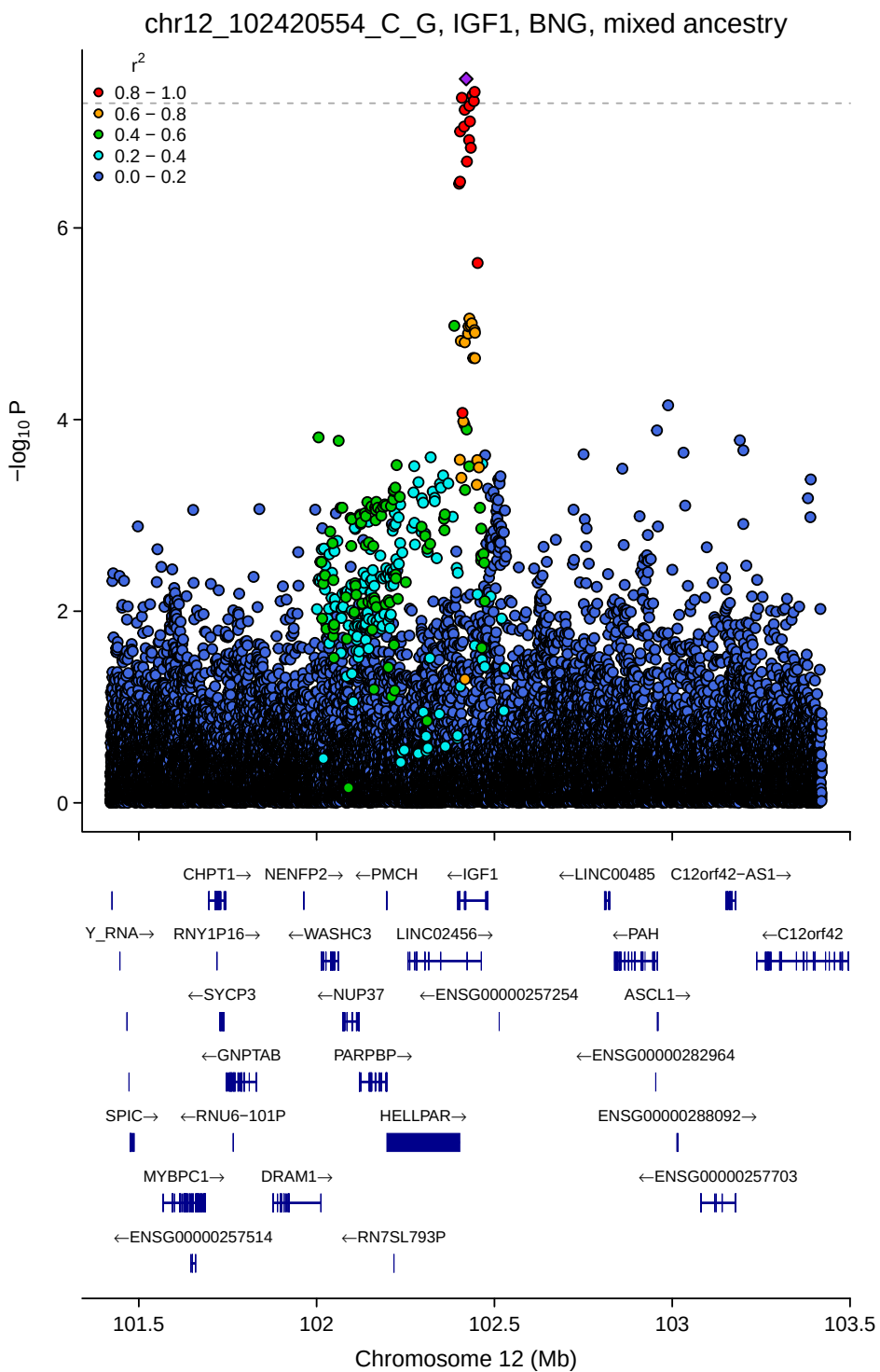
chr19\_2634825\_T\_C, GNG7, BNG, mixed ancestry



chr19\_2634825\_T\_C, GNG7, ThC, mixed ancestry

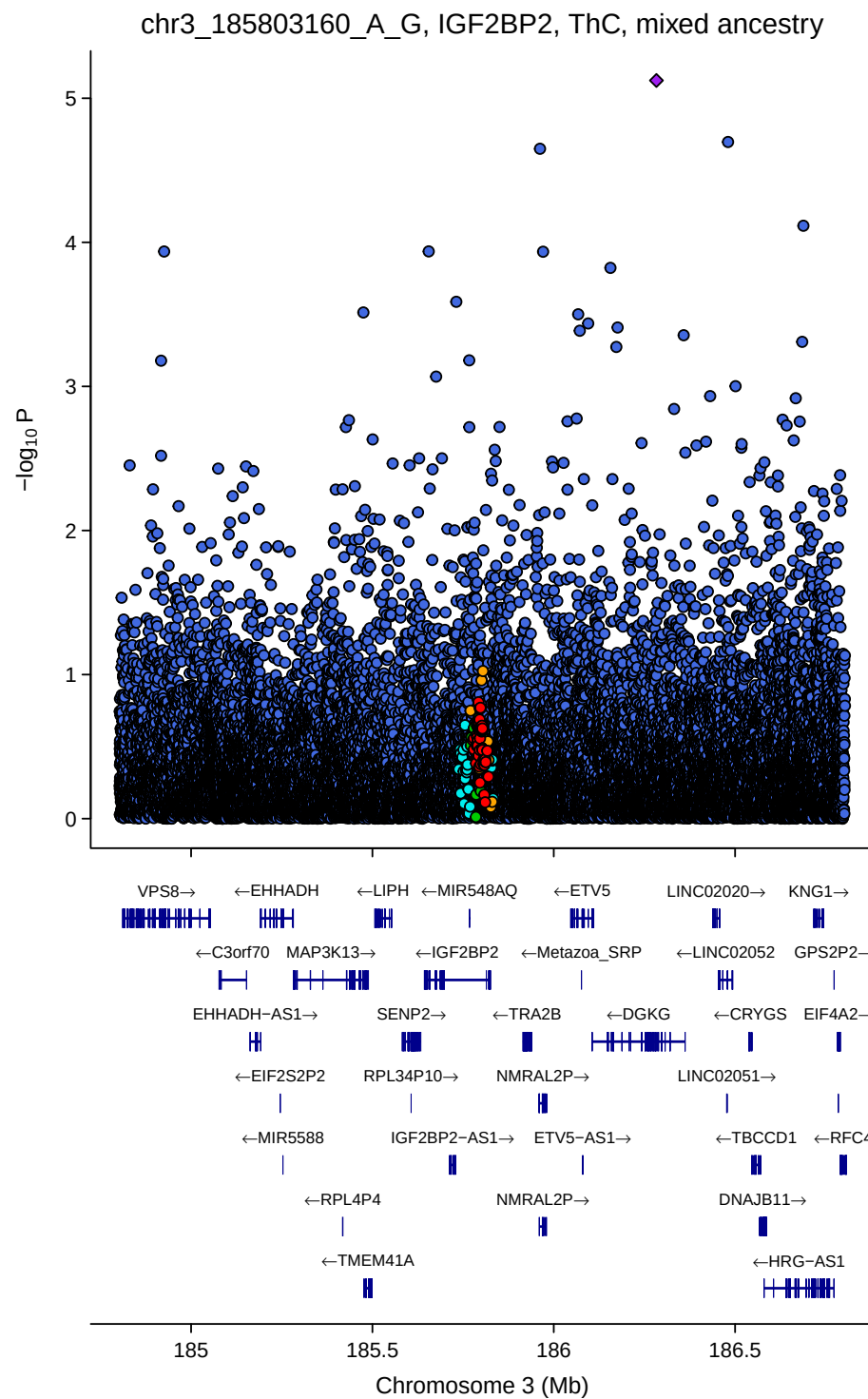
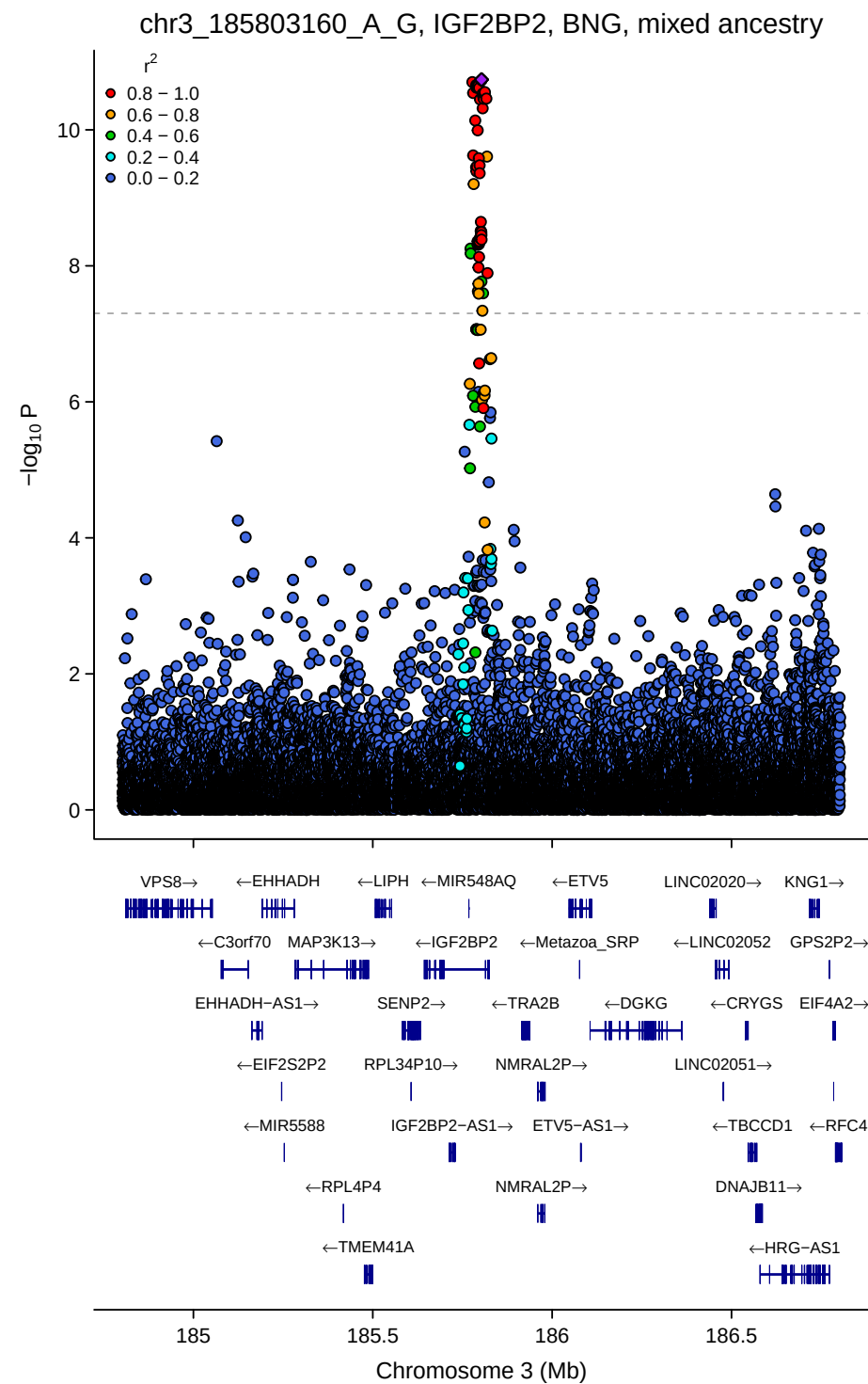


# Supplementary Figure 2.2



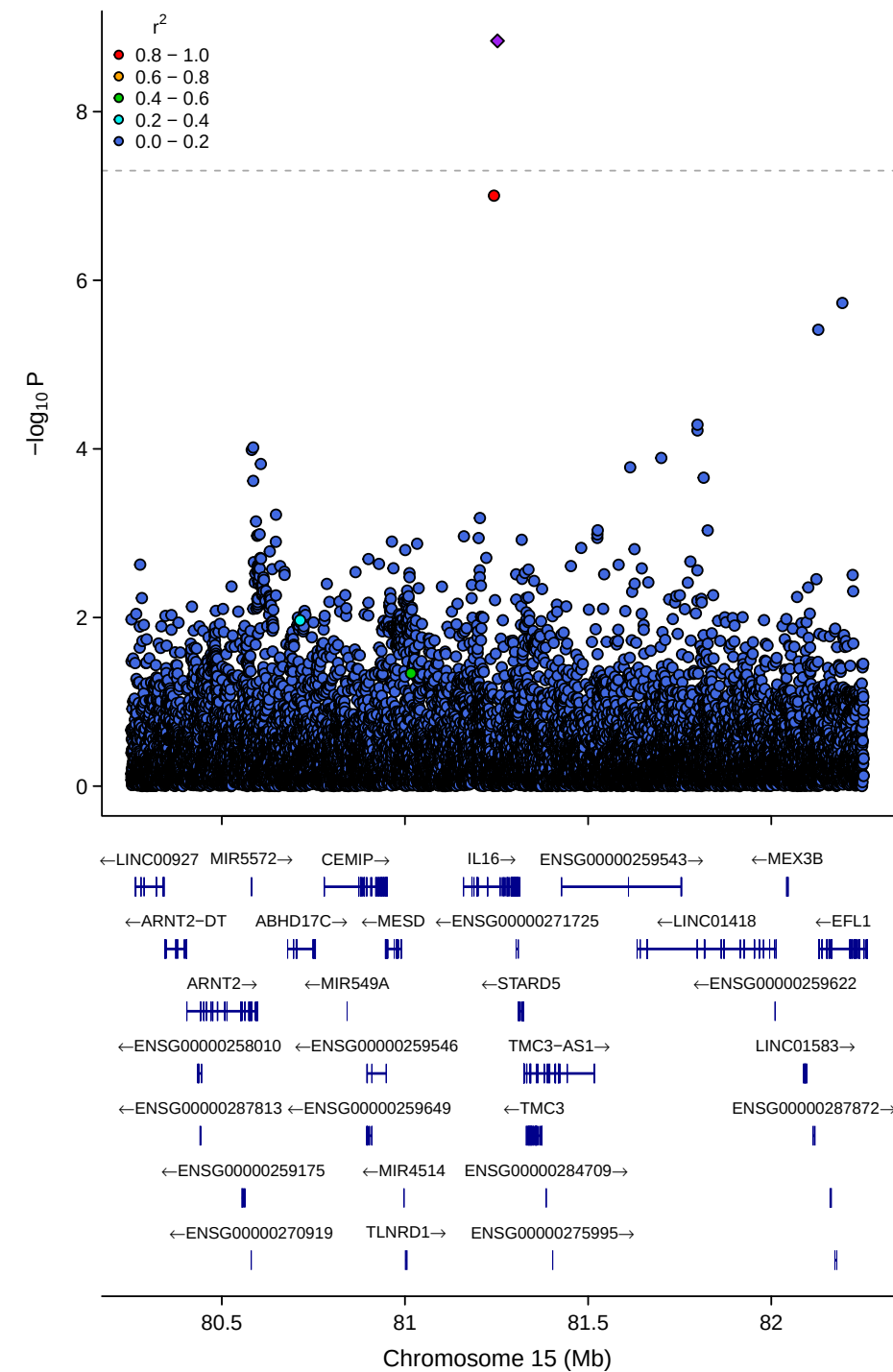


Supplementary Figure 2.2

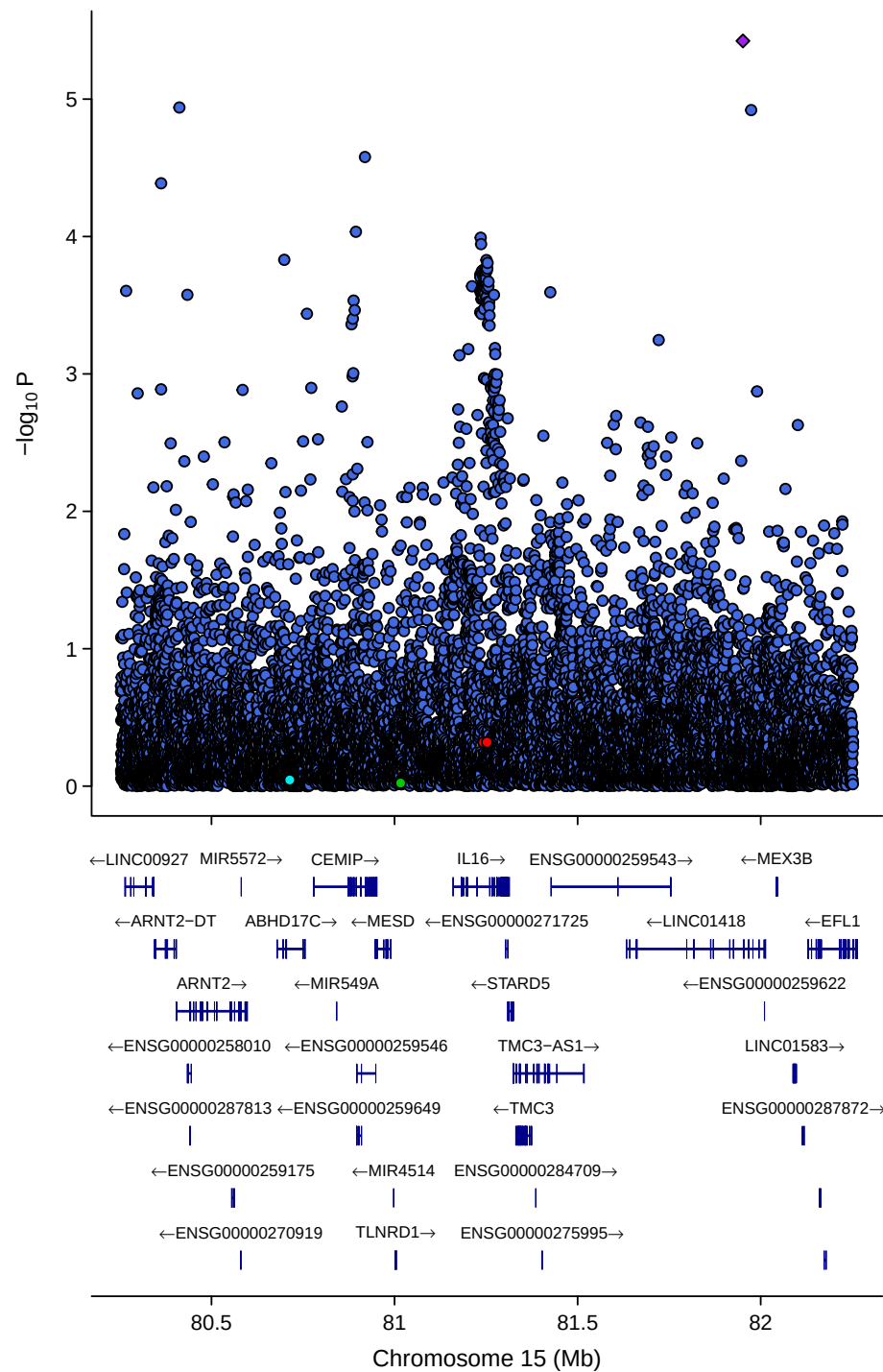


Supplementary Figure 2.2

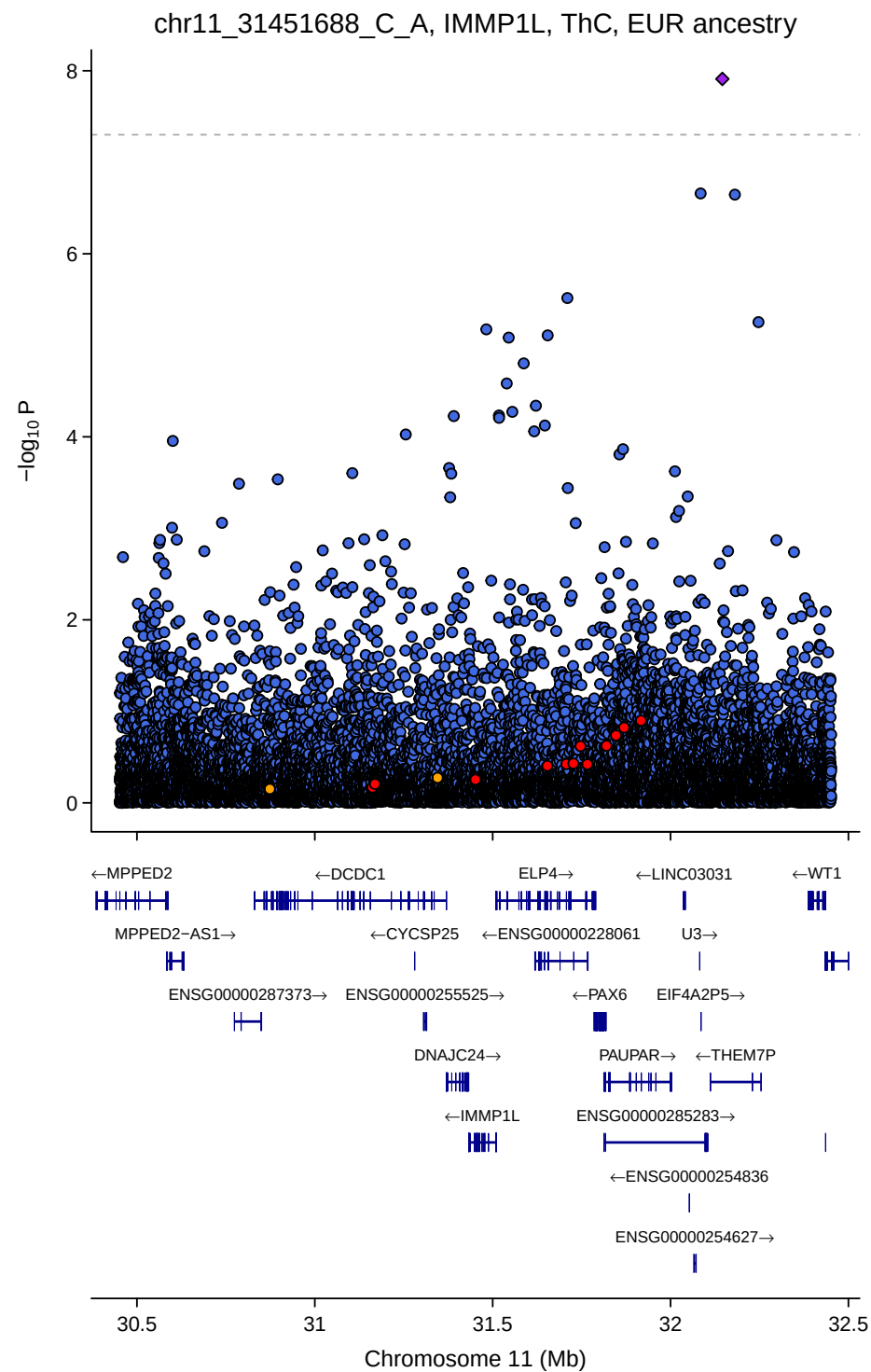
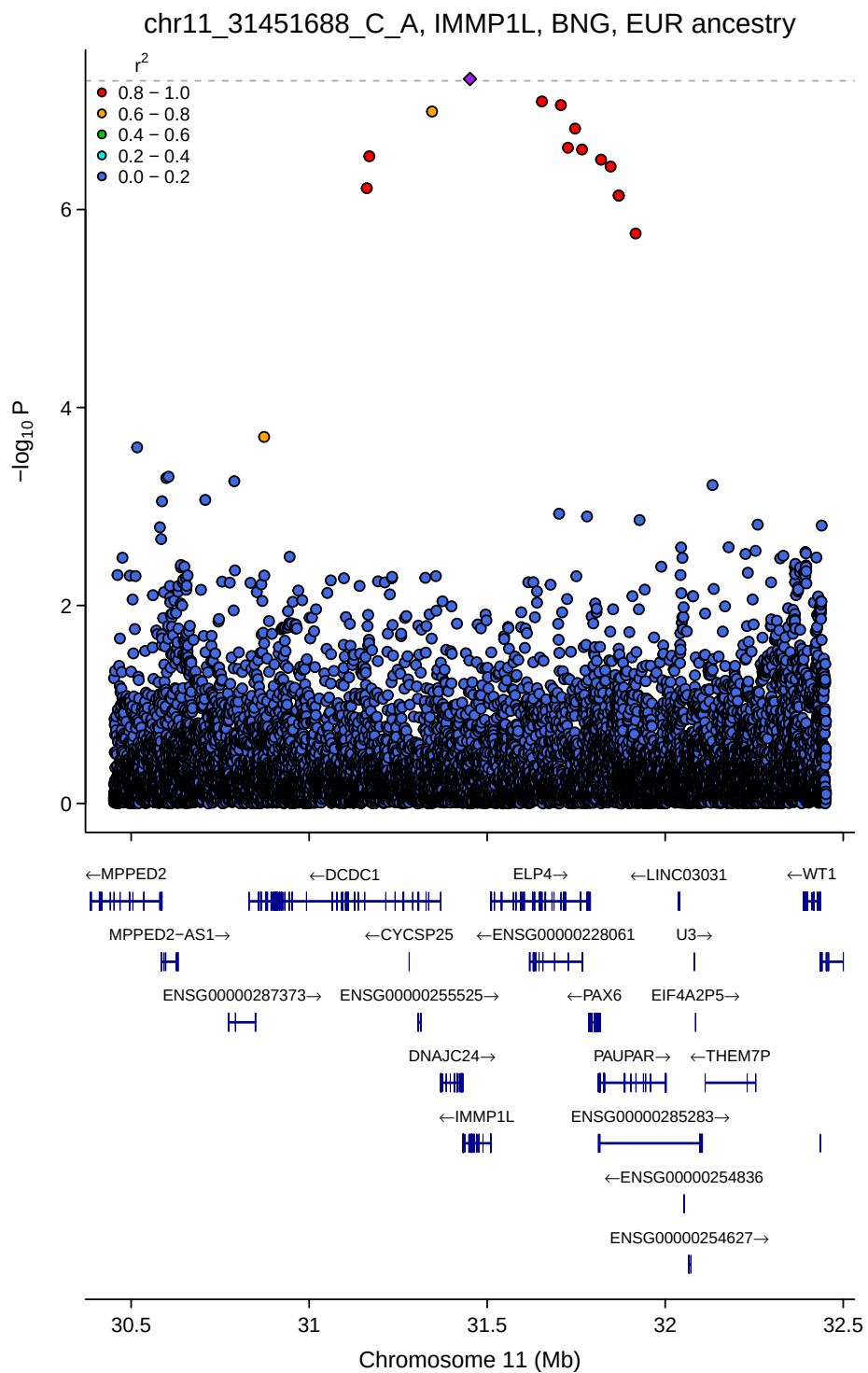
chr15\_81252528\_A\_C, IL16, BNG, EUR ancestry



chr15\_81252528\_A\_C, IL16, ThC, EUR ancestry

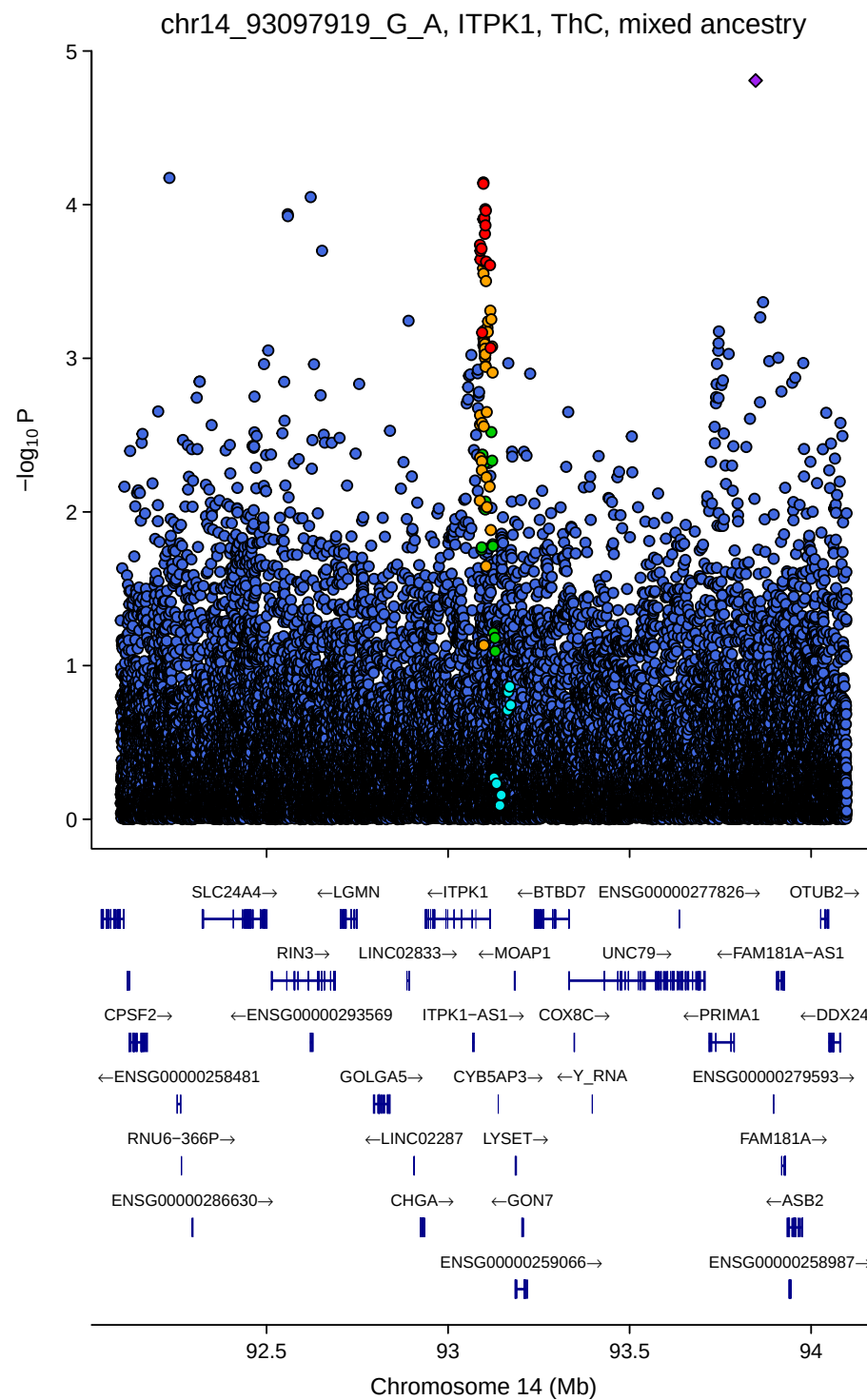
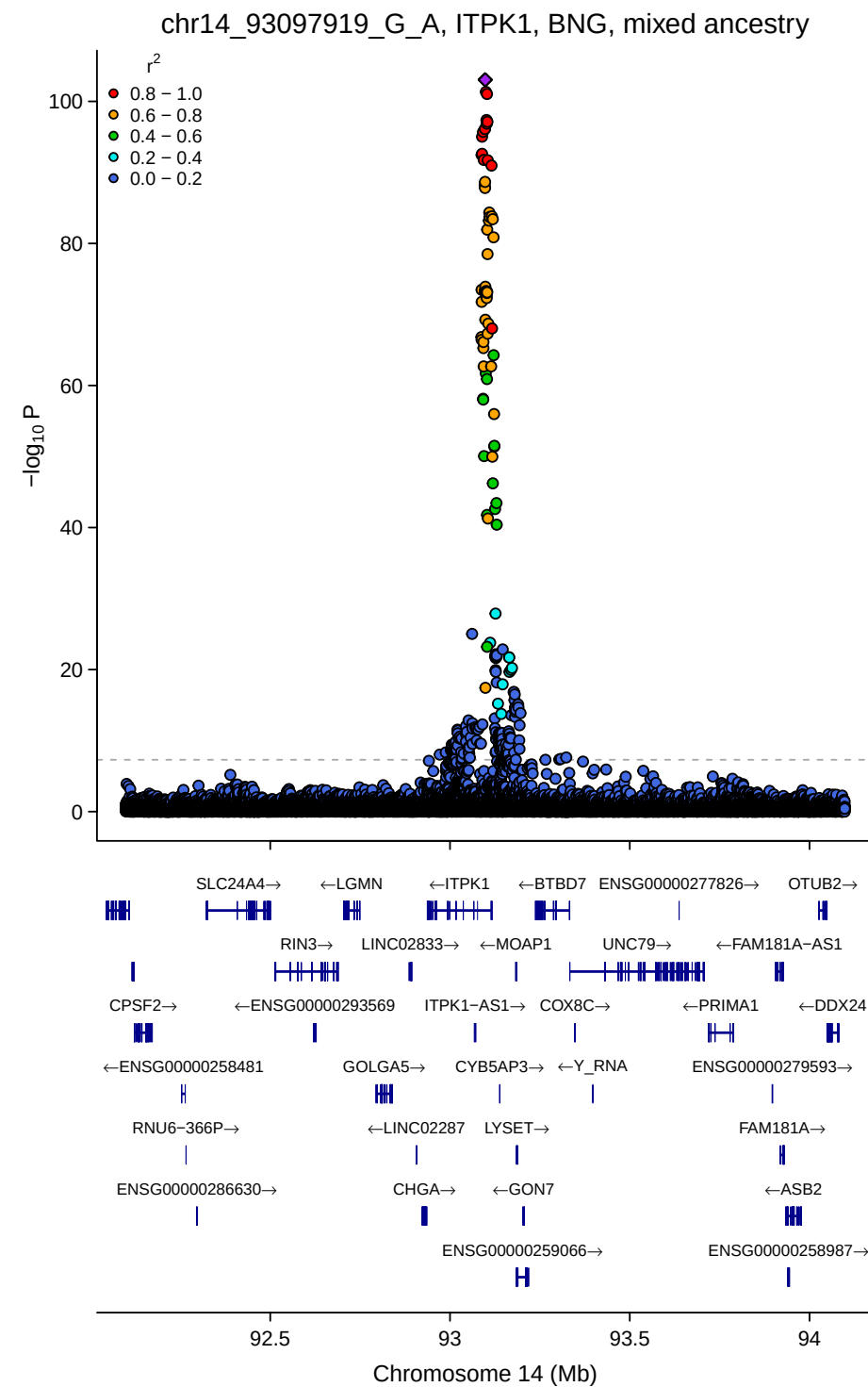


Supplementary Figure 2.2

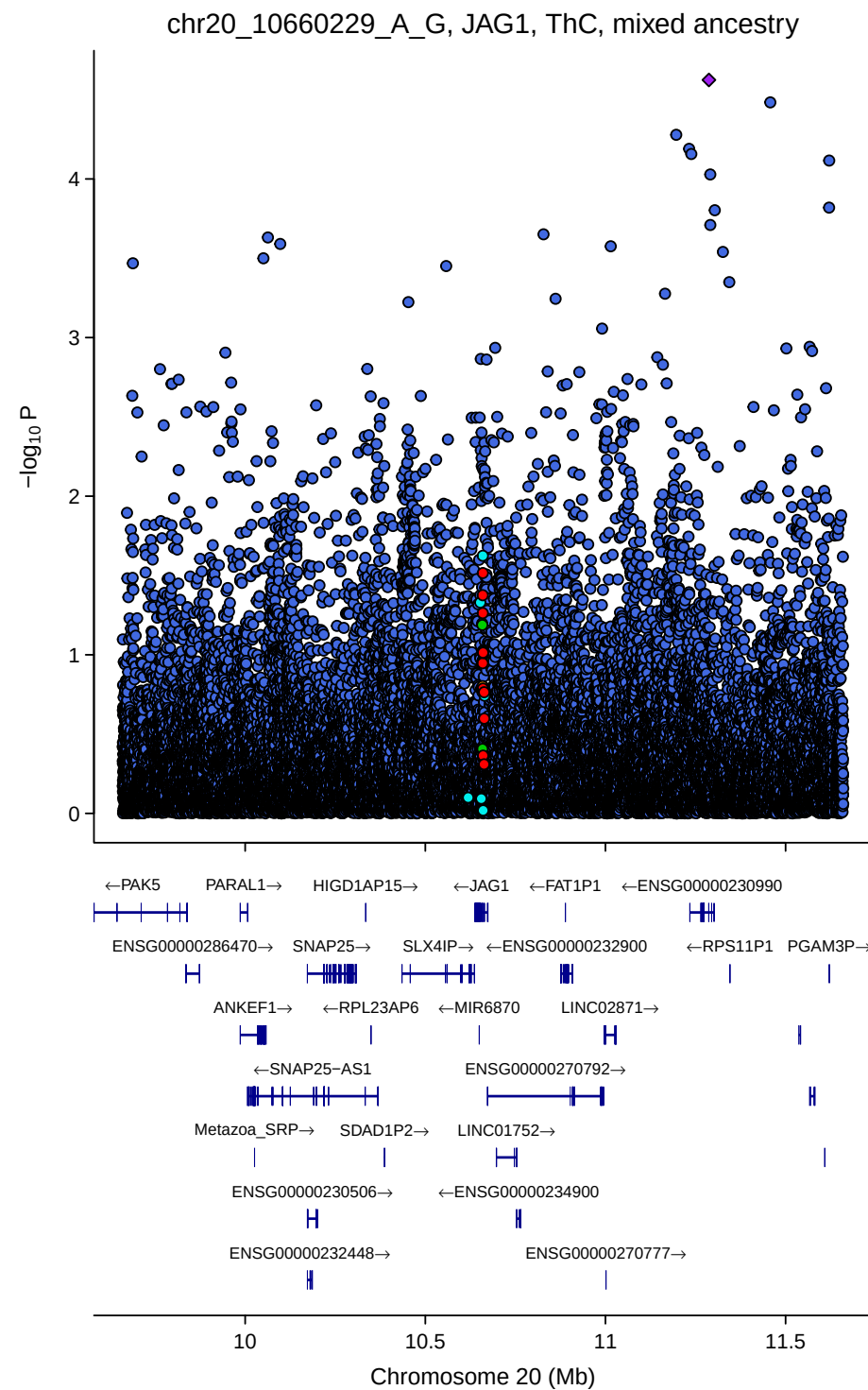
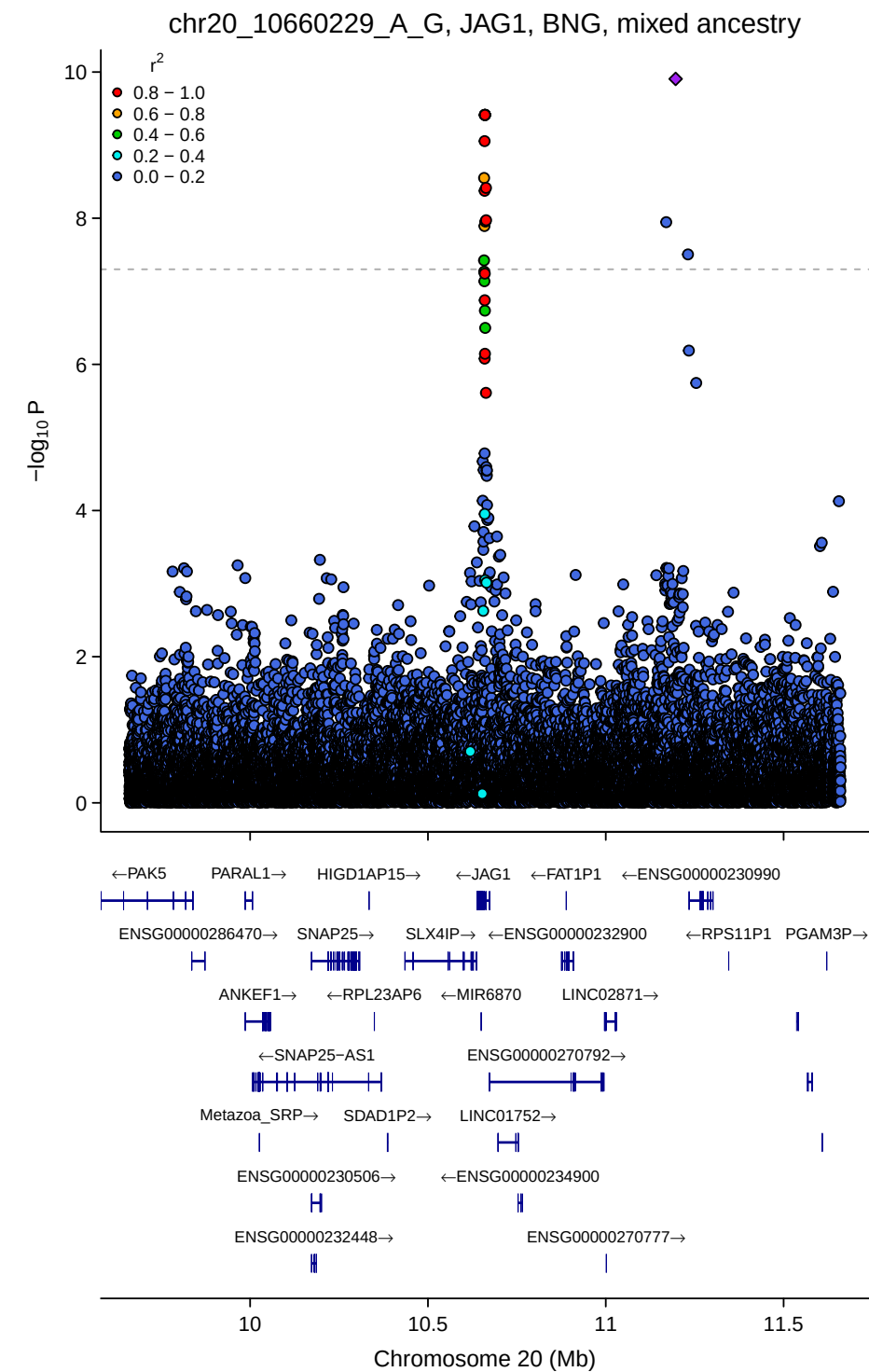




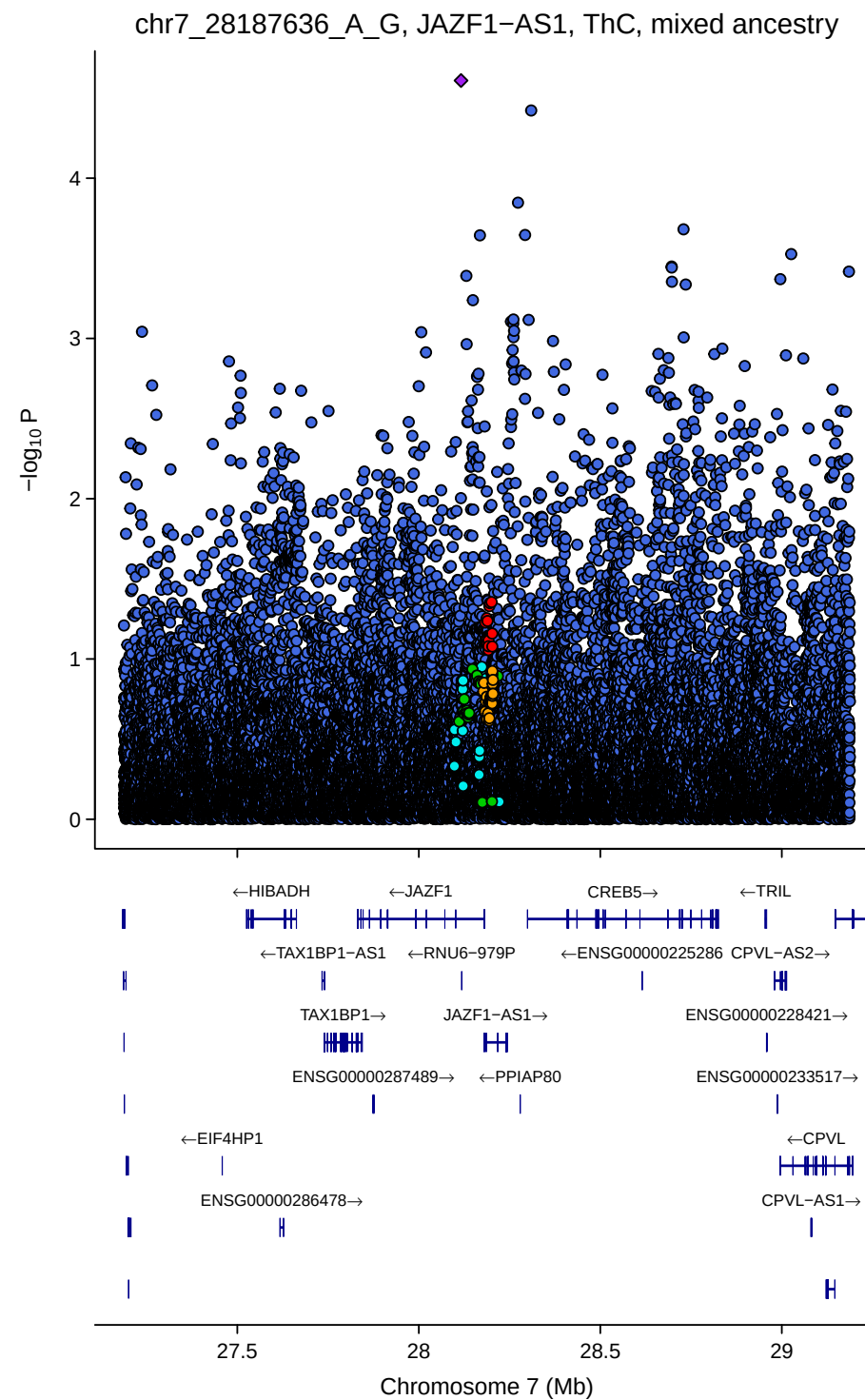
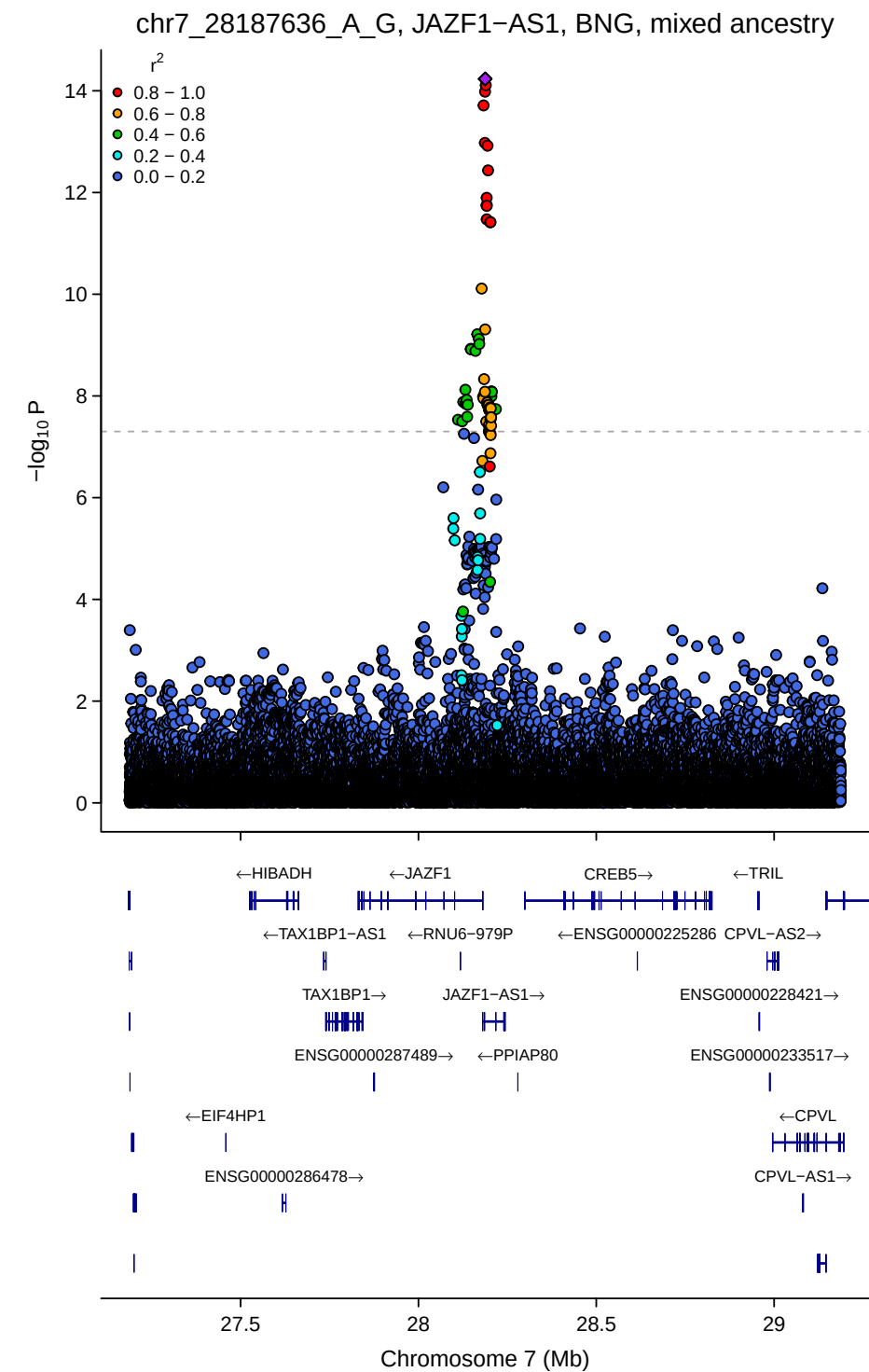
Supplementary Figure 2.2



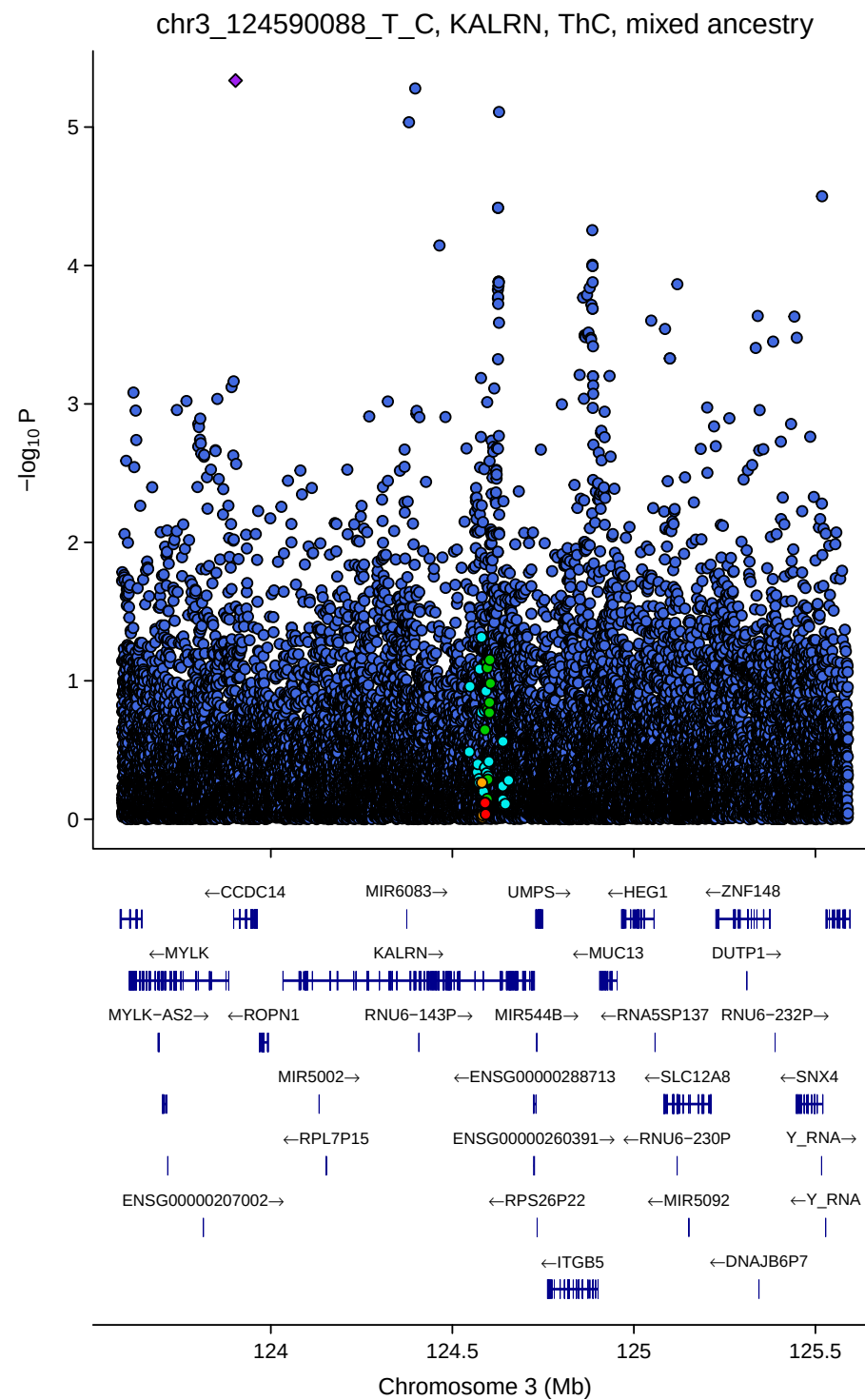
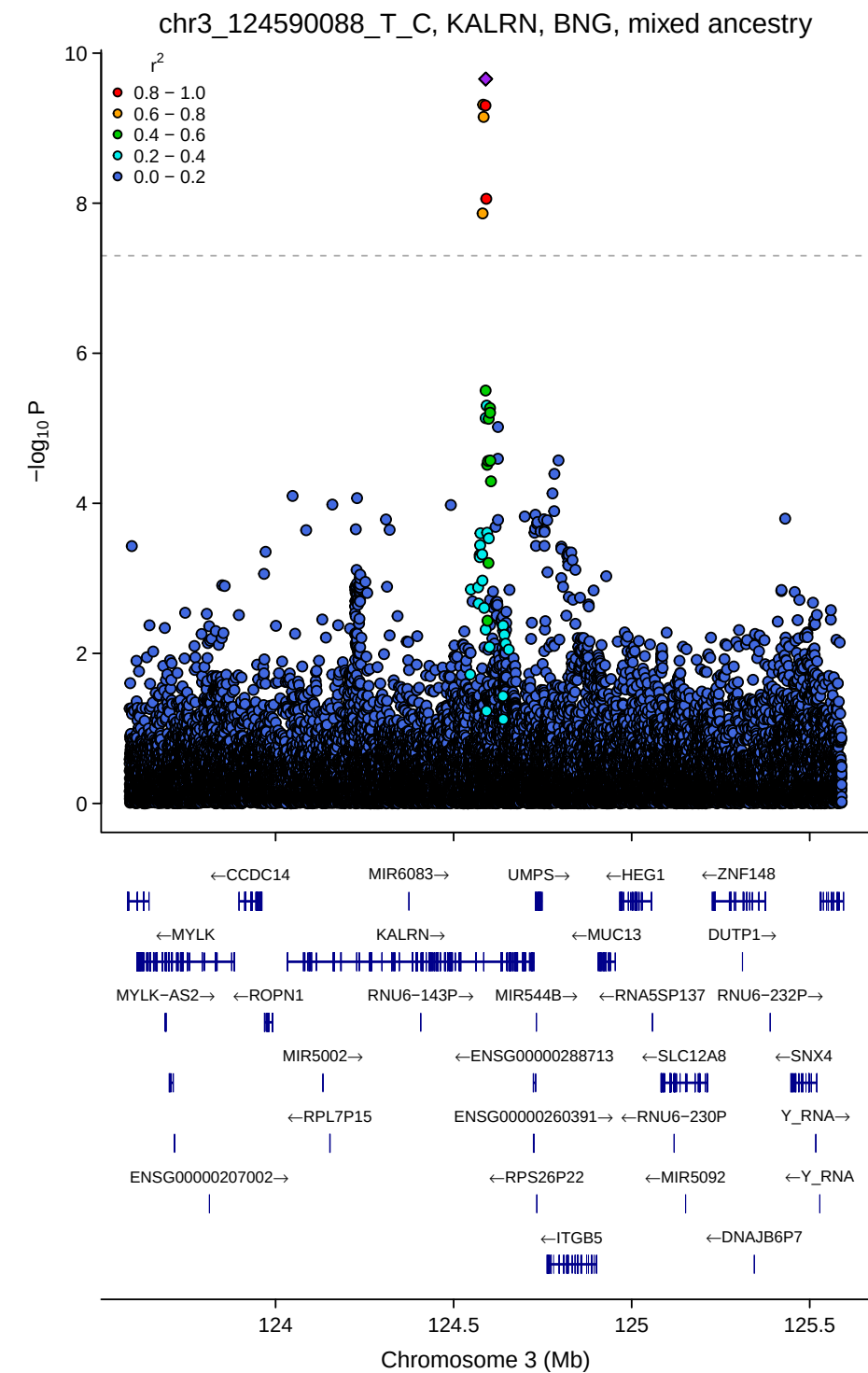
# Supplementary Figure 2.2



Supplementary Figure 2.2

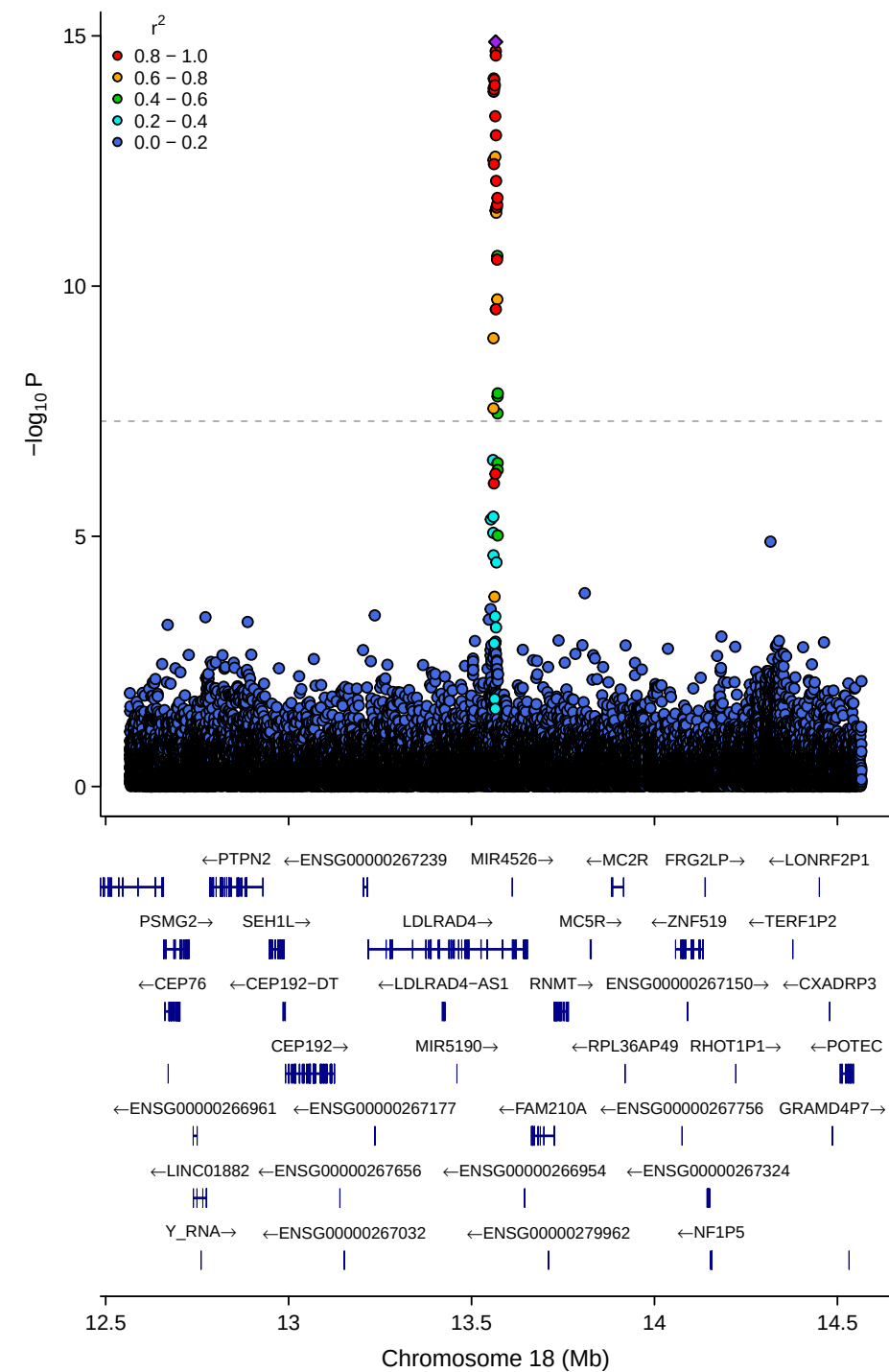


Supplementary Figure 2.2

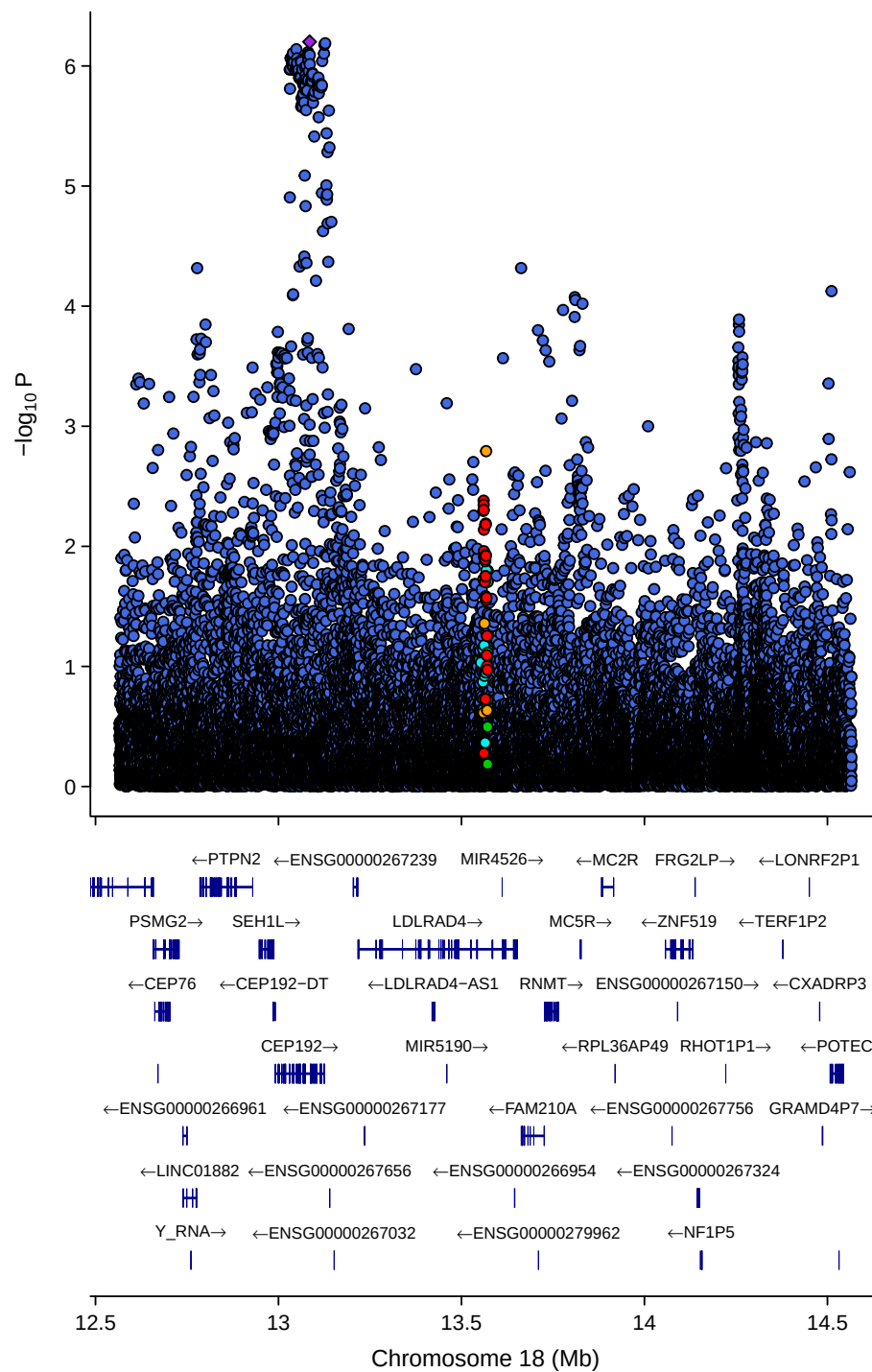


Supplementary Figure 2.2

chr18\_13565922\_G\_A, LDLRAD4, BNG, mixed ancestry



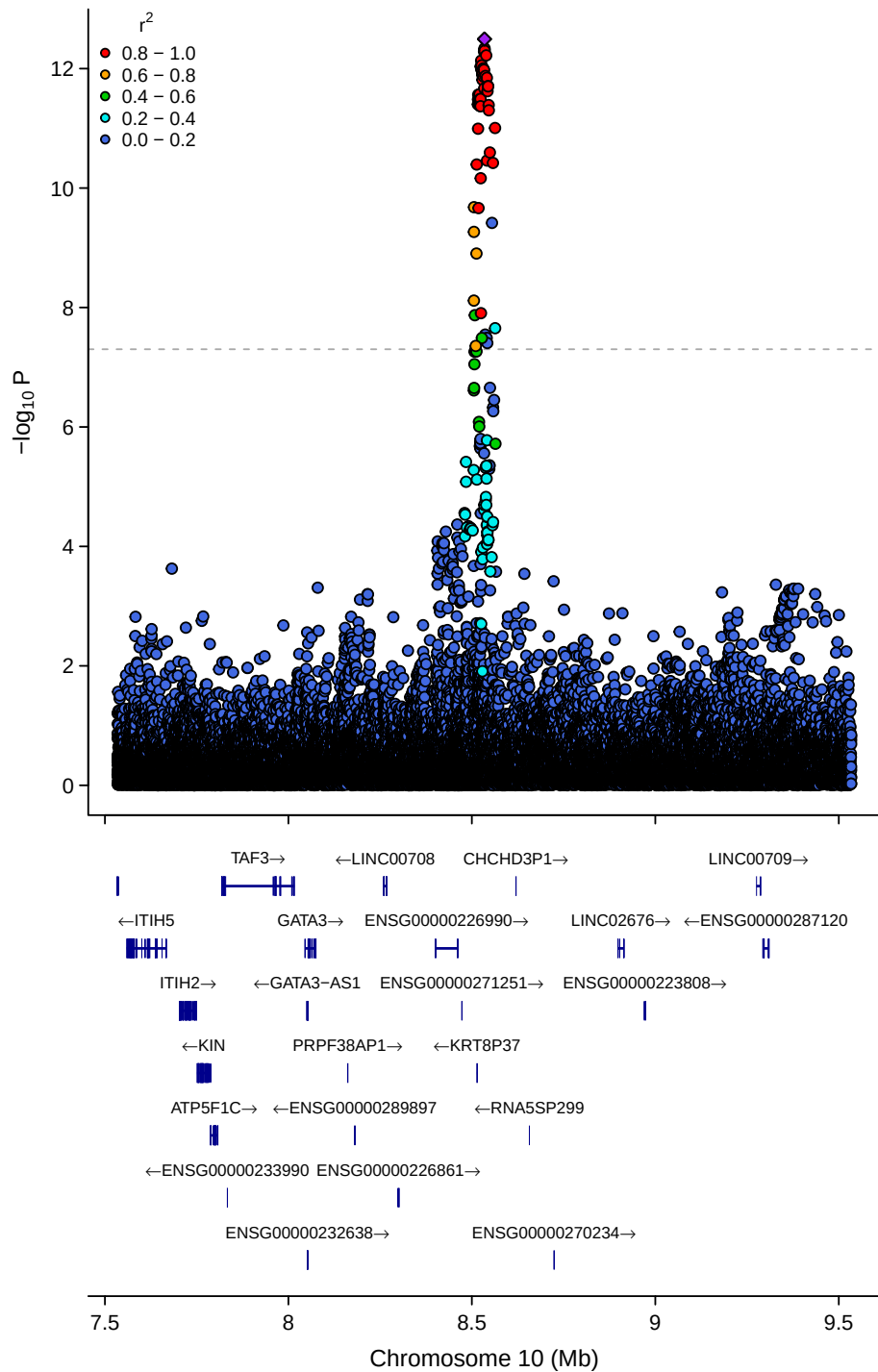
chr18\_13565922\_G\_A, LDLRAD4, ThC, mixed ancestry



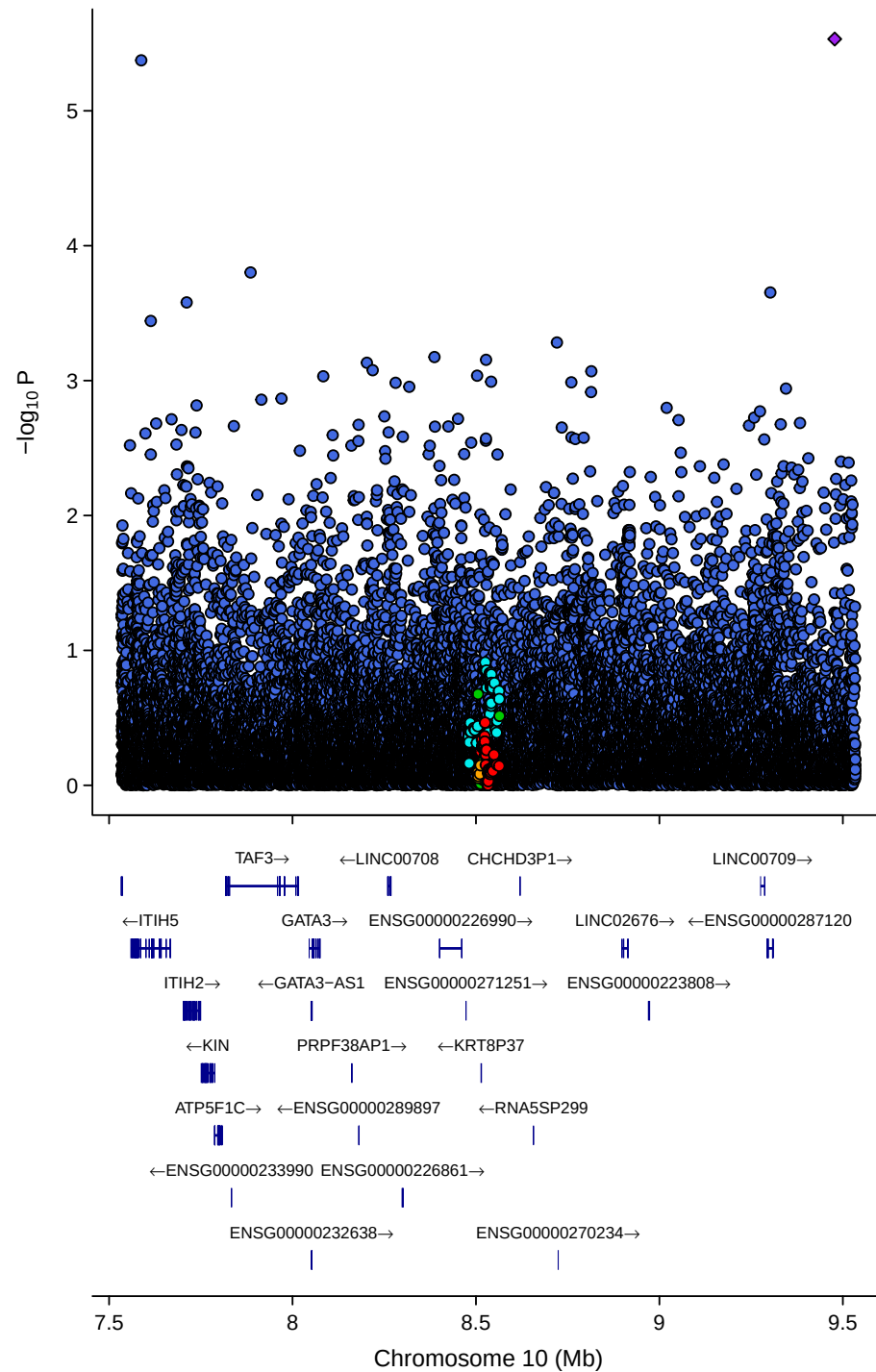


# Supplementary Figure 2.2

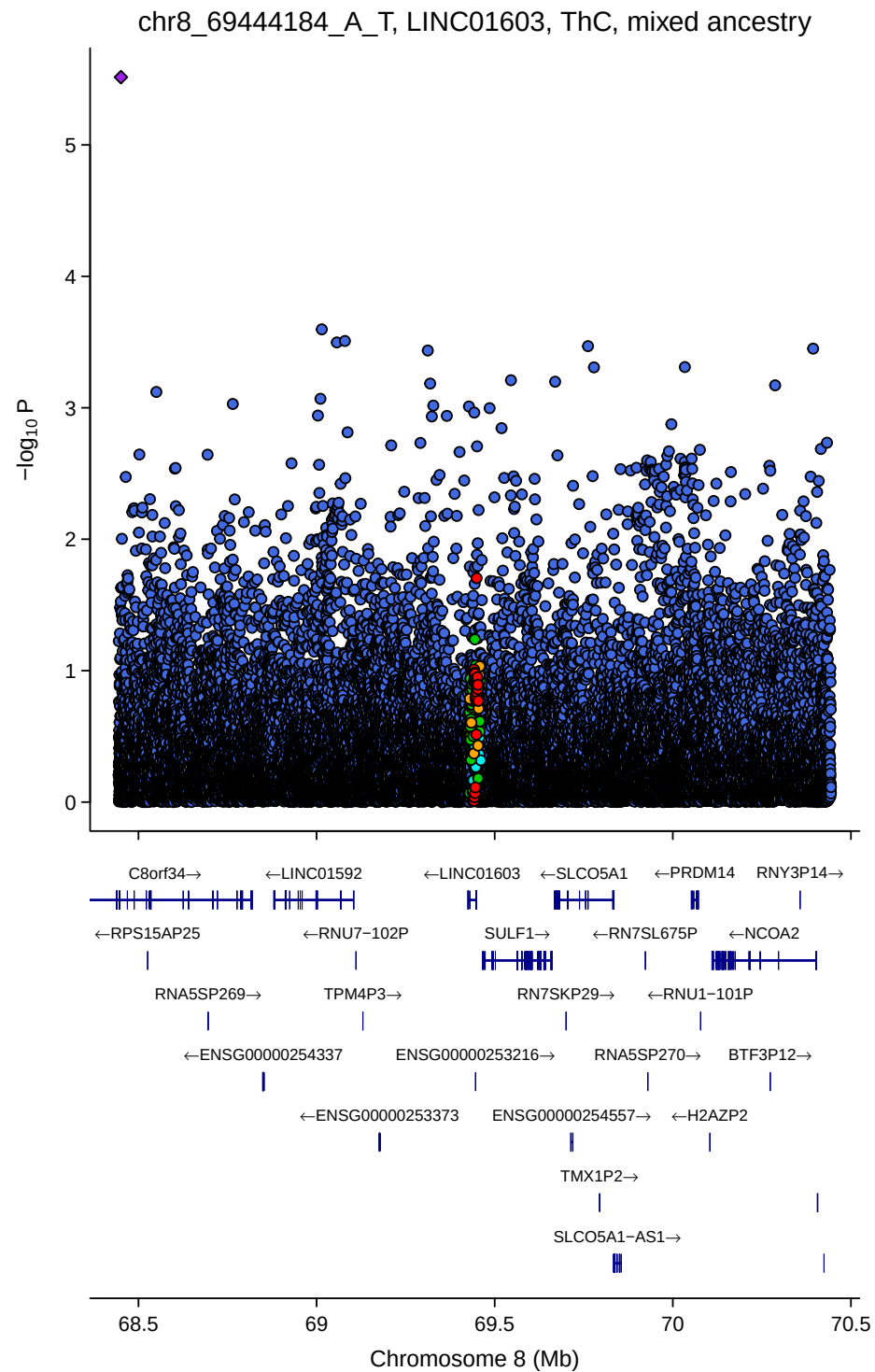
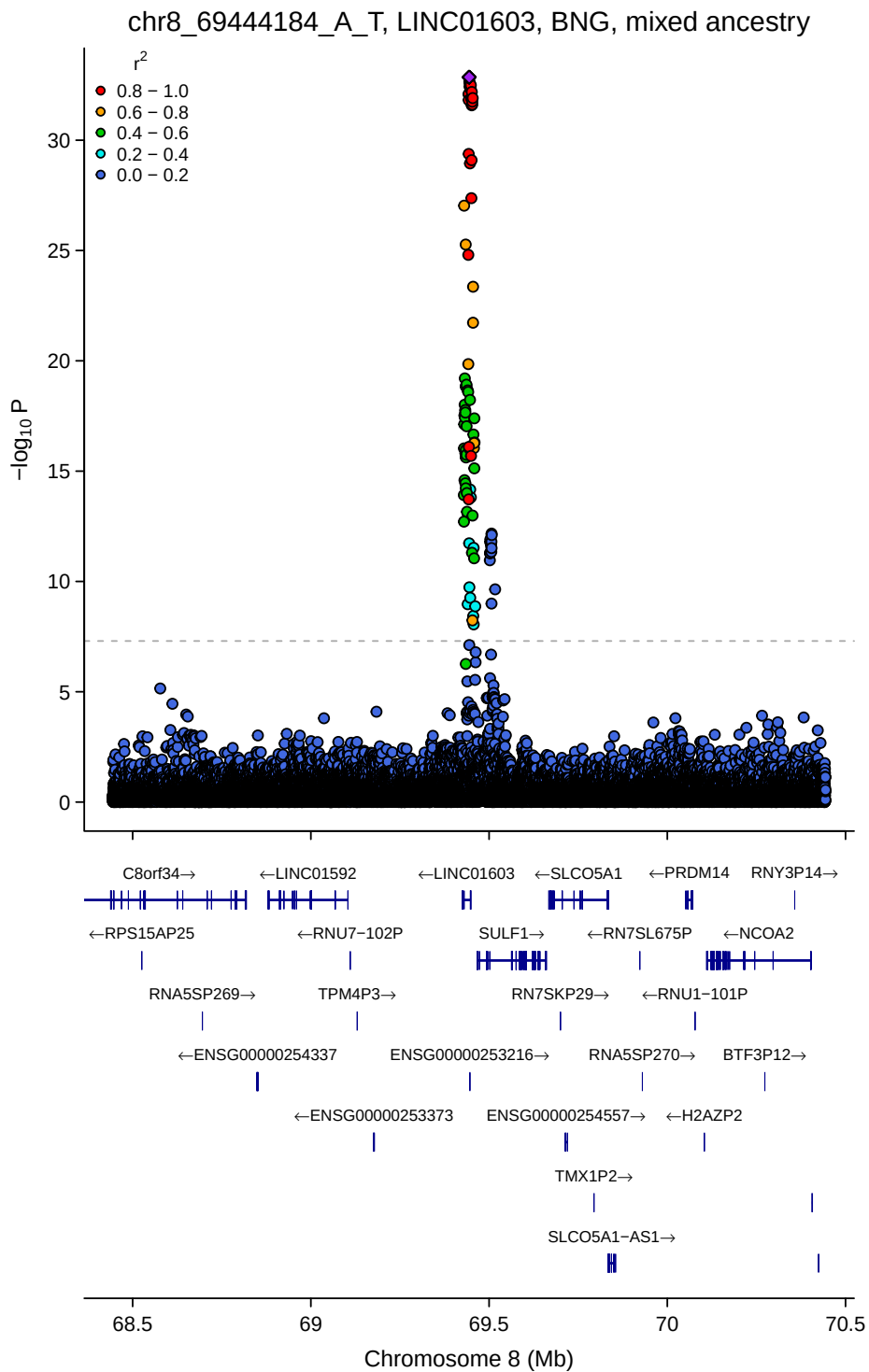
chr10\_8534469\_T\_C, LINC00708;LOC105376398, BNG, mixed ancest



chr10\_8534469\_T\_C, LINC00708;LOC105376398, ThC, mixed ancest



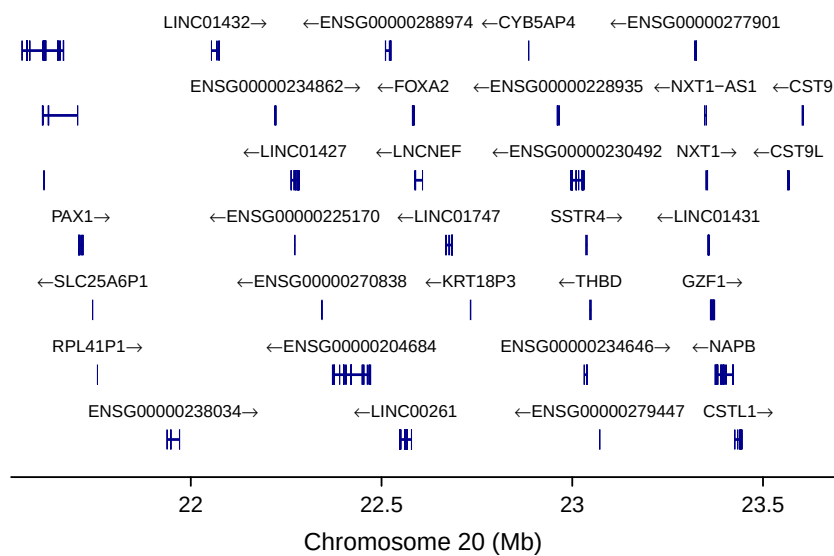
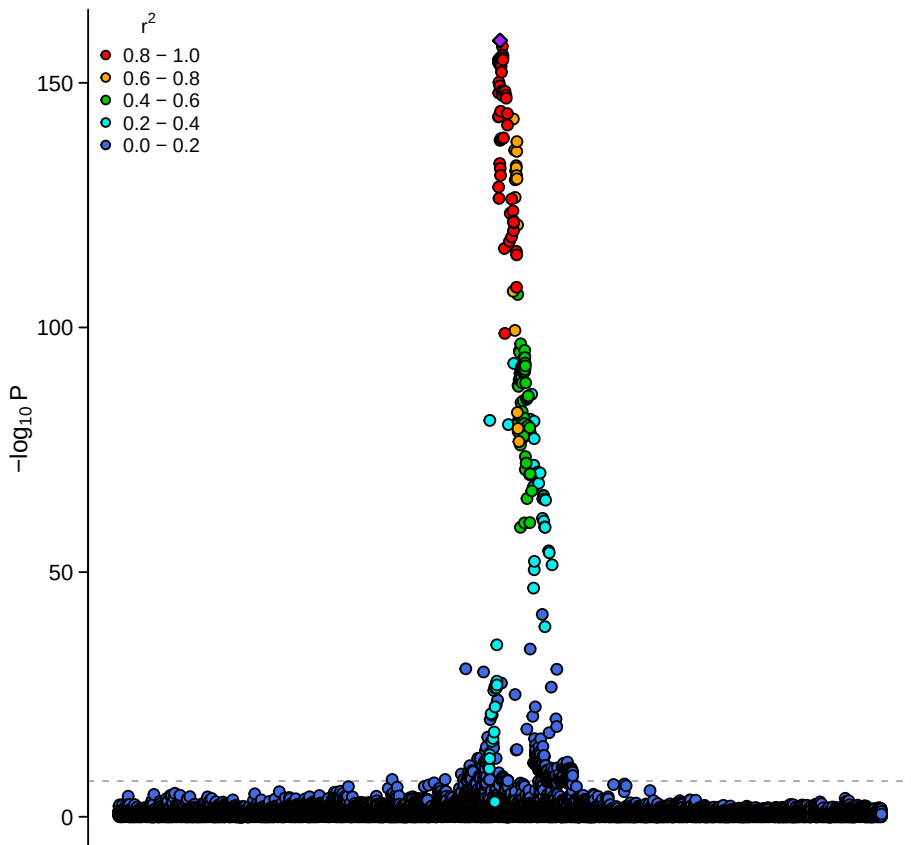
# Supplementary Figure 2.2



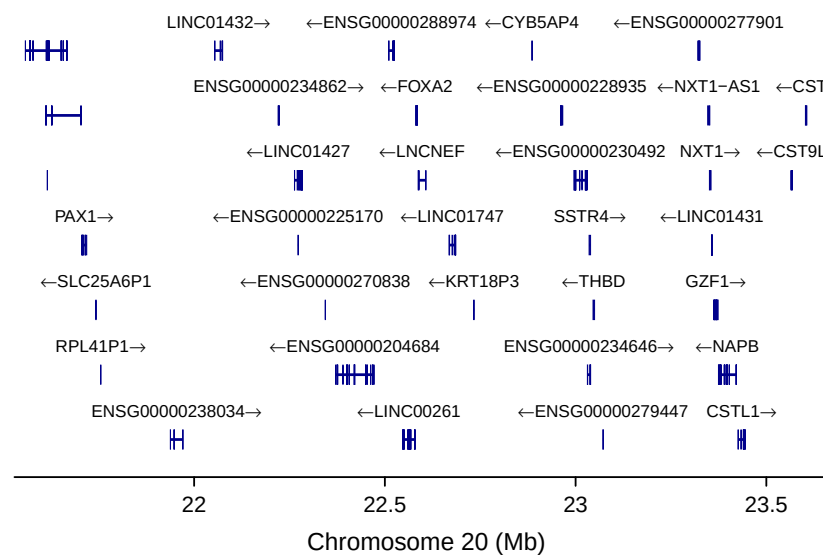
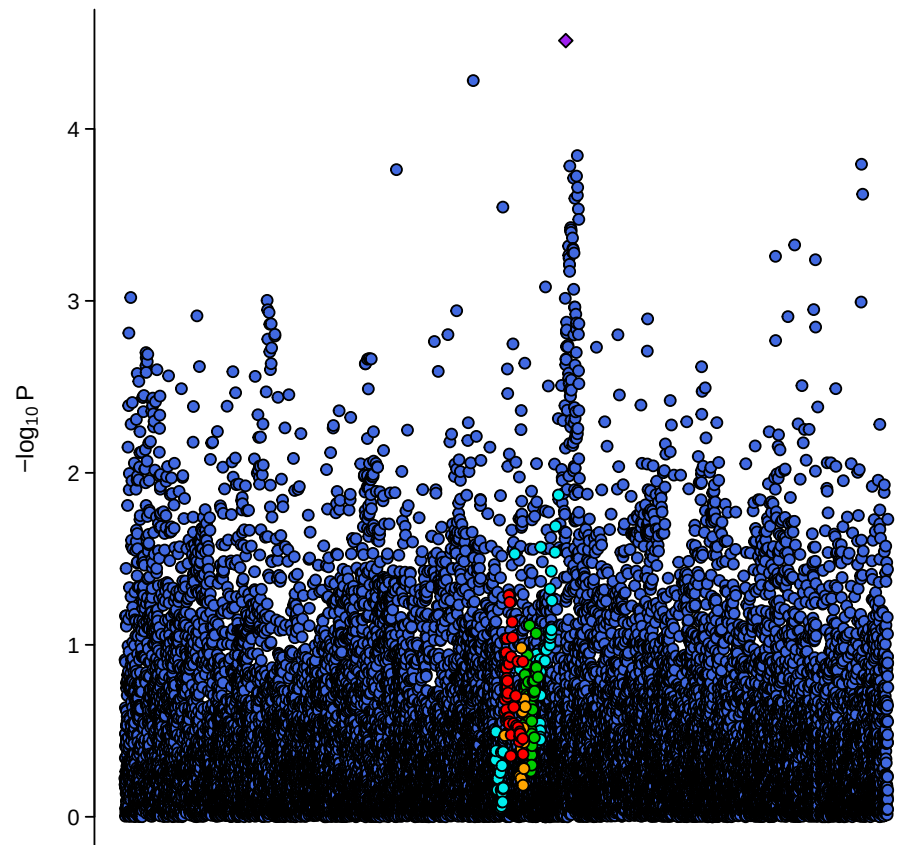


# Supplementary Figure 2.2

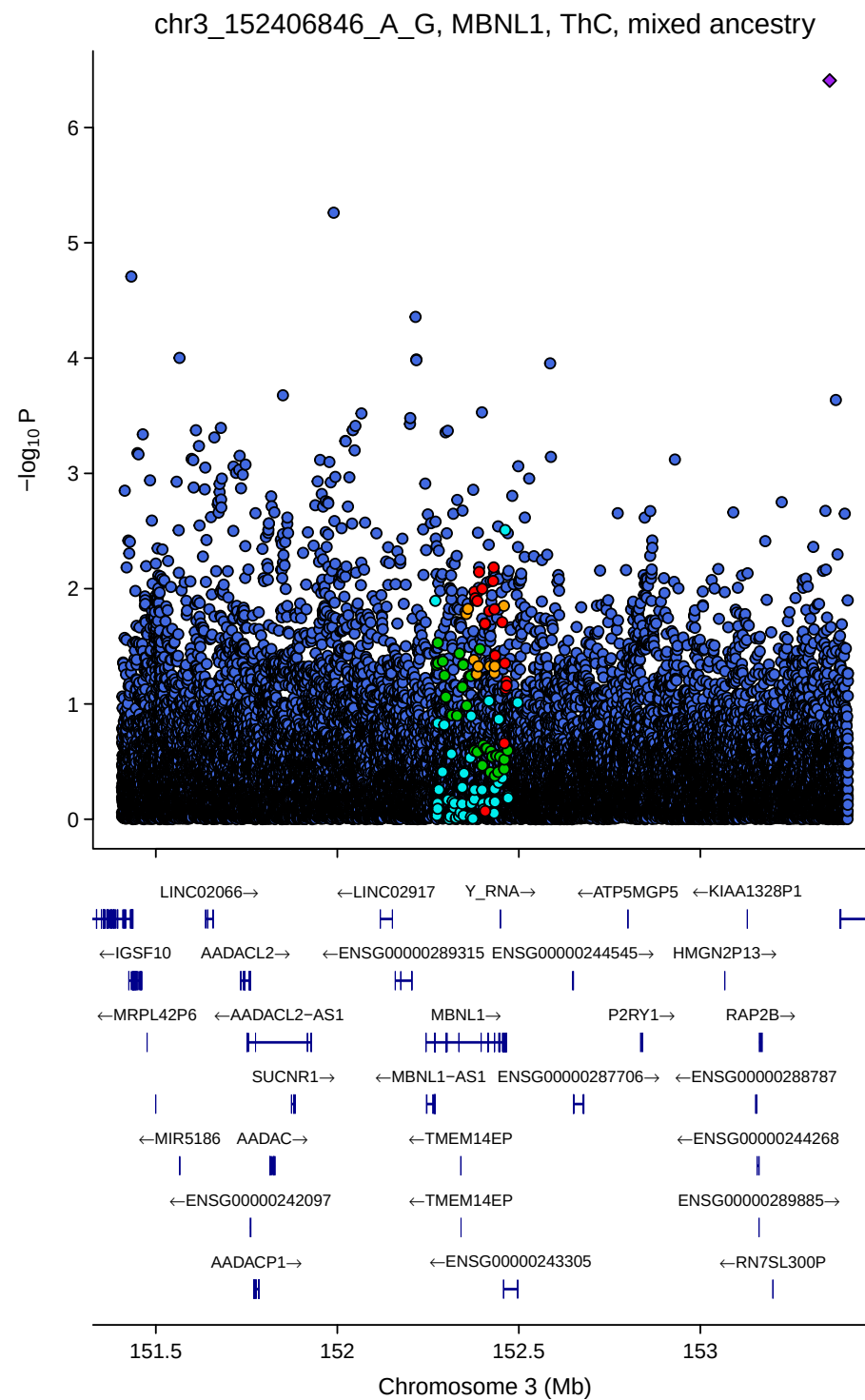
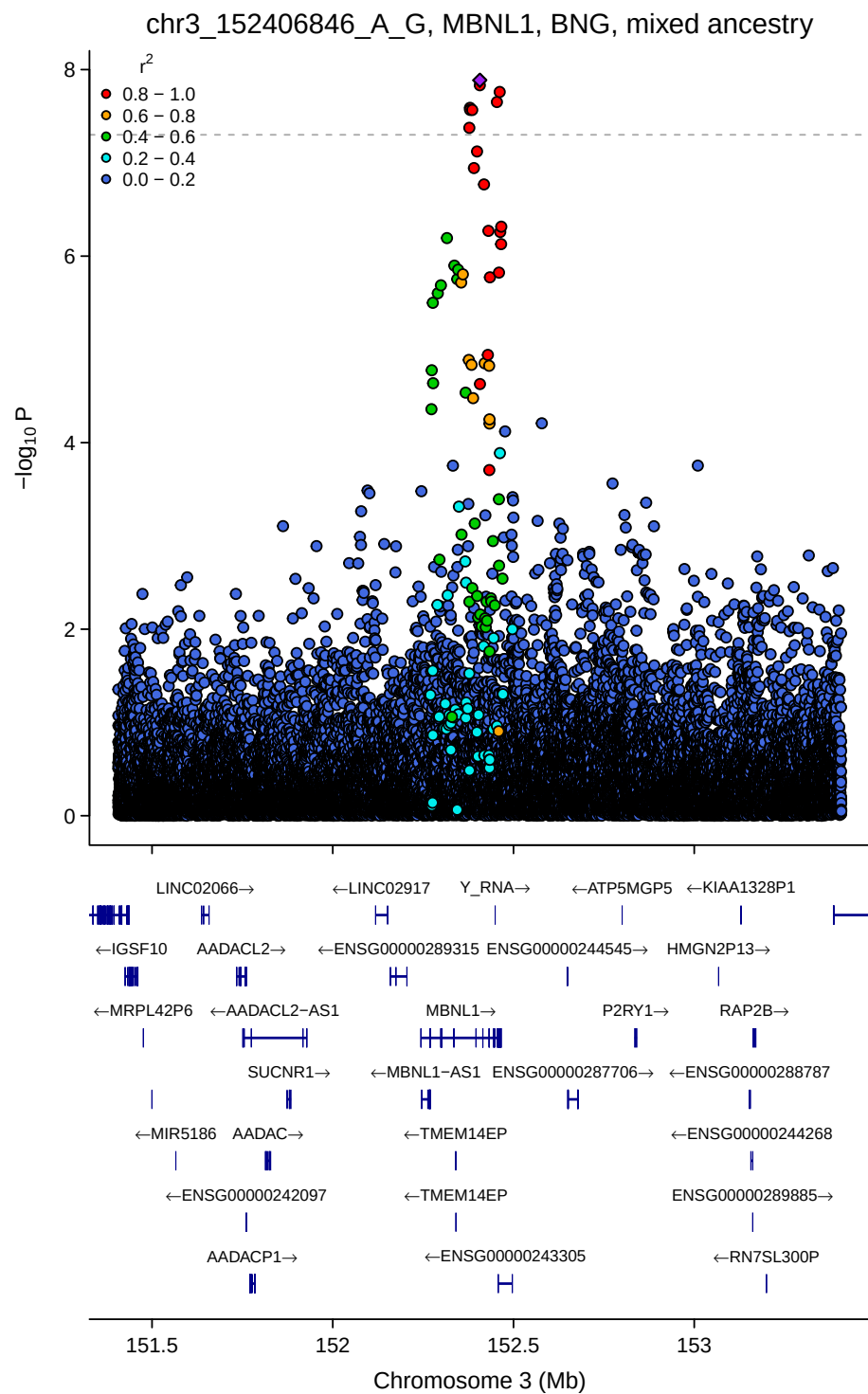
chr20\_22608882\_T\_G, LINCNEF;LINC01747, BNG, mixed ancestry



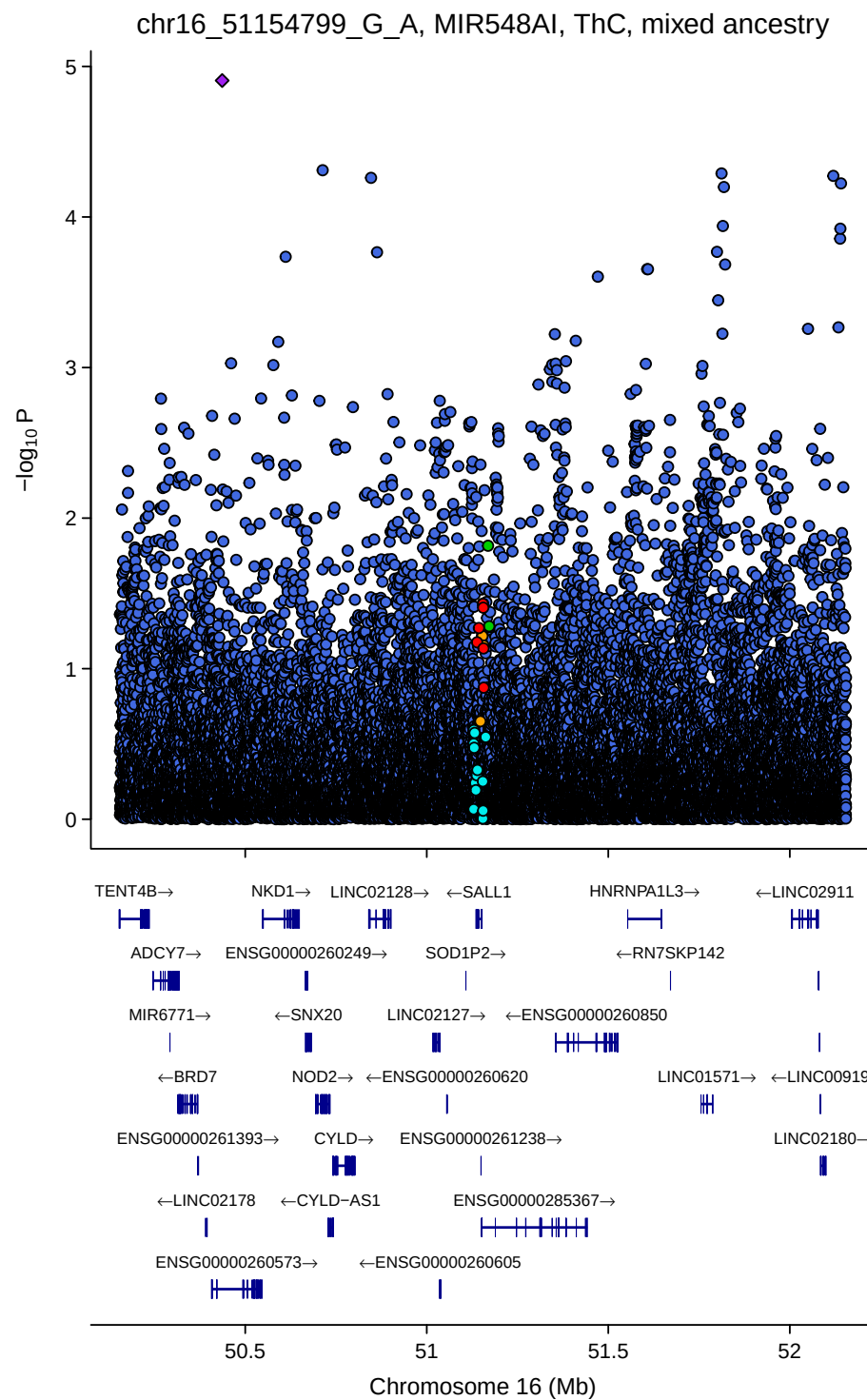
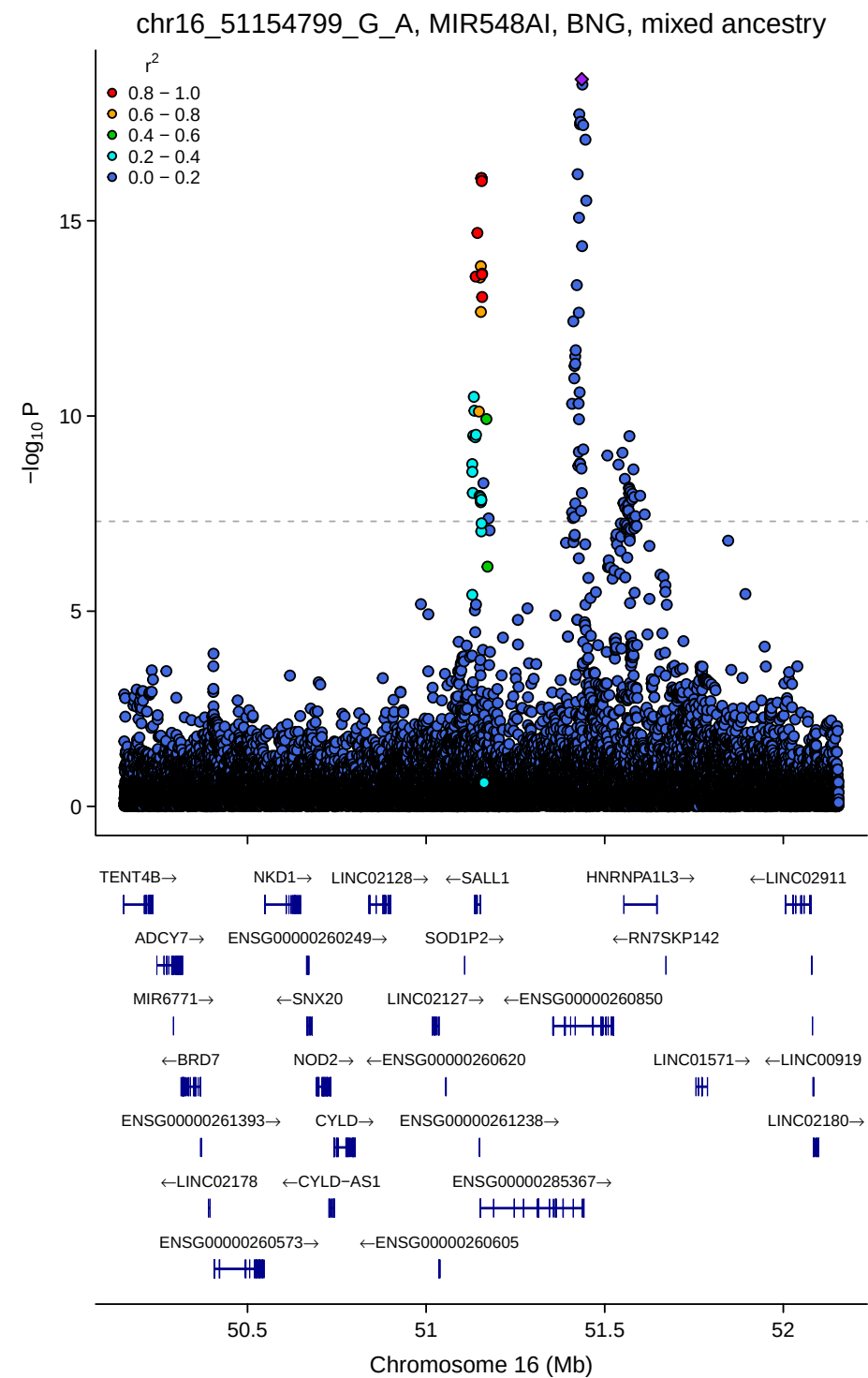
chr20\_22608882\_T\_G, LINCNEF;LINC01747, ThC, mixed ancestry



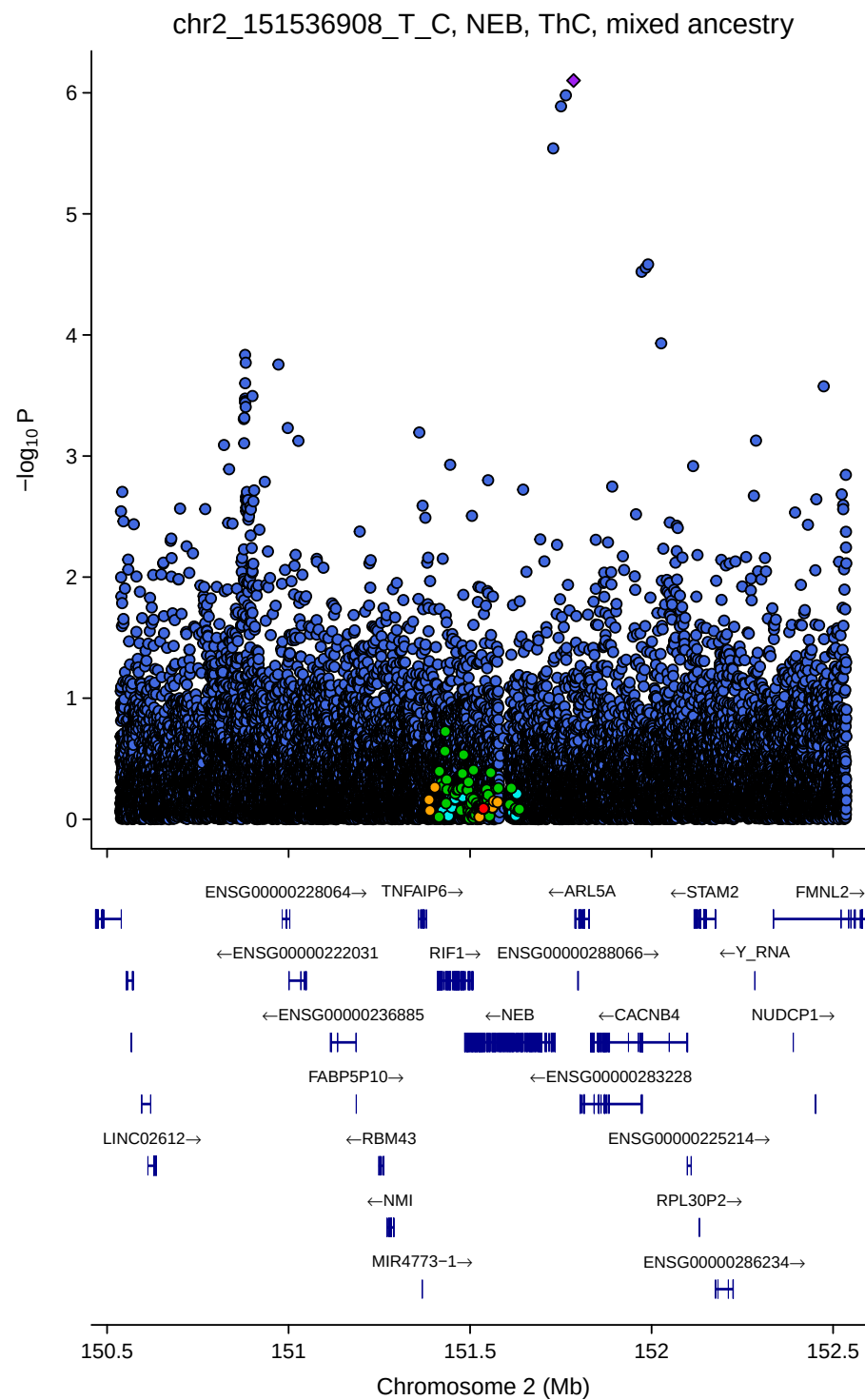
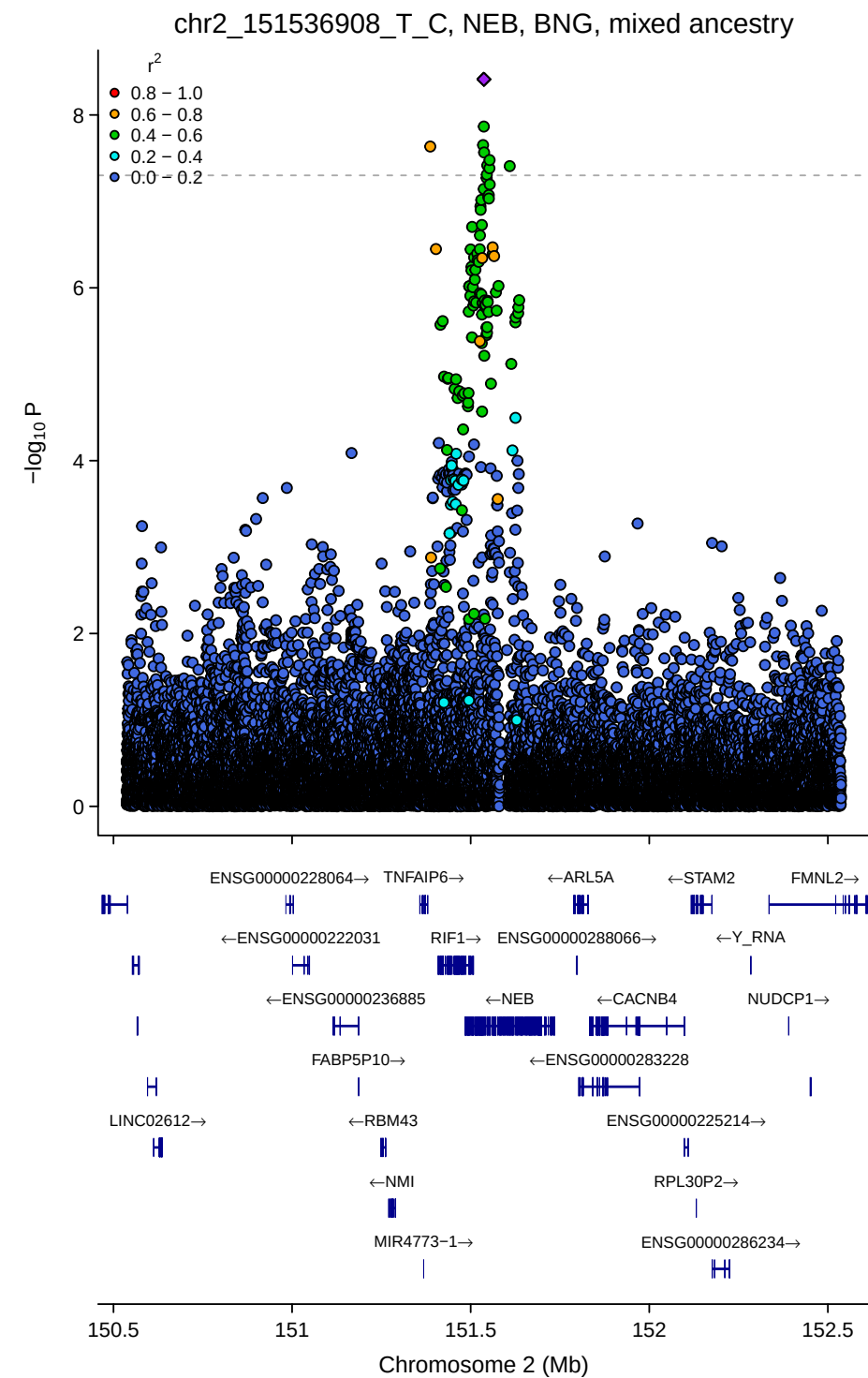
# Supplementary Figure 2.2



Supplementary Figure 2.2



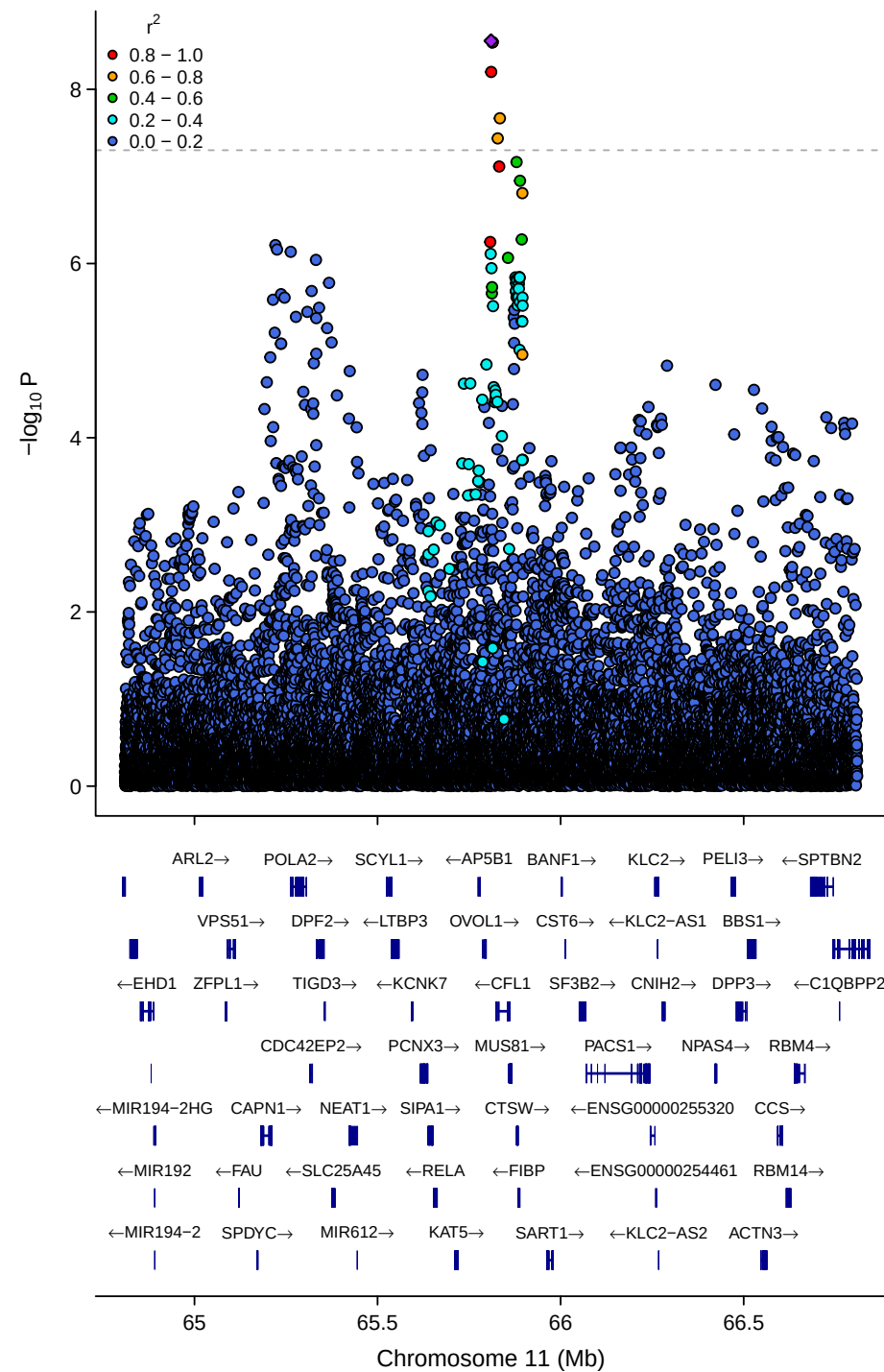
# Supplementary Figure 2.2



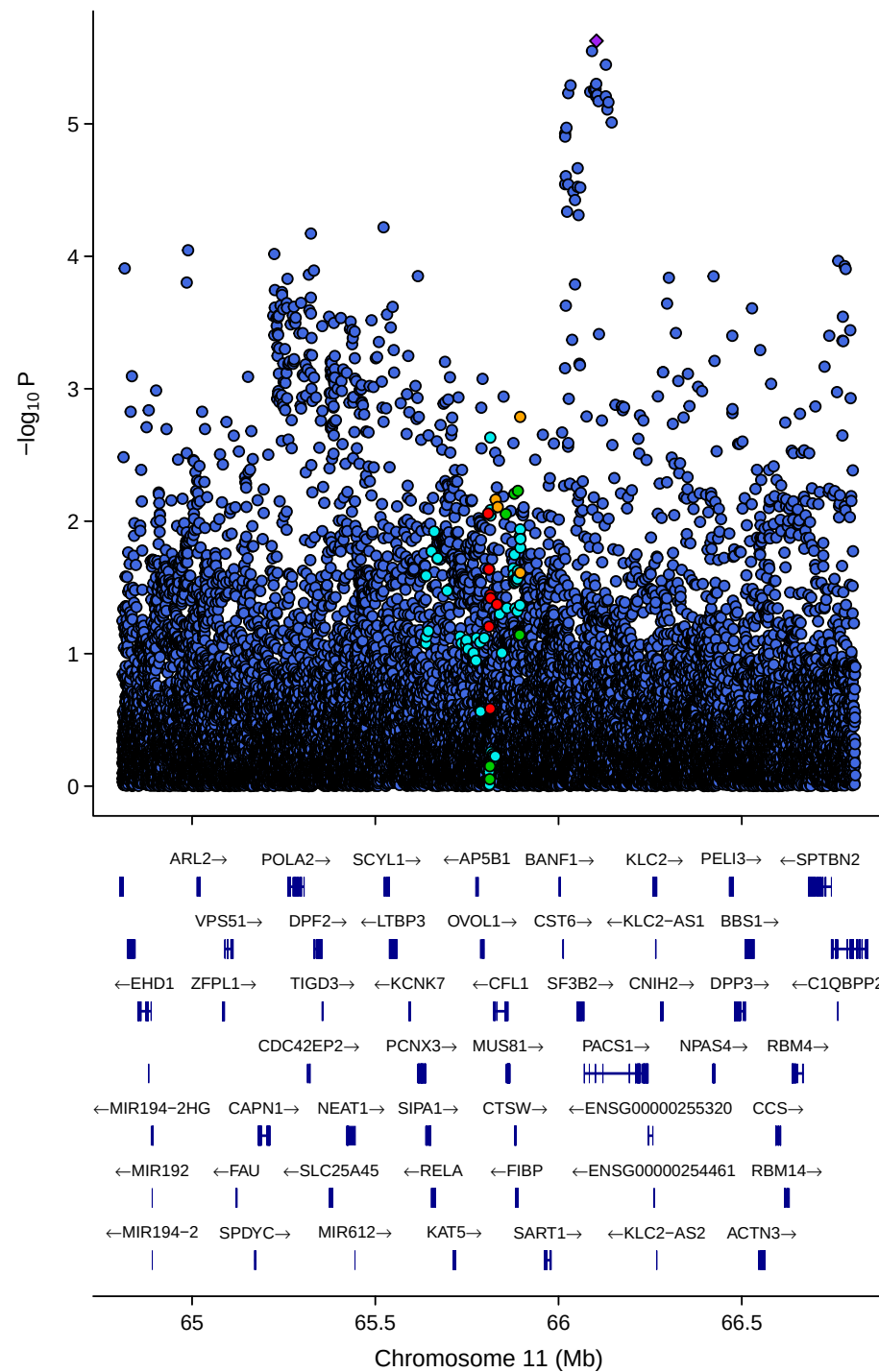


Supplementary Figure 2.2

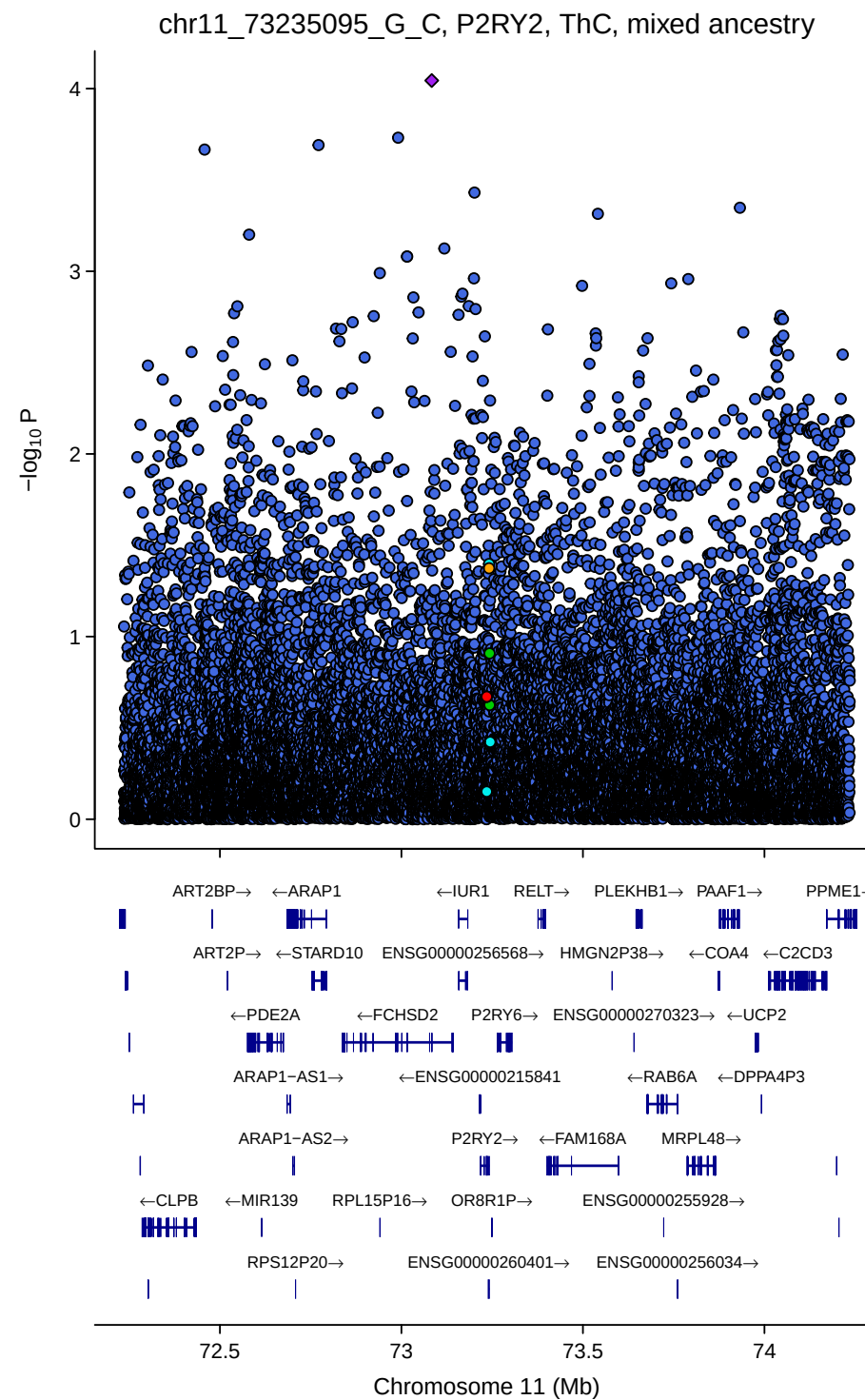
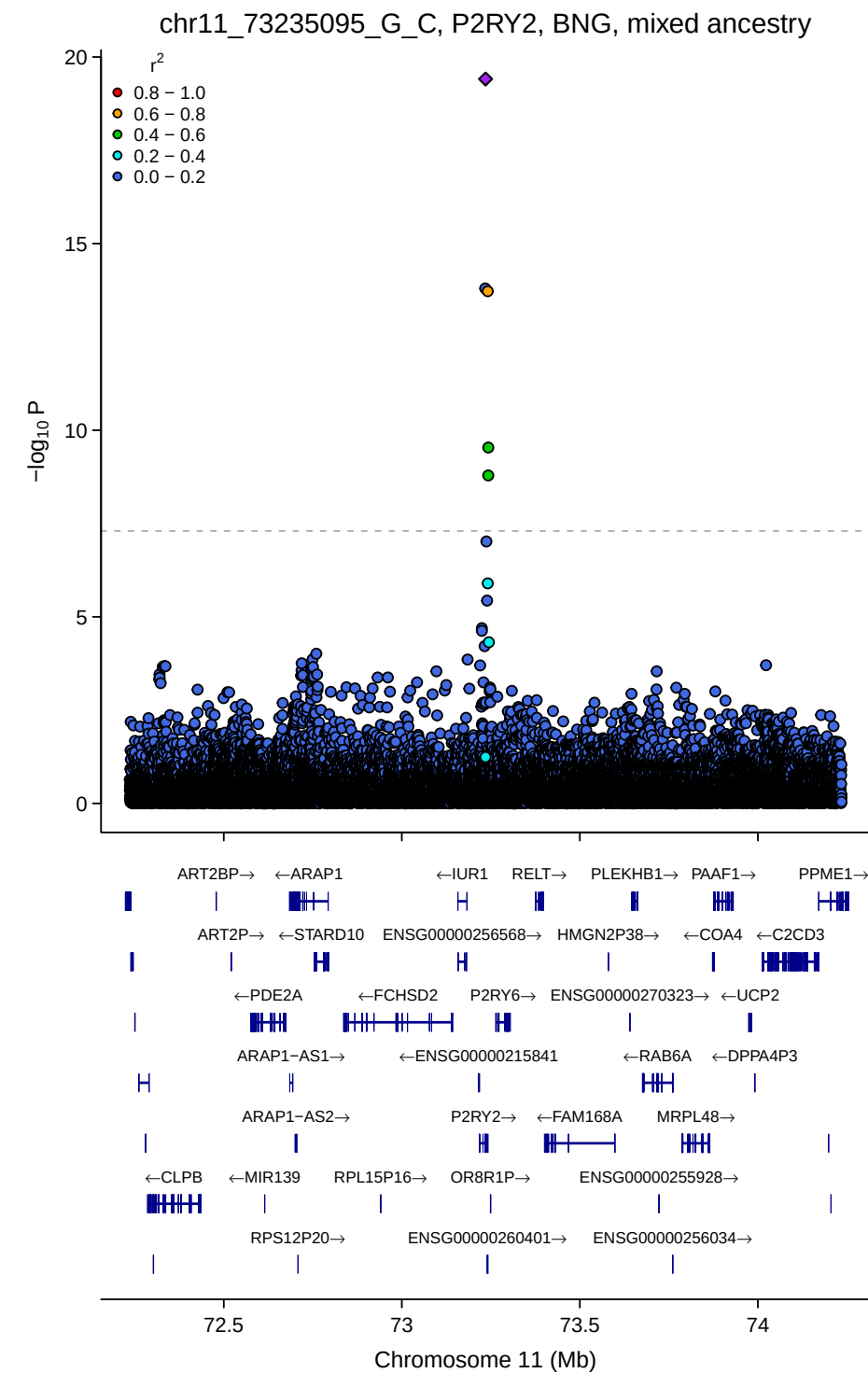
chr11\_65810045\_G\_T, OVOL1;SNX32, BNG, mixed ancestry



chr11\_65810045\_G\_T, OVOL1;SNX32, ThC, mixed ancestry

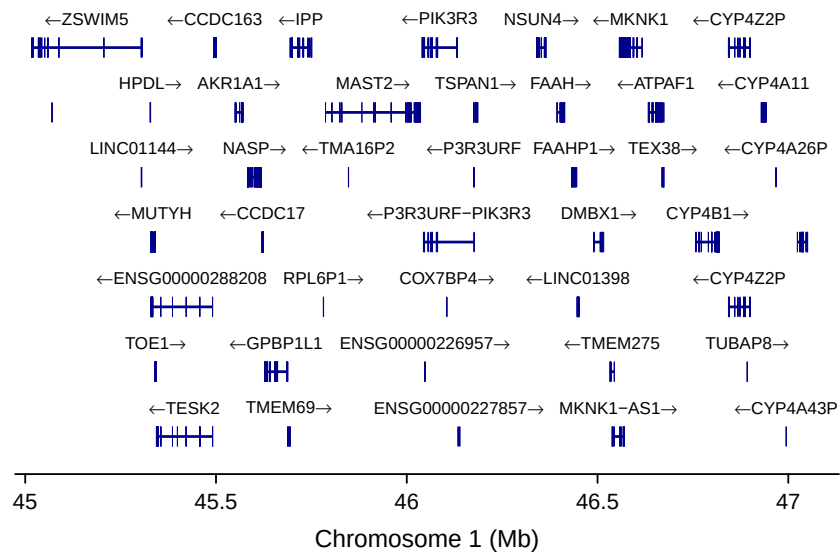
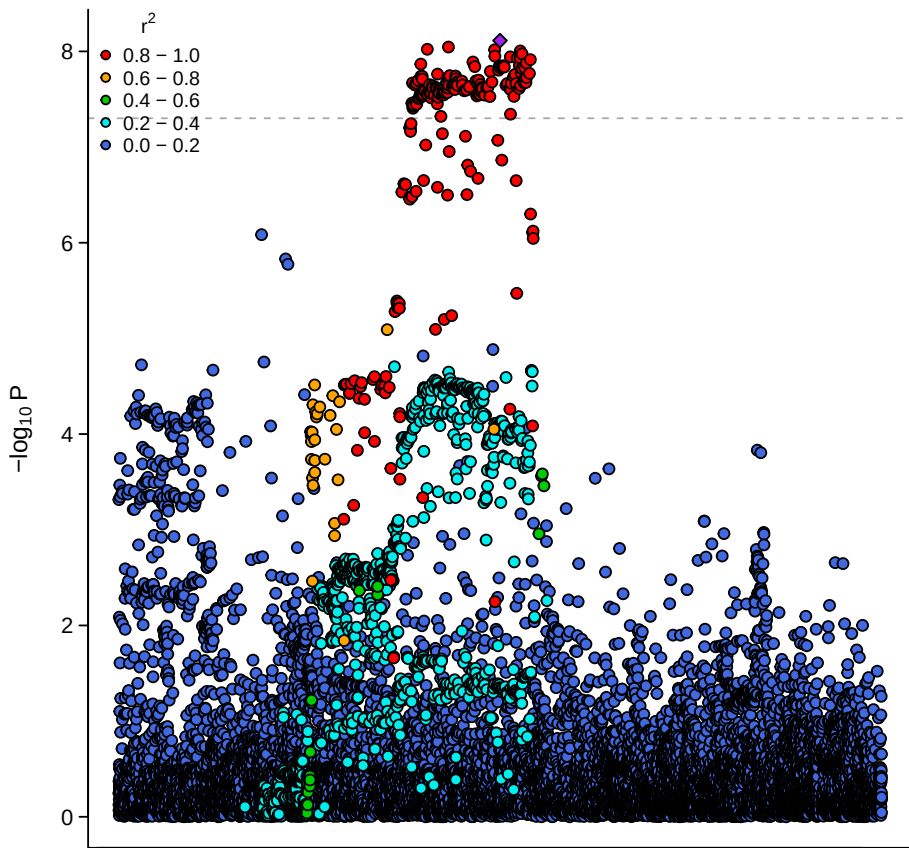


# Supplementary Figure 2.2

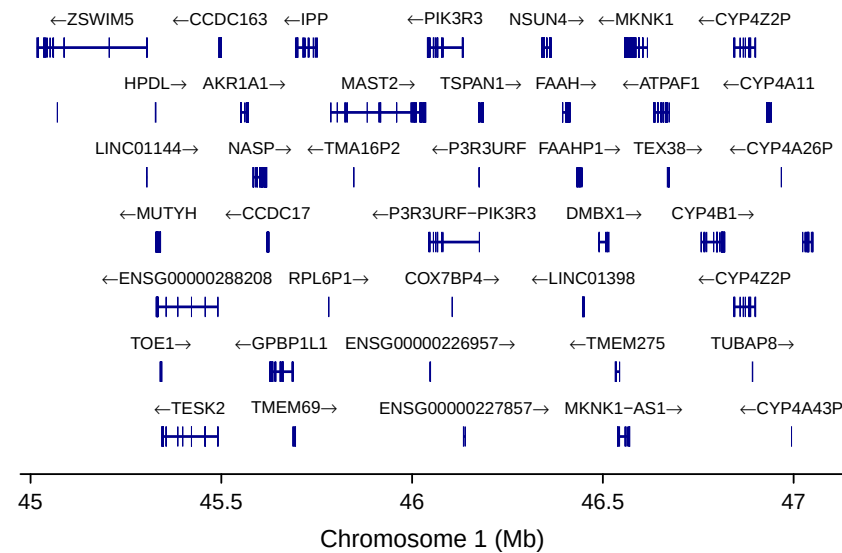
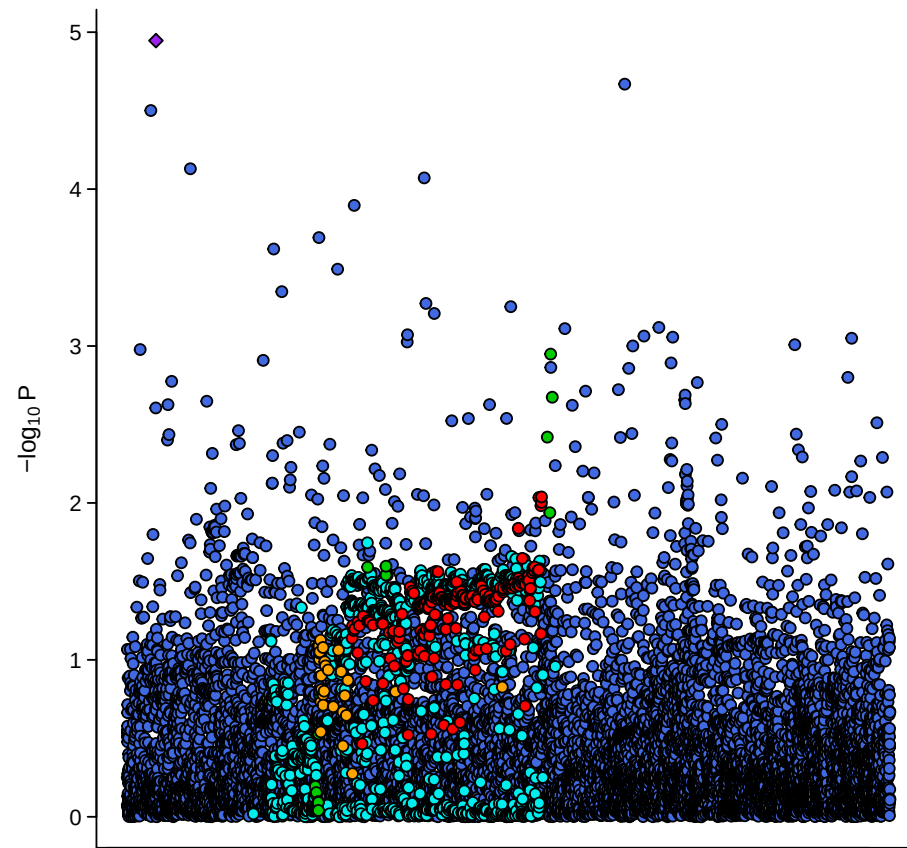


# Supplementary Figure 2.2

chr1\_46053005\_T\_C, P3R3URF-PIK3R3;PIK3R3, BNG, EUR ancestry



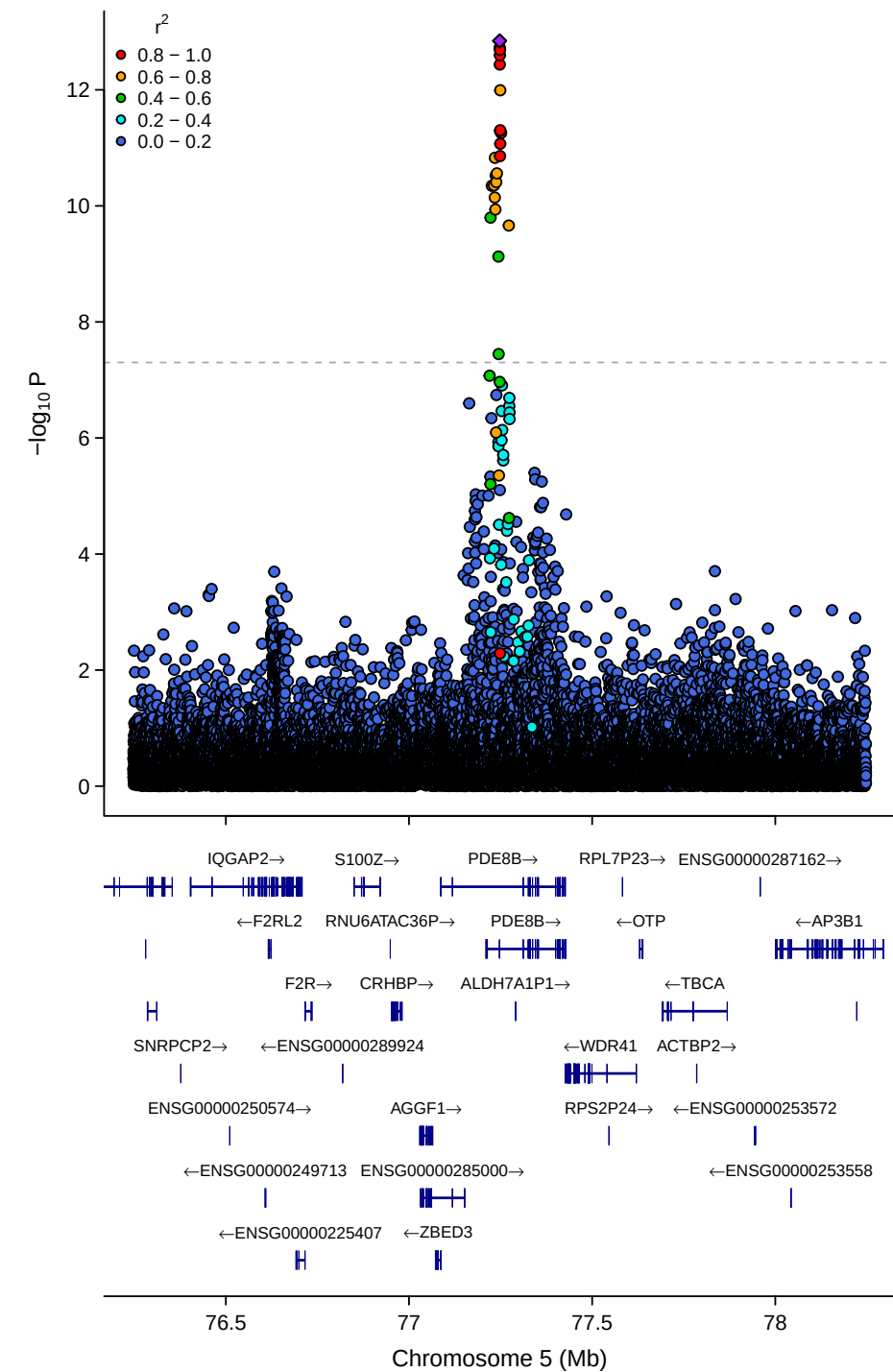
chr1\_46053005\_T\_C, P3R3URF-PIK3R3;PIK3R3, ThC, EUR ancestry



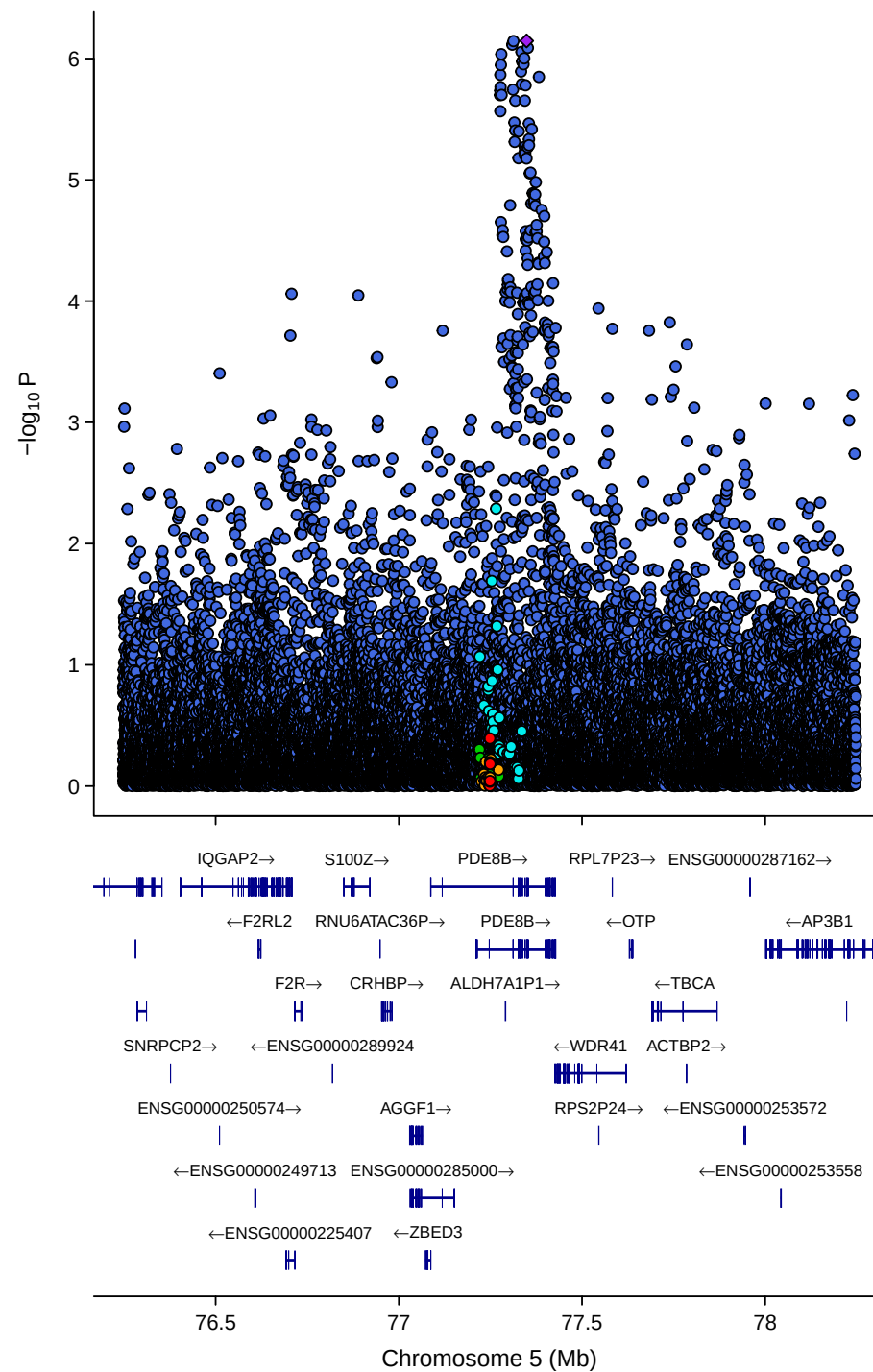


# Supplementary Figure 2.2

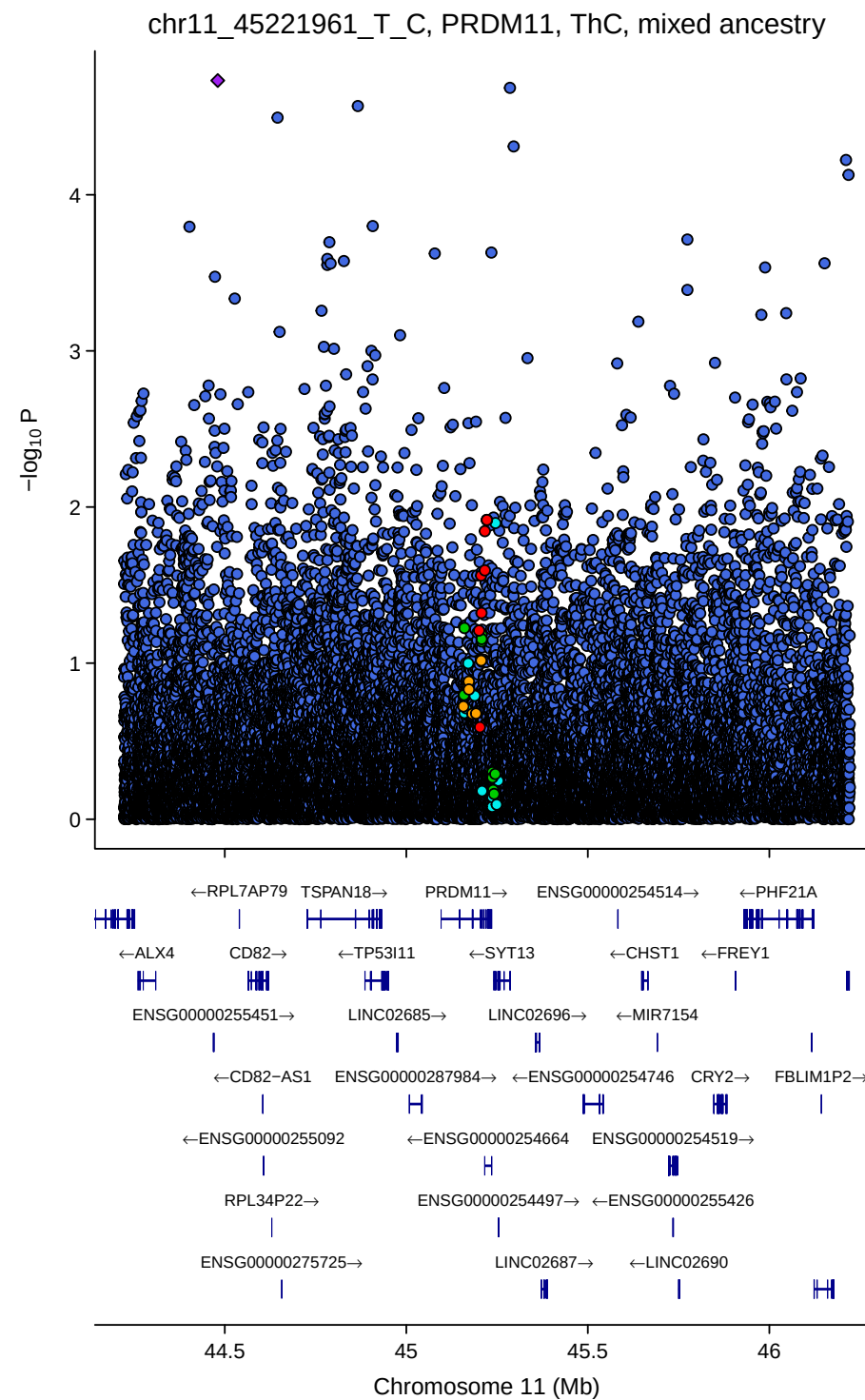
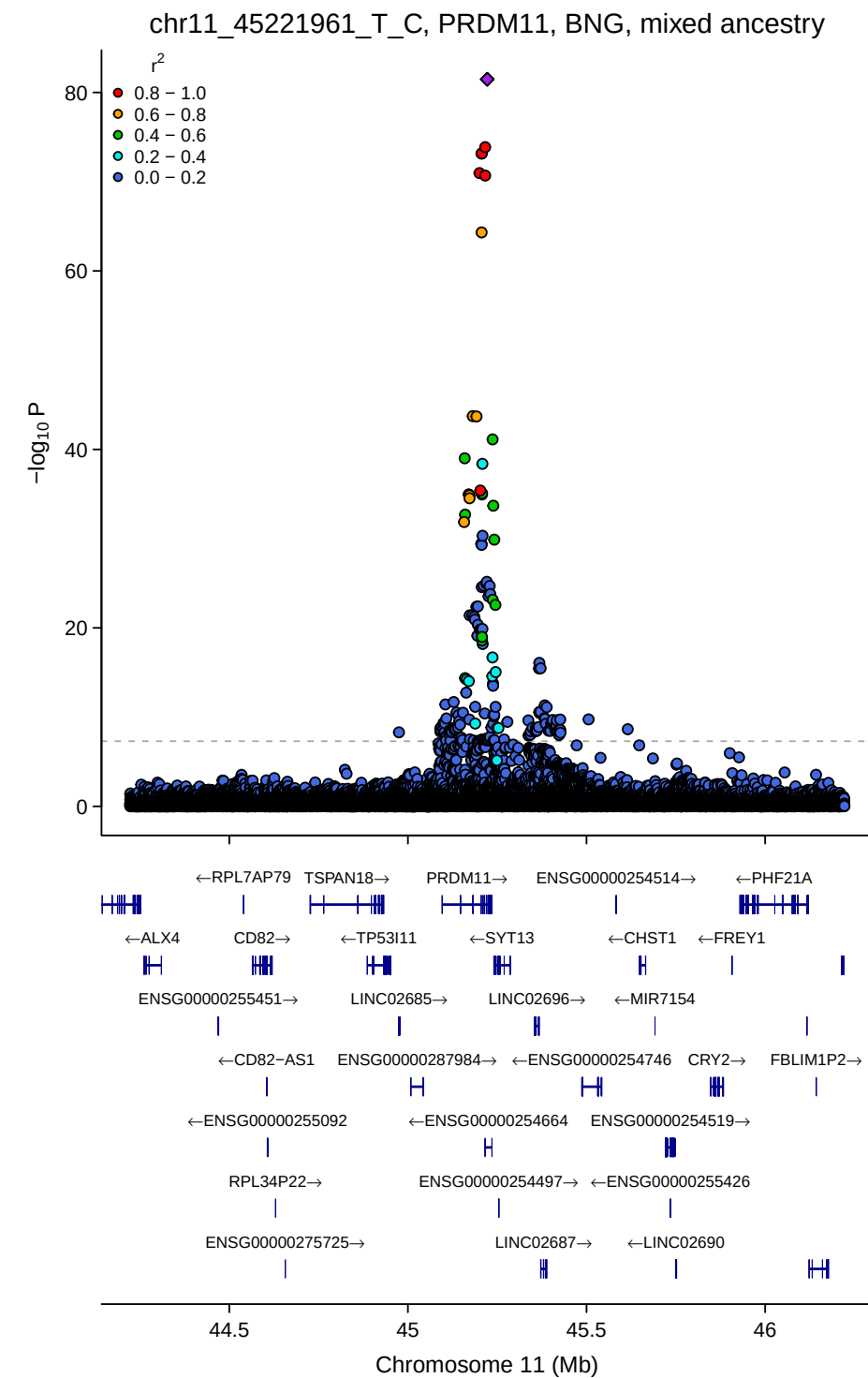
chr5\_77247384\_A\_T, PDE8B, BNG, mixed ancestry



chr5\_77247384\_A\_T, PDE8B, ThC, mixed ancestry

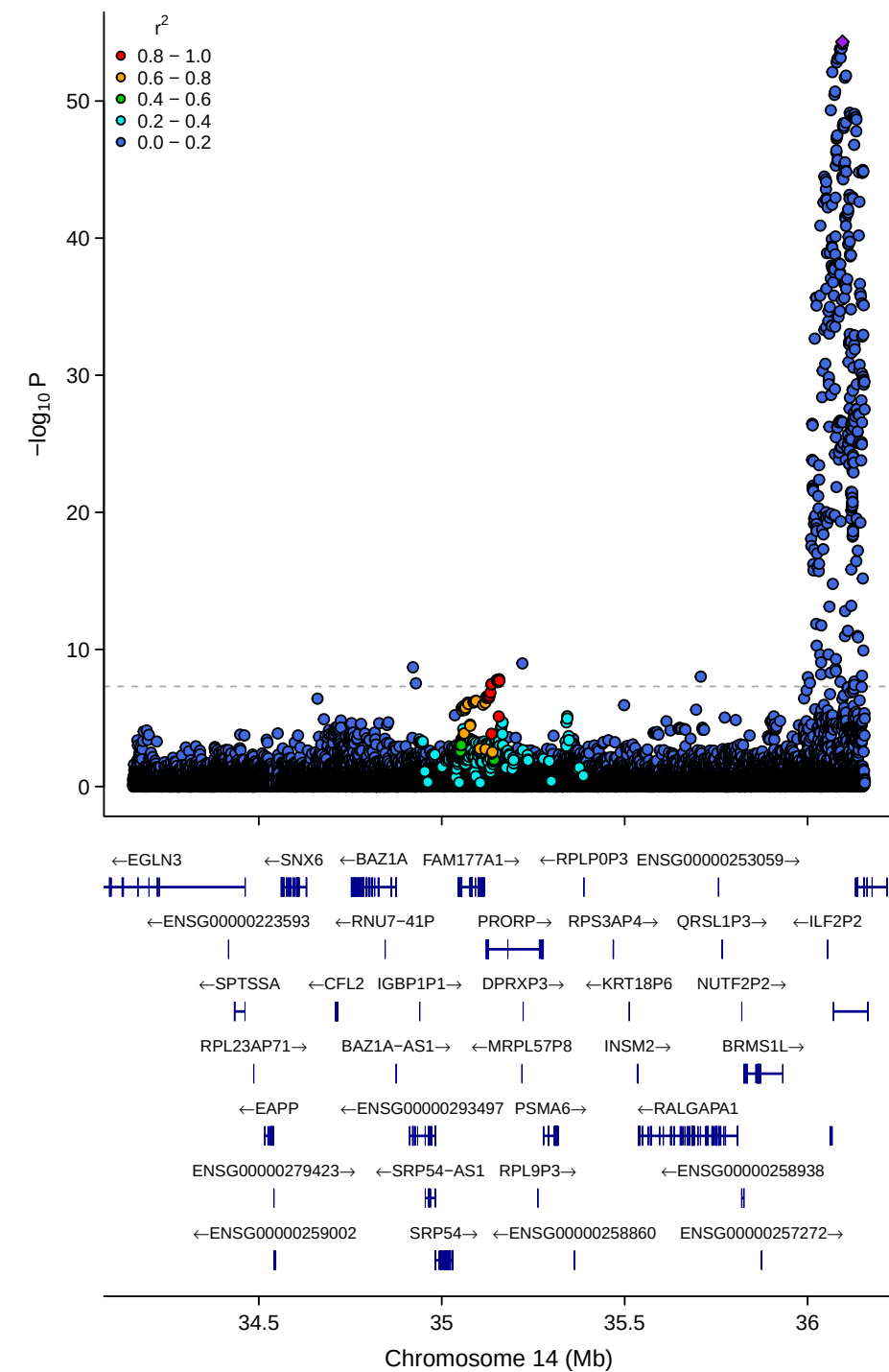


# Supplementary Figure 2.2

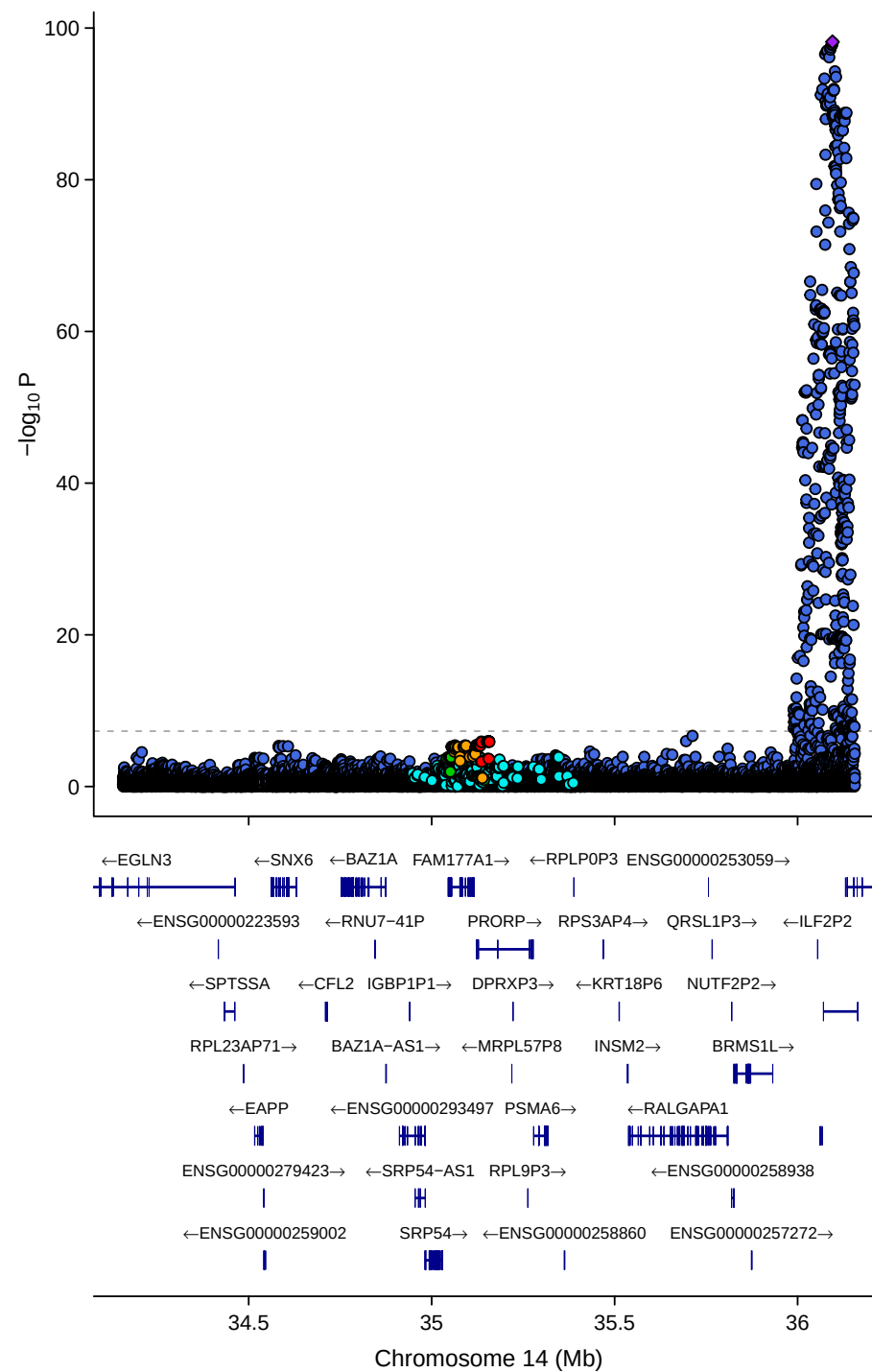


Supplementary Figure 2.2

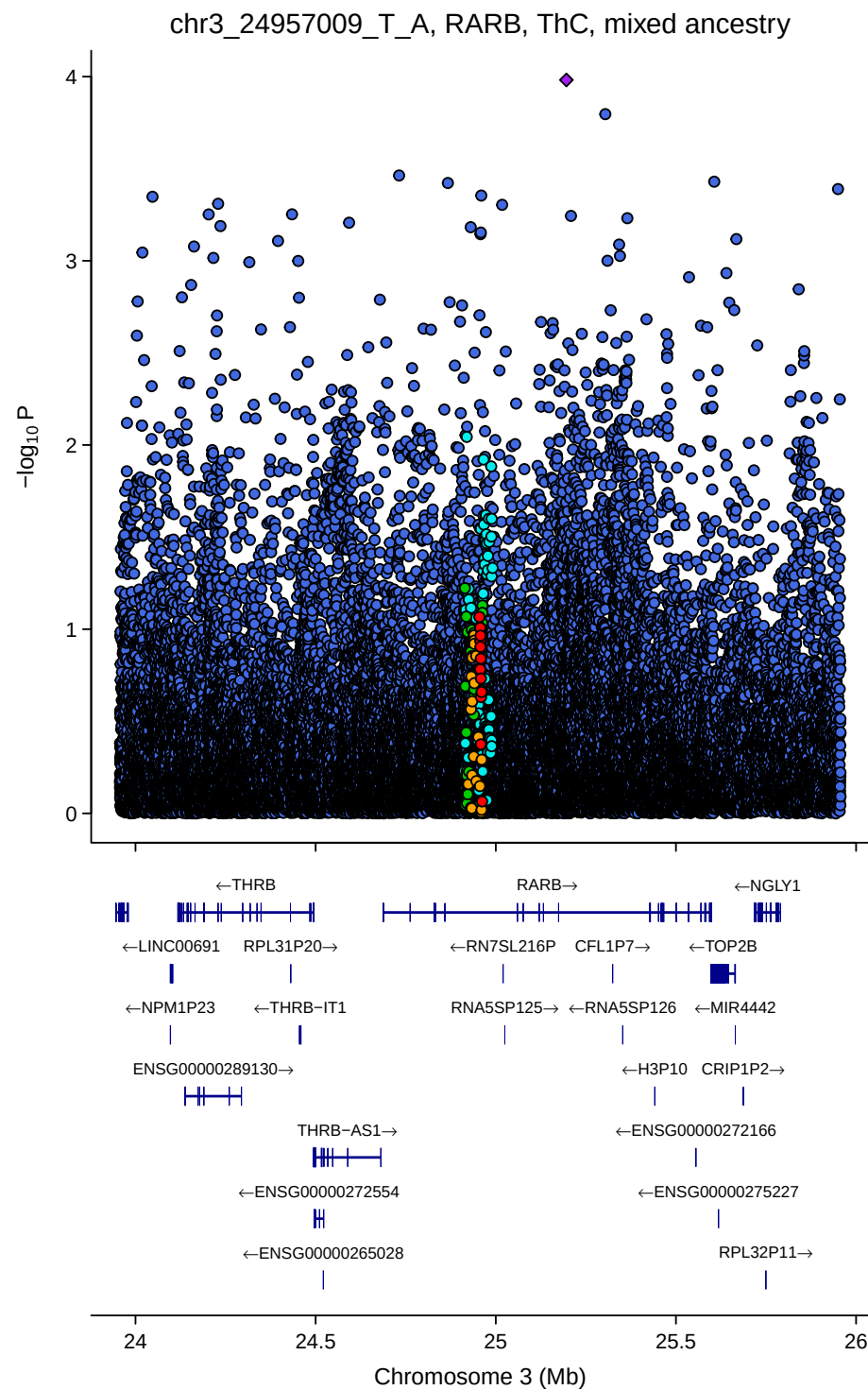
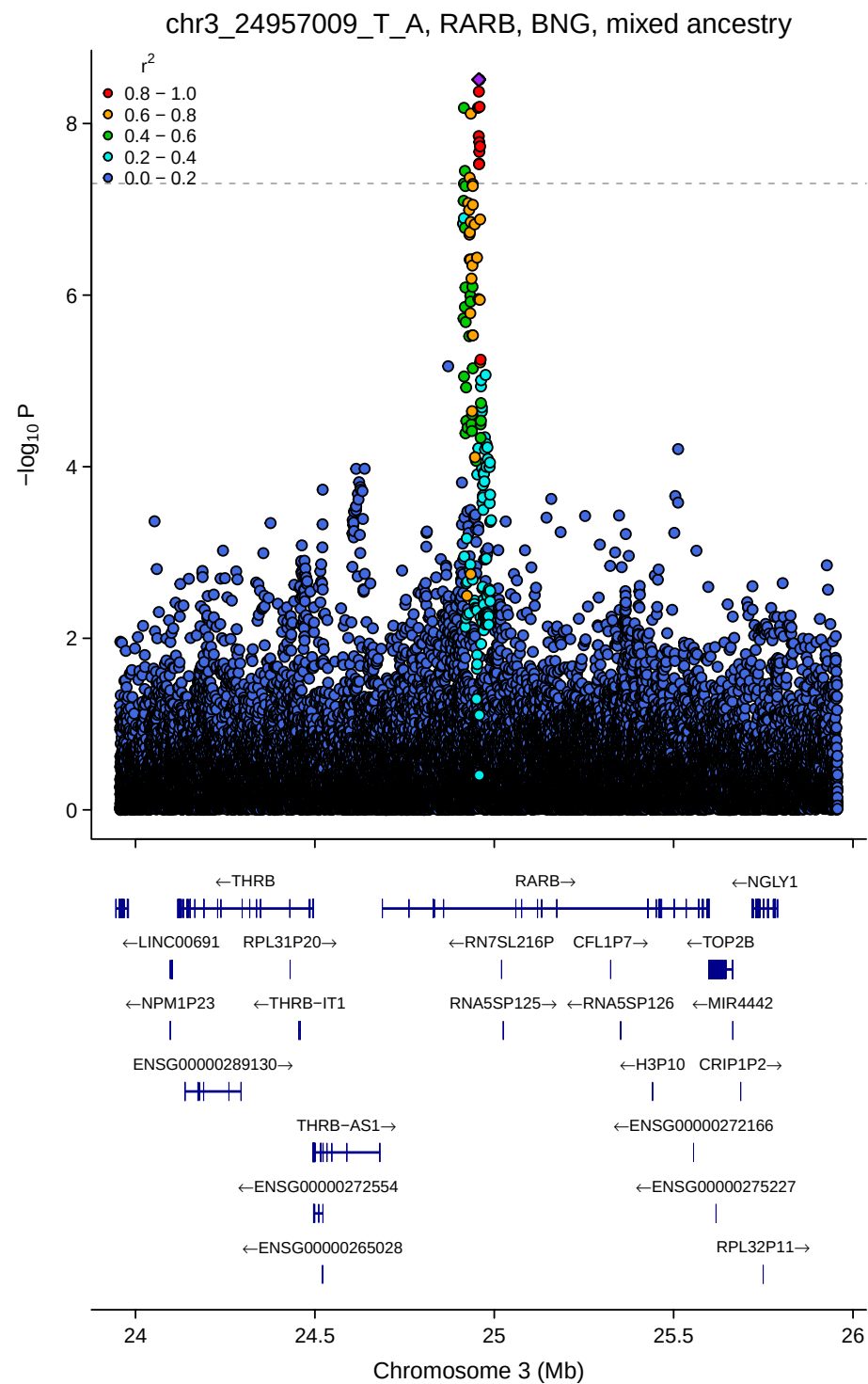
chr14\_35156402\_A\_G, PRORP, BNG, mixed ancestry



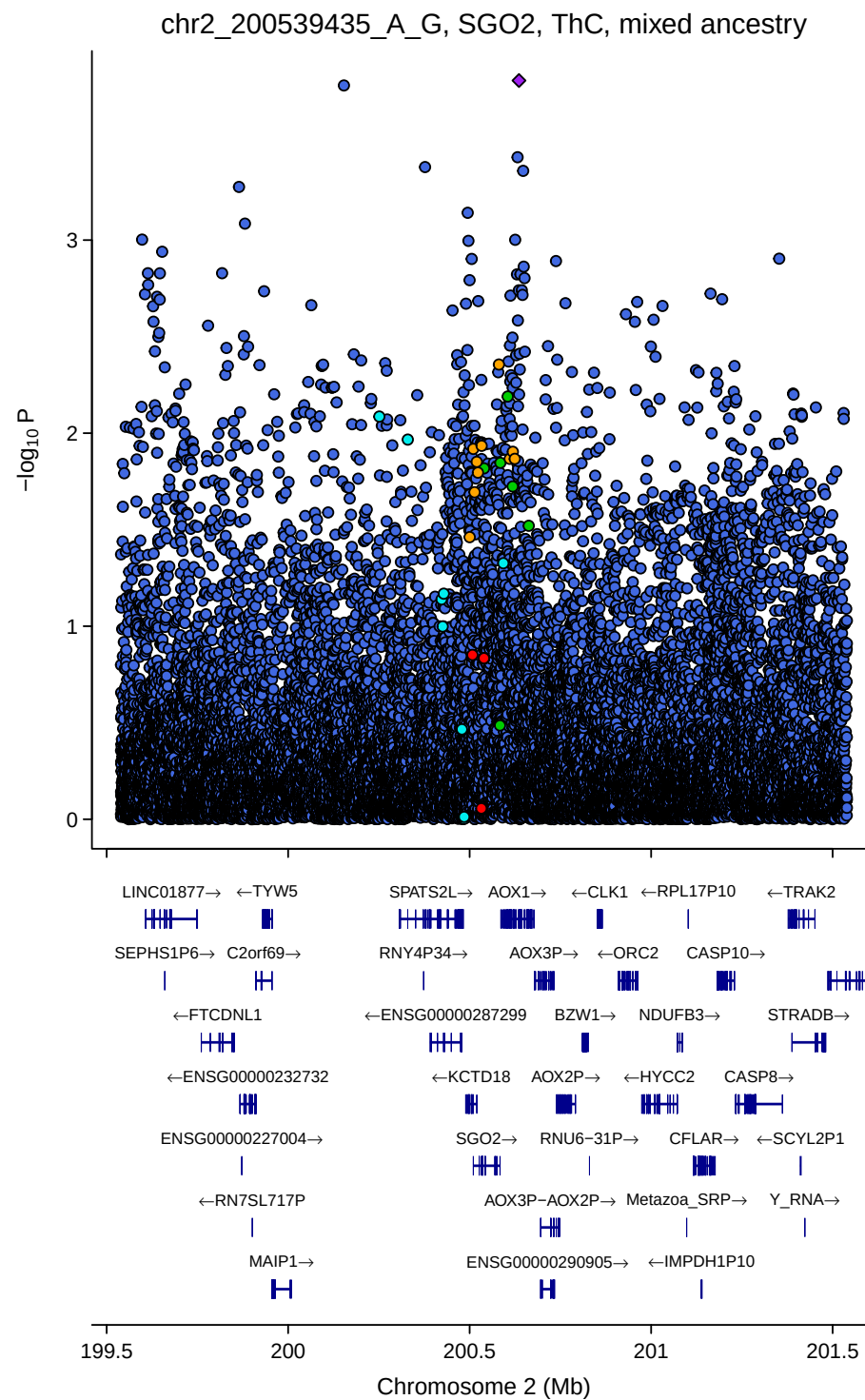
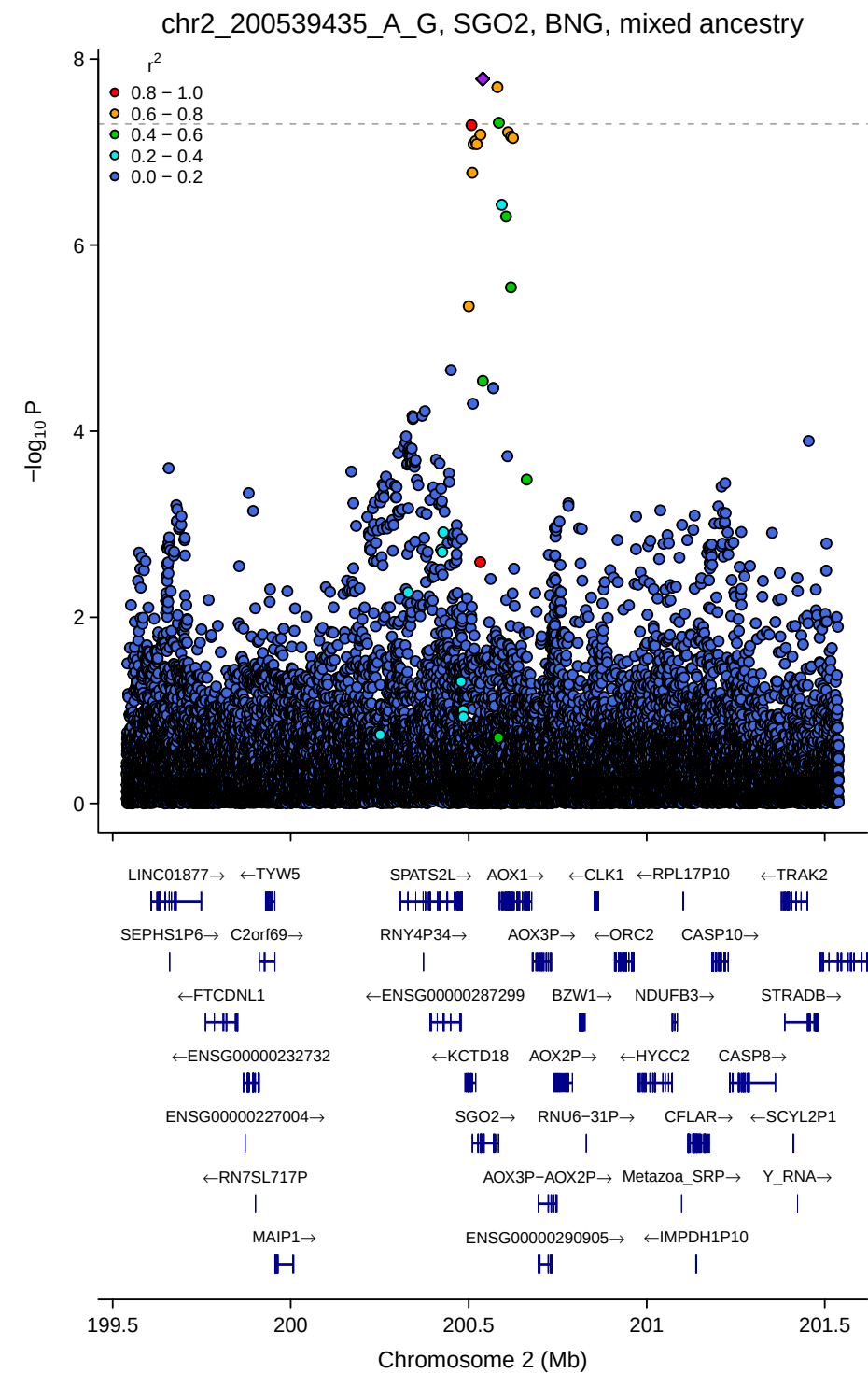
chr14\_35156402\_A\_G, PRORP, ThC, mixed ancestry



Supplementary Figure 2.2

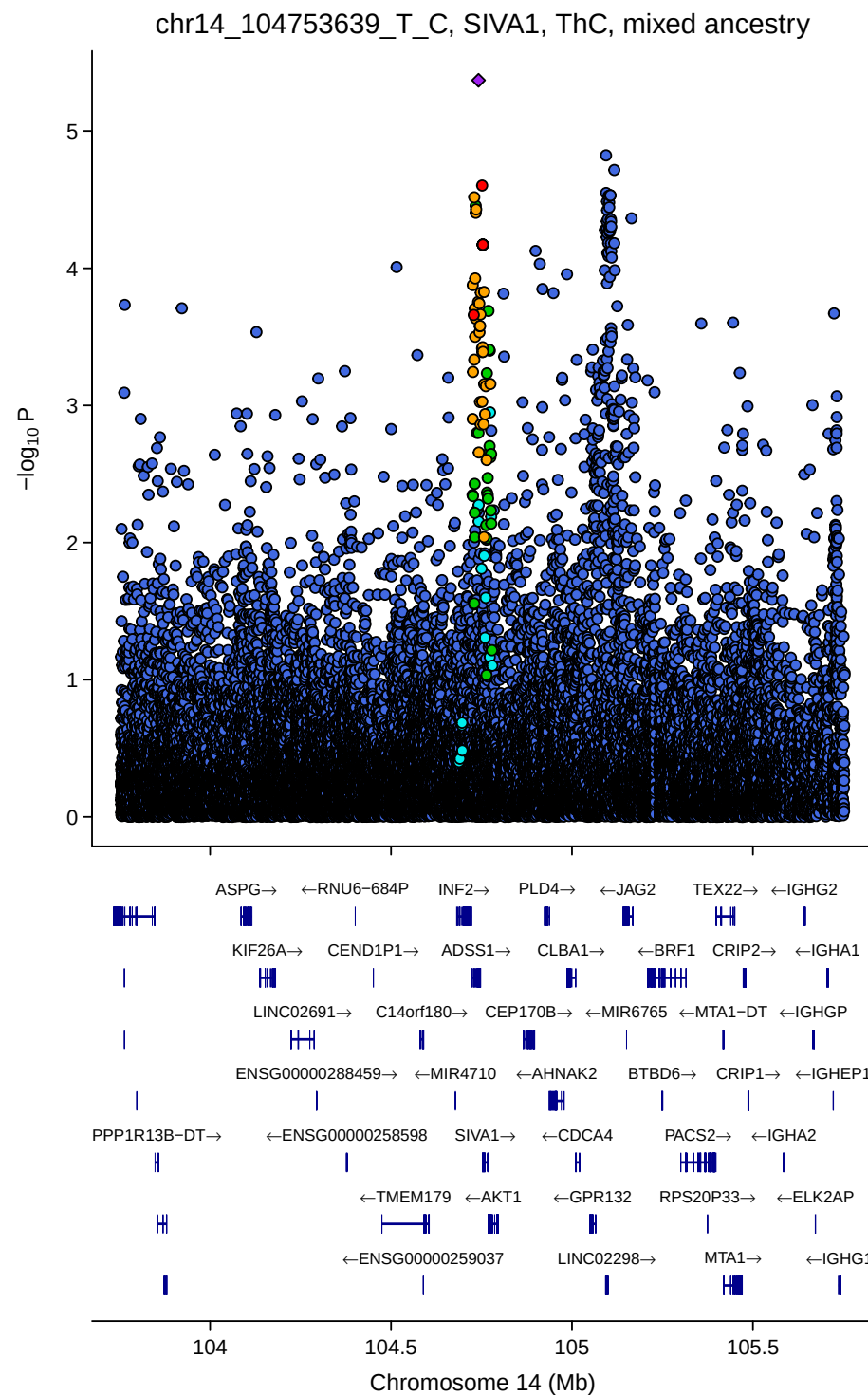
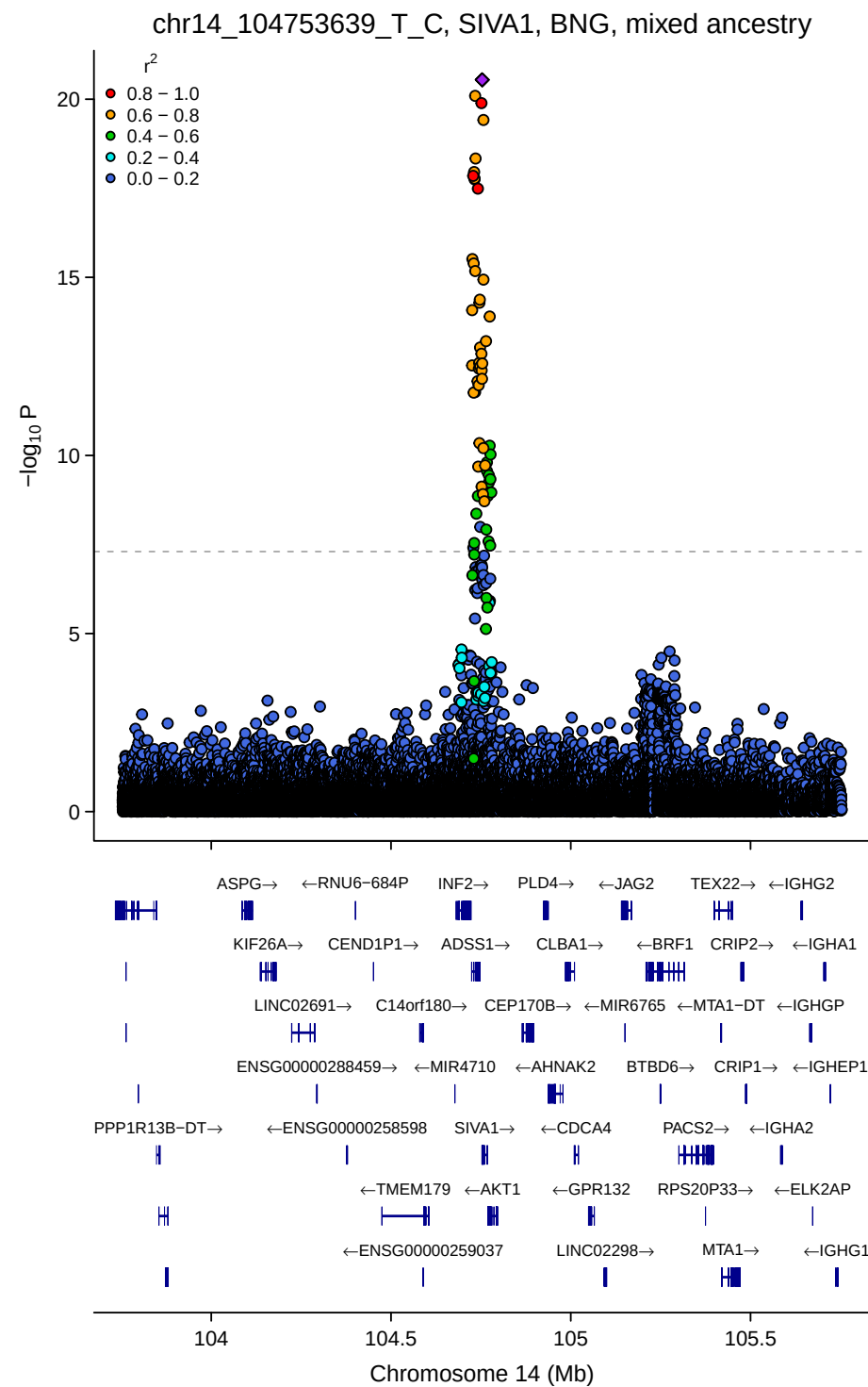


Supplementary Figure 2.2





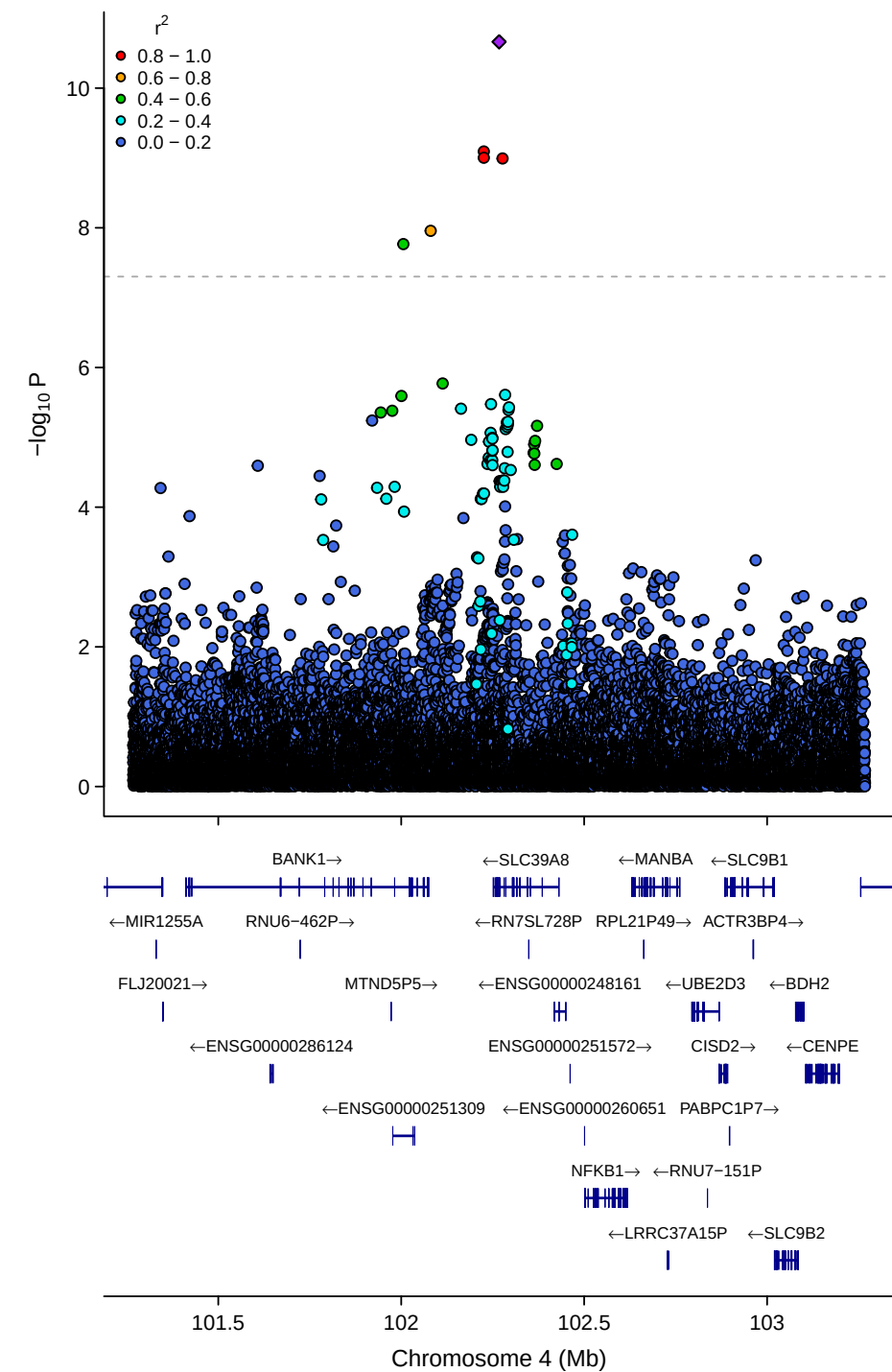
# Supplementary Figure 2.2



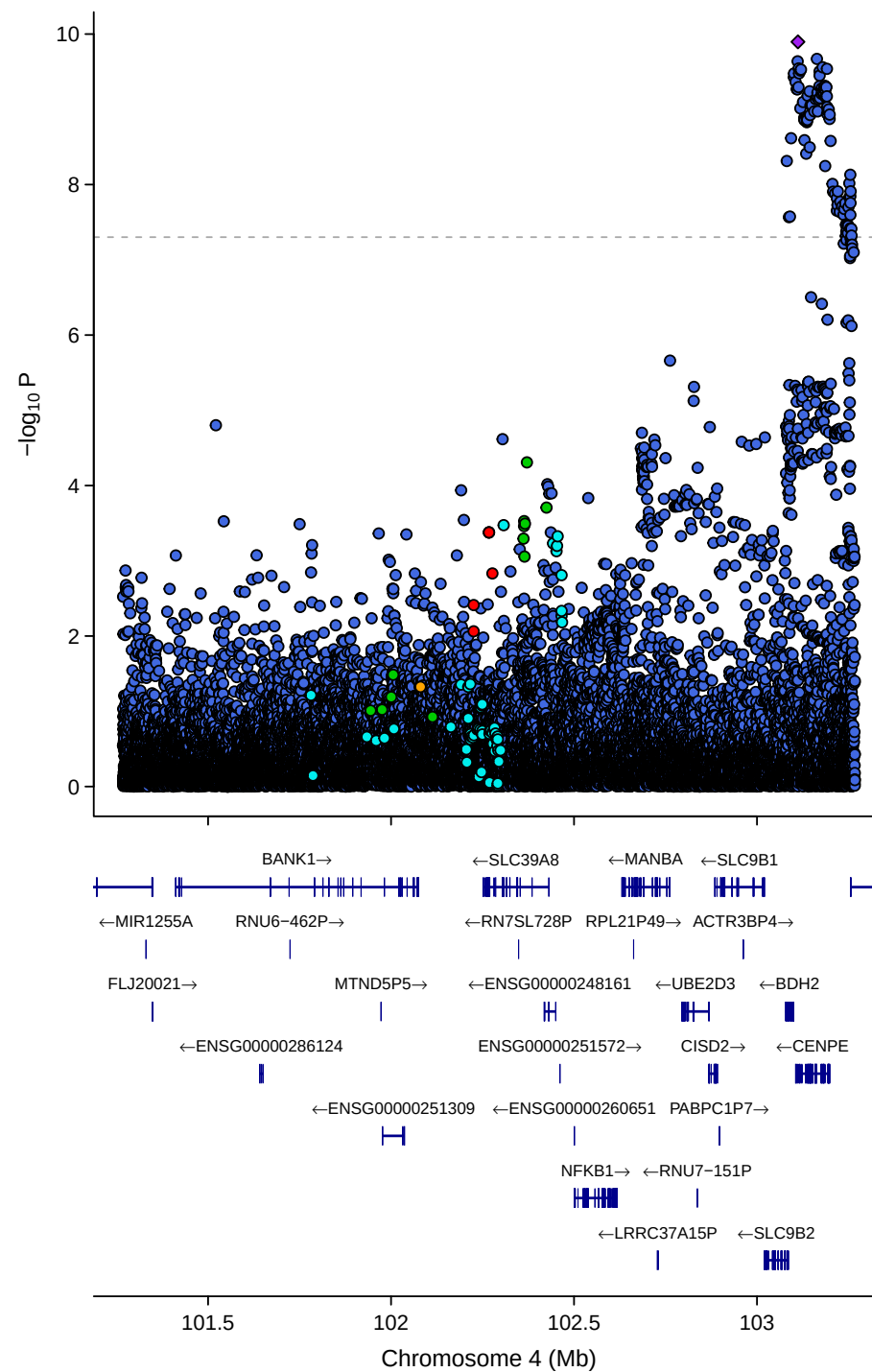


Supplementary Figure 2.2

chr4\_102267552\_C\_T, SLC39A8, BNG, mixed ancestry

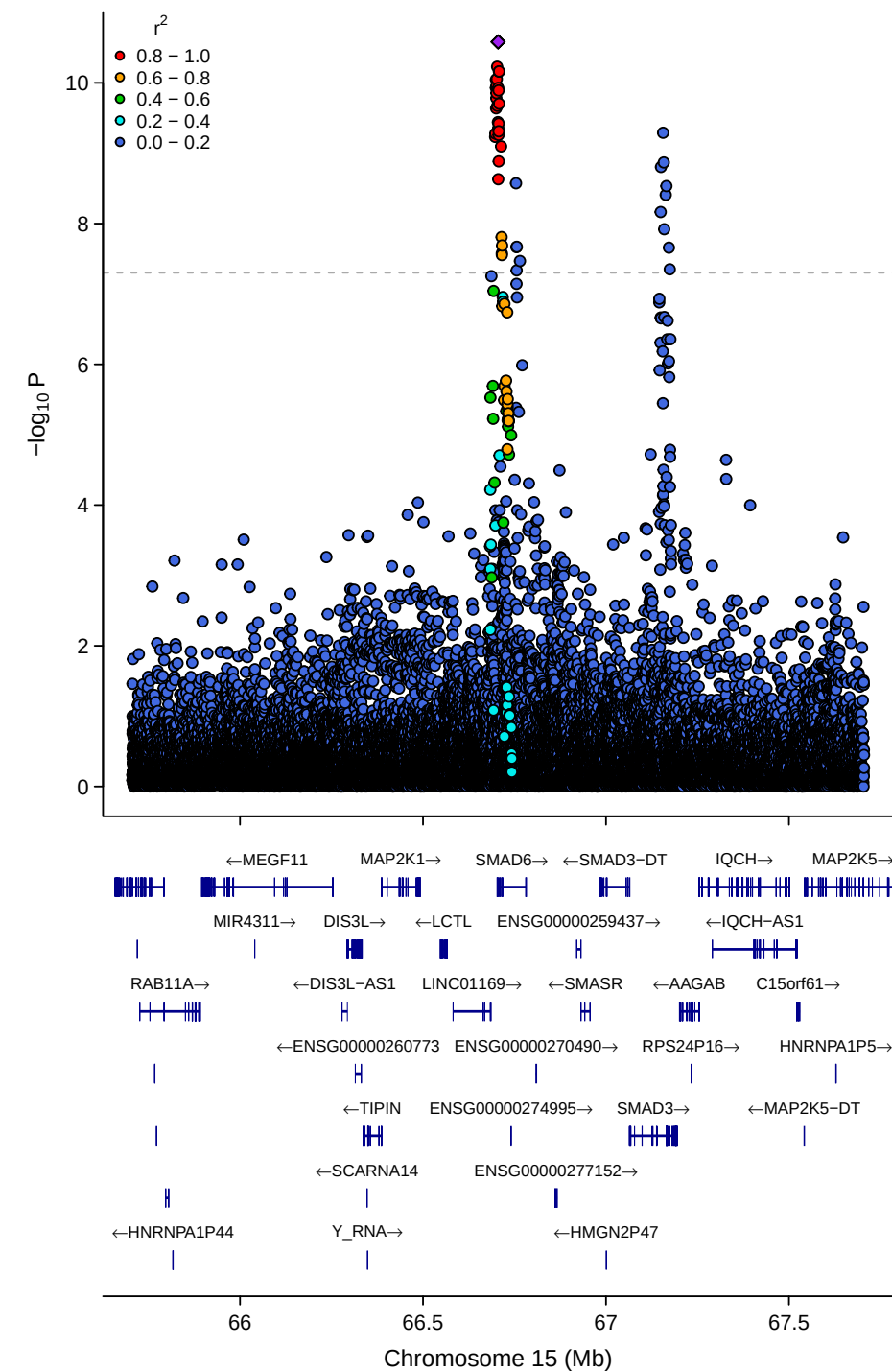


chr4\_102267552\_C\_T, SLC39A8, ThC, mixed ancestry

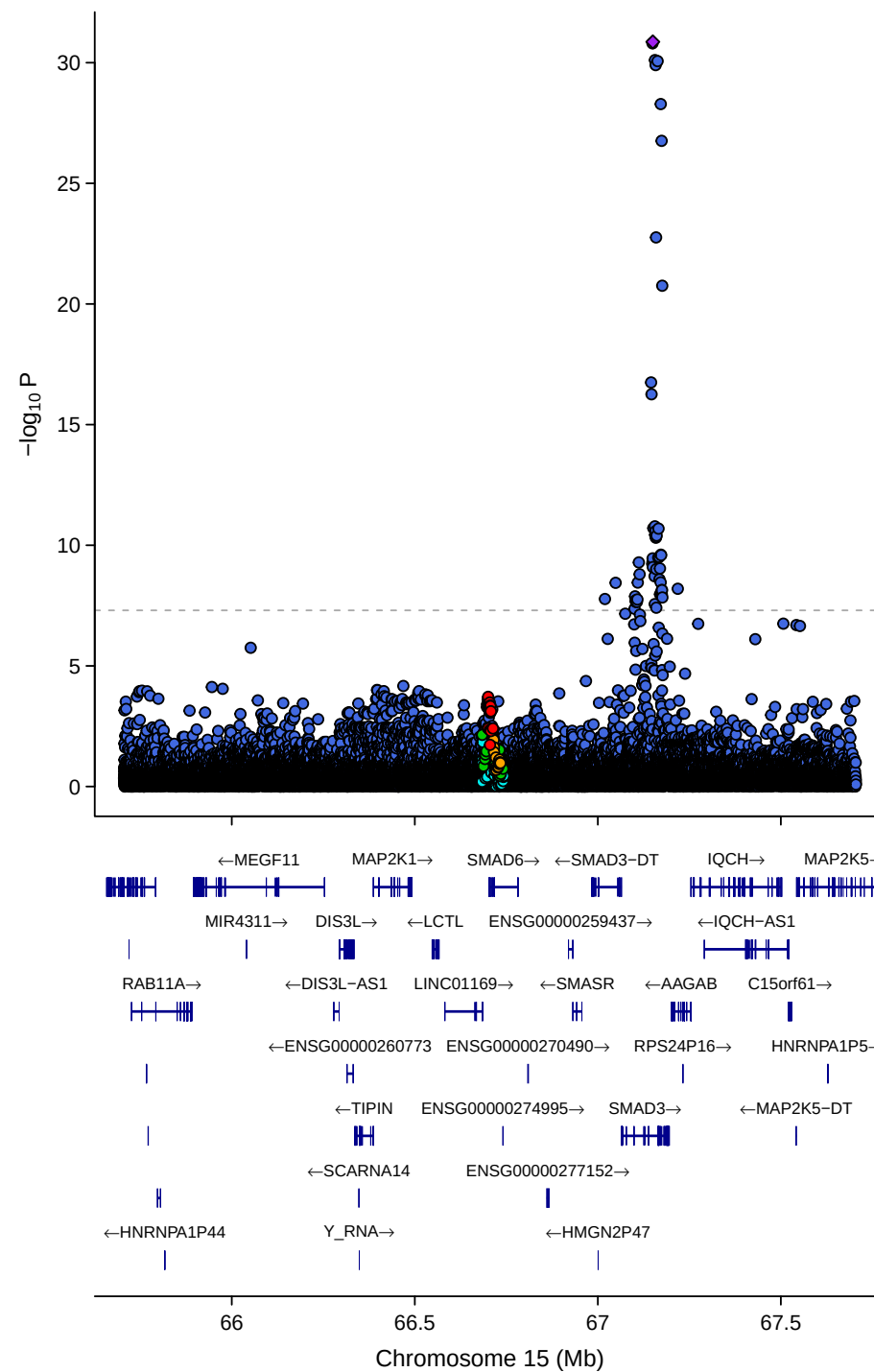


# Supplementary Figure 2.2

chr15\_66705258\_A\_C, SMAD6, BNG, mixed ancestry

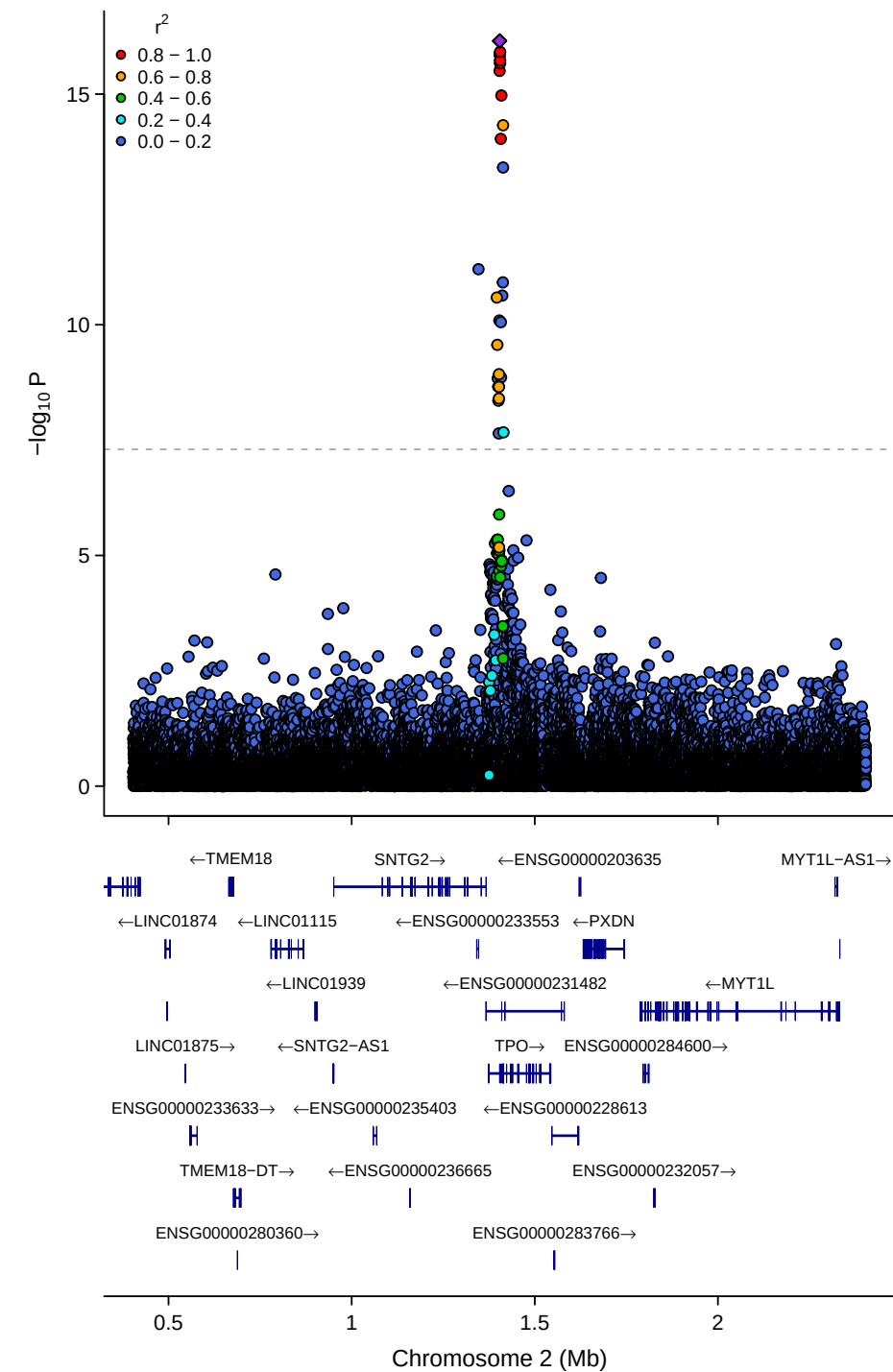


chr15\_66705258\_A\_C, SMAD6, ThC, mixed ancestry

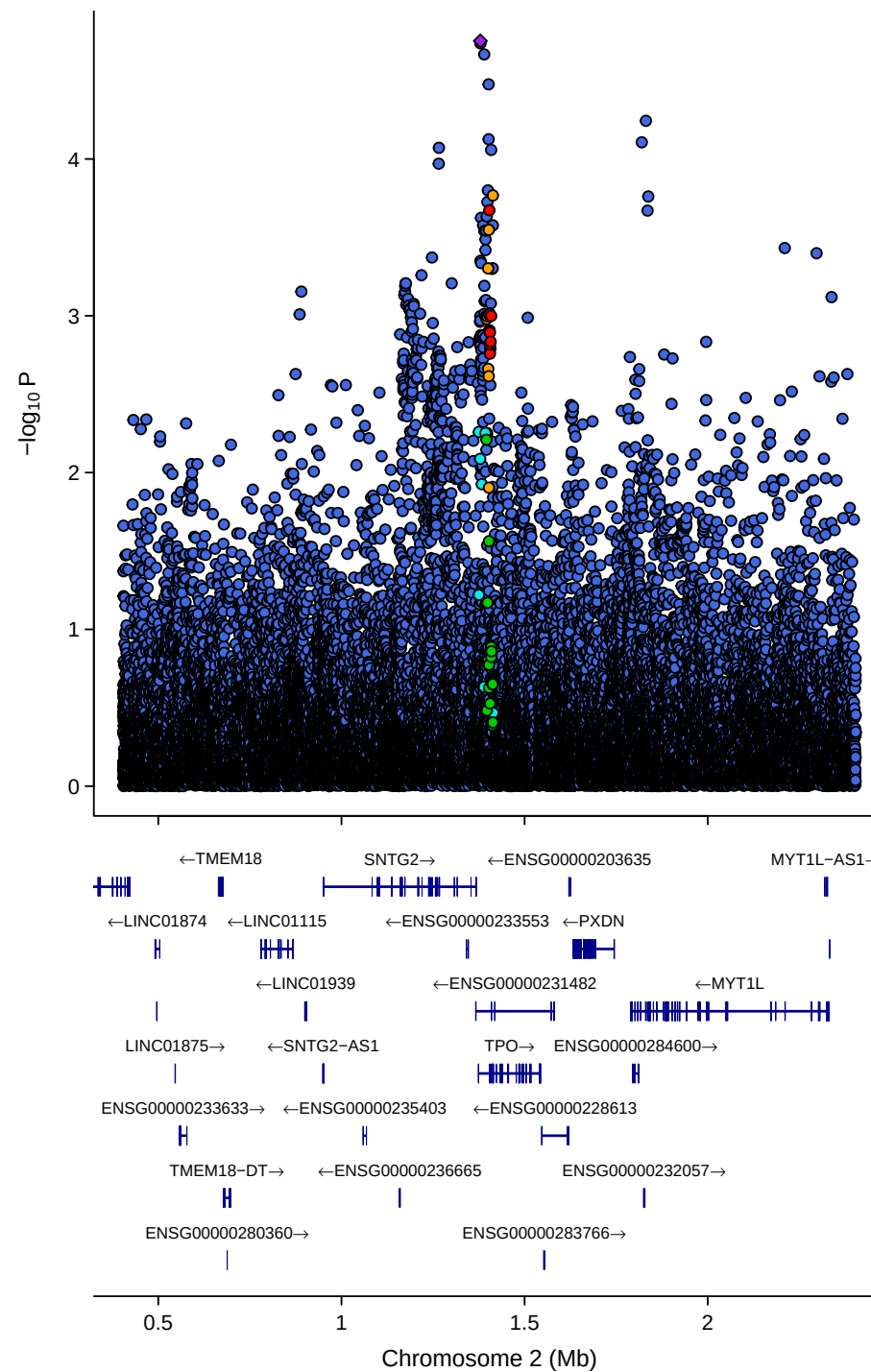


Supplementary Figure 2.2

chr2\_1404043\_C\_T, SNTG2;TPO, BNG, mixed ancestry

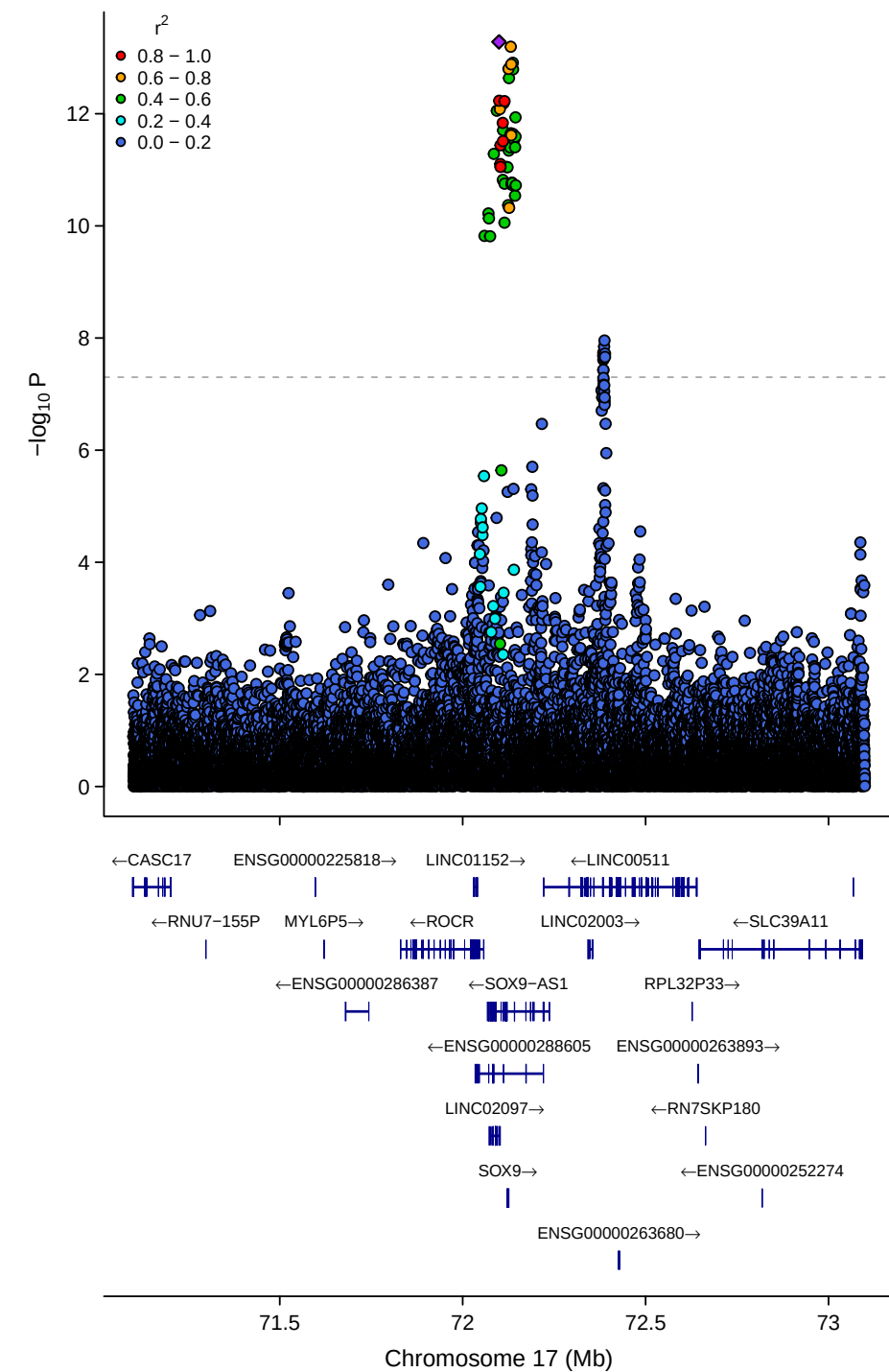


chr2\_1404043\_C\_T, SNTG2;TPO, ThC, mixed ancestry

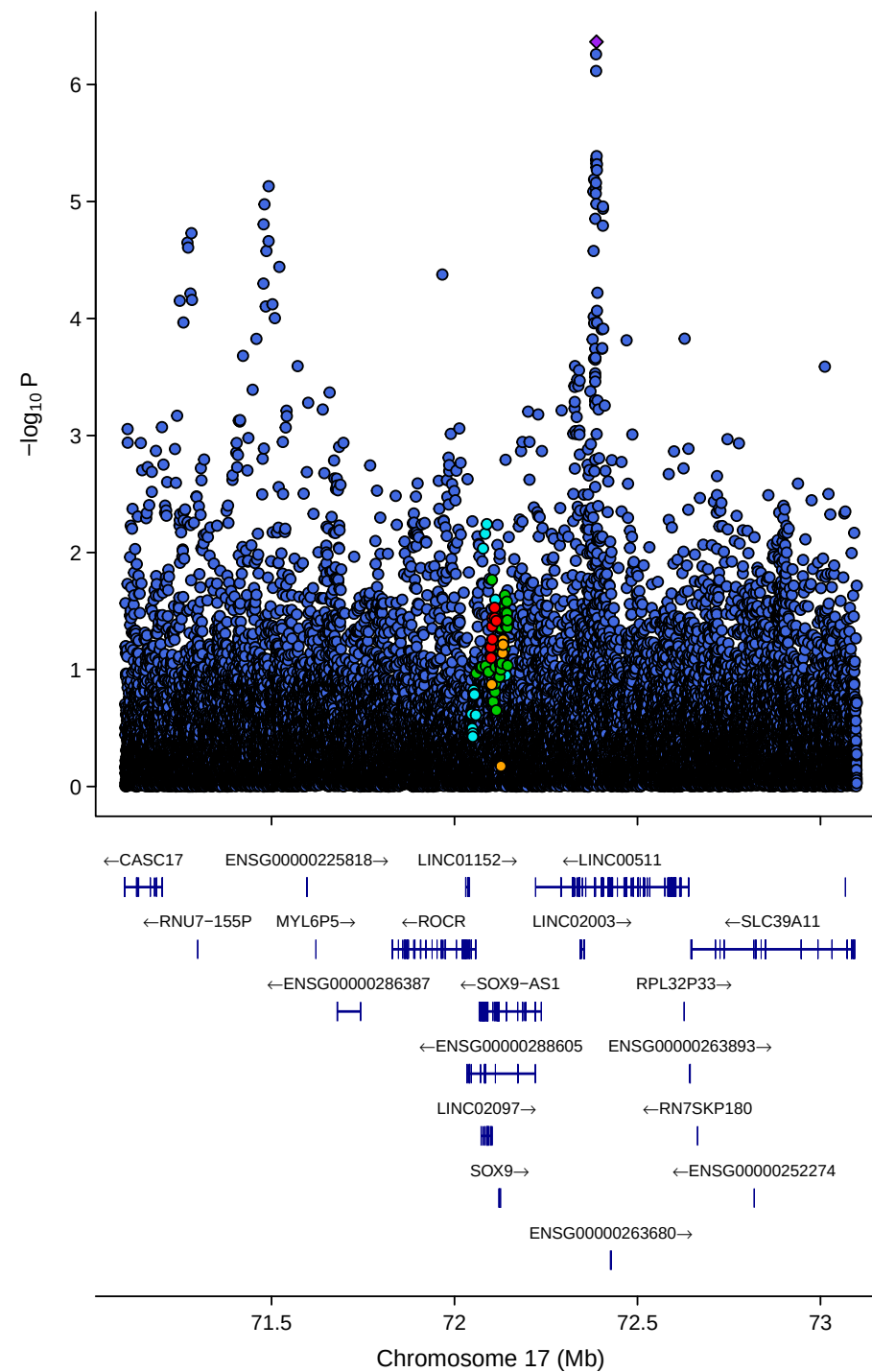


Supplementary Figure 2.2

chr17\_72099224\_C\_T, SOX9-AS1, BNG, mixed ancestry

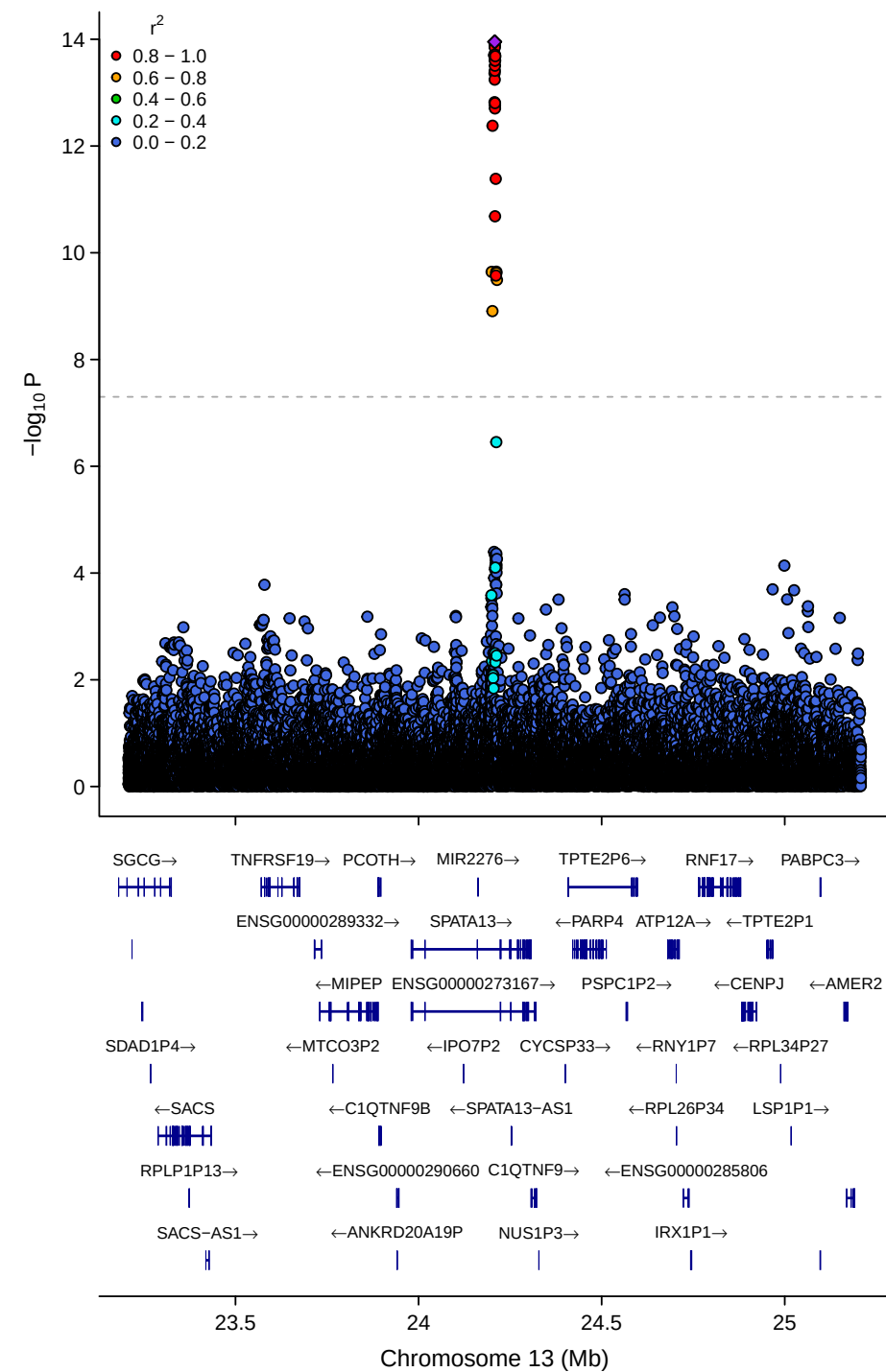


chr17\_72099224\_C\_T, SOX9-AS1, ThC, mixed ancestry

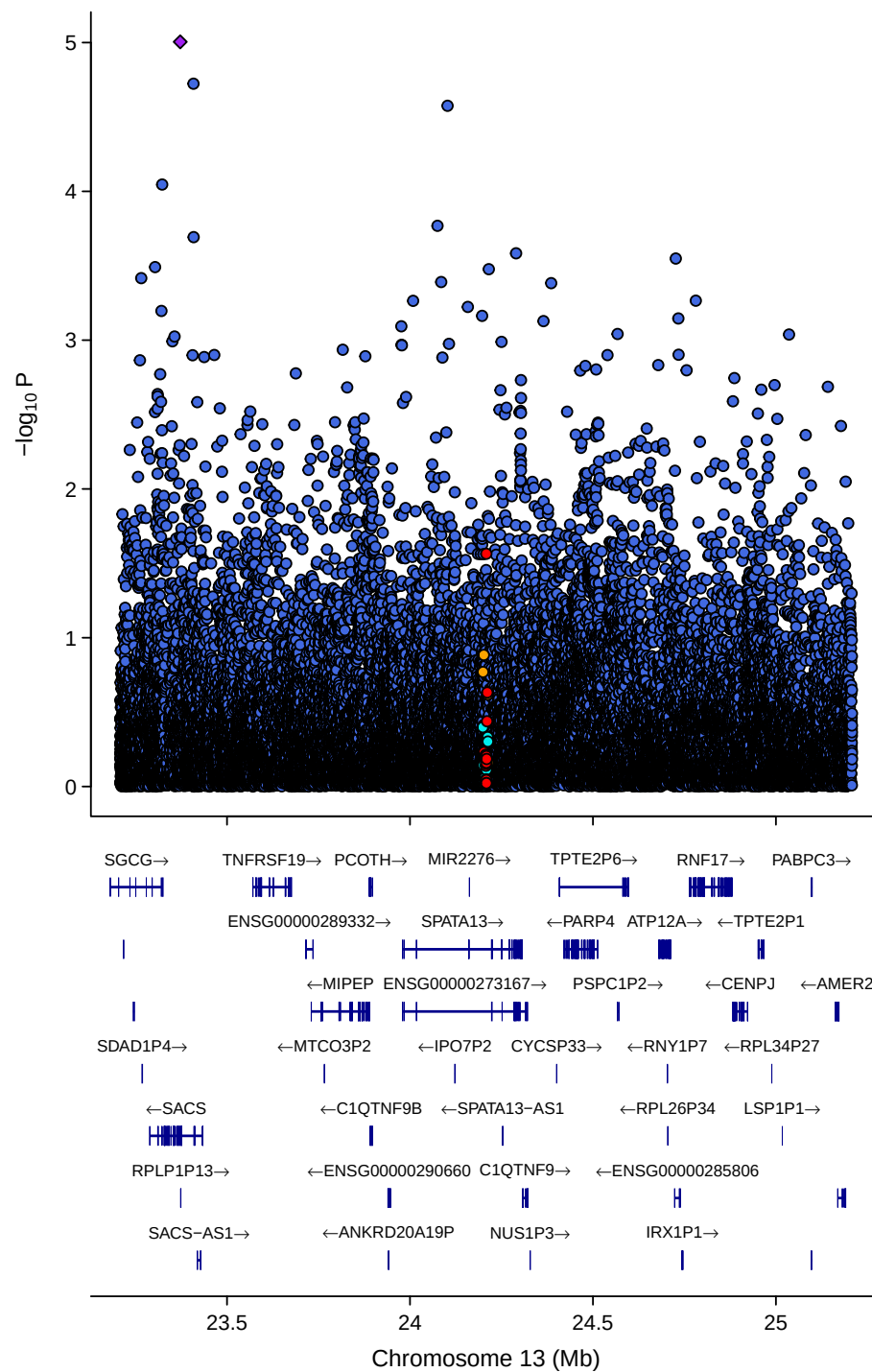


# Supplementary Figure 2.2

chr13\_24207942\_T\_C, SPATA13, BNG, mixed ancestry



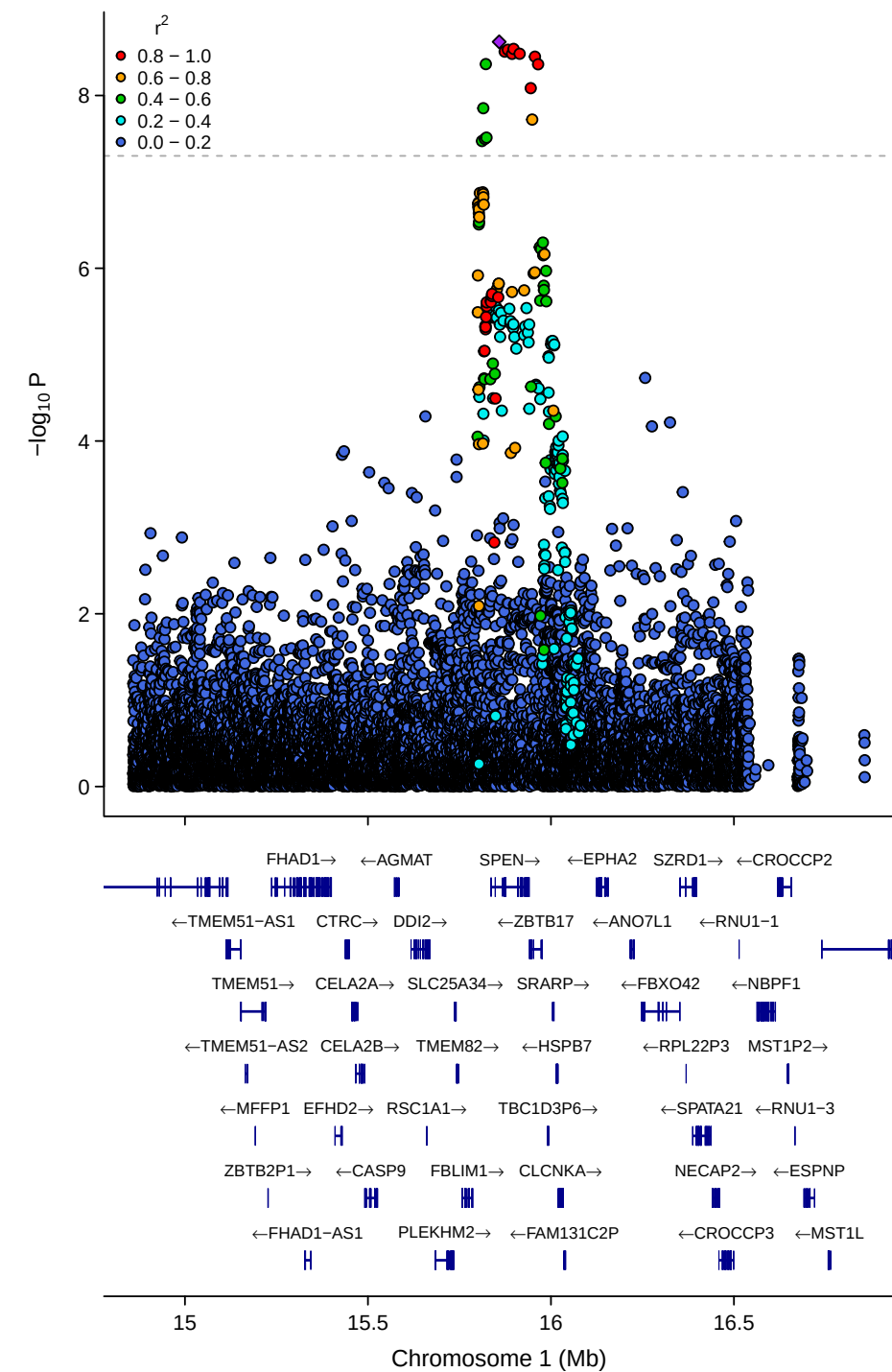
chr13\_24207942\_T\_C, SPATA13, ThC, mixed ancestry



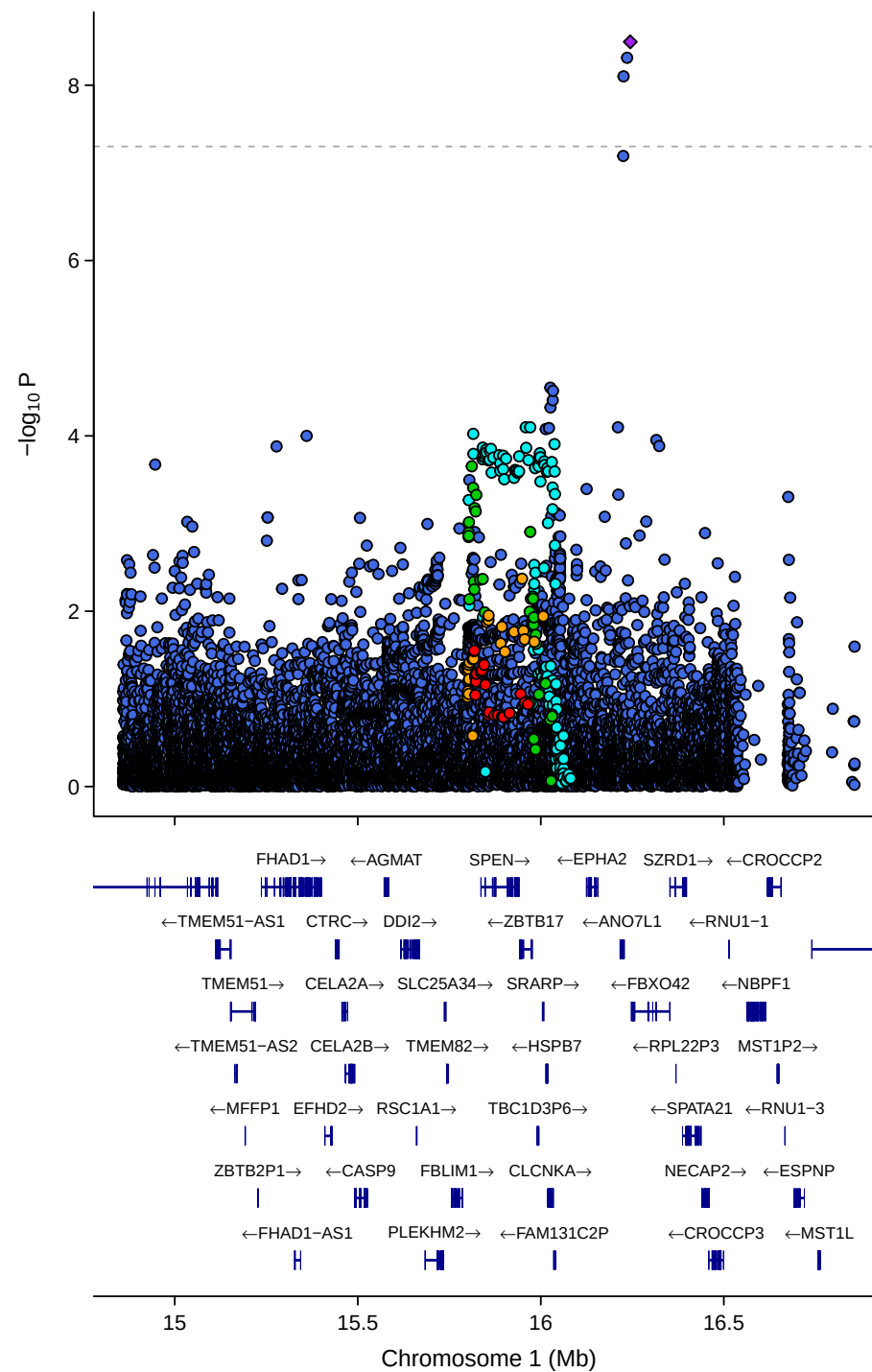


# Supplementary Figure 2.2

chr1\_15858628\_T\_C, SPEN, BNG, EUR ancestry

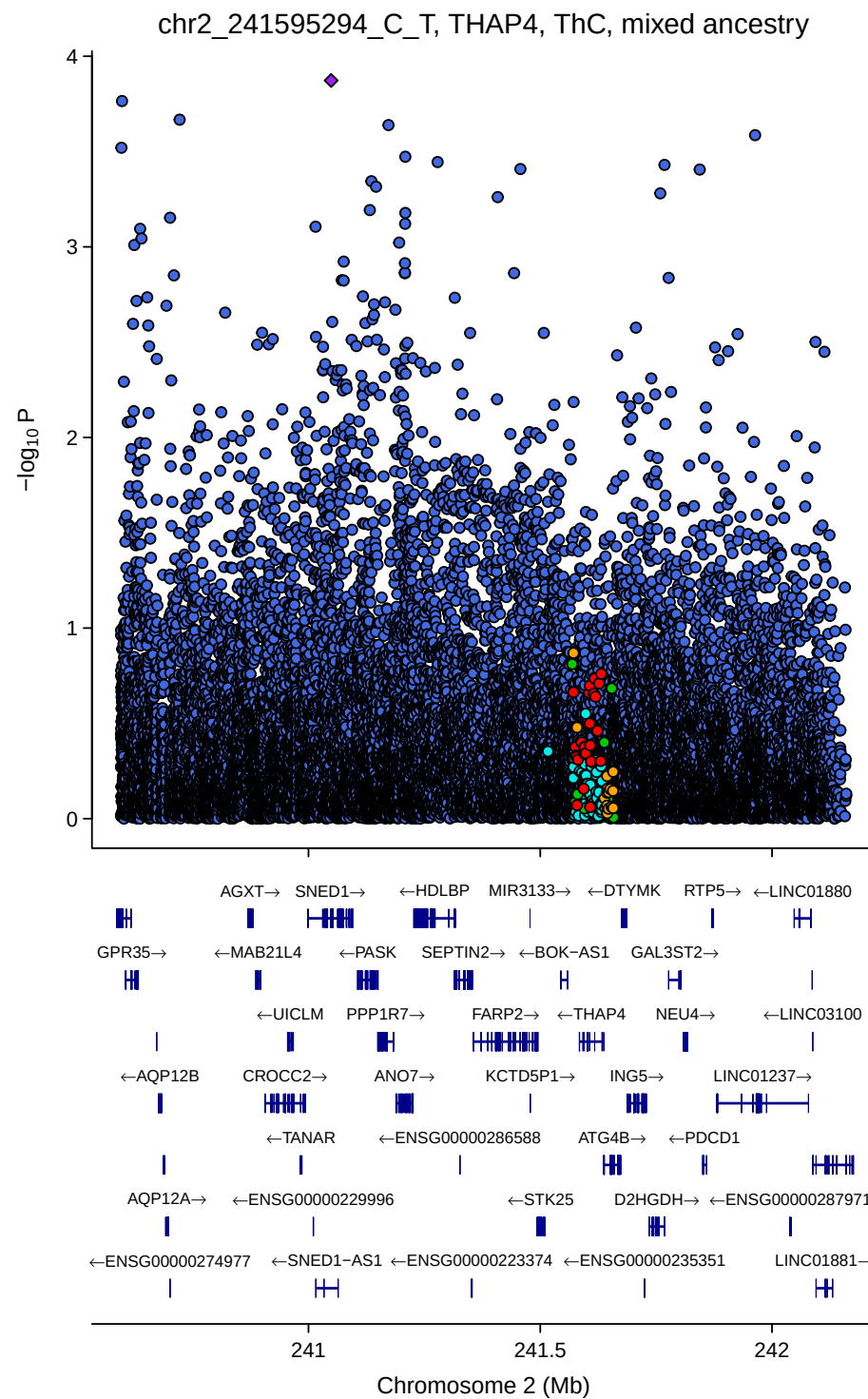
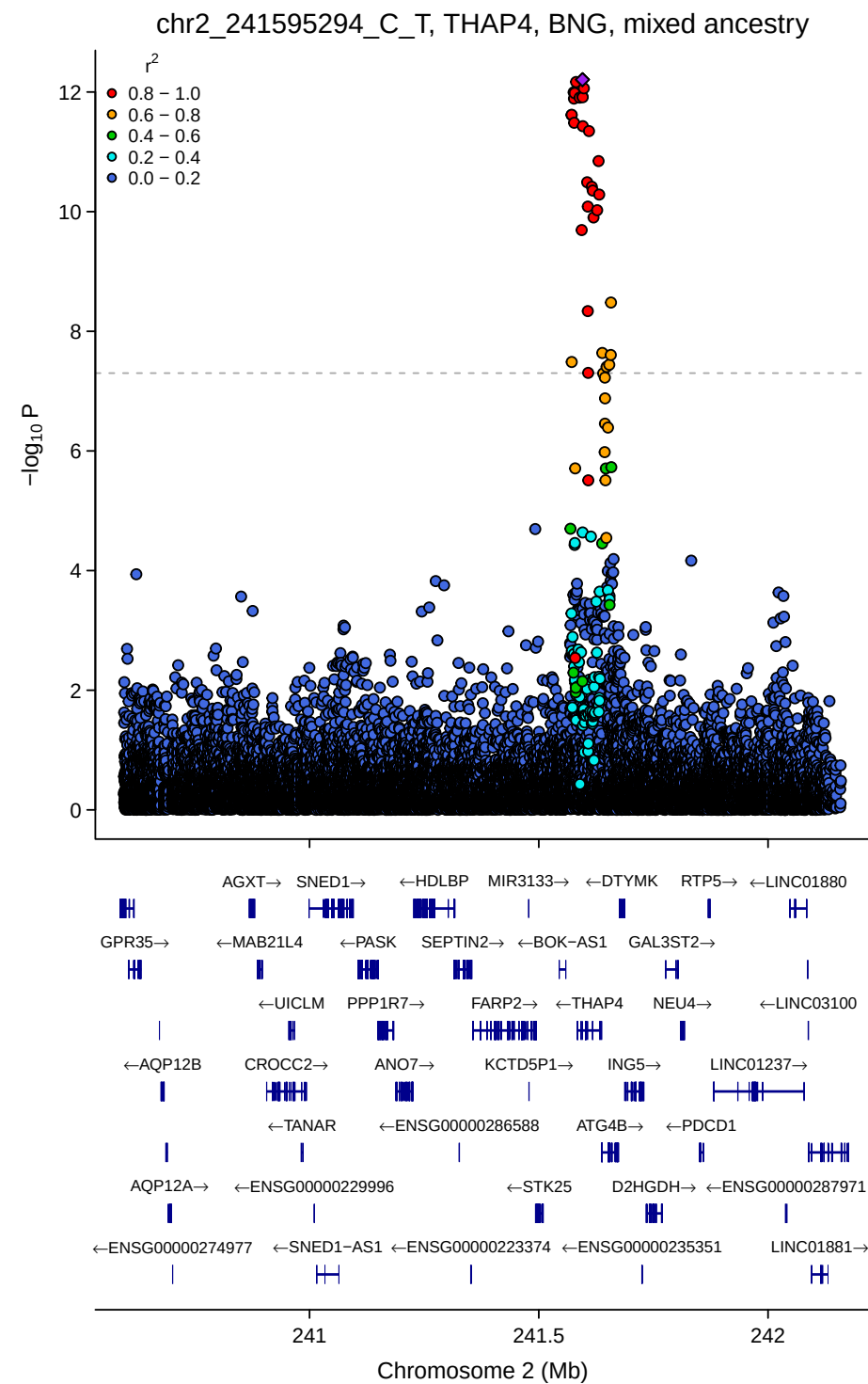


chr1\_15858628\_T\_C, SPEN, ThC, EUR ancestry



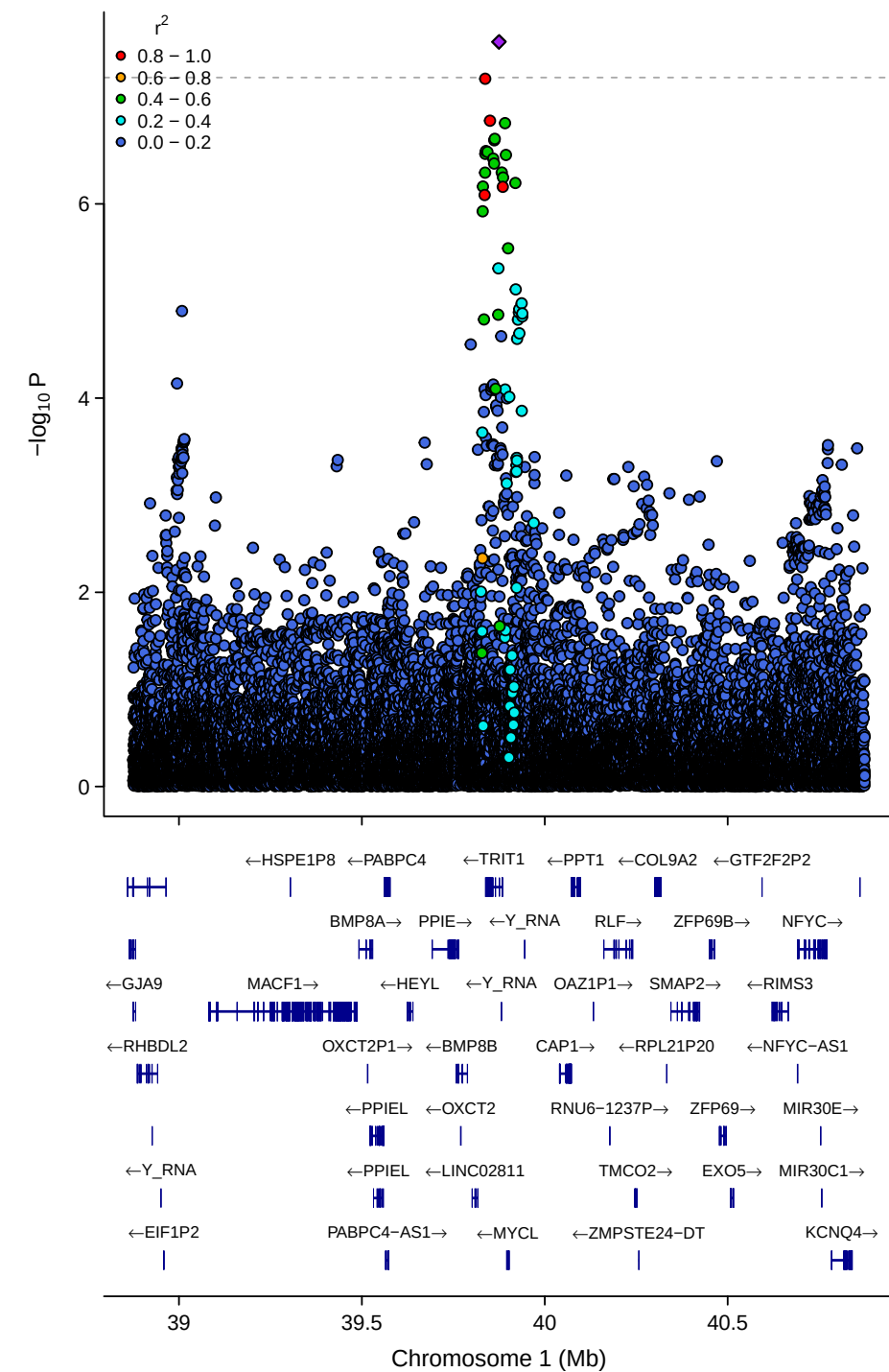


Supplementary Figure 2.2

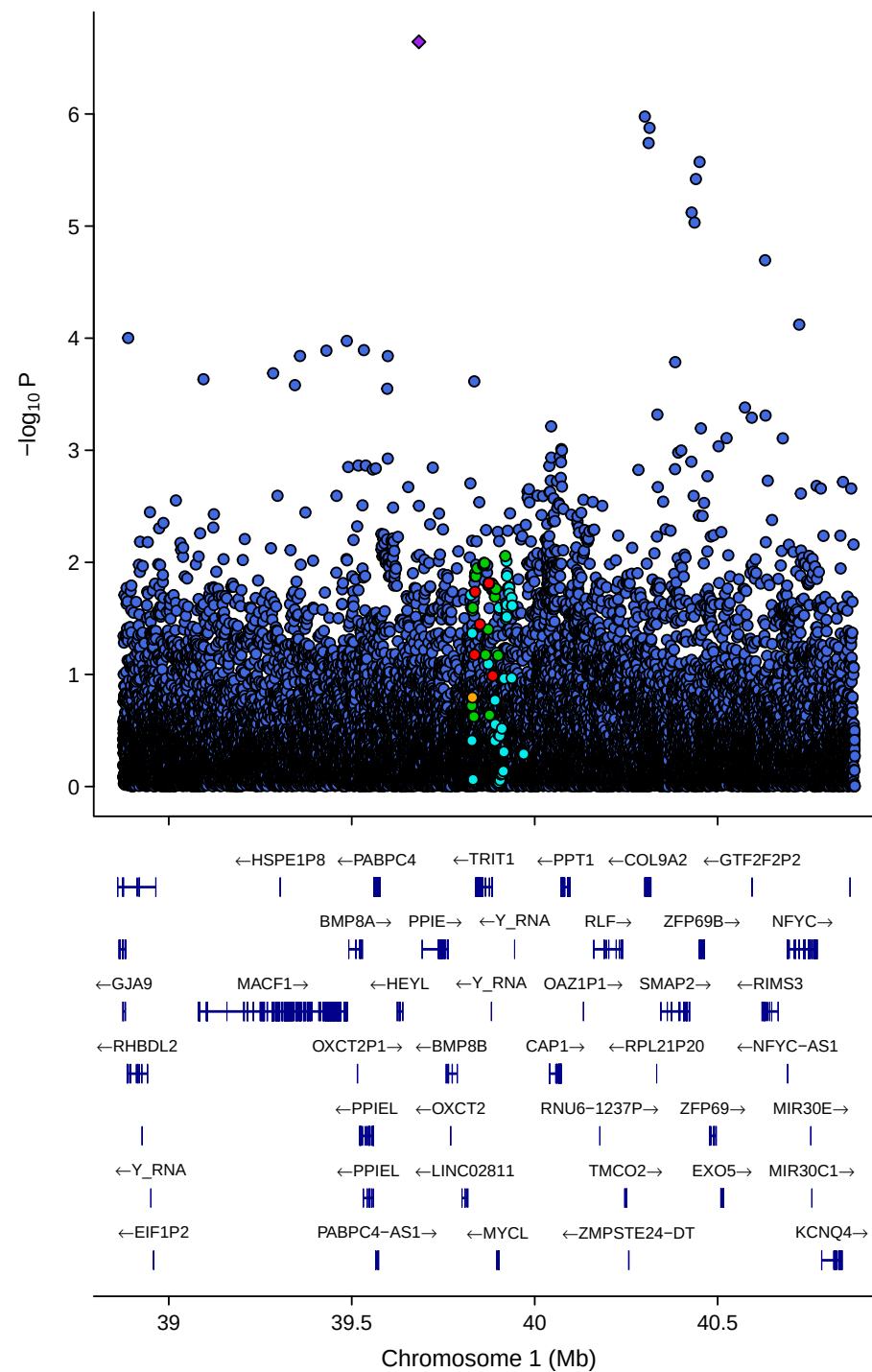


# Supplementary Figure 2.2

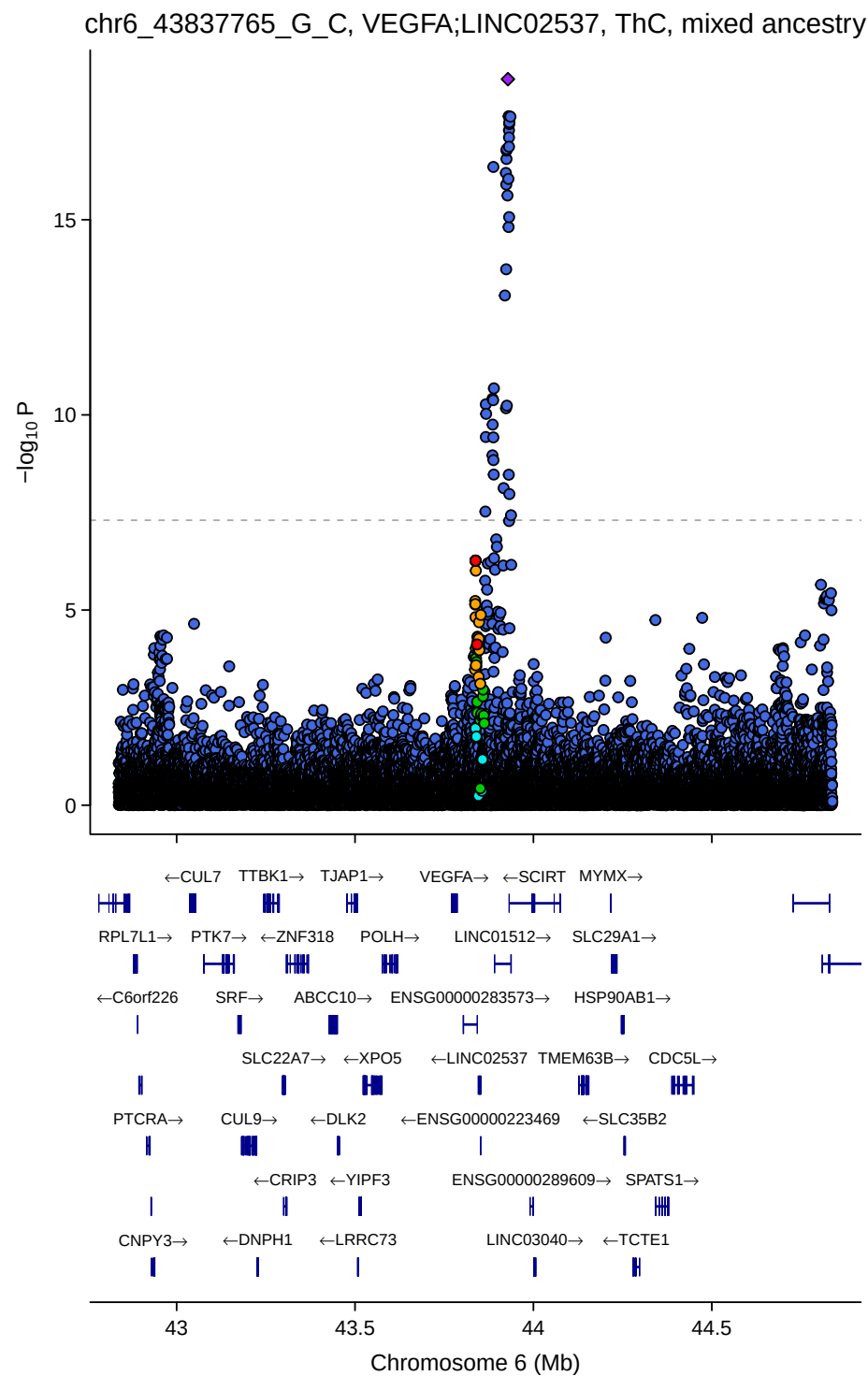
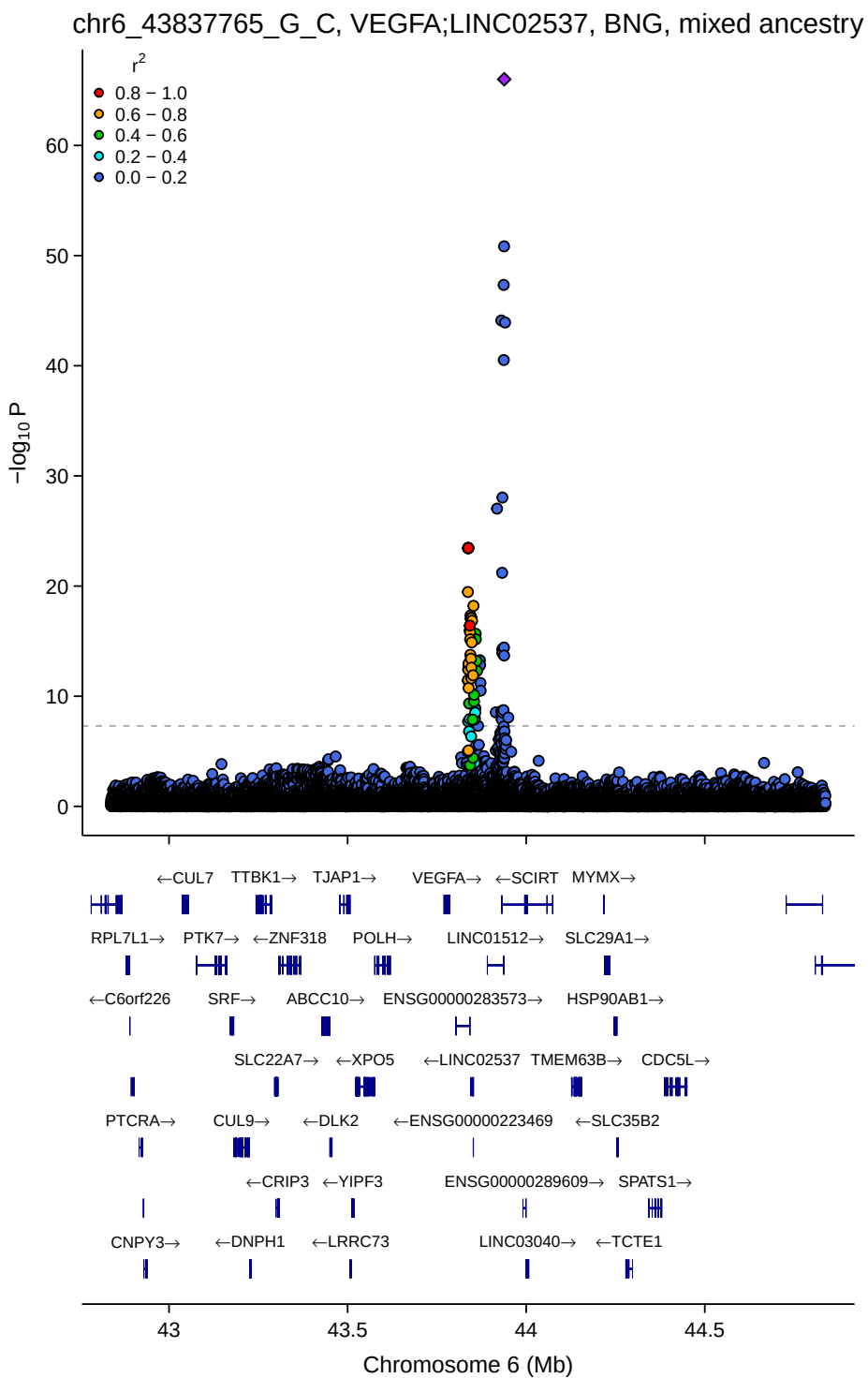
chr1\_39874915\_G\_A, TRIT1, BNG, mixed ancestry



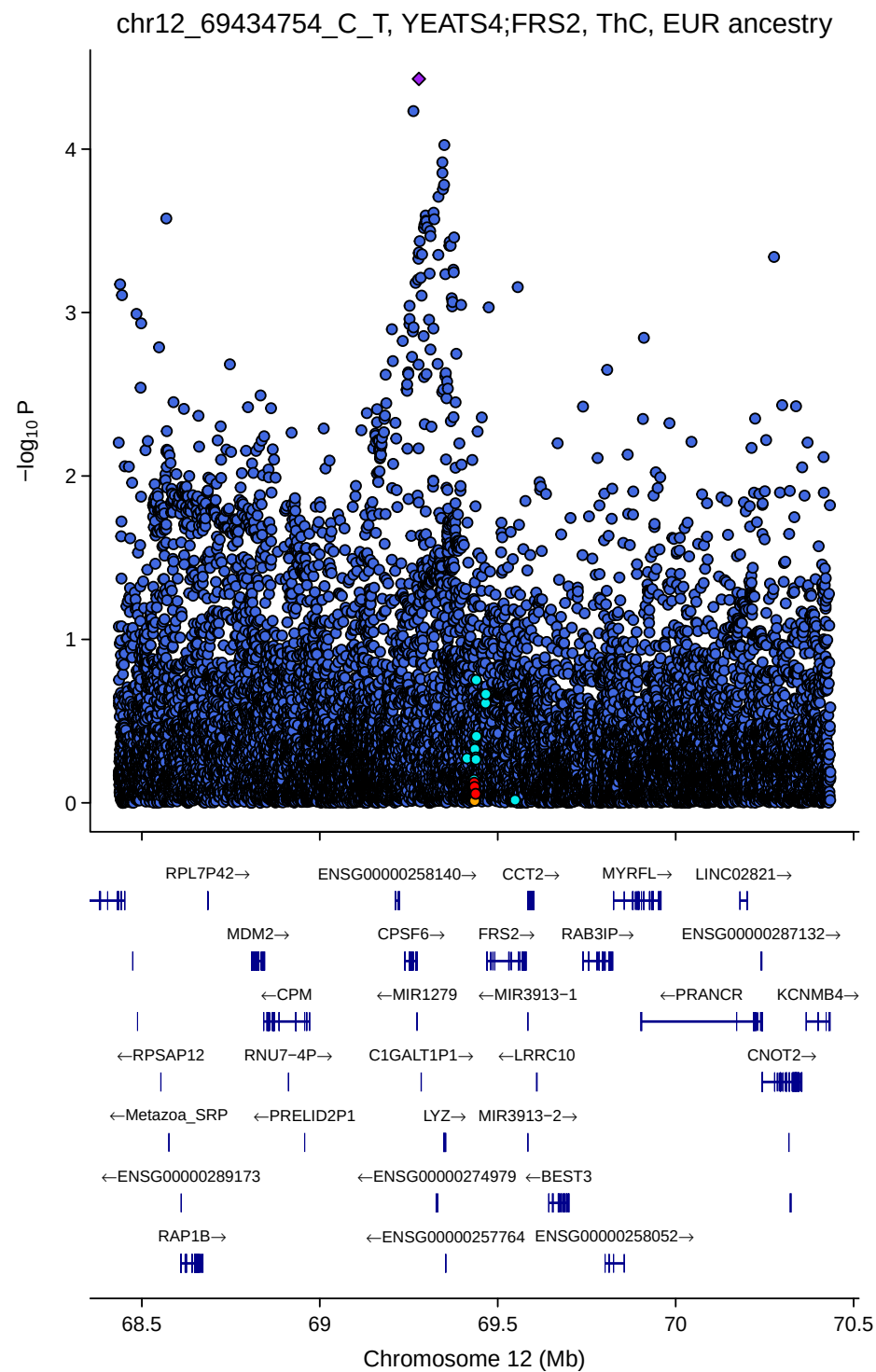
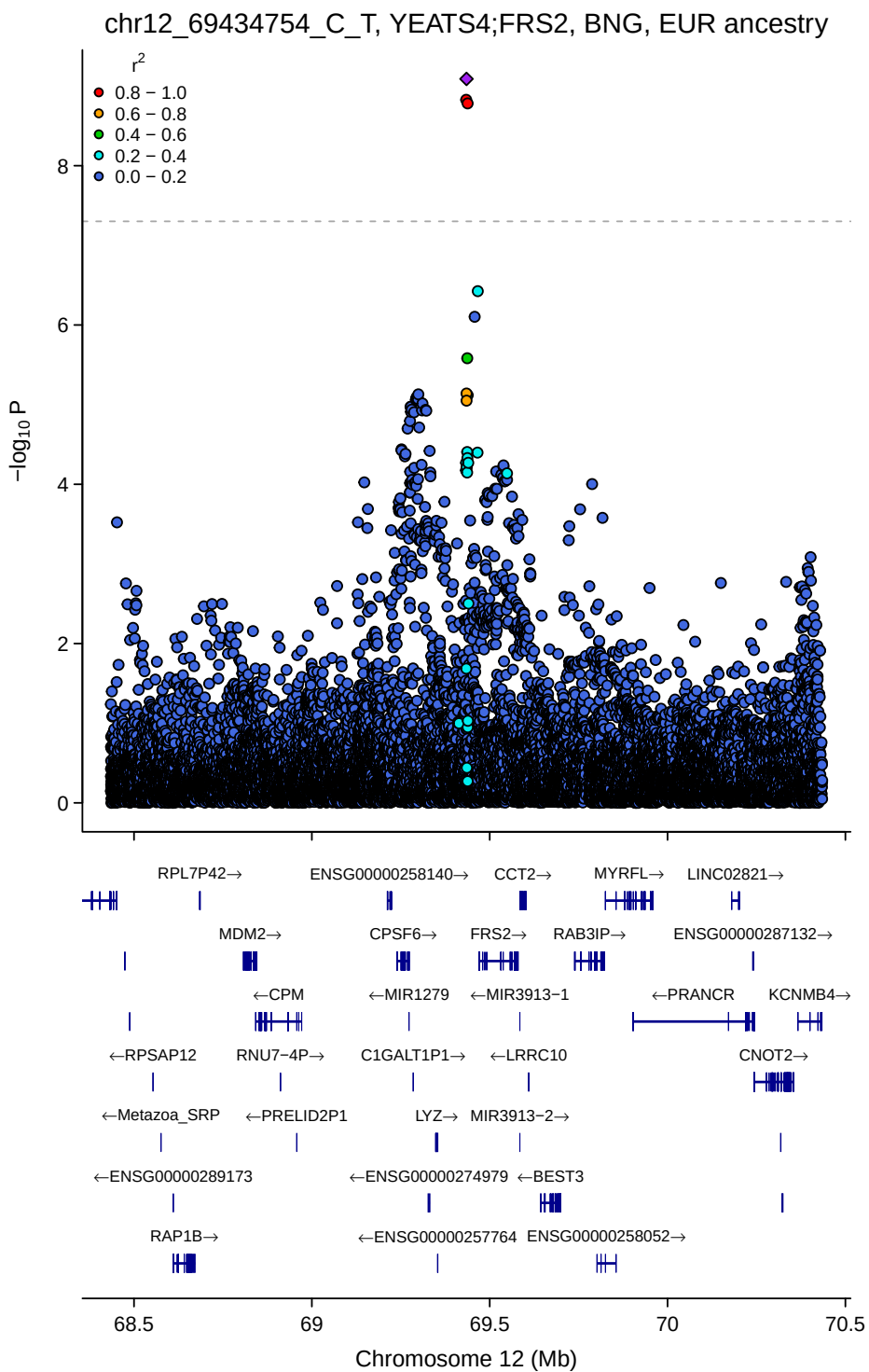
chr1\_39874915\_G\_A, TRIT1, ThC, mixed ancestry



# Supplementary Figure 2.2



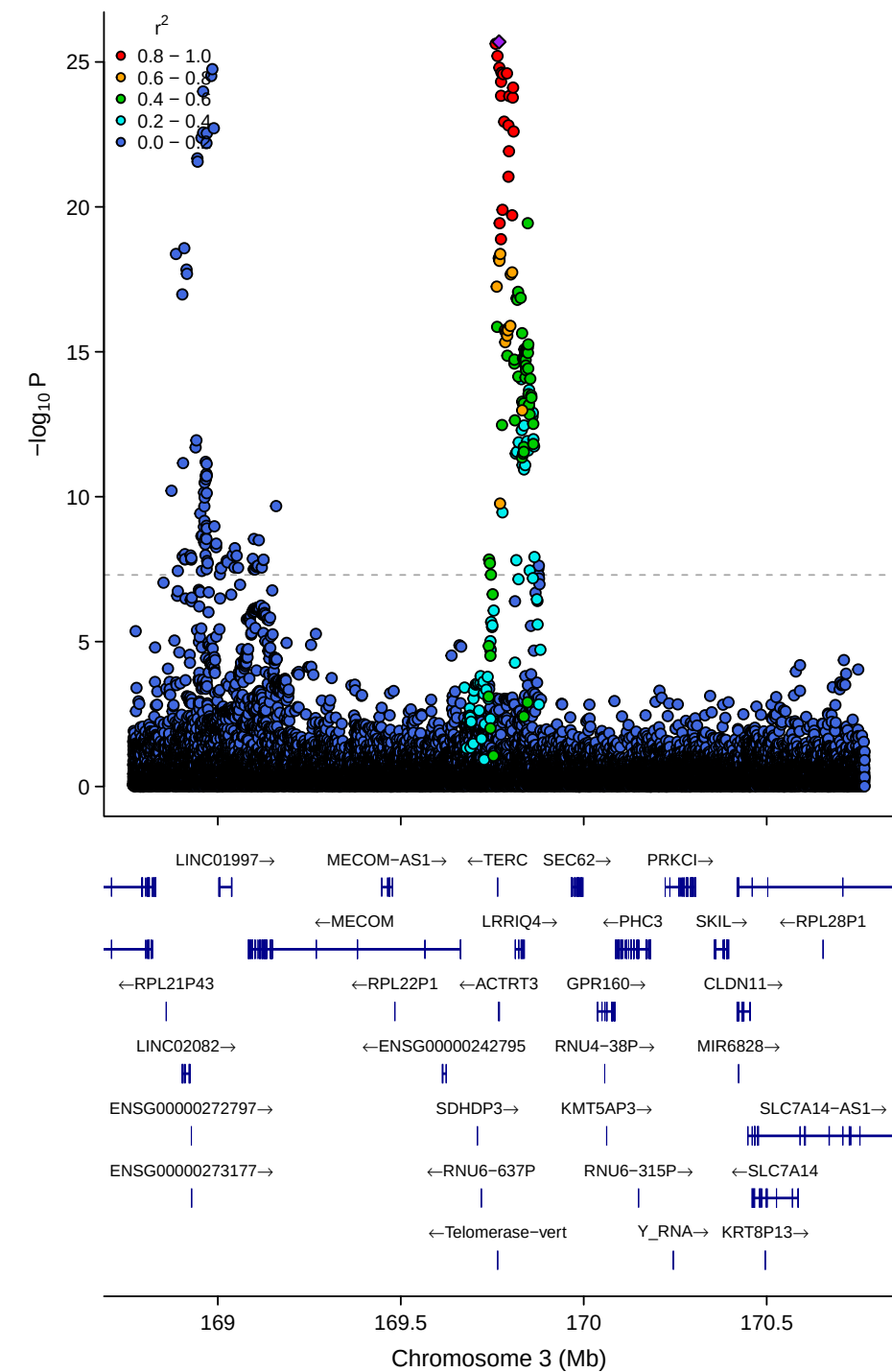
# Supplementary Figure 2.2



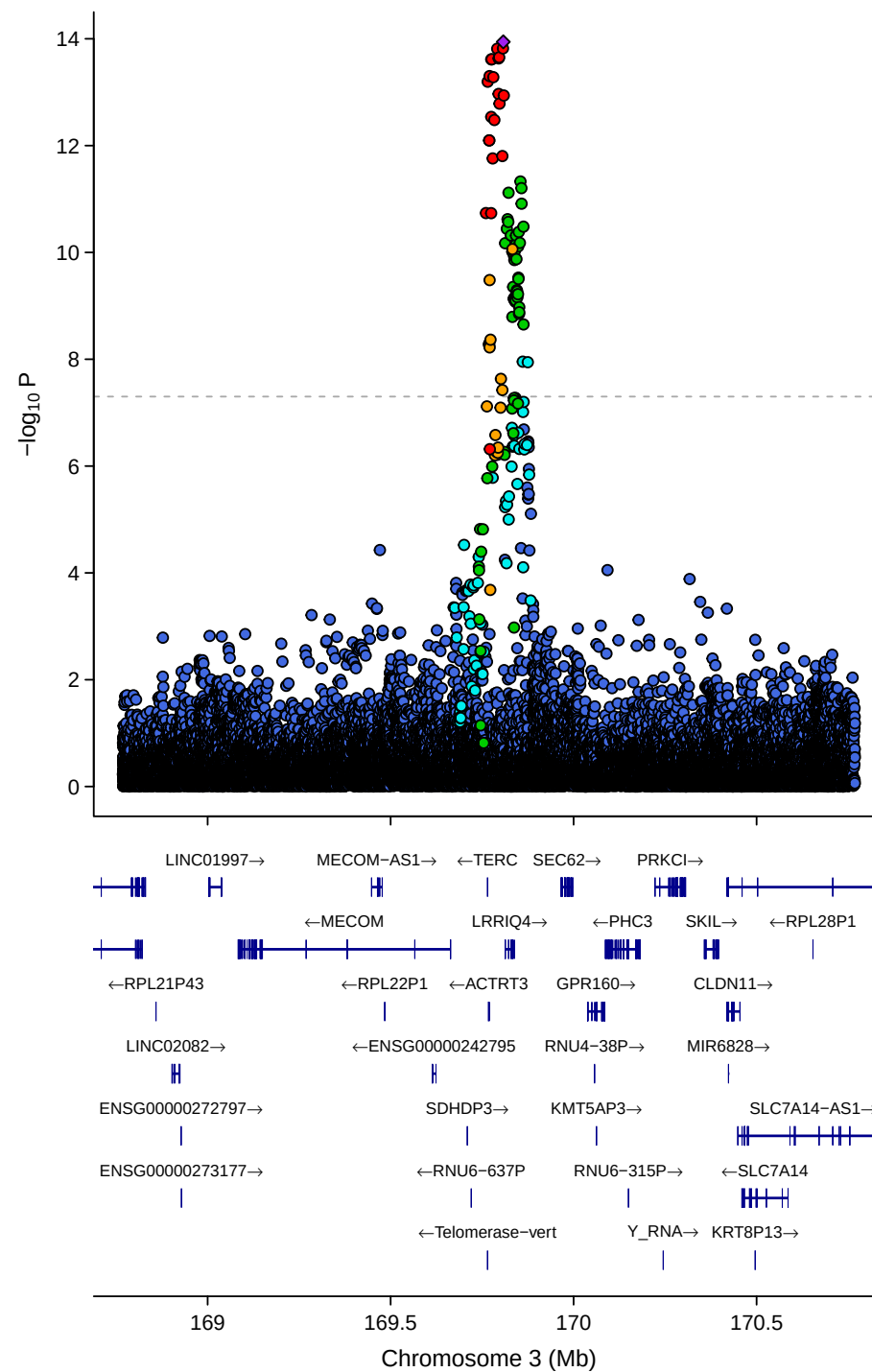
Supplementary Figure 2.3. Locus plots for loci significantly associated with both benign and malignant thyroid nodules. The left plot displays  $-\log_{10}(\text{p-values})$  for variants from thyroid cancer meta-analysis, the right plot displays  $-\log_{10}(\text{p-values})$  for variants within the same genomic region from the benign nodular goiter meta-analysis. The lead variant is shown with a purple diamond. Genome wide significance is indicated by the dashed horizontal line at  $-\log_{10}(5\text{e-}8)$ .

Supplementary Figure 2.3

chr3\_169768720\_G\_A, ACTRT3, ThC, mixed ancestry

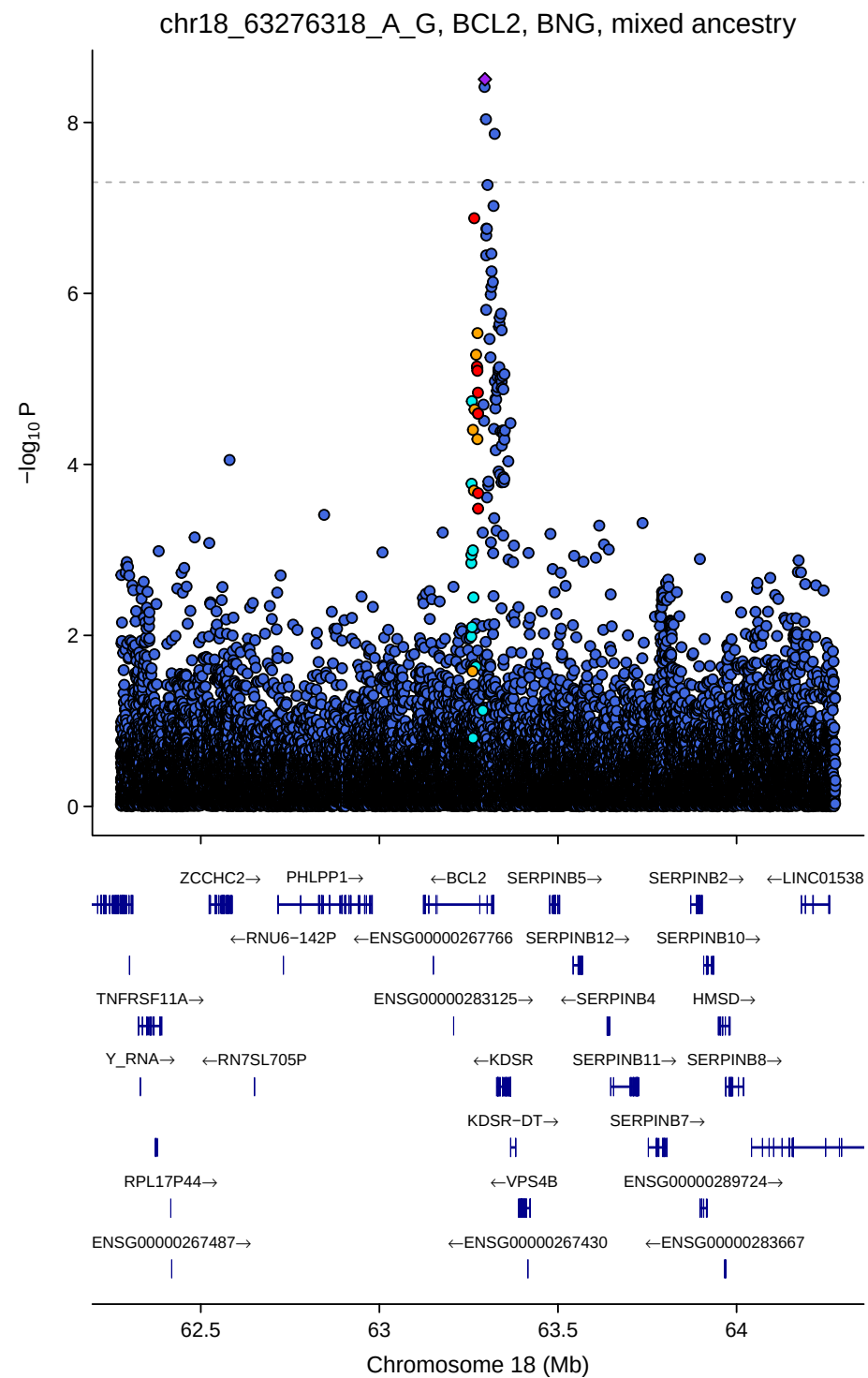
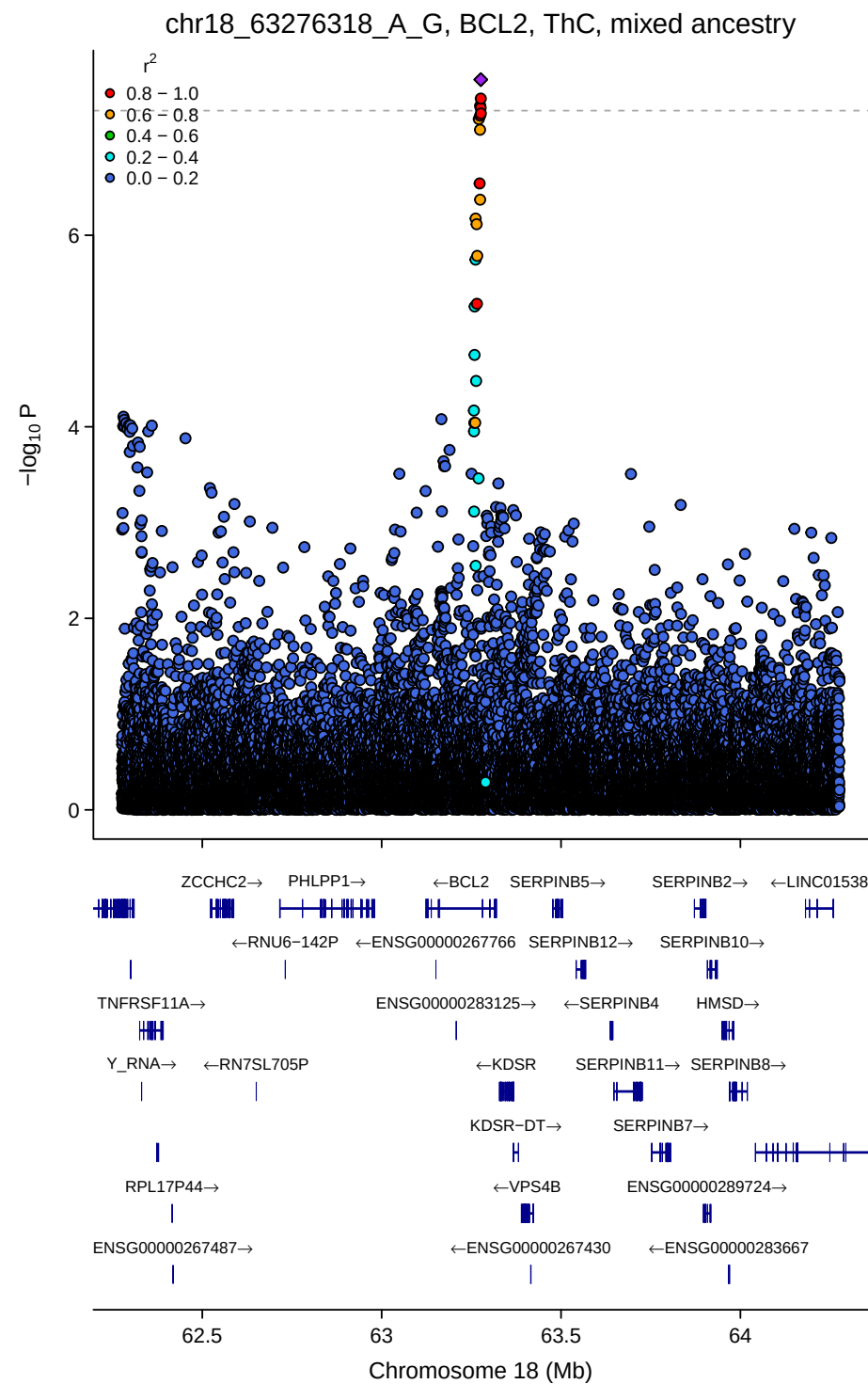


chr3\_169768720\_G\_A, ACTRT3, BNG, mixed ancestry



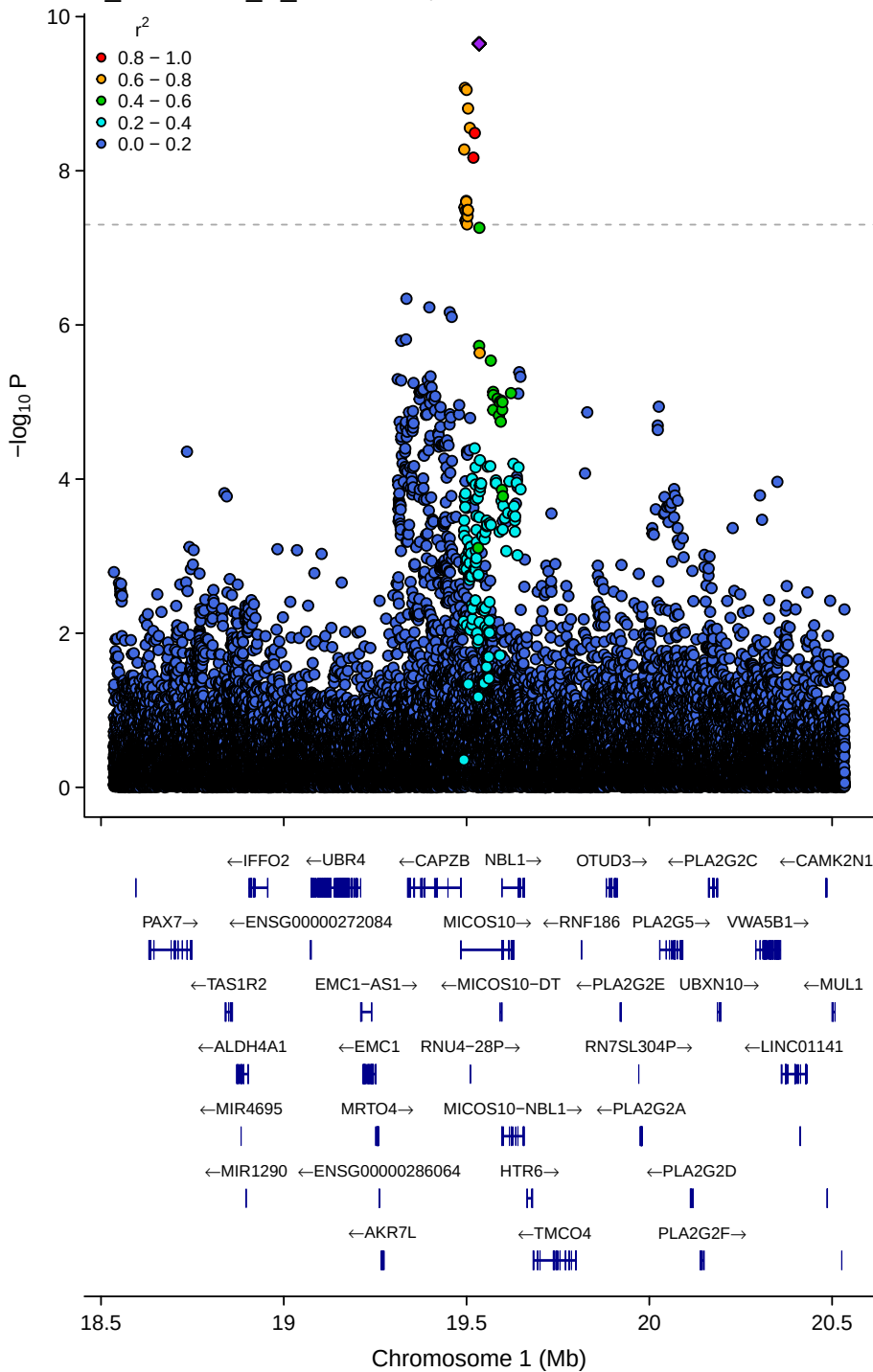


Supplementary Figure 2.3

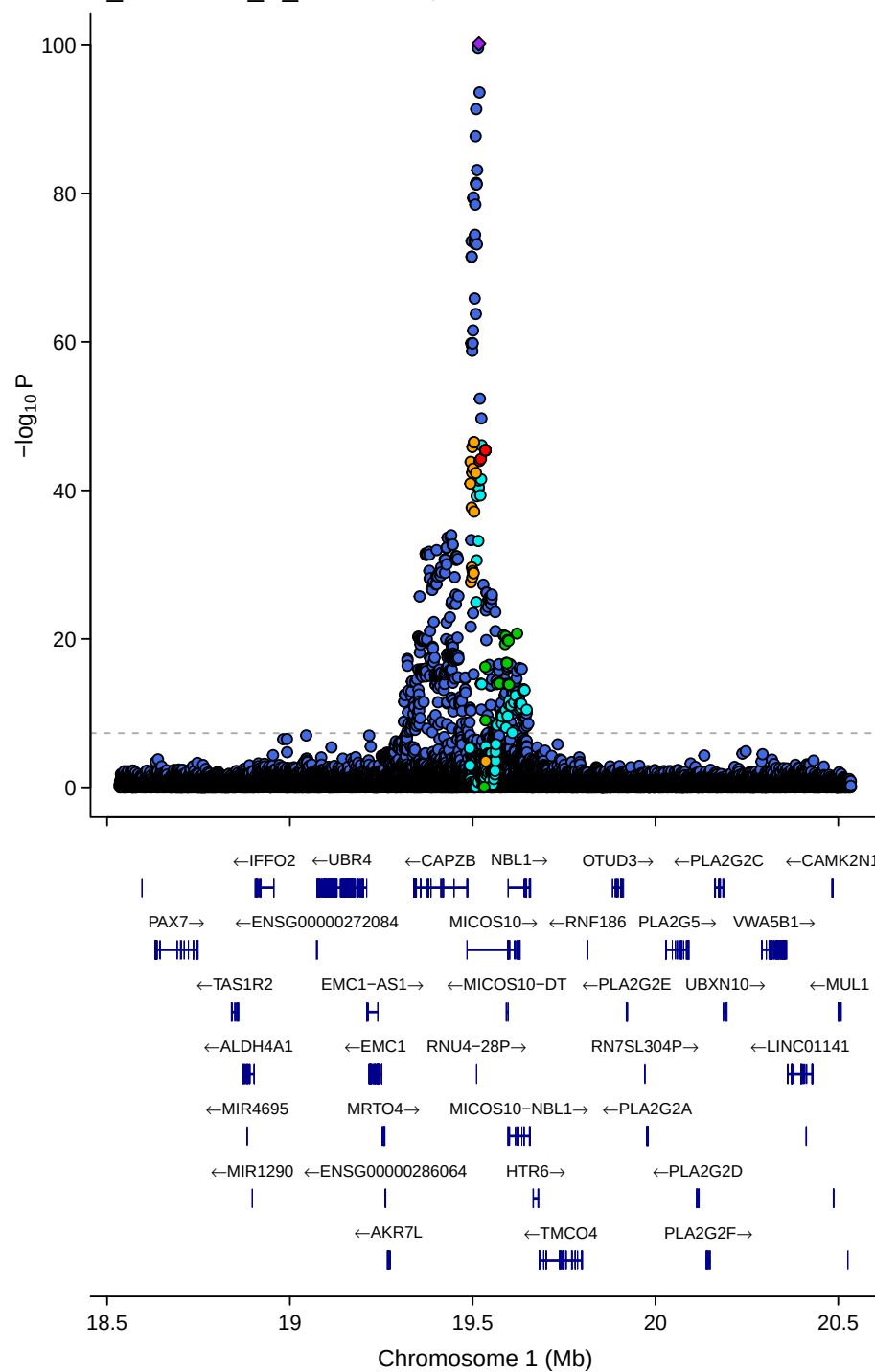


# Supplementary Figure 2.3

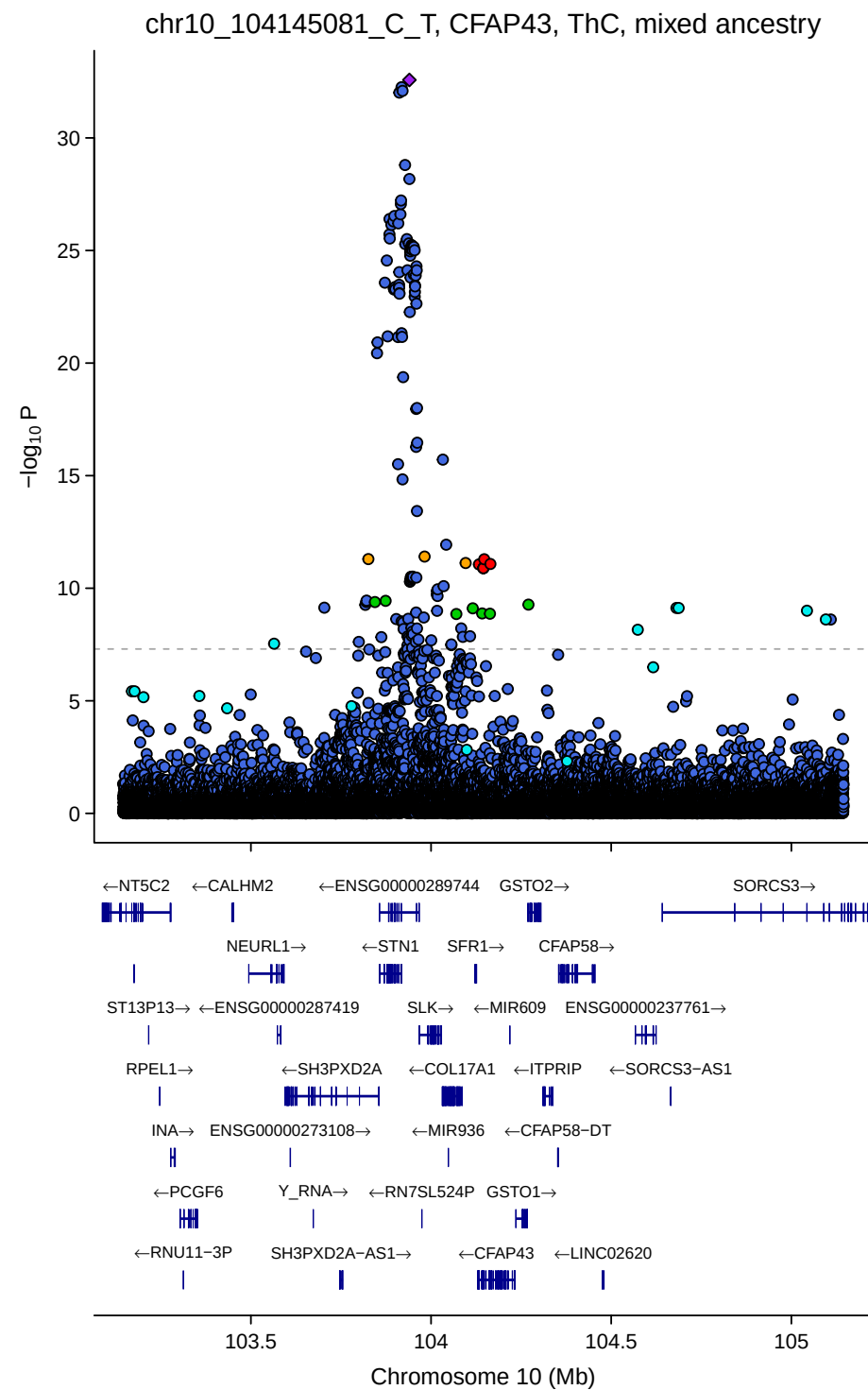
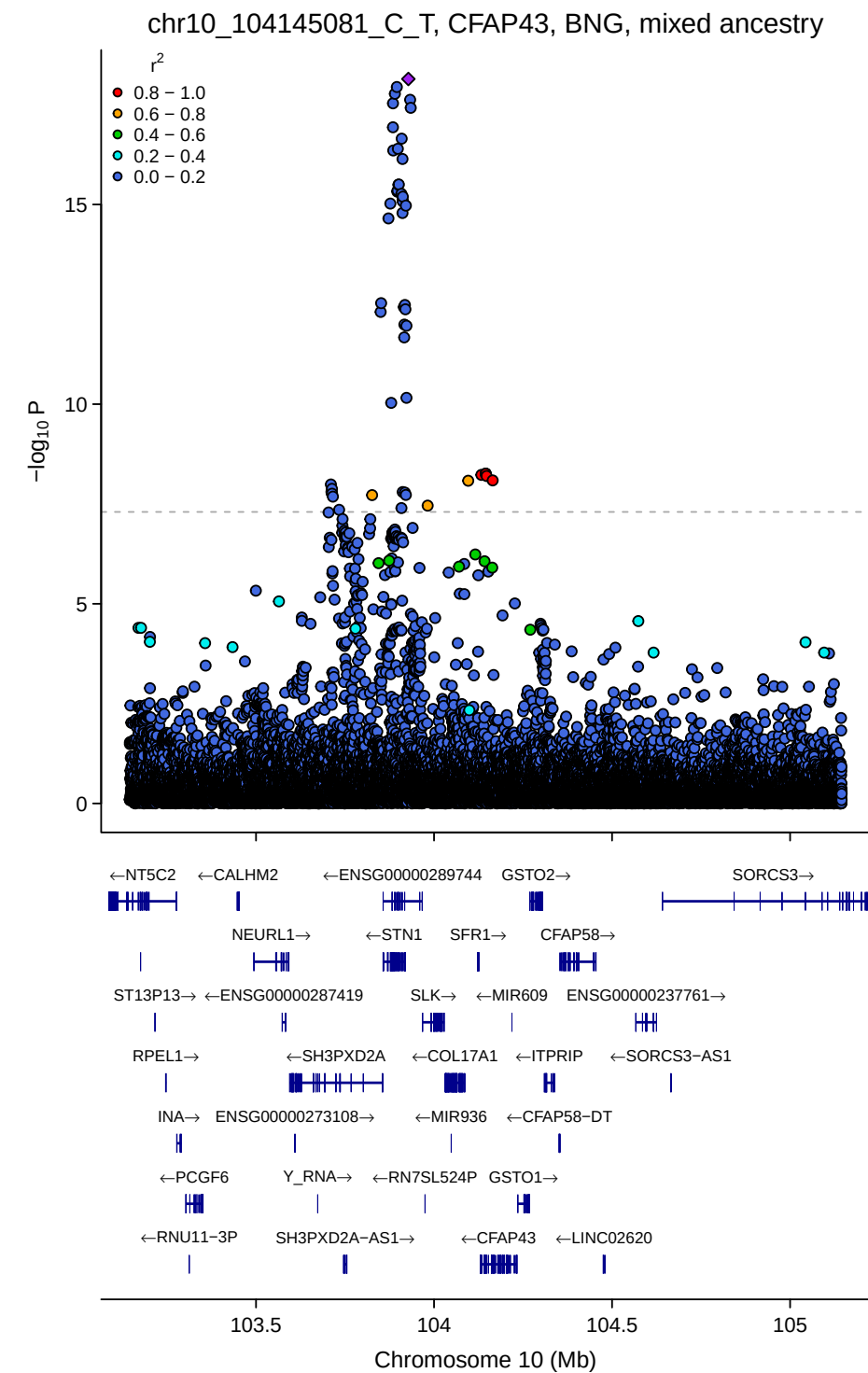
chr1\_19534612\_A\_G, CAPZB;LOC105378614, ThC, mixed ancestry



chr1\_19534612\_A\_G, CAPZB;LOC105378614, BNG, mixed ancestry

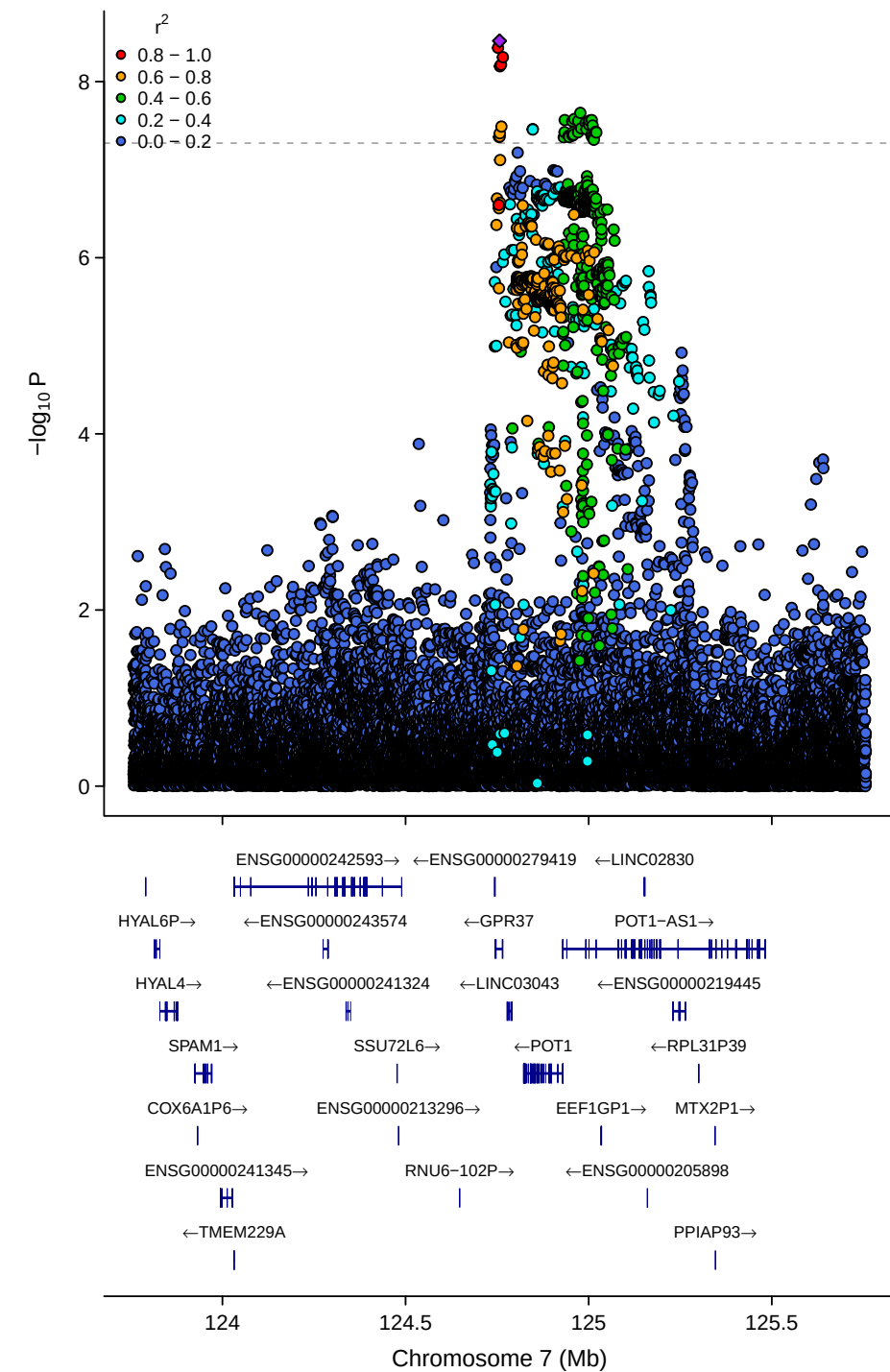


Supplementary Figure 2.3

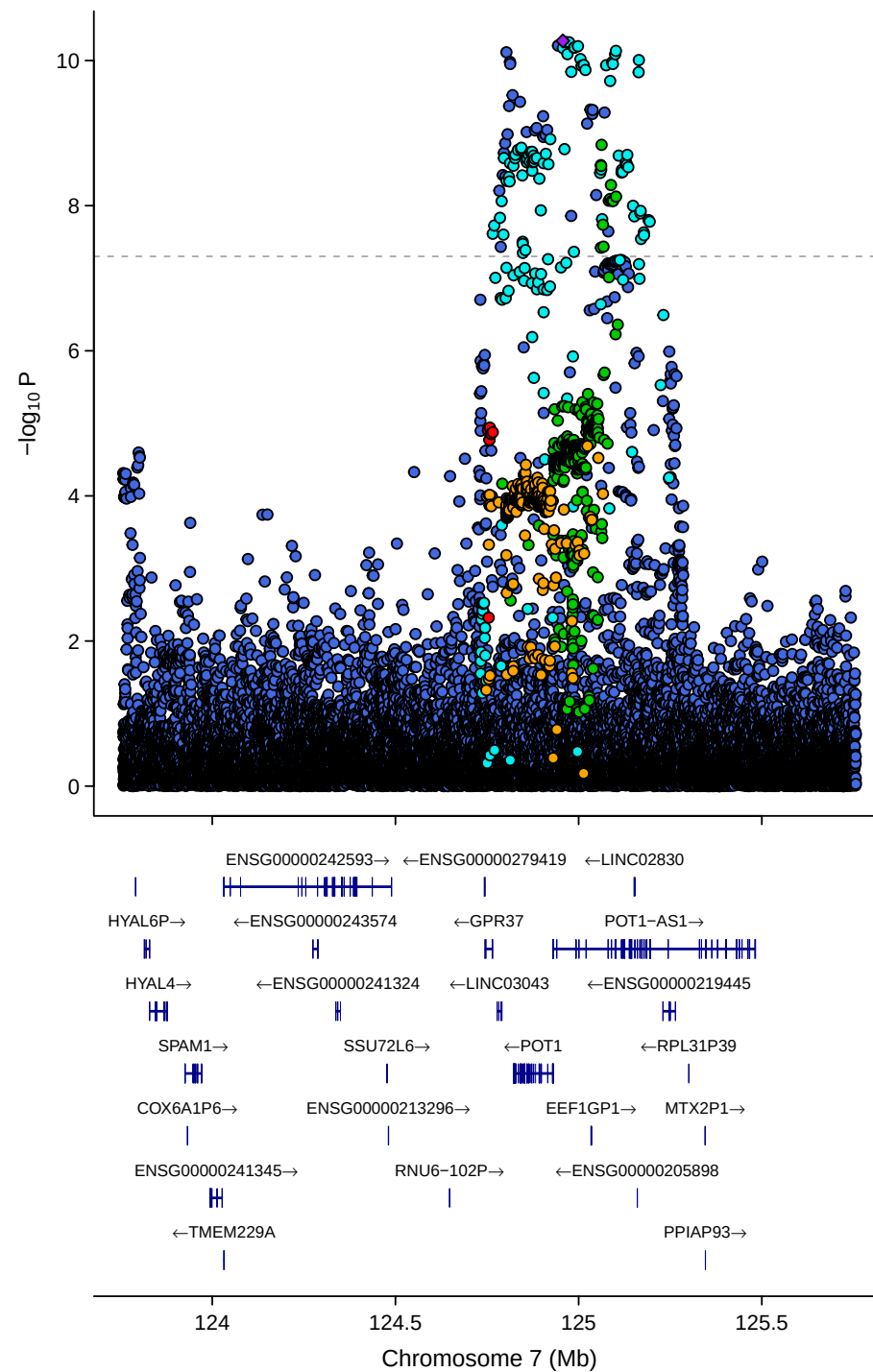


Supplementary Figure 2.3

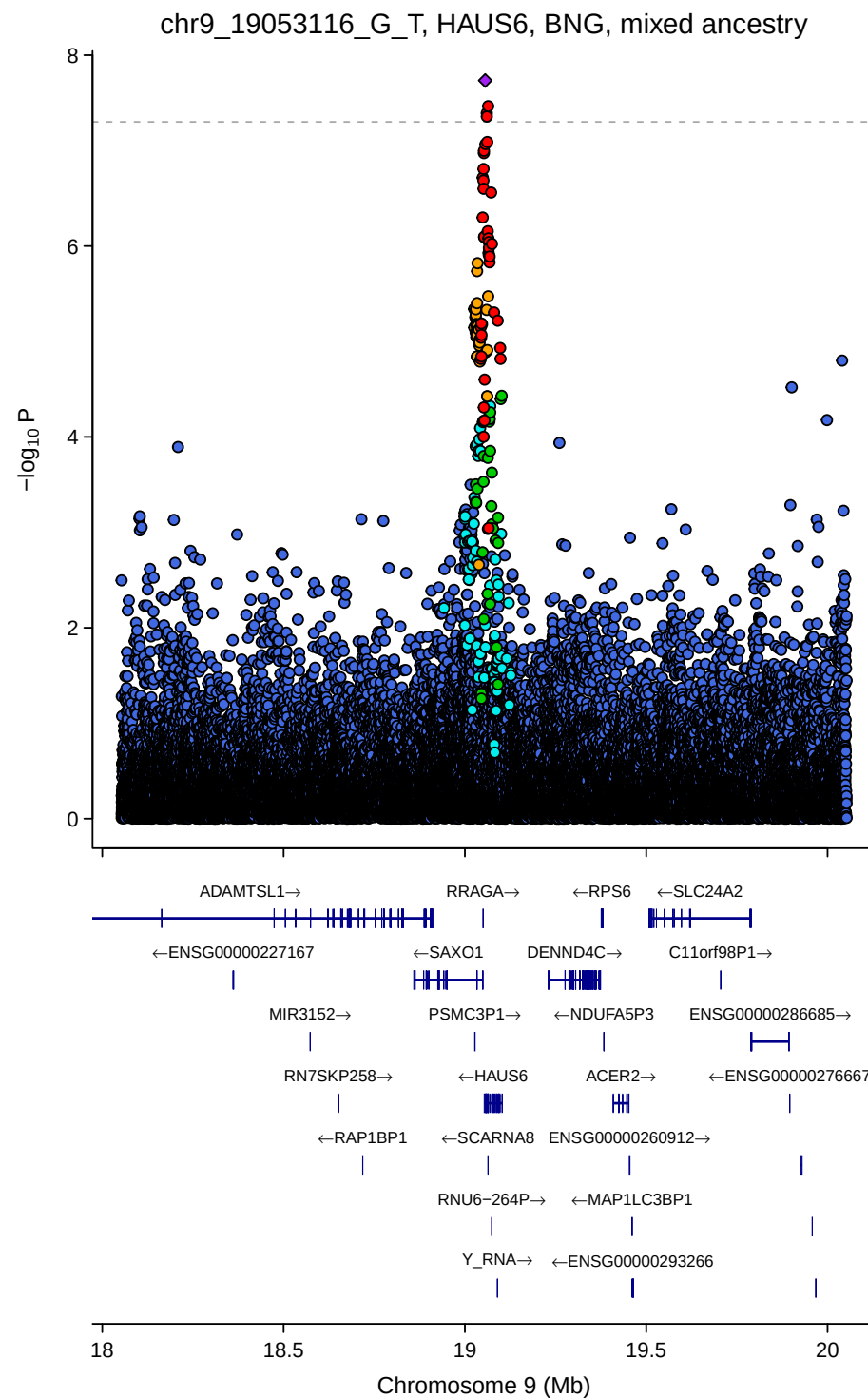
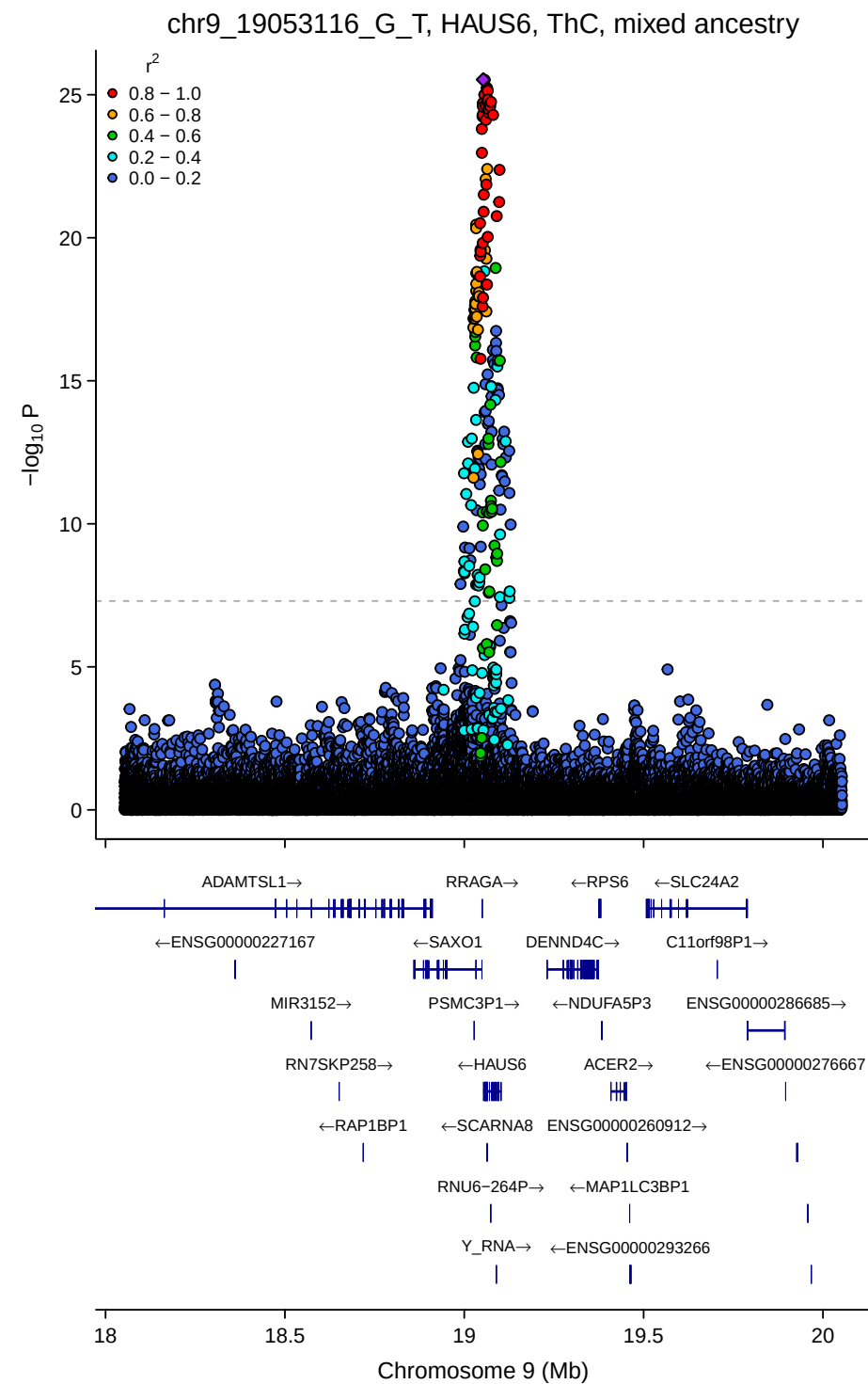
chr7\_124756591\_G\_A, GPR37, ThC, mixed ancestry



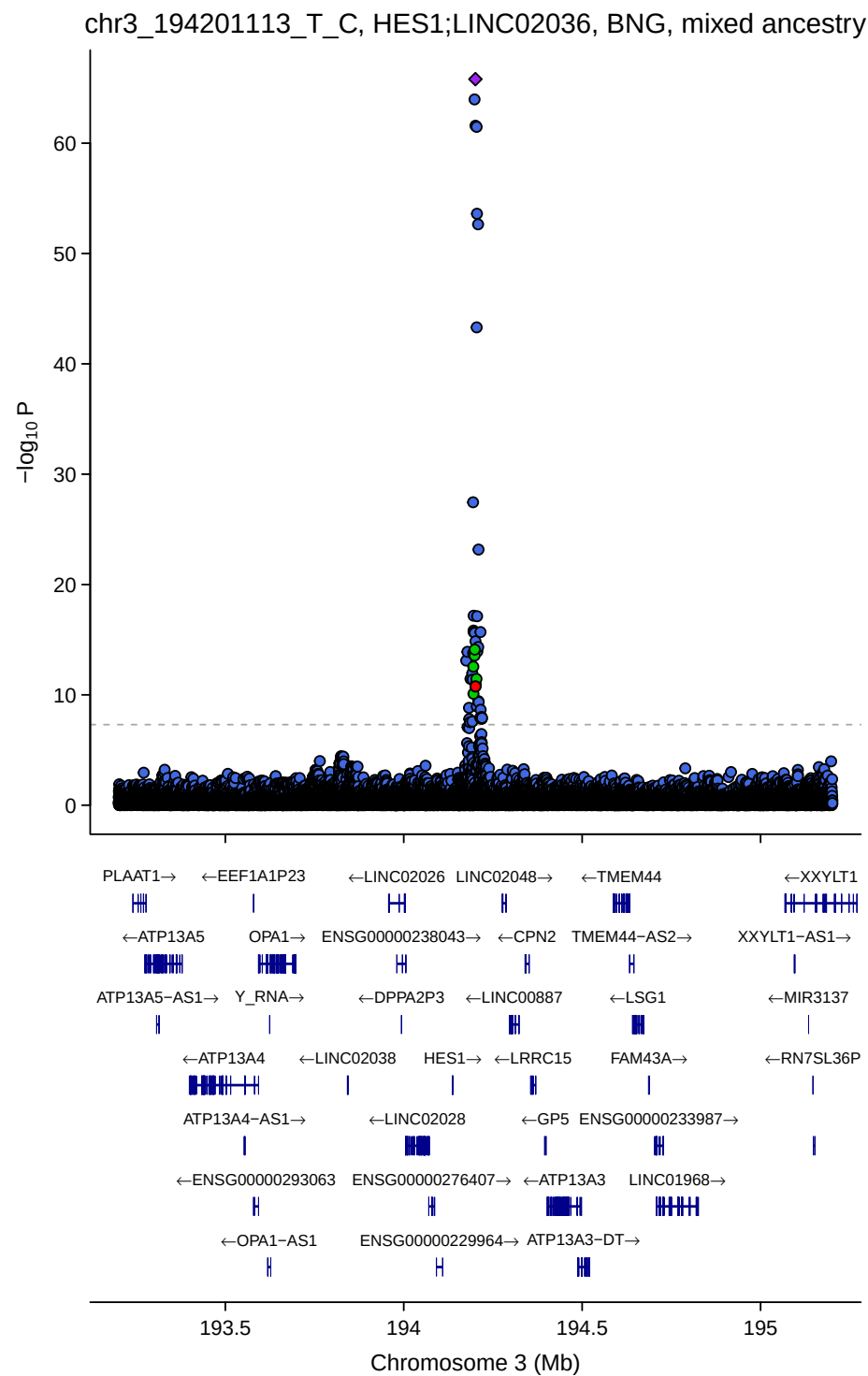
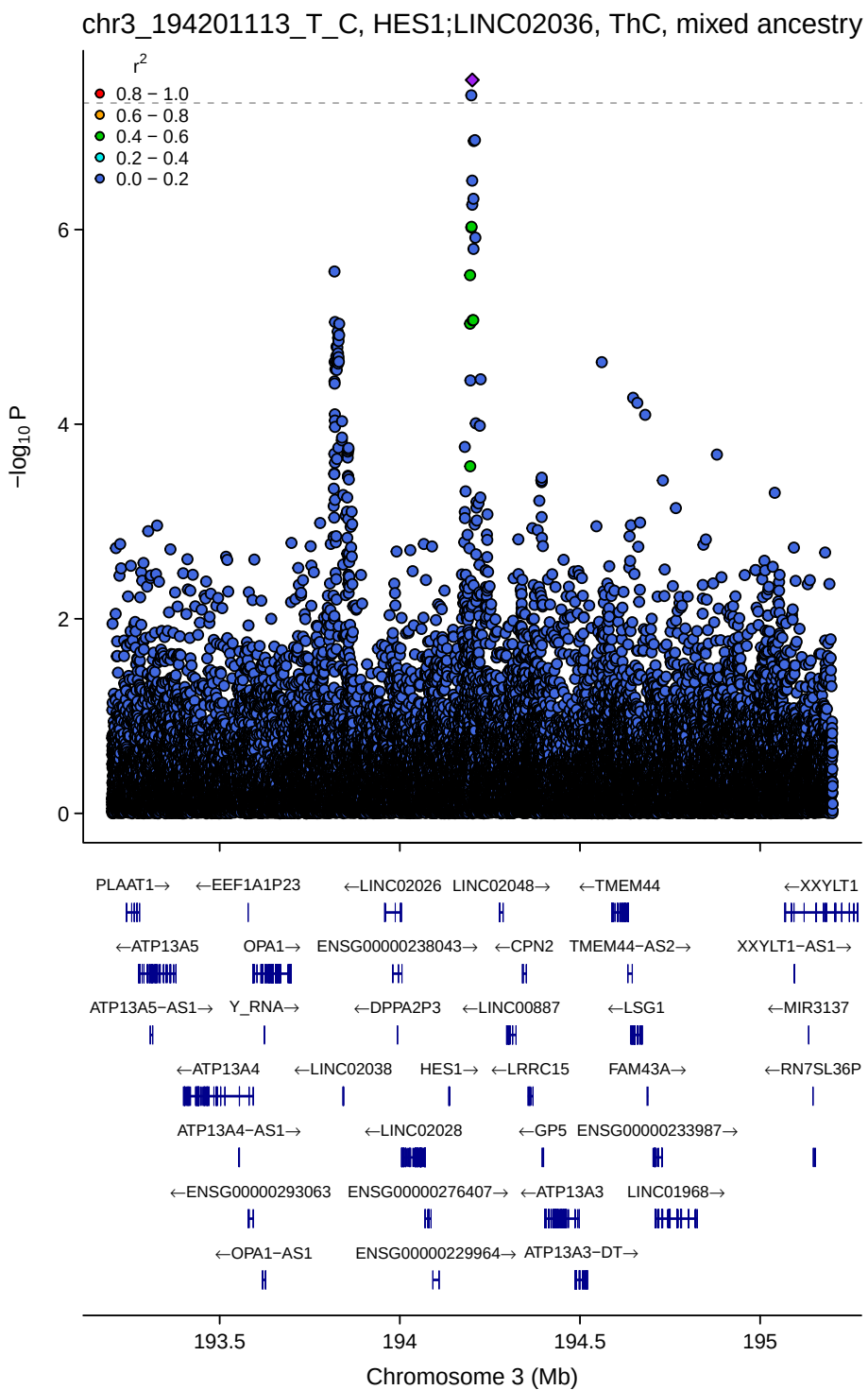
chr7\_124756591\_G\_A, GPR37, BNG, mixed ancestry



Supplementary Figure 2.3



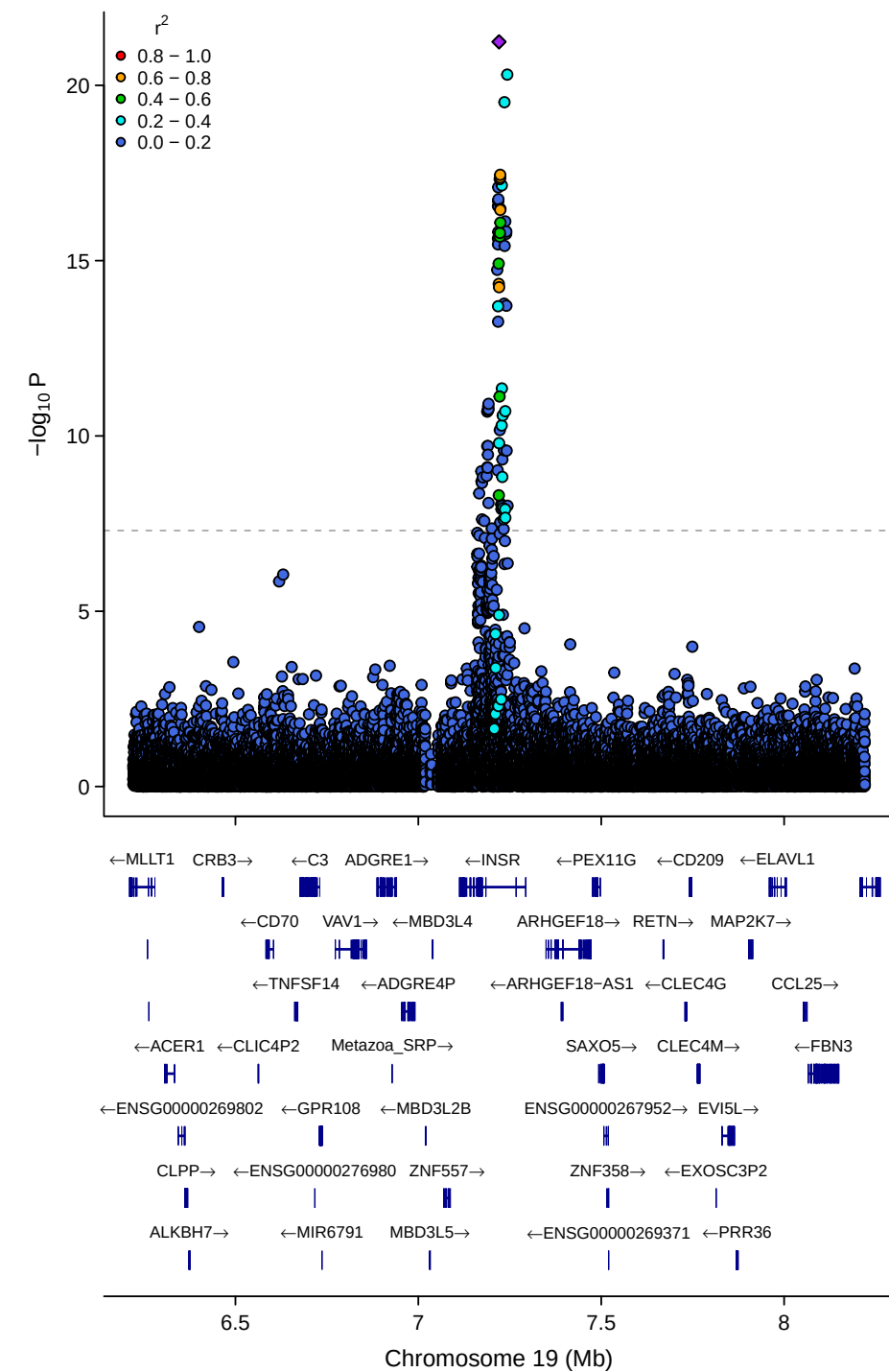
# Supplementary Figure 2.3



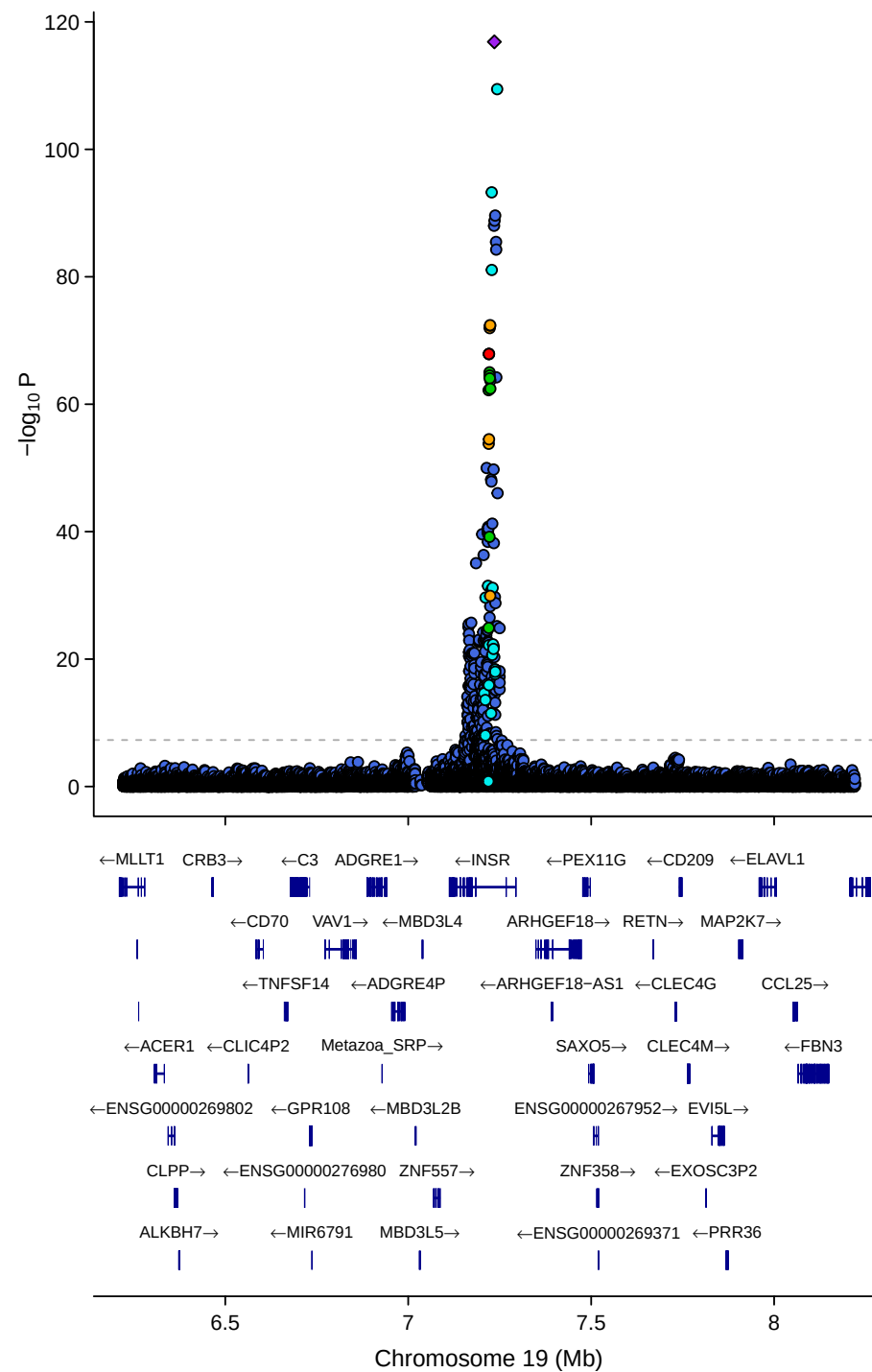


Supplementary Figure 2.3

chr19\_7220585\_G\_T, INSR, ThC, mixed ancestry

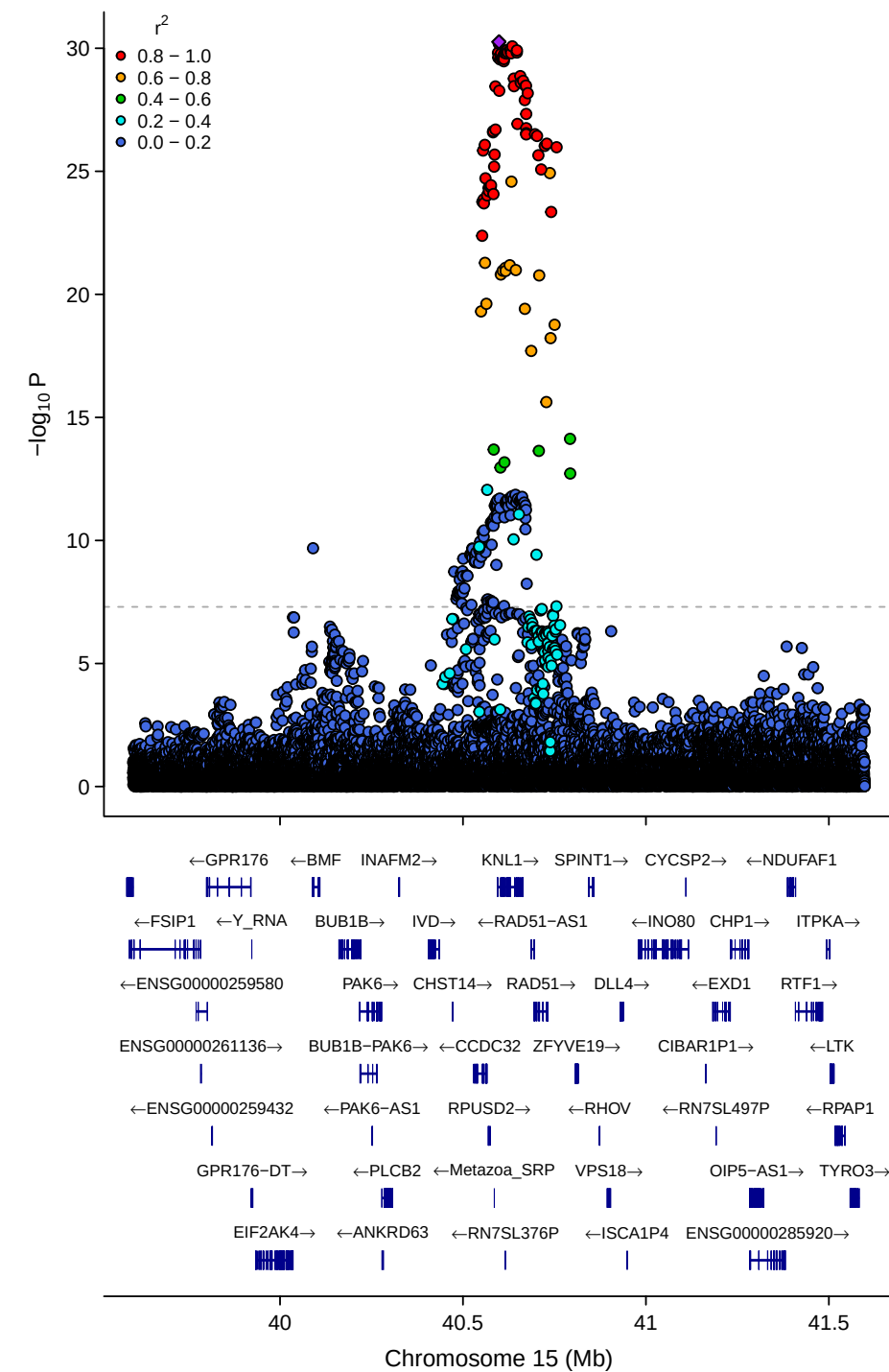


chr19\_7220585\_G\_T, INSR, BNG, mixed ancestry

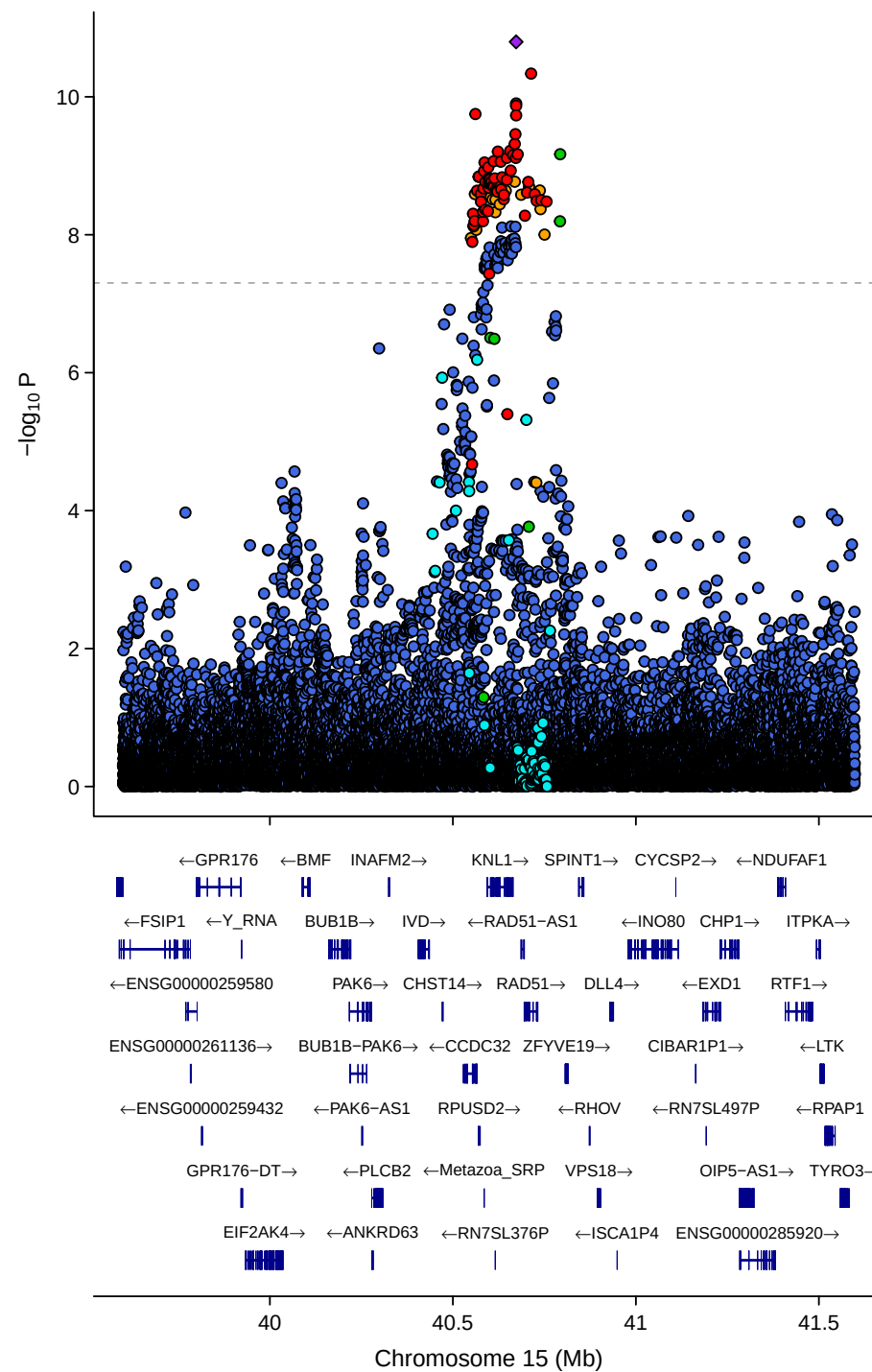


Supplementary Figure 2.3

chr15\_40598312\_G\_T, KNL1, ThC, mixed ancestry

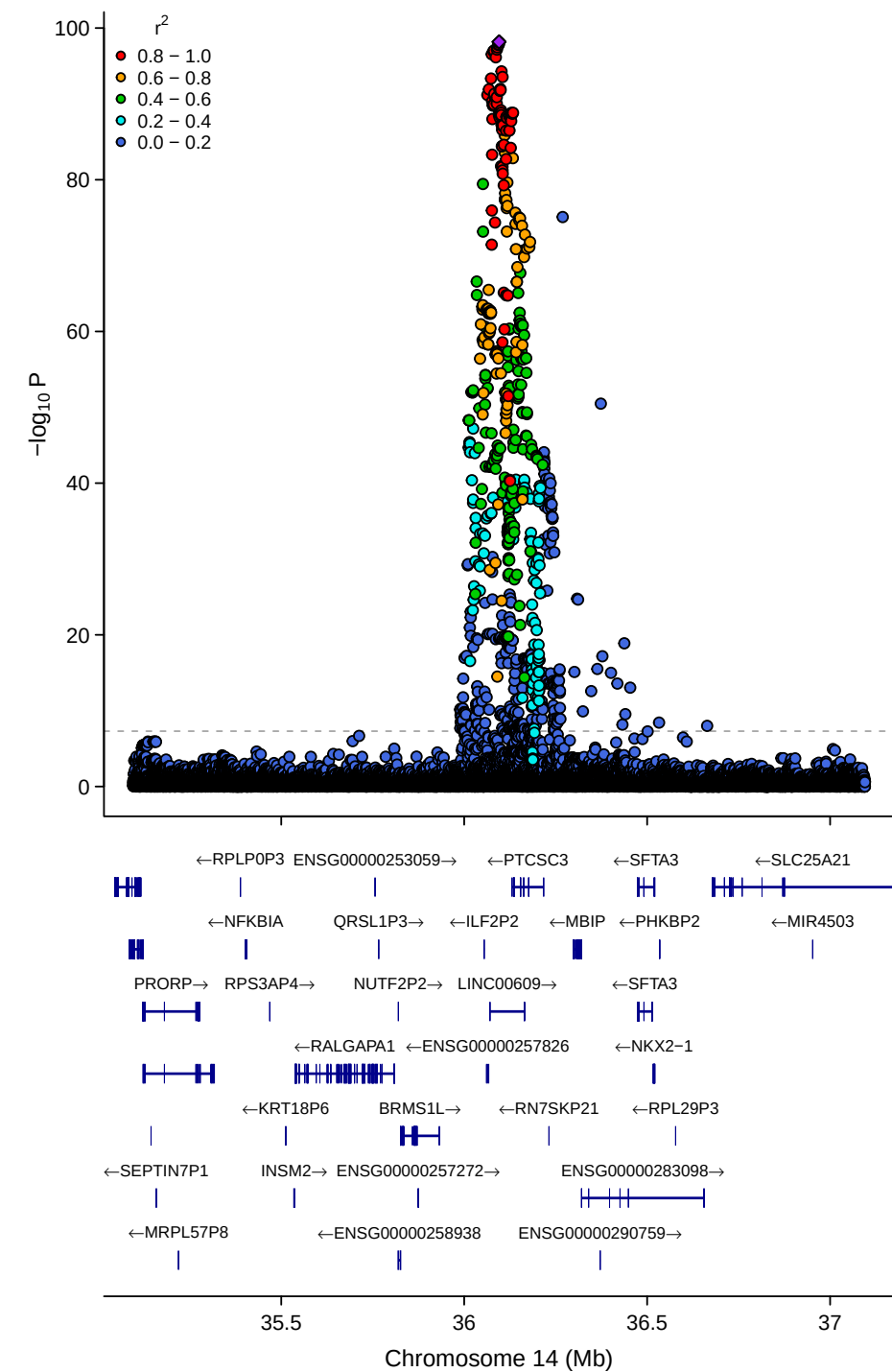


chr15\_40598312\_G\_T, KNL1, BNG, mixed ancestry

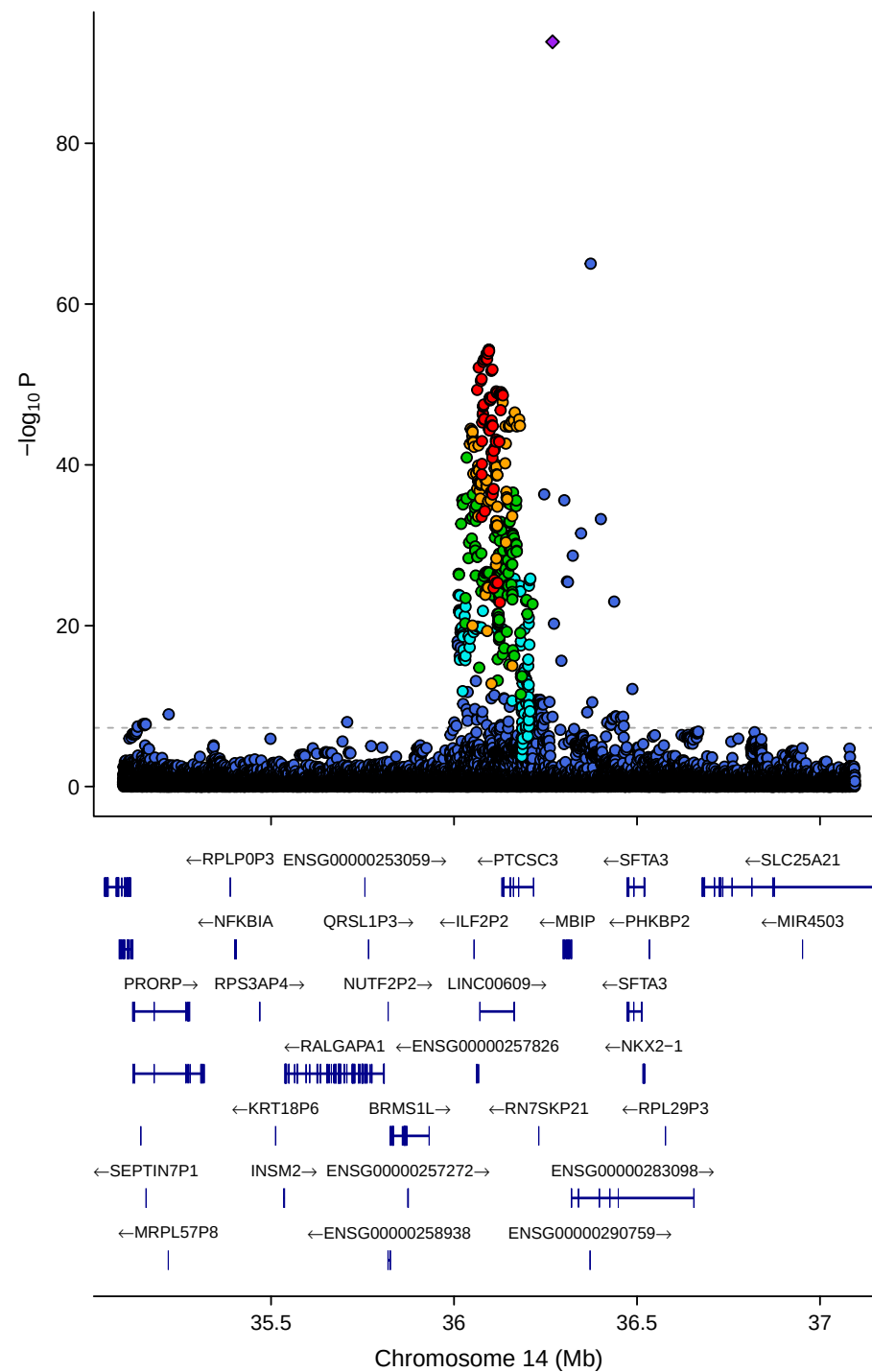


# Supplementary Figure 2.3

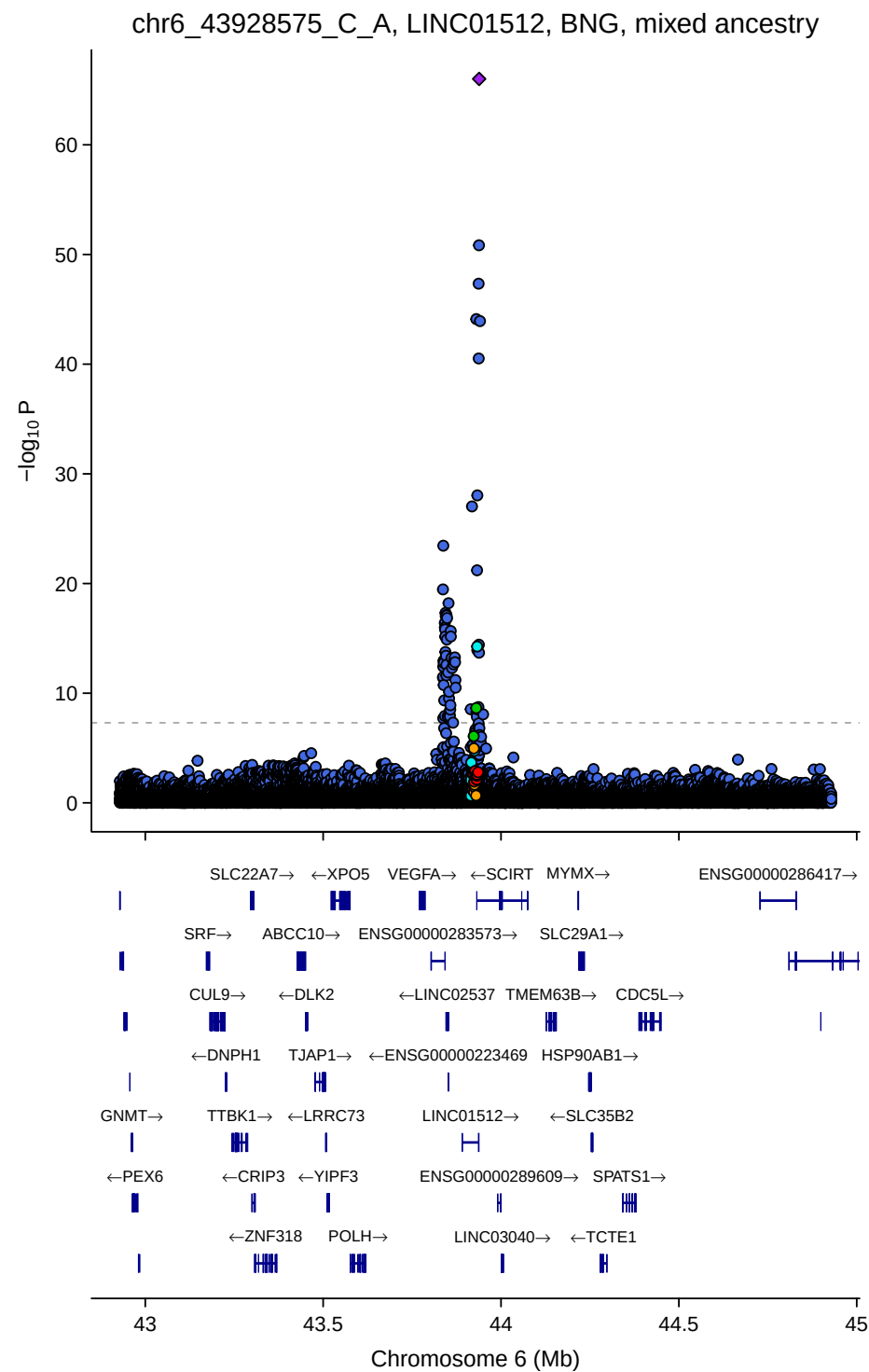
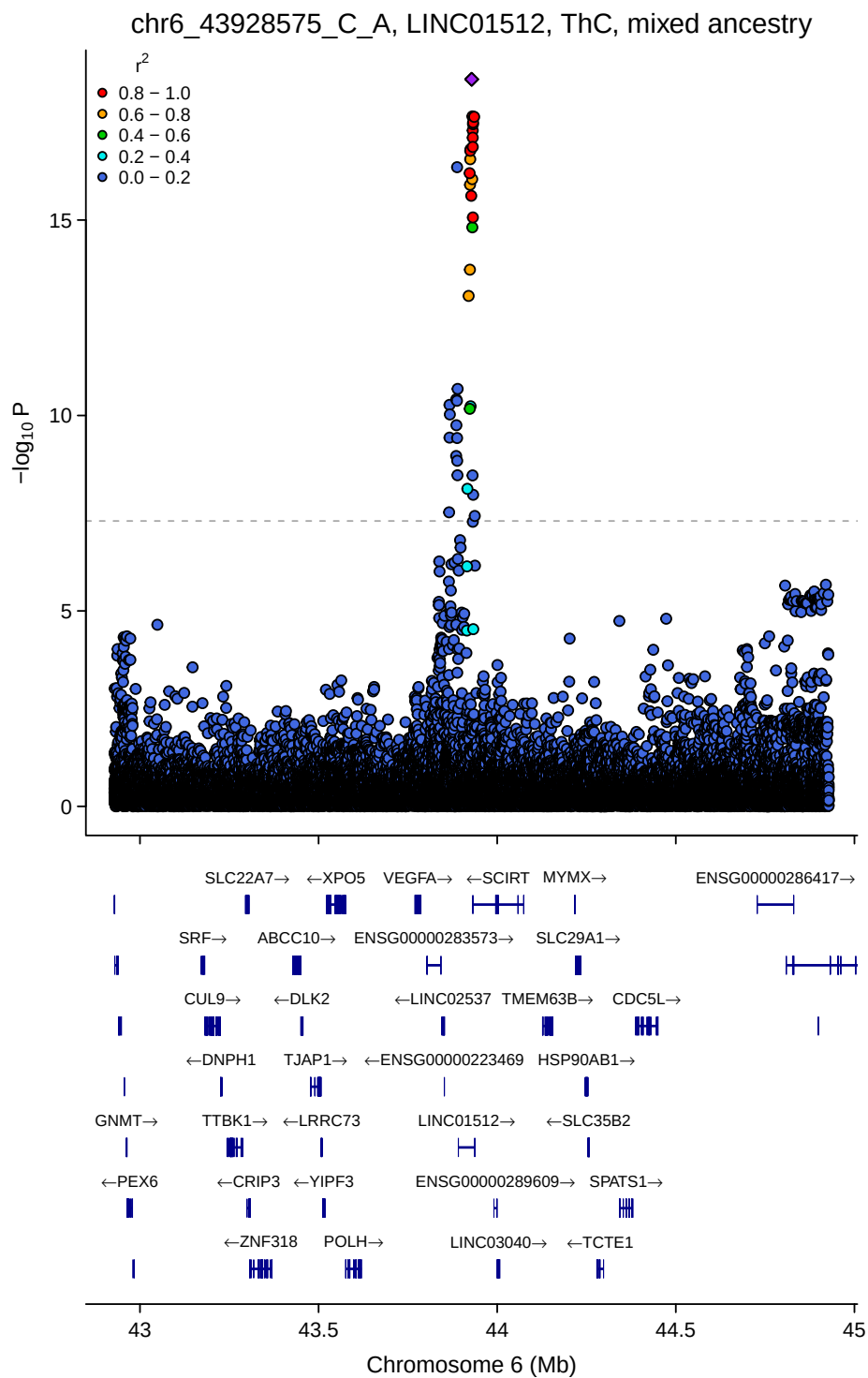
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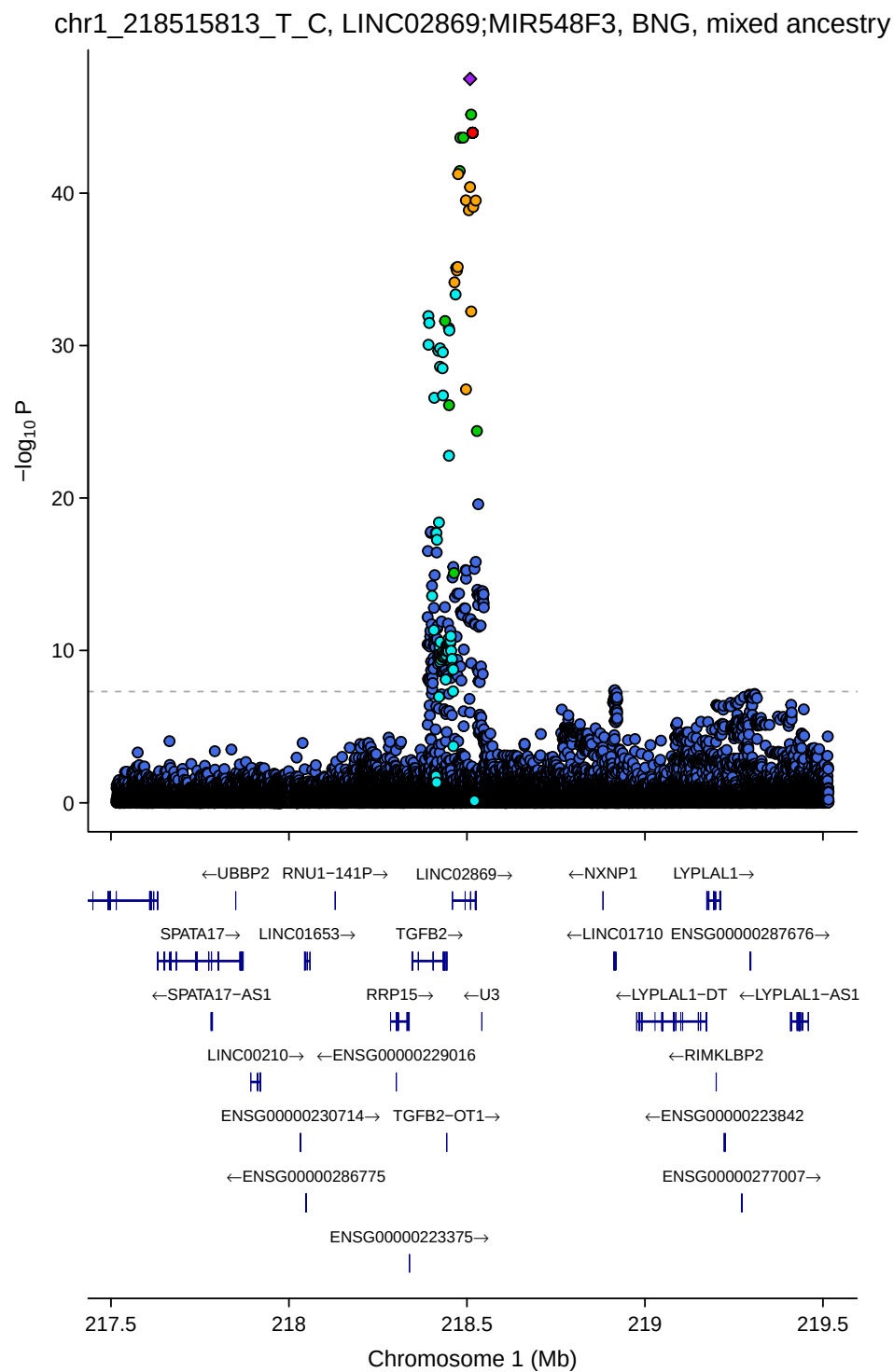
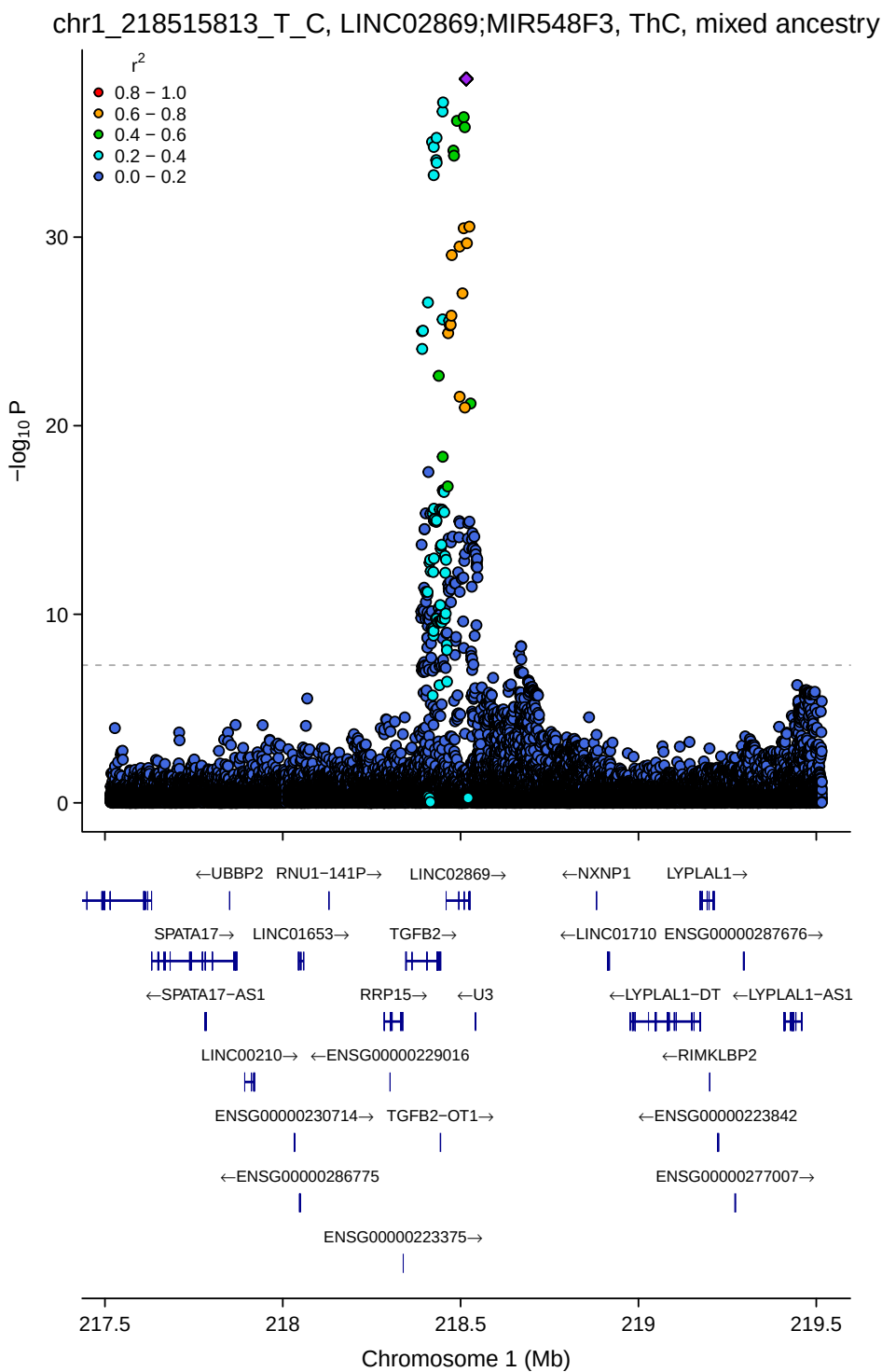
chr14\_36095227\_T\_G, LINC00609, BNG, mixed ancestry



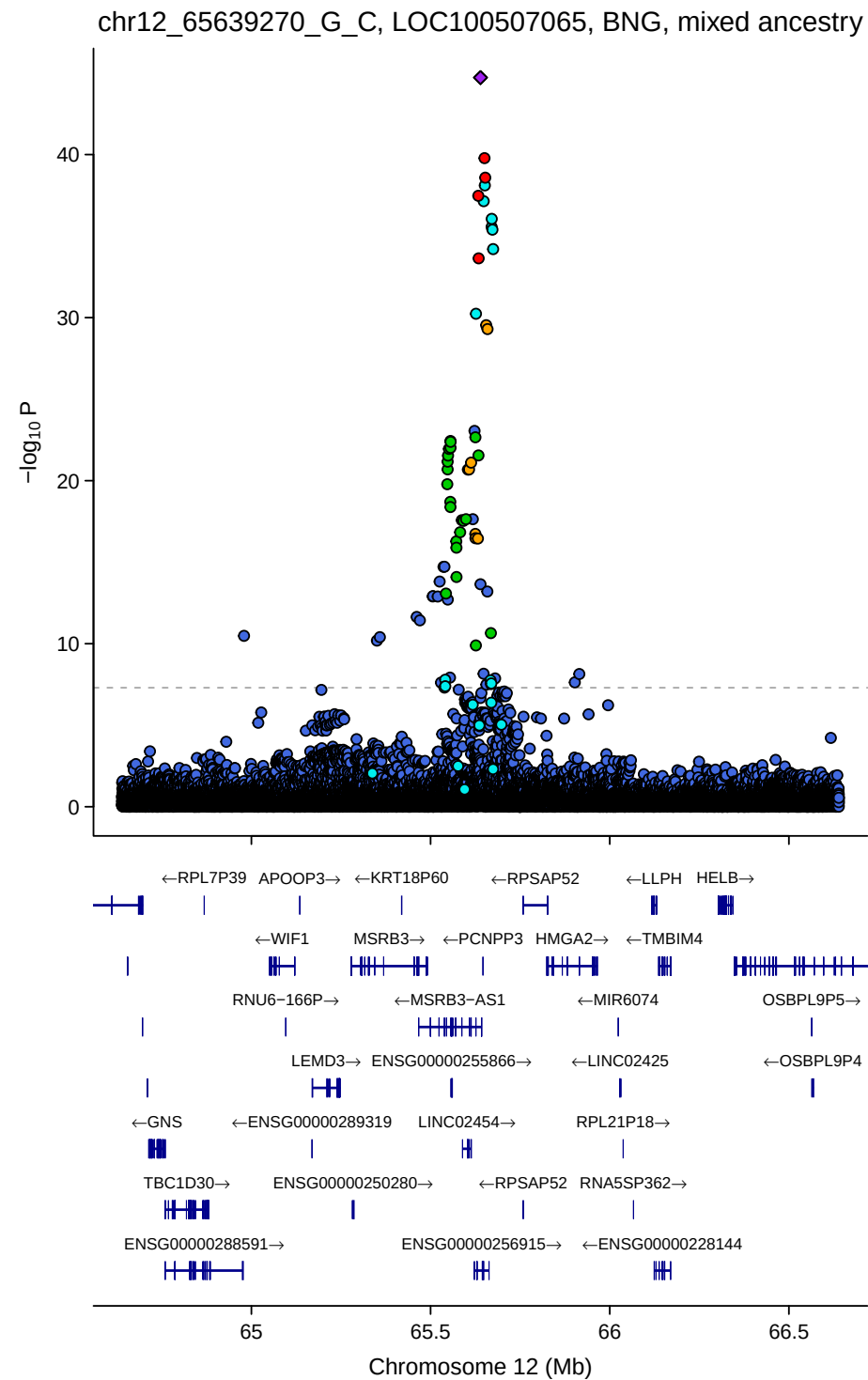
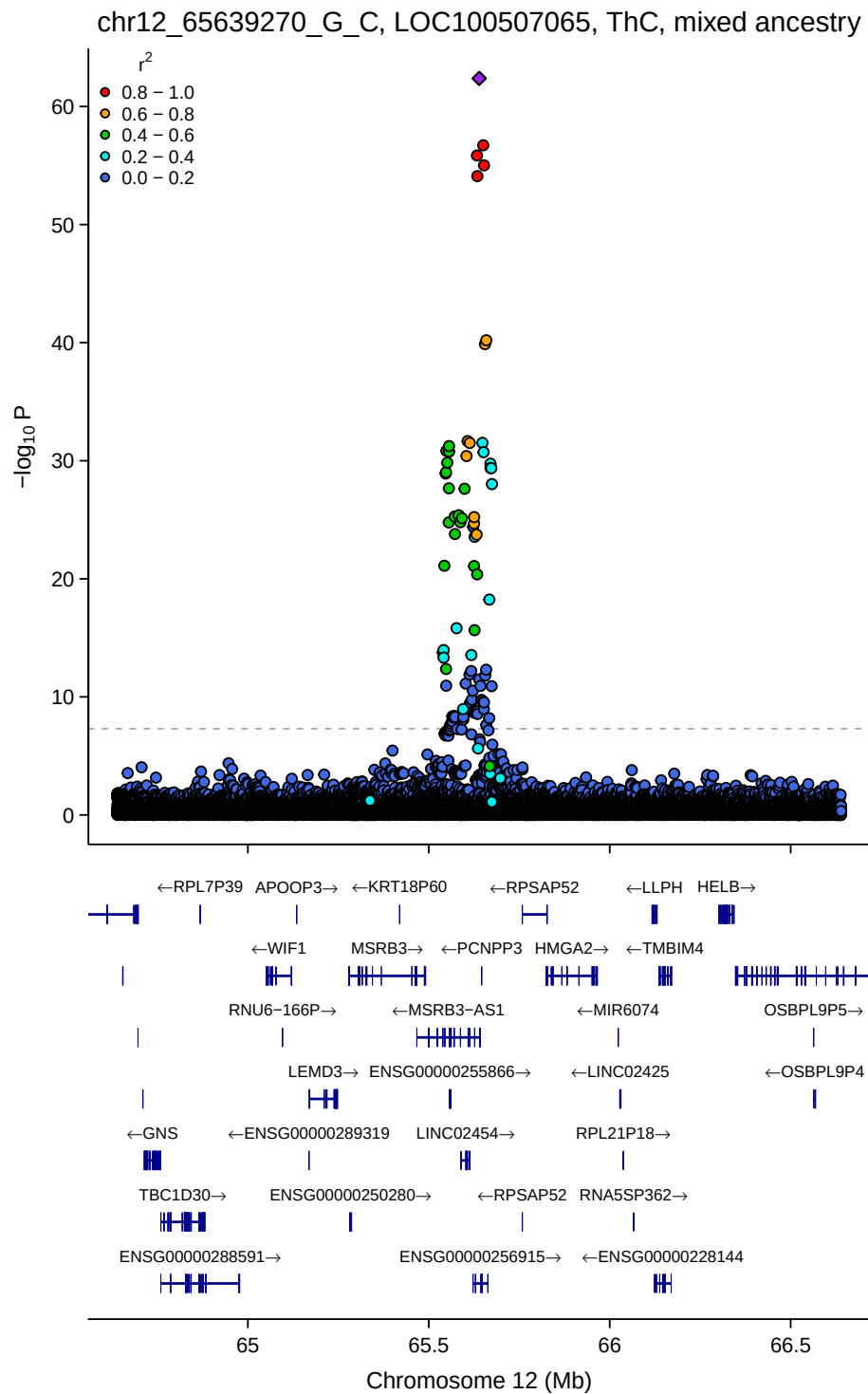
Supplementary Figure 2.3



Supplementary Figure 2.3

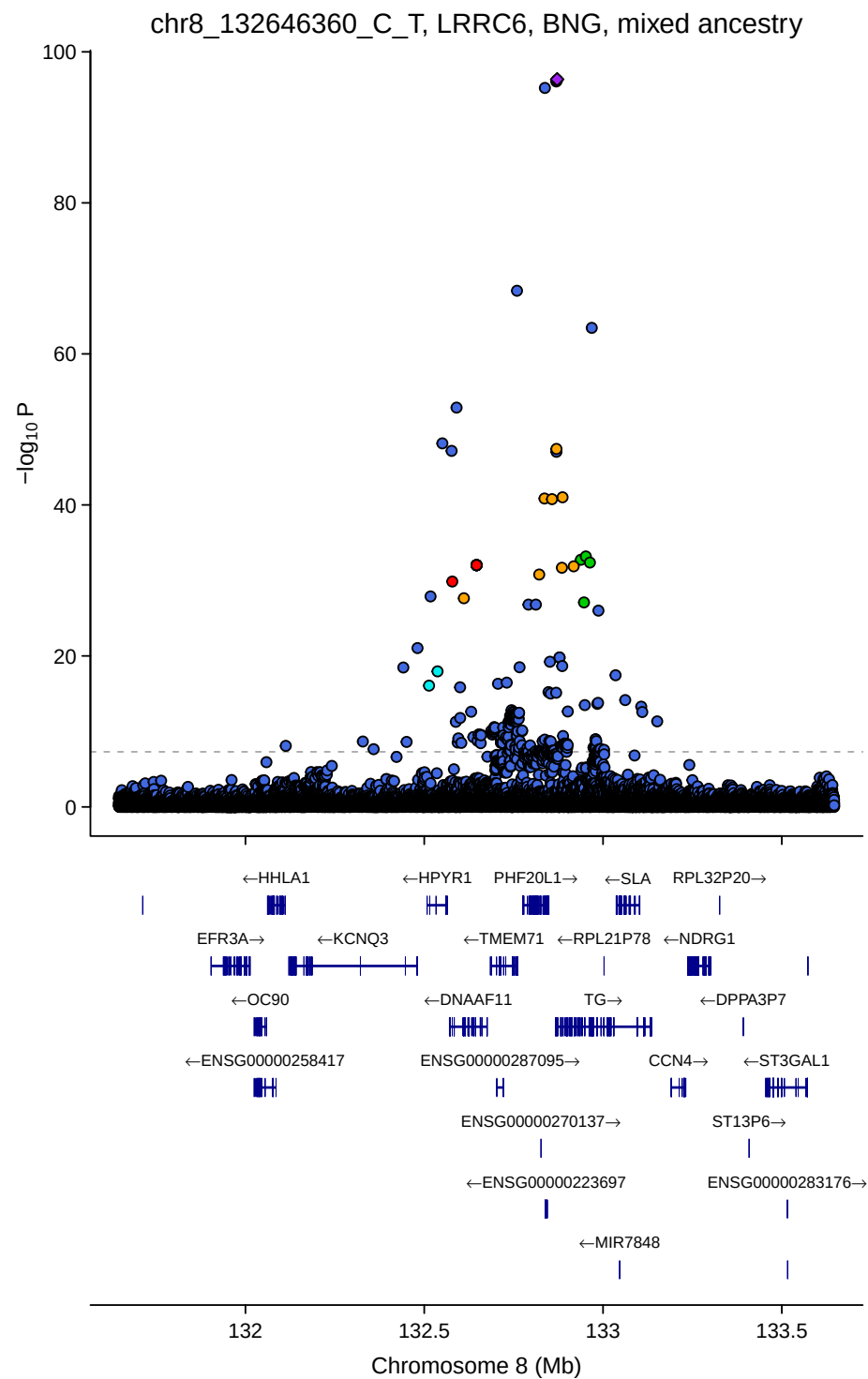
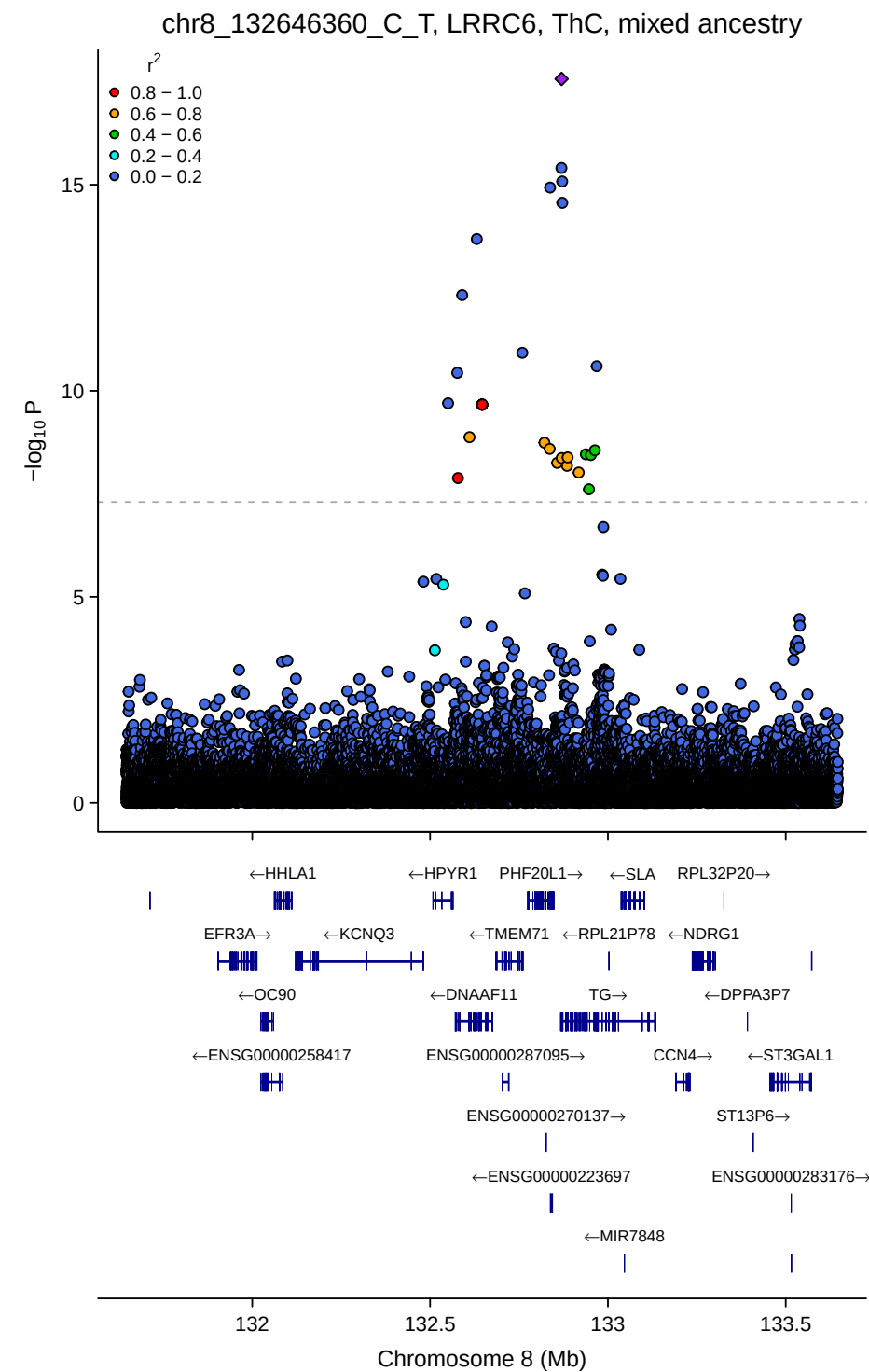


# Supplementary Figure 2.3



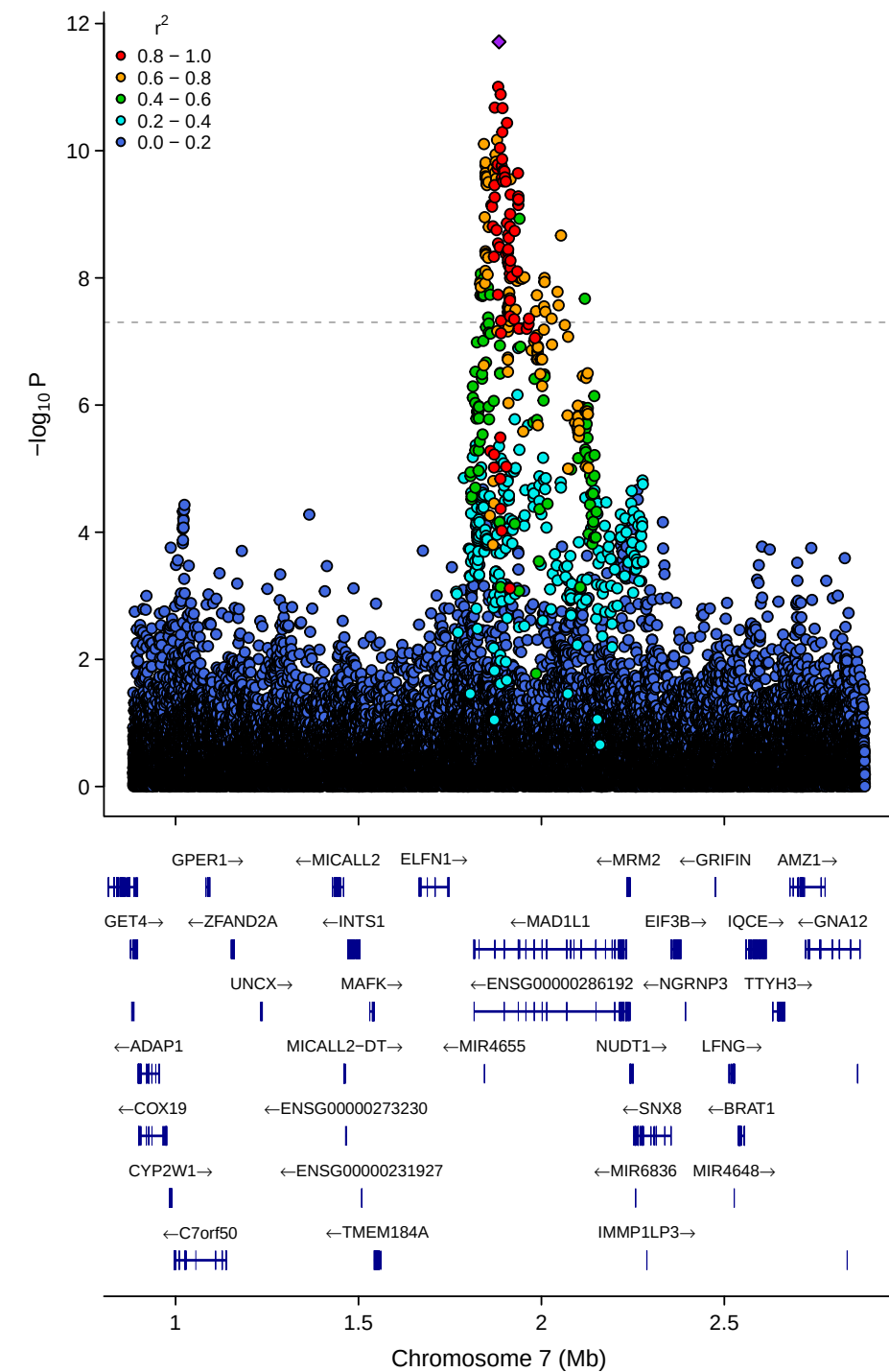


Supplementary Figure 2.3

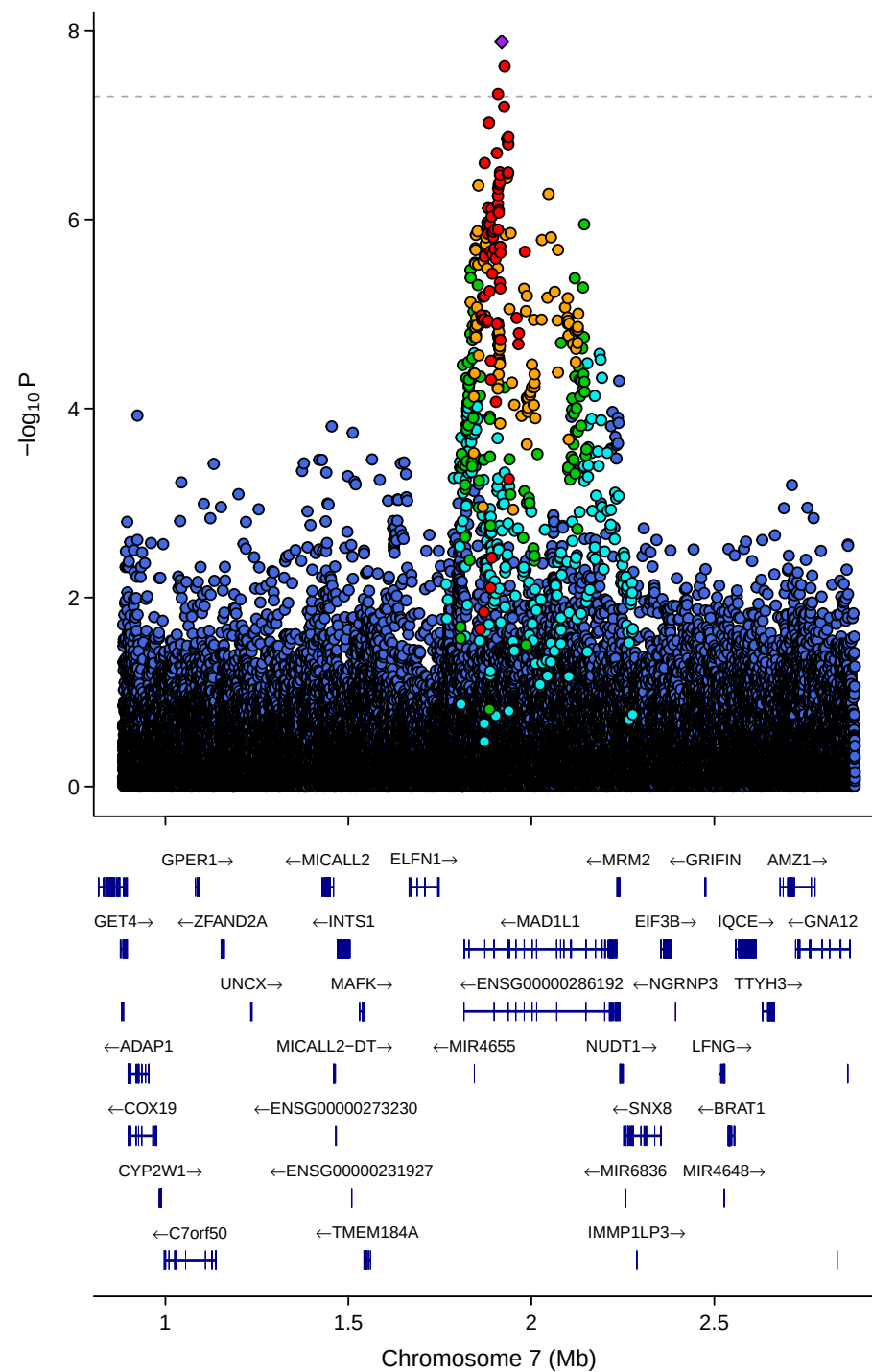


Supplementary Figure 2.3

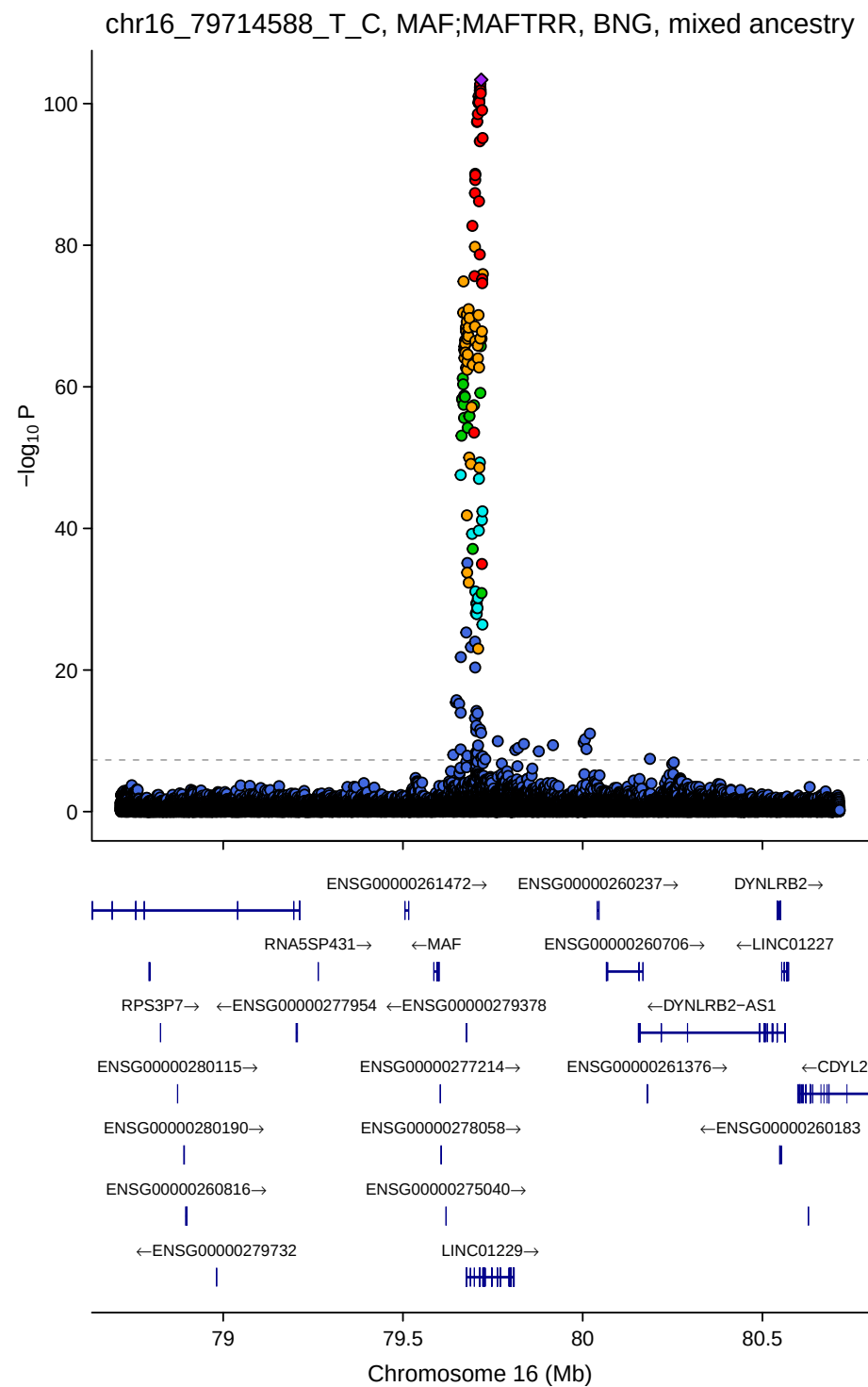
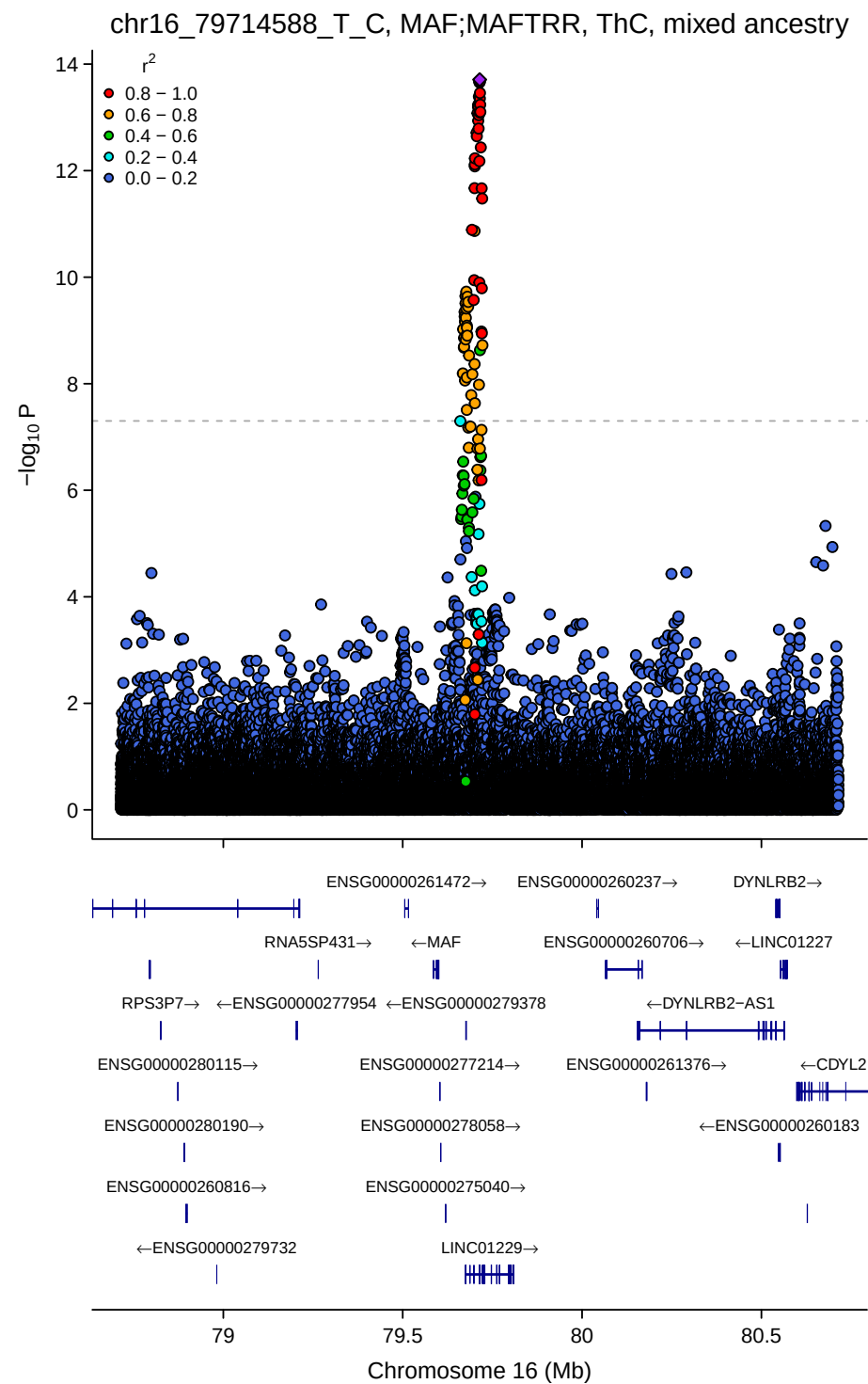
chr7\_1884059\_C\_T, MAD1L1, ThC, mixed ancestry



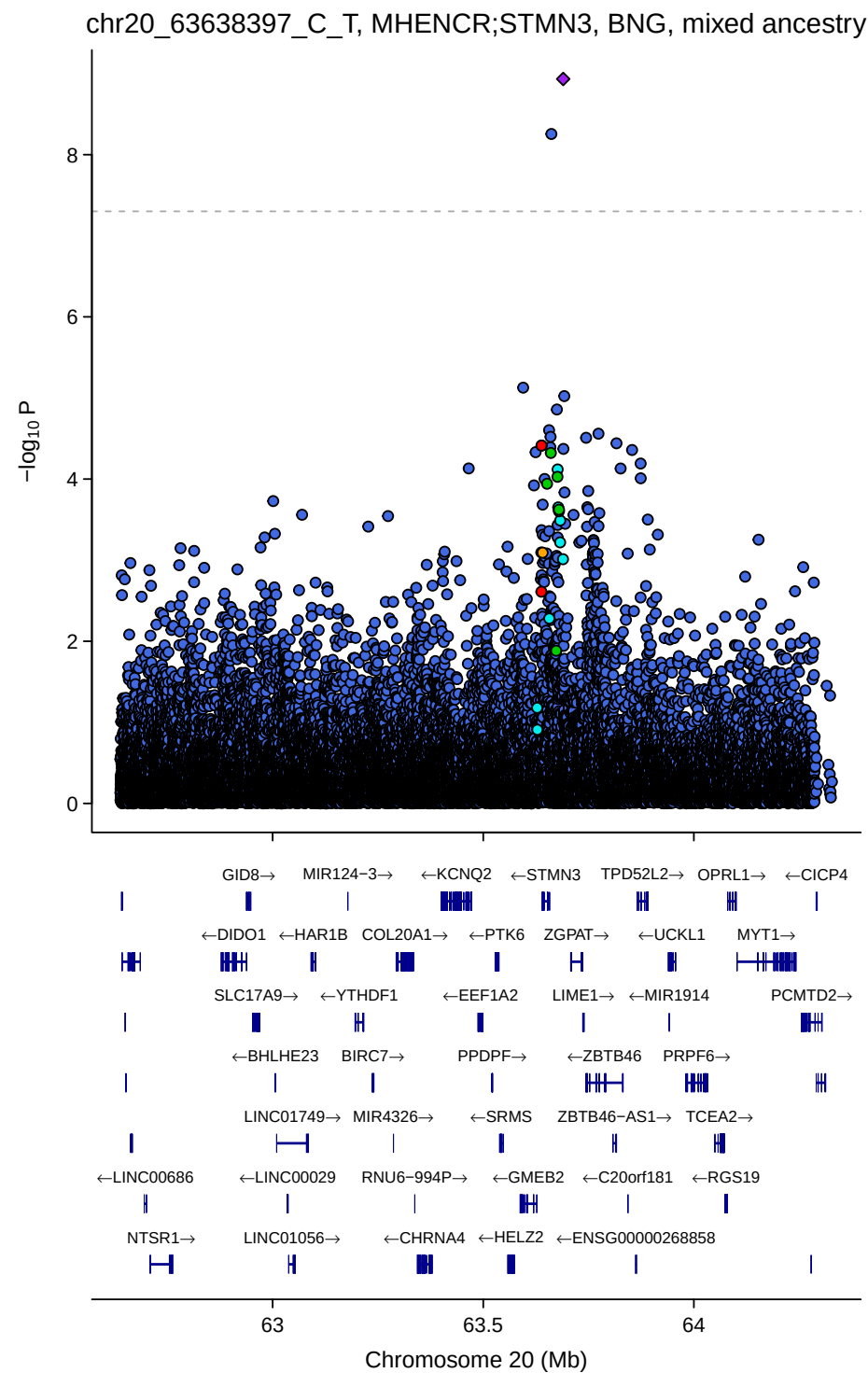
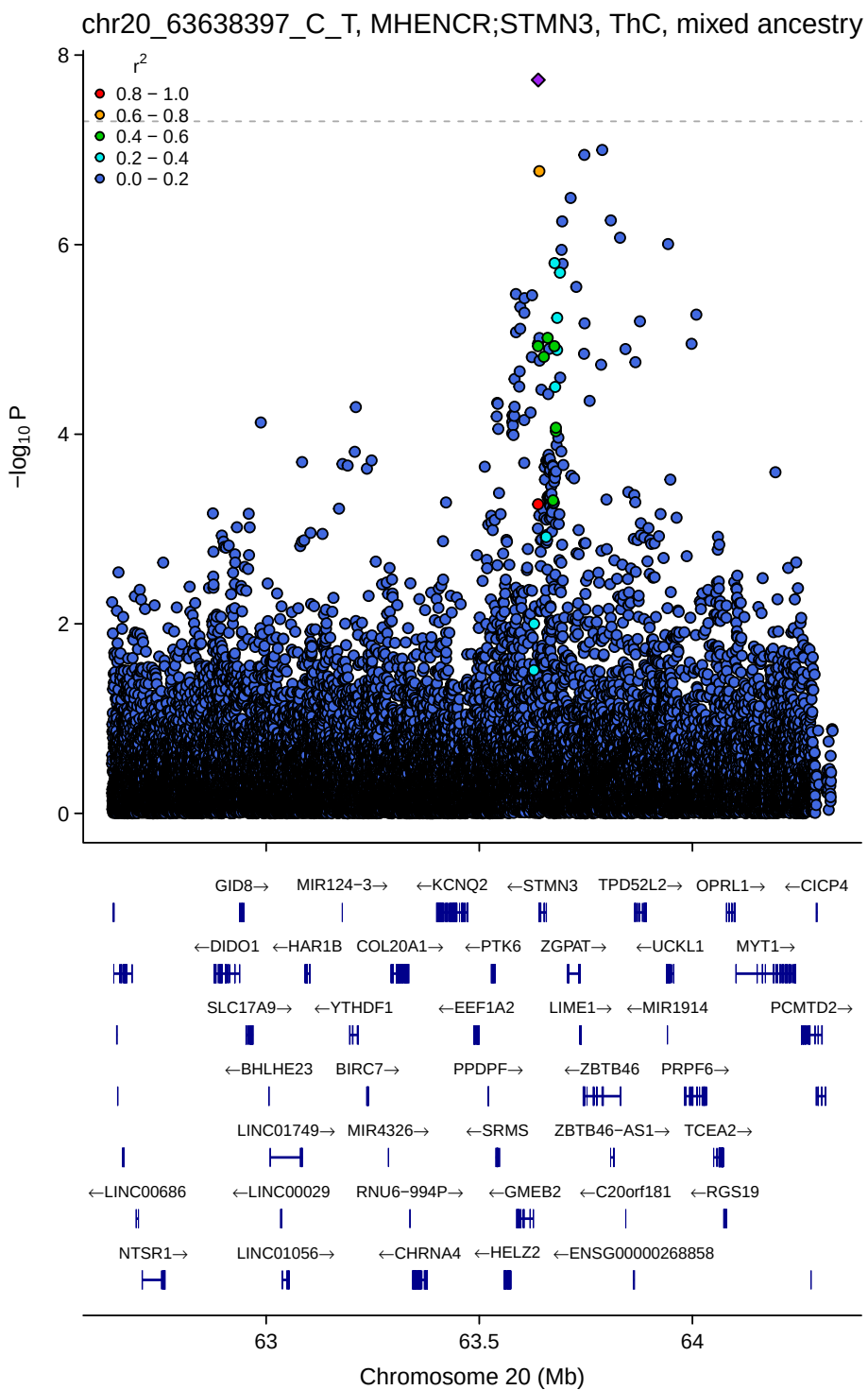
chr7\_1884059\_C\_T, MAD1L1, BNG, mixed ancestry



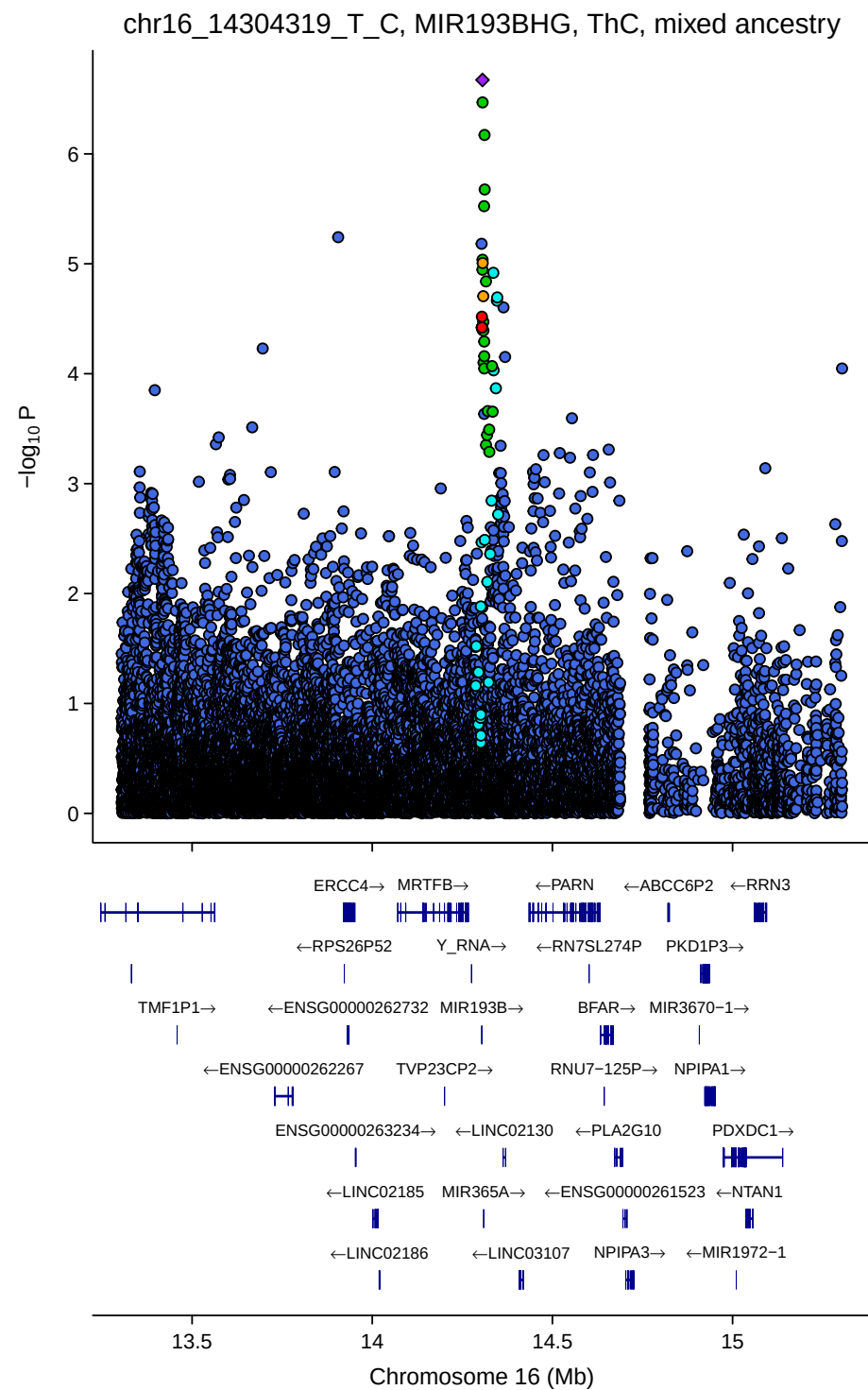
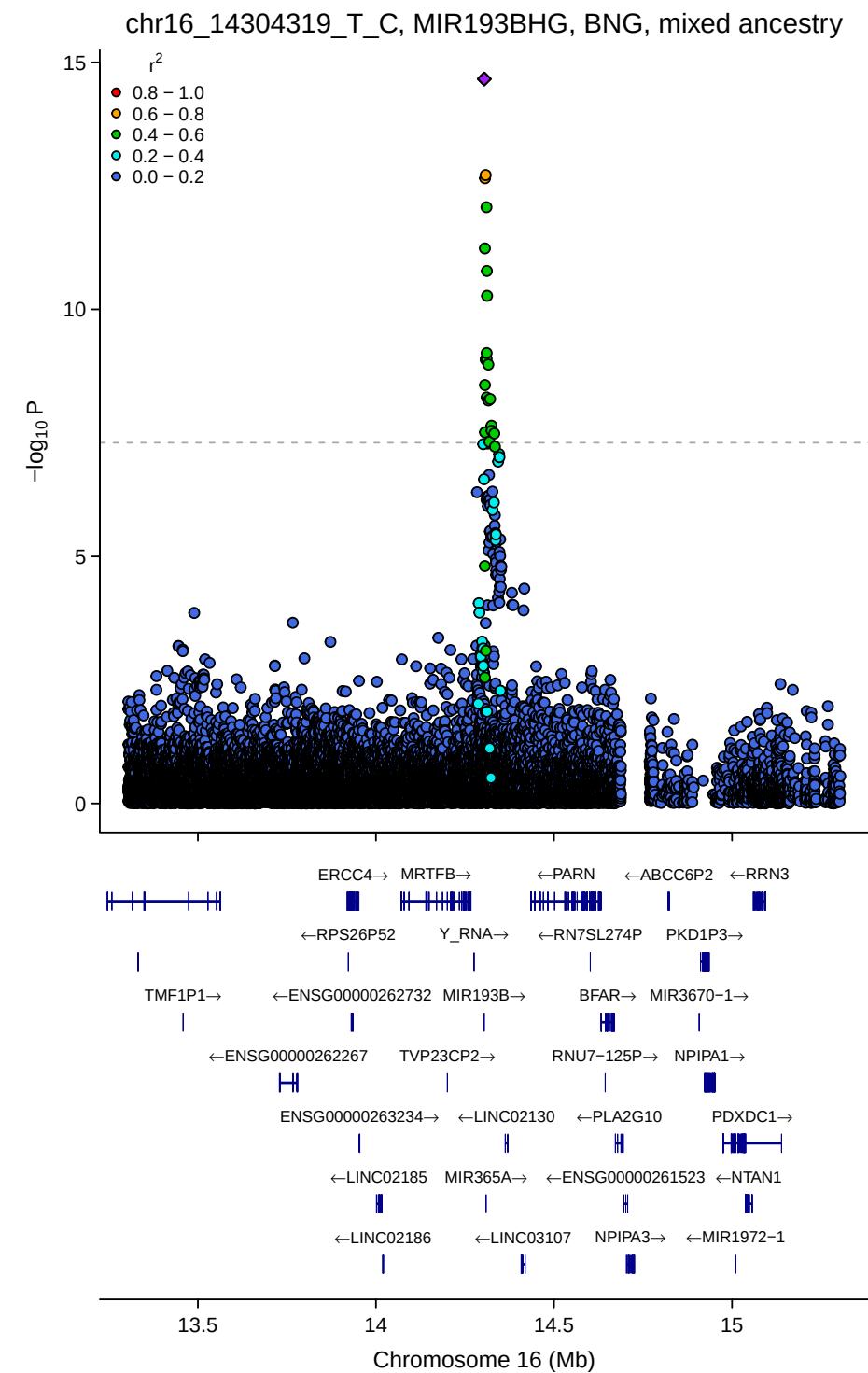
# Supplementary Figure 2.3



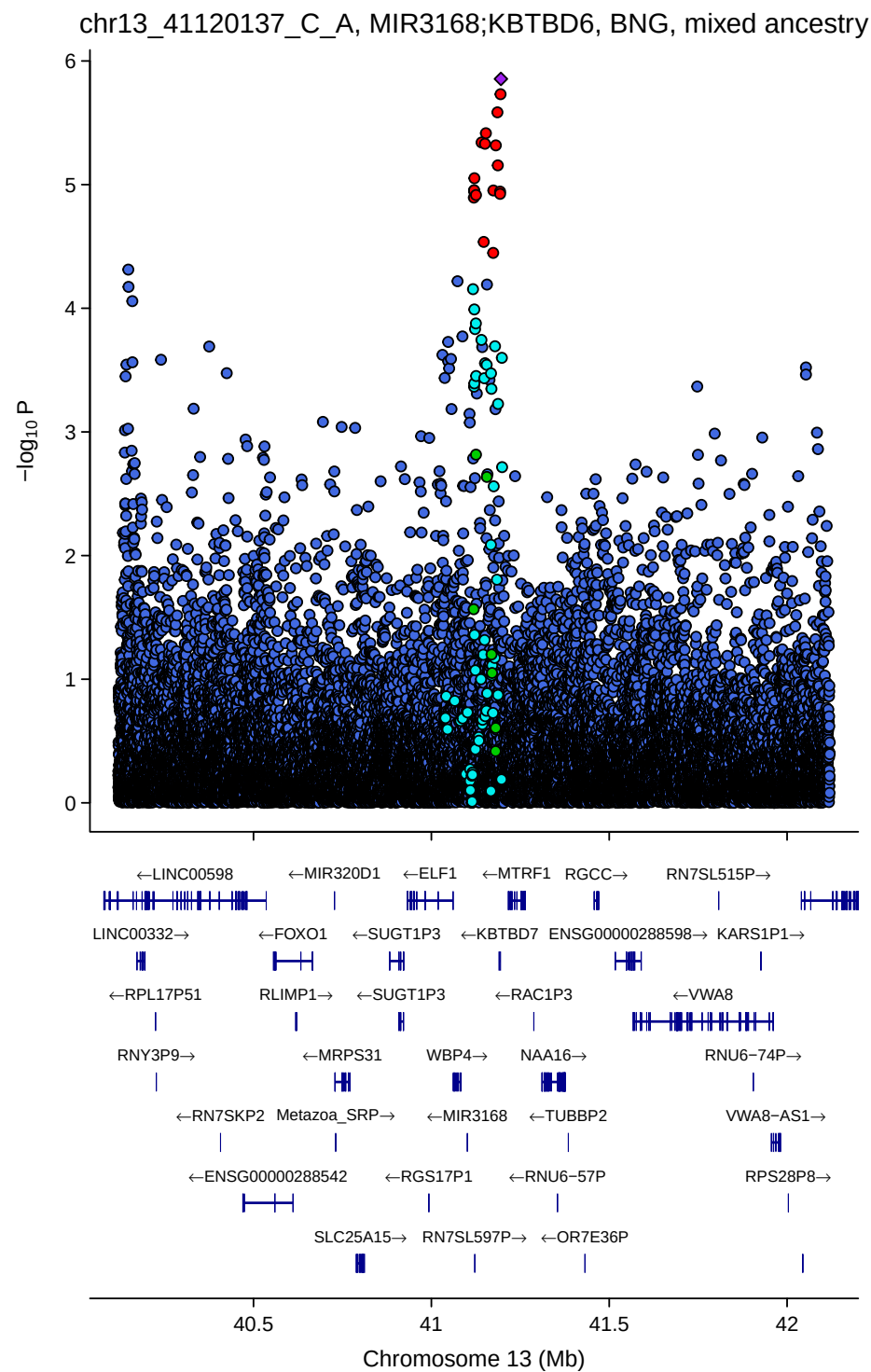
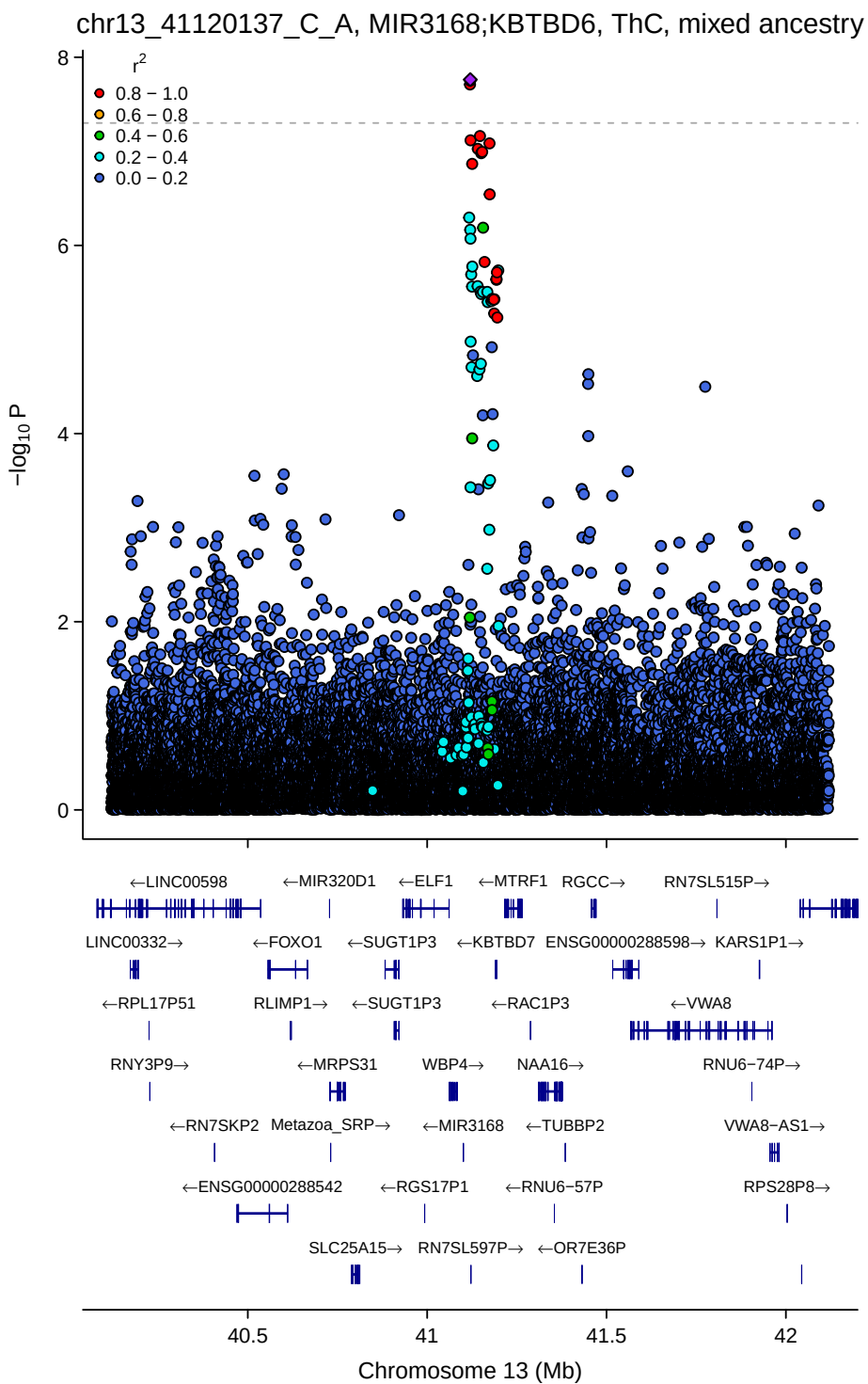
# Supplementary Figure 2.3



Supplementary Figure 2.3

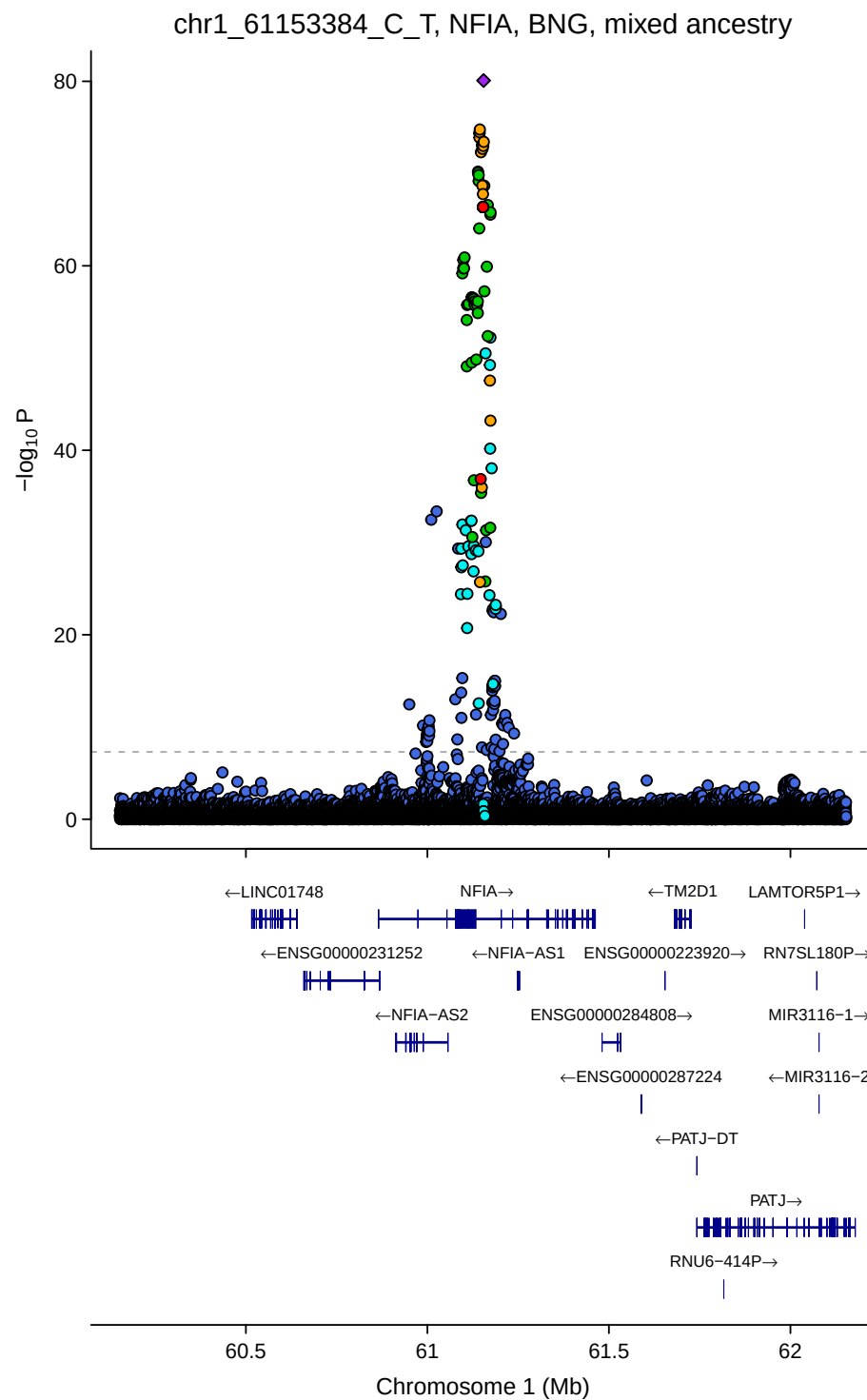
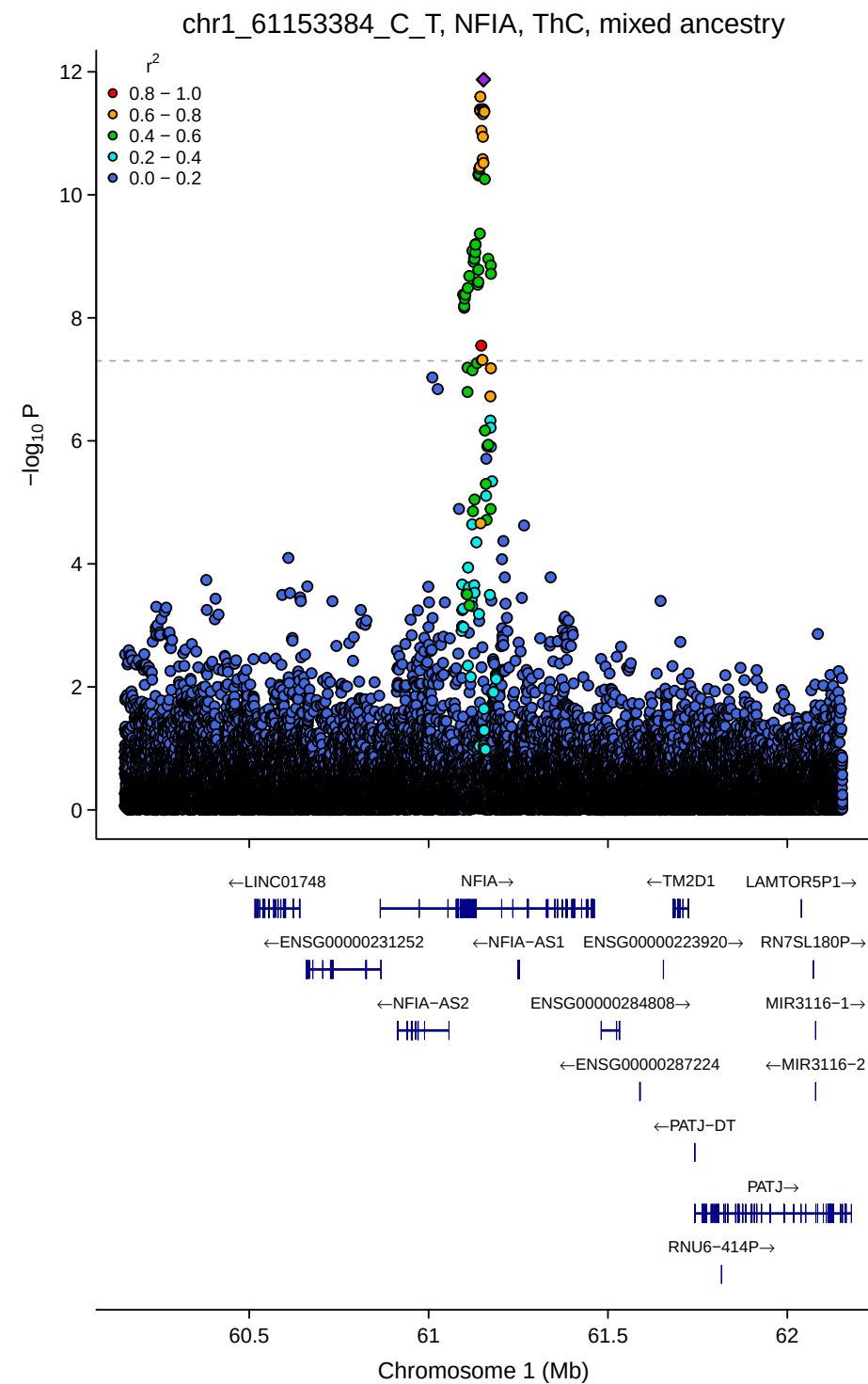


# Supplementary Figure 2.3

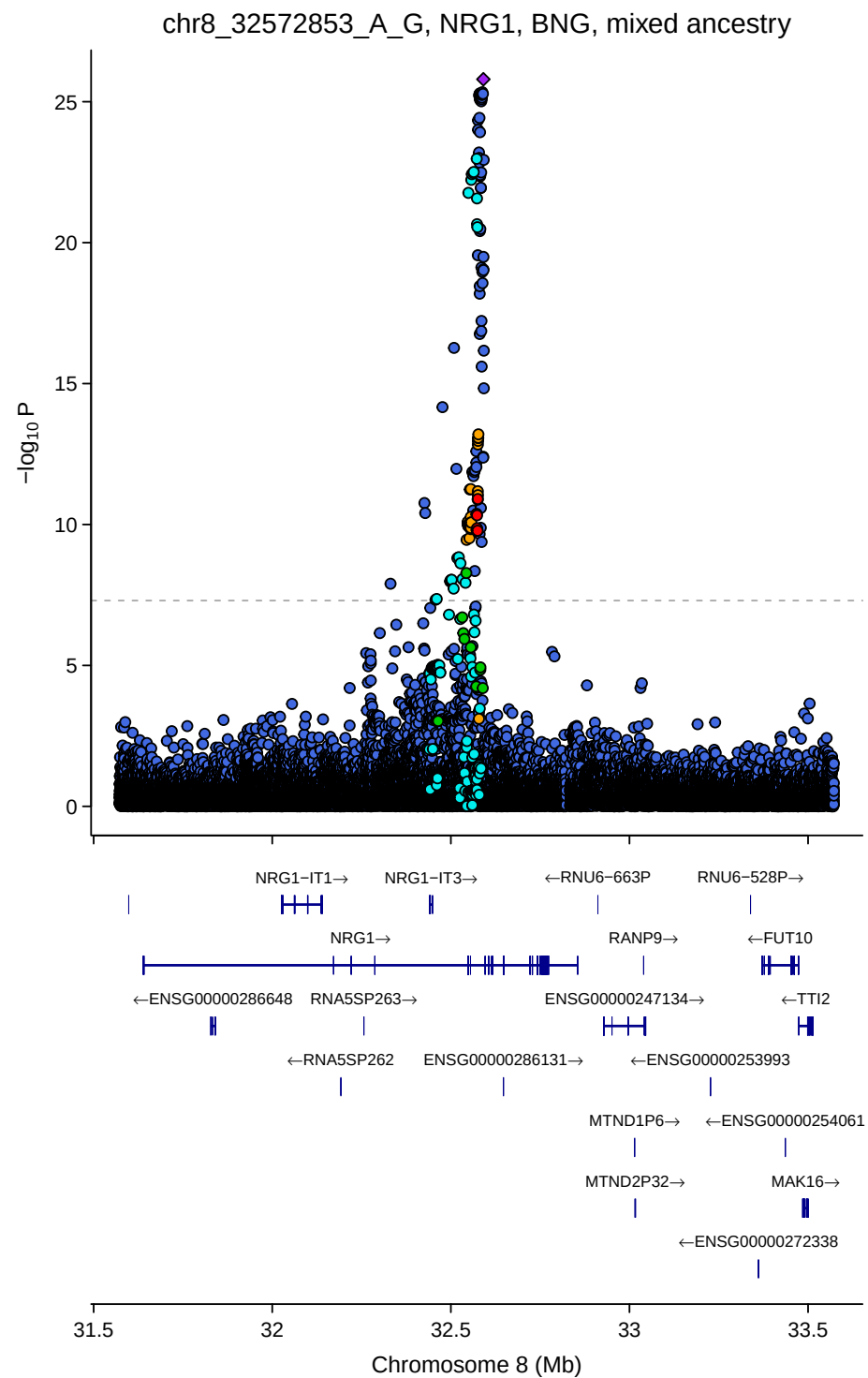
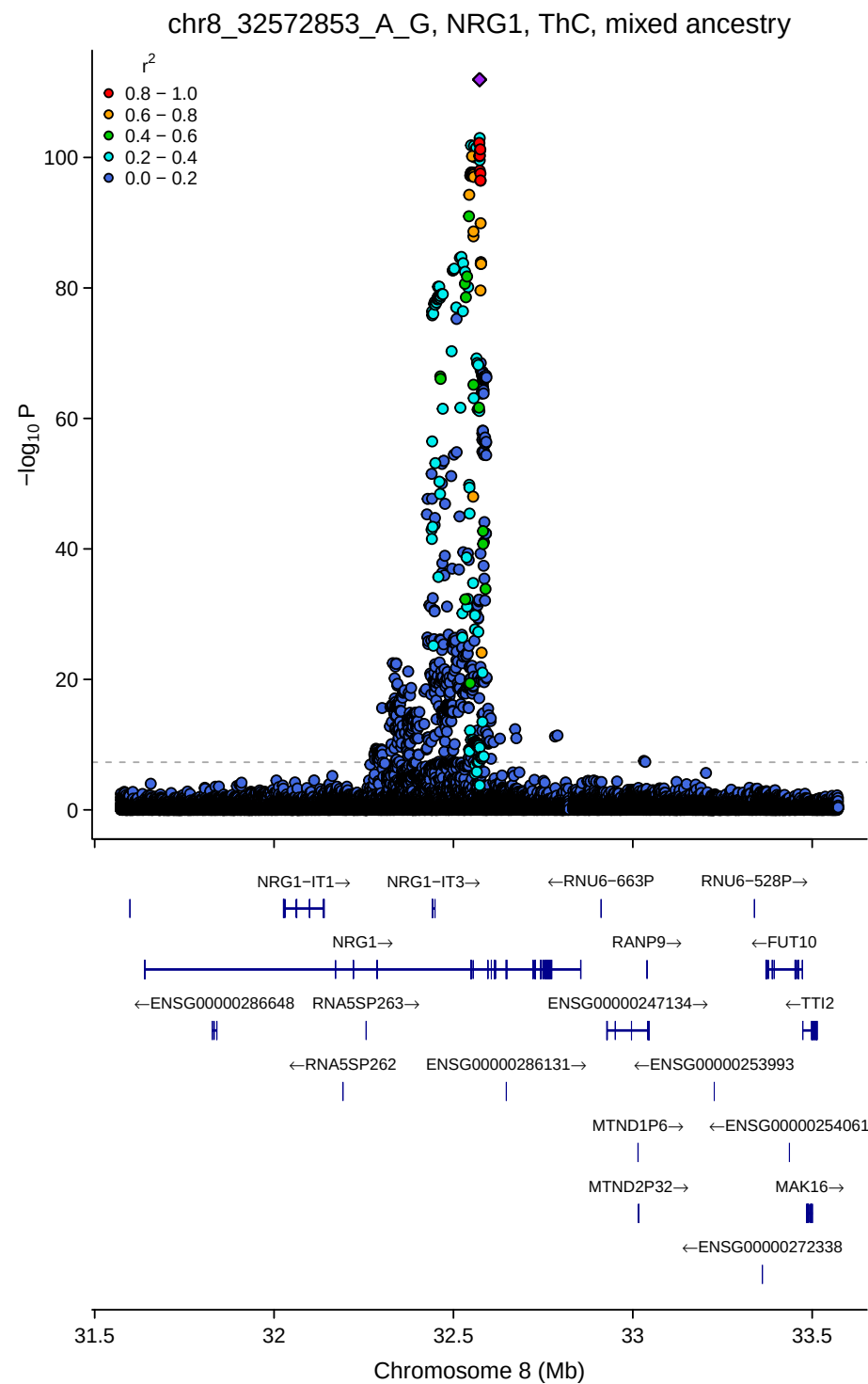




Supplementary Figure 2.3

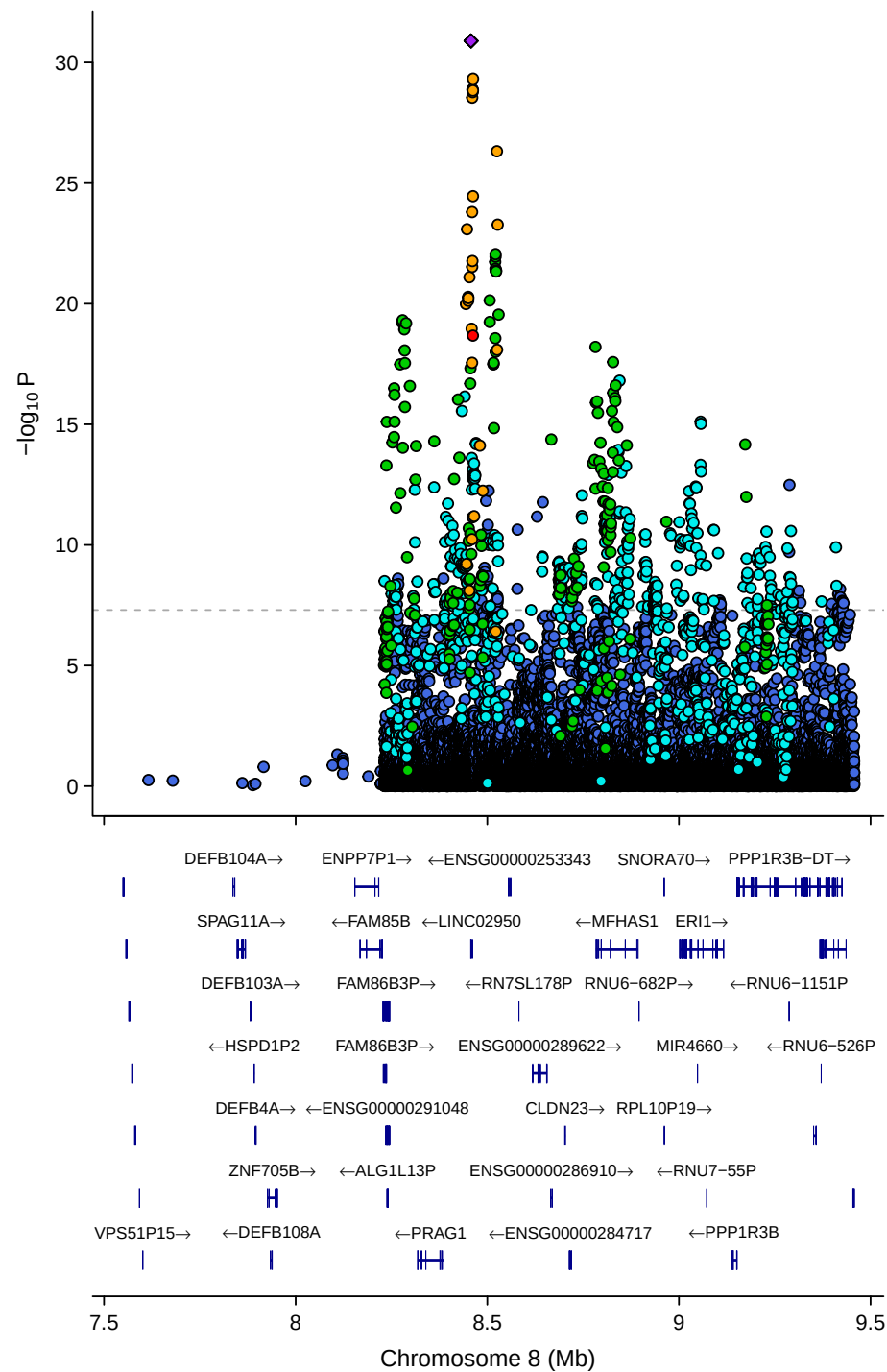
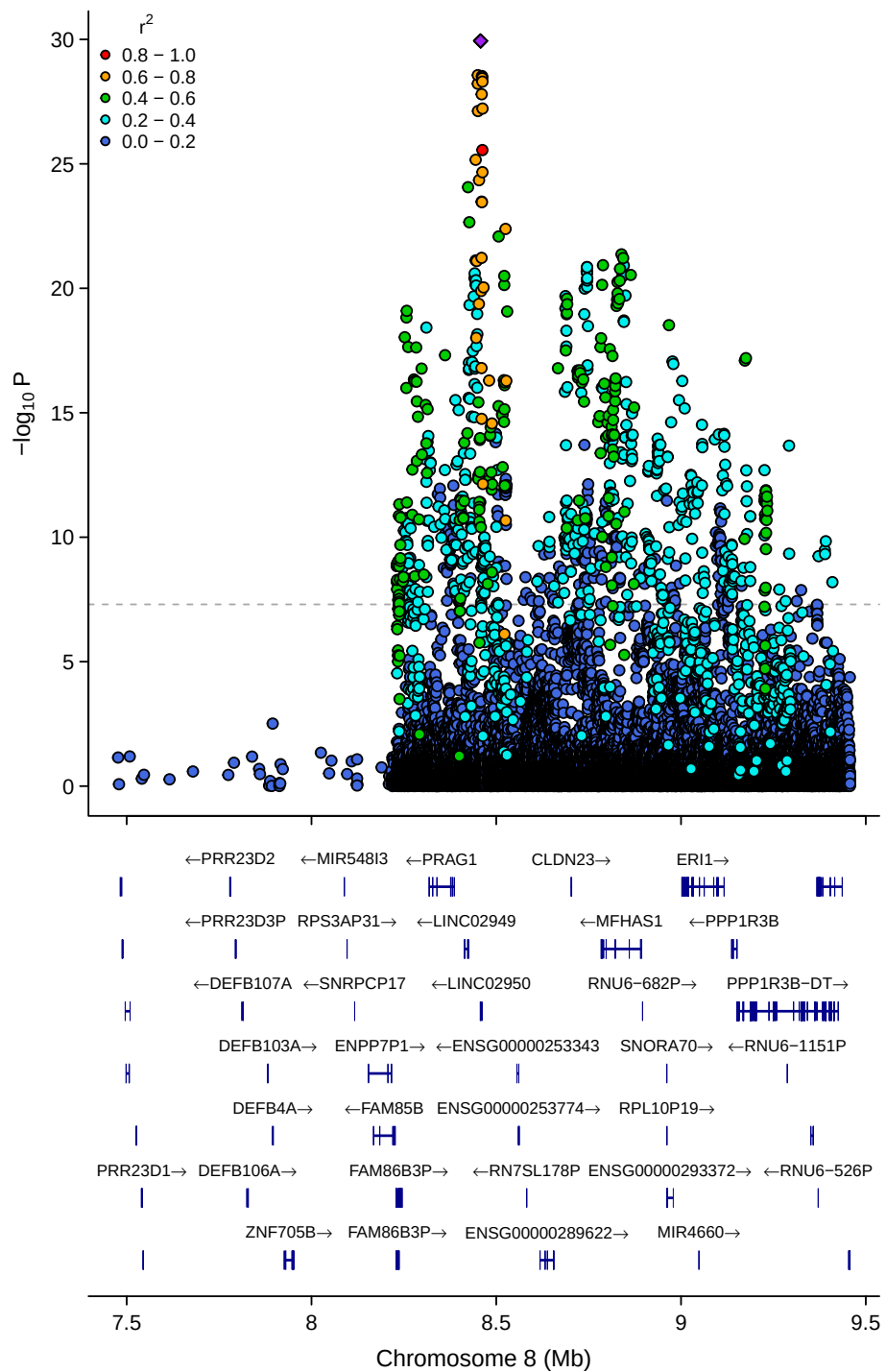


Supplementary Figure 2.3

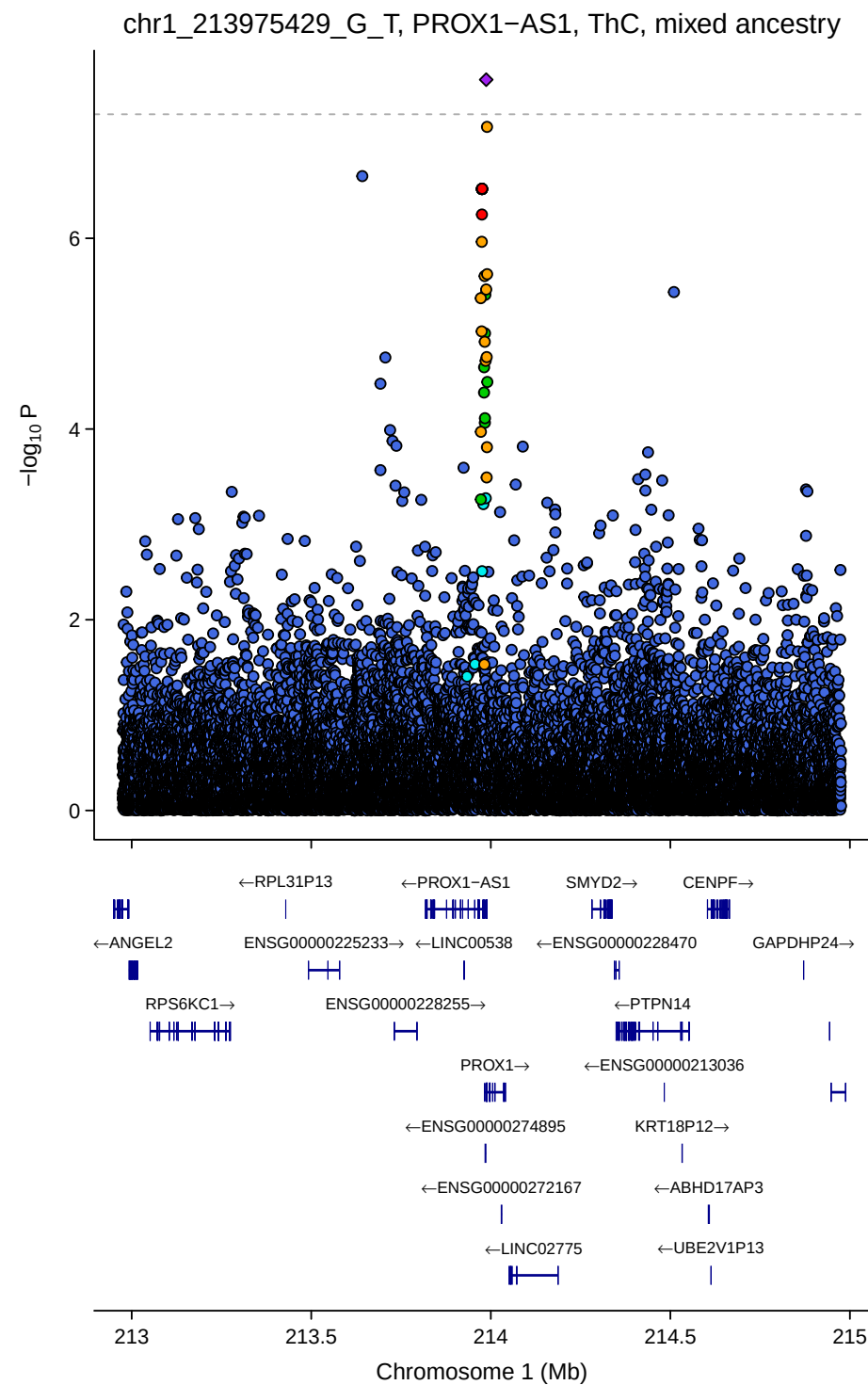
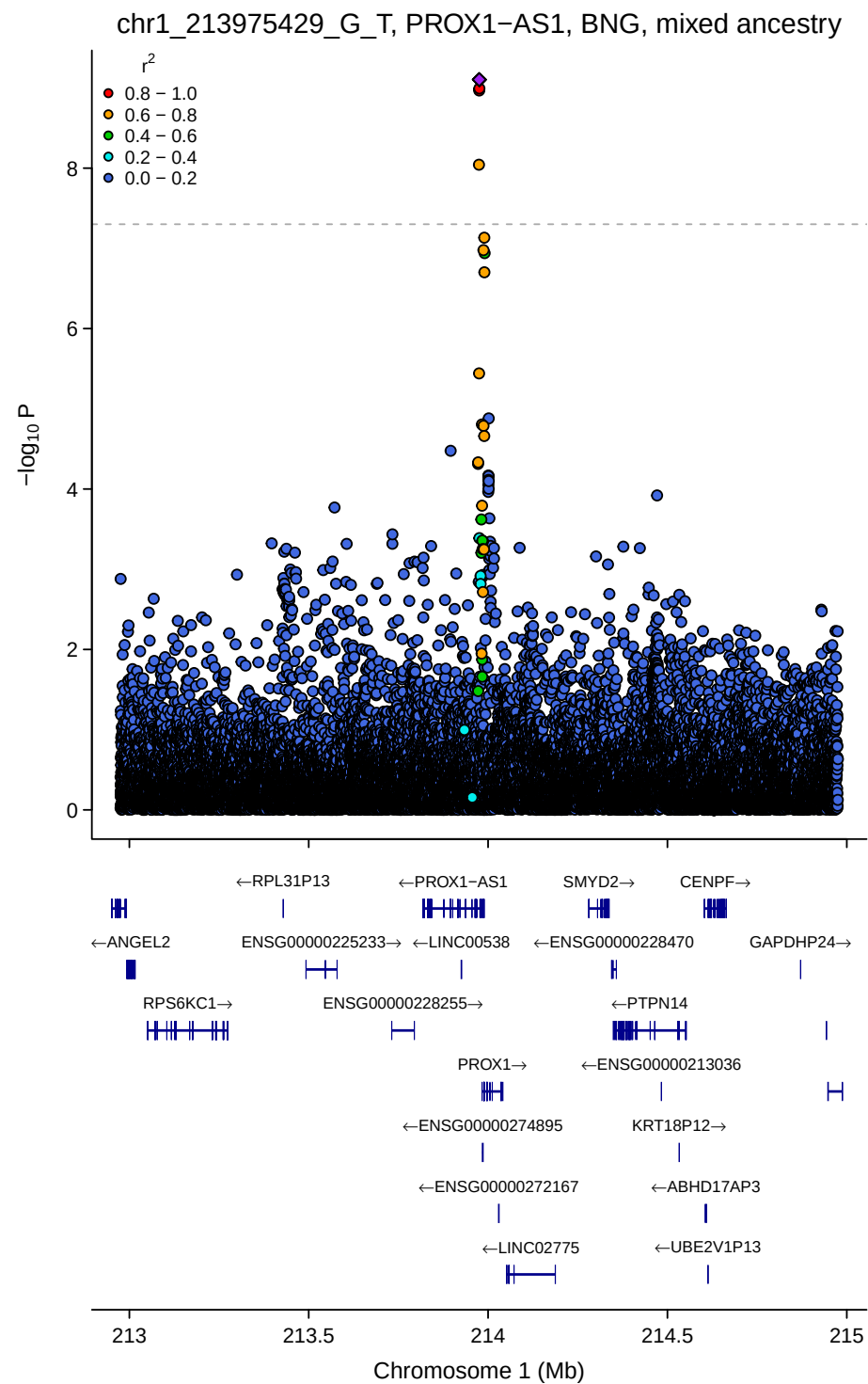


# Supplementary Figure 2.3

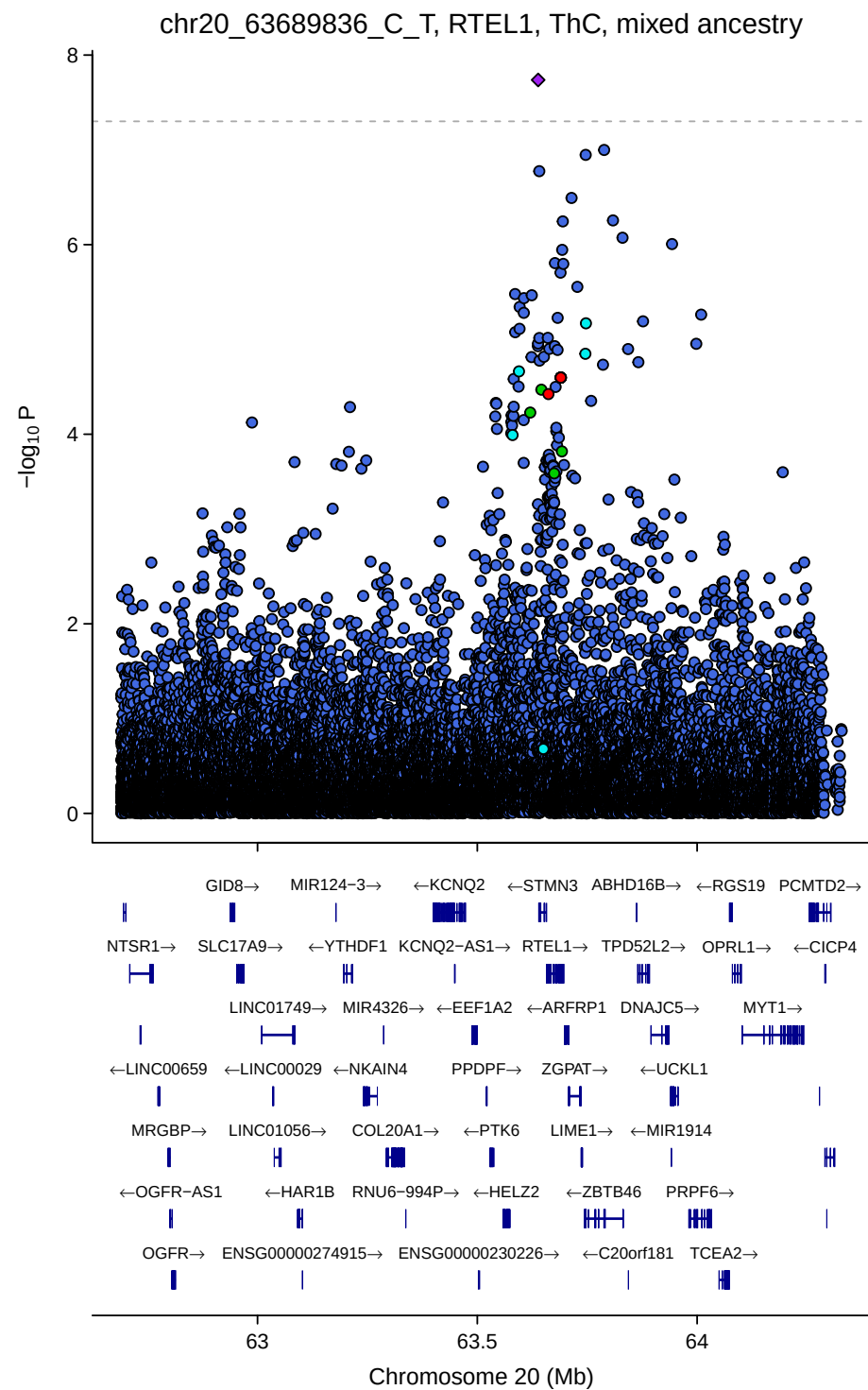
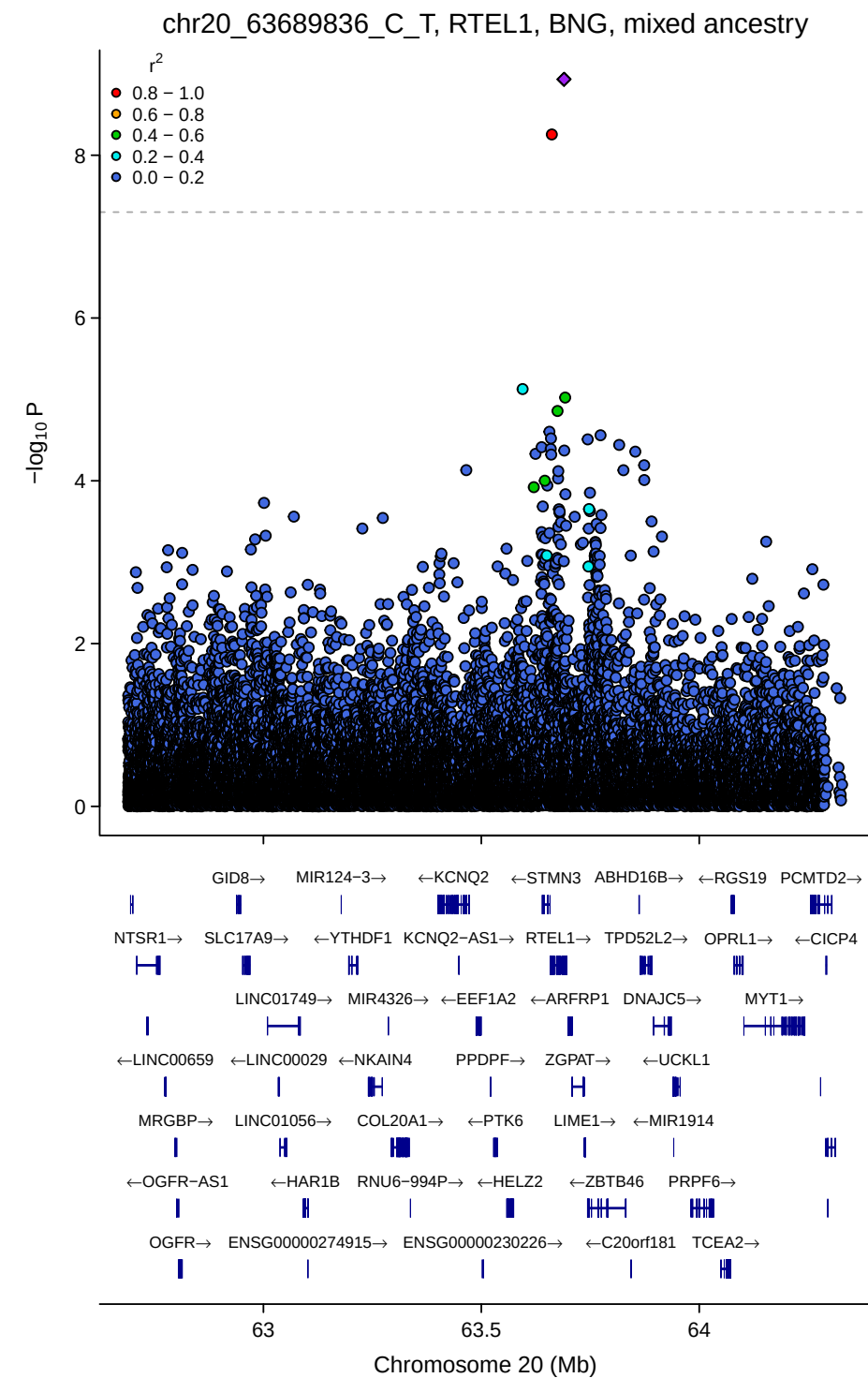
chr8\_8457501\_CCAGAGAGGCT\_C, PRAG1;CLDN23, ThC, mixed ances chr8\_8457501\_CCAGAGAGGCT\_C, PRAG1;CLDN23, BNG, mixed ances



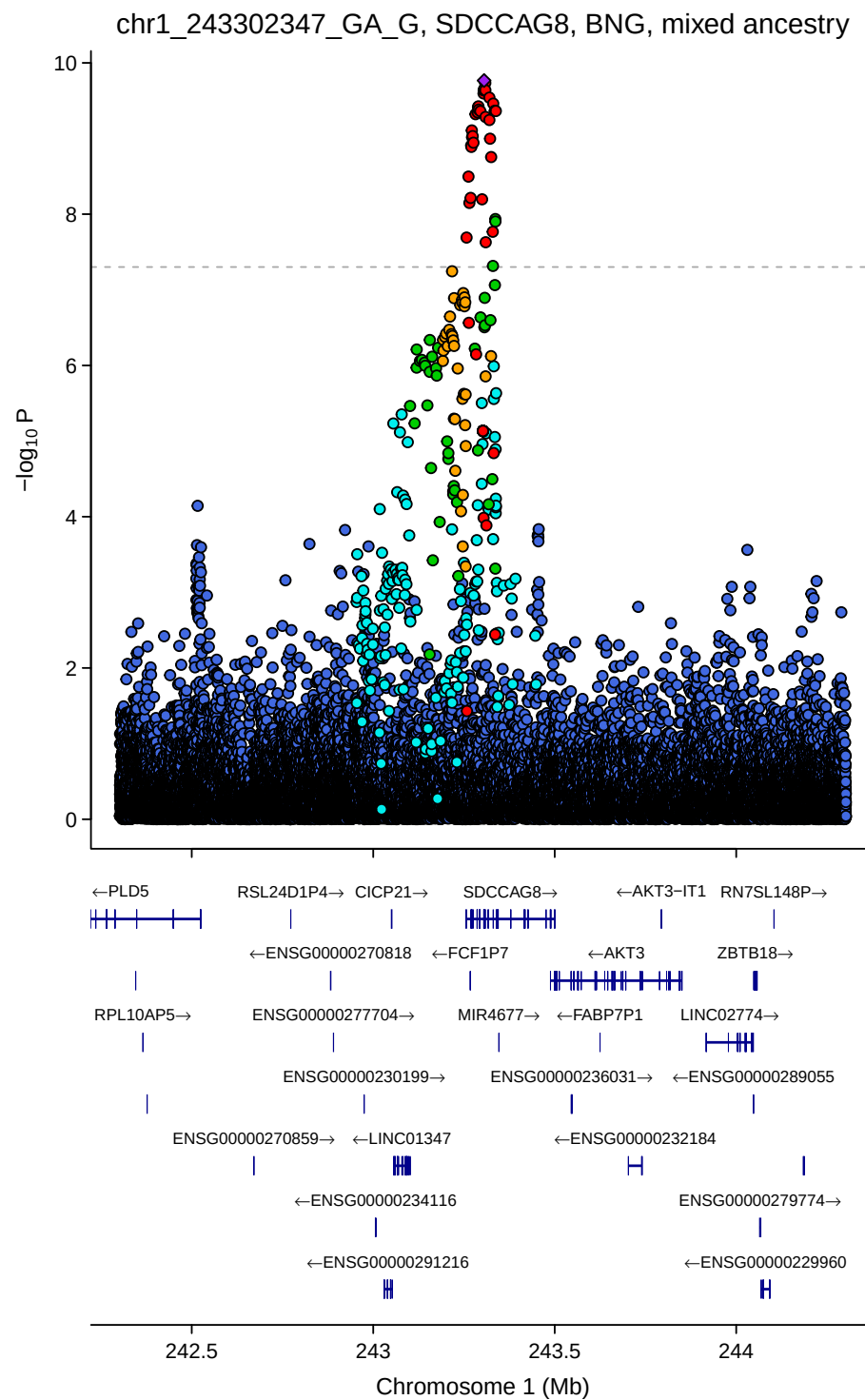
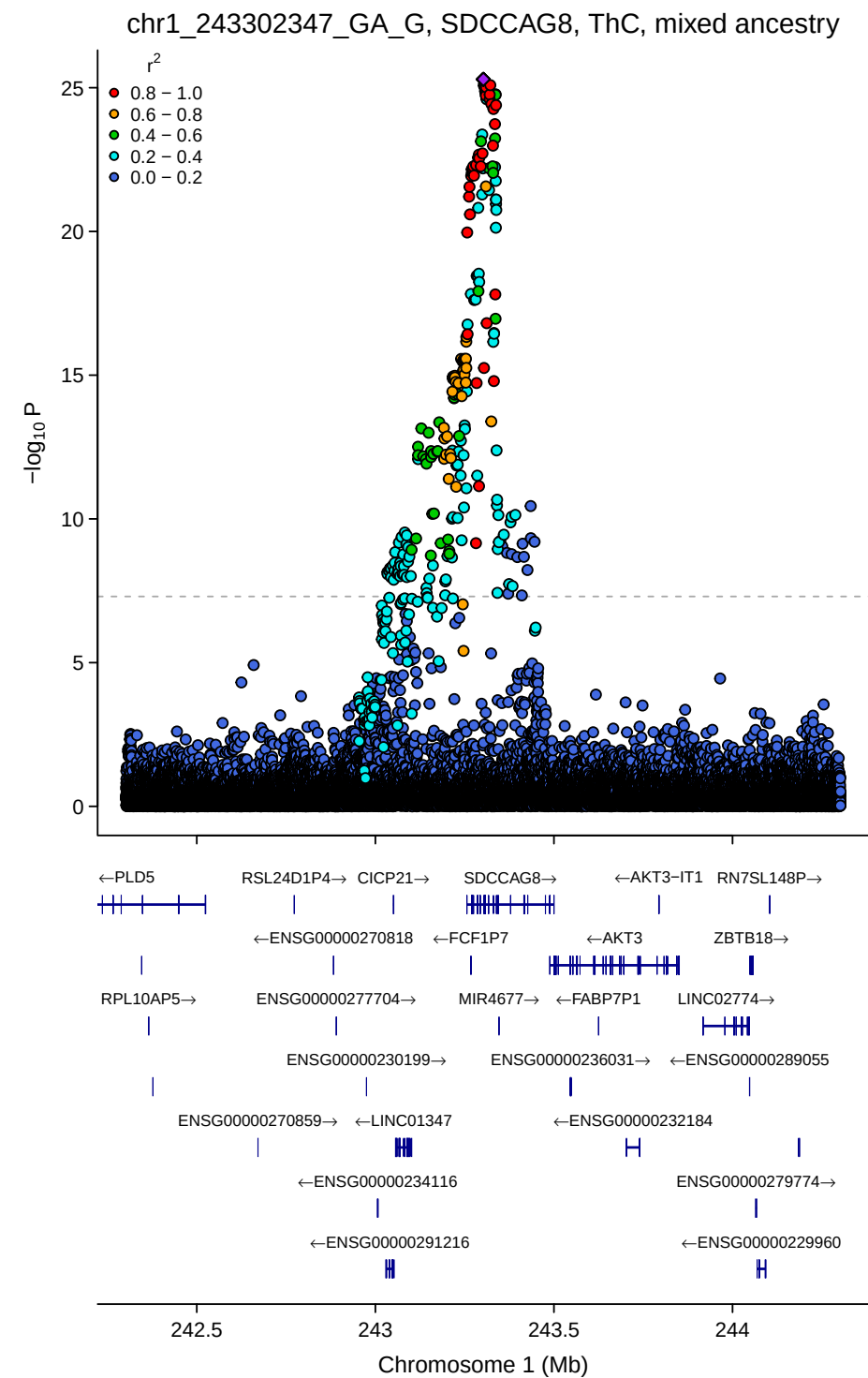
Supplementary Figure 2.3



Supplementary Figure 2.3

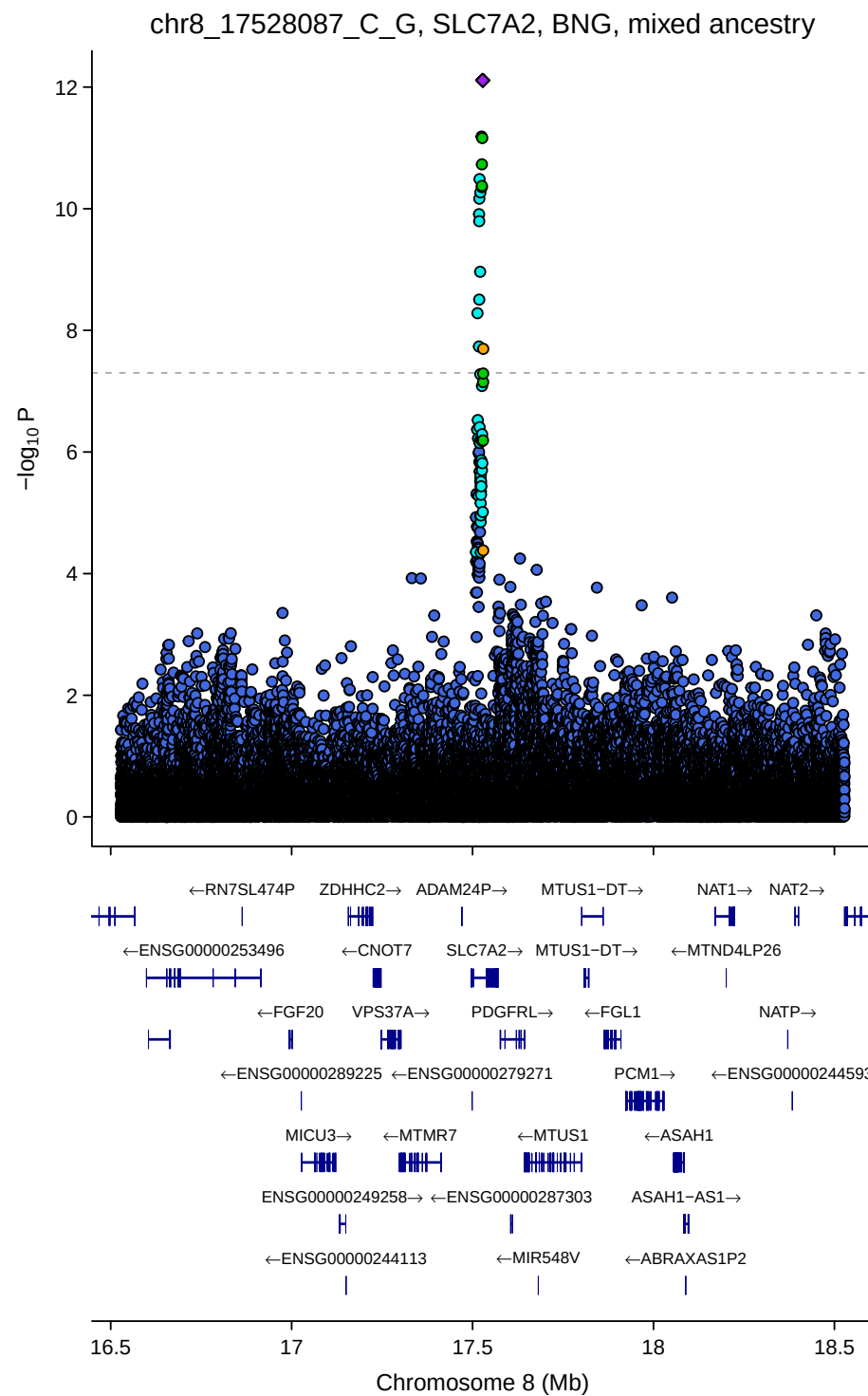
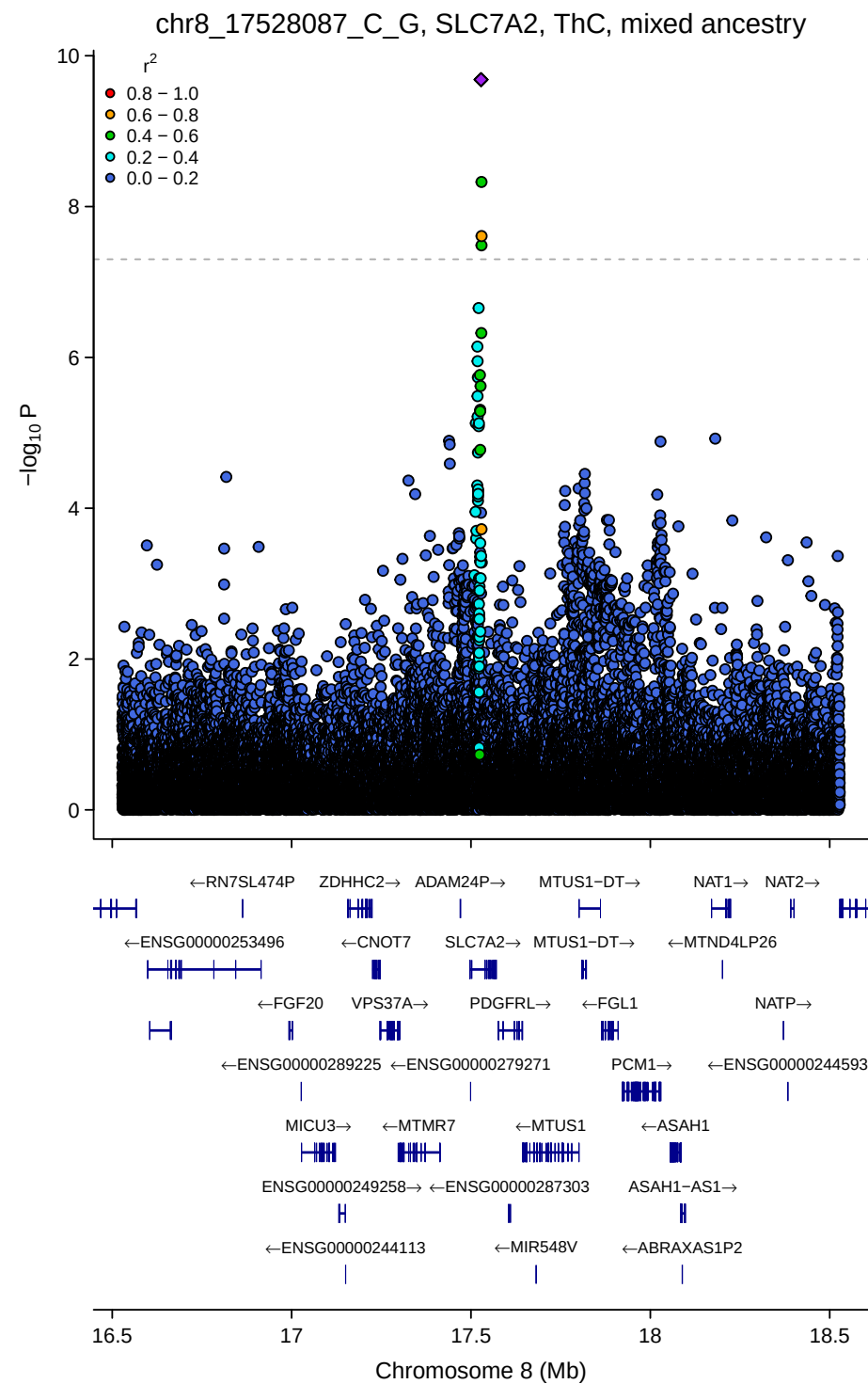


Supplementary Figure 2.3



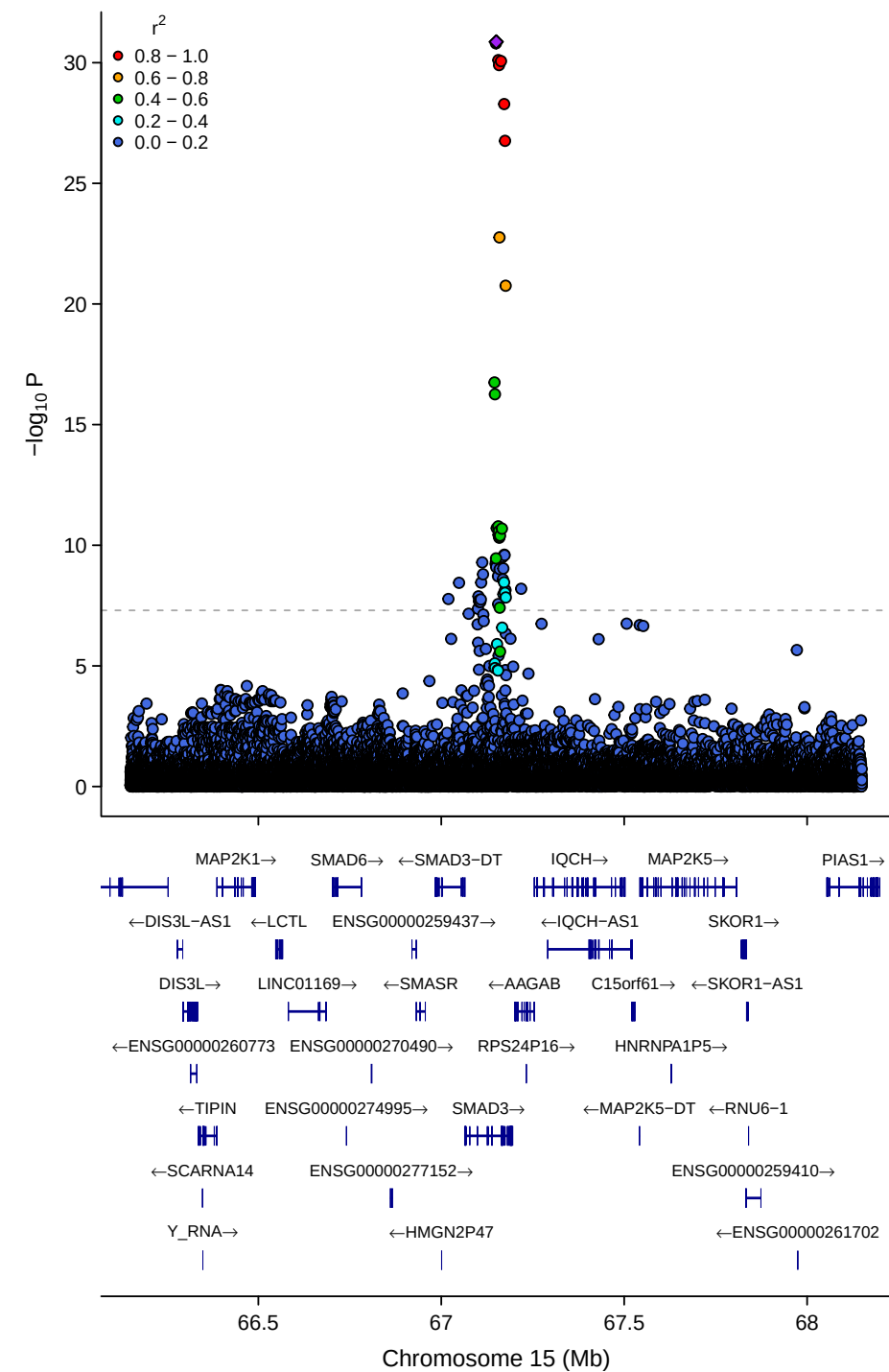


# Supplementary Figure 2.3

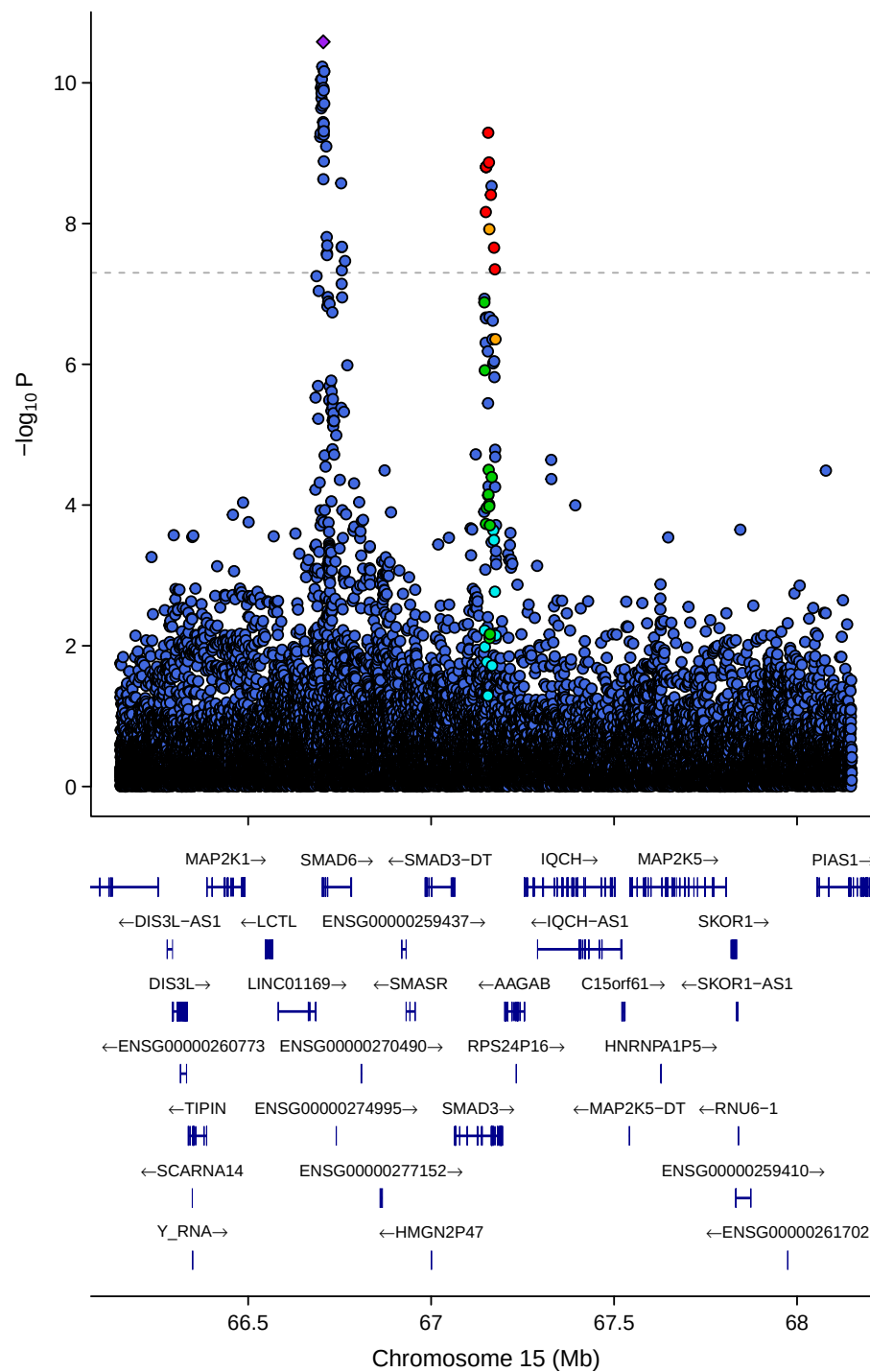


Supplementary Figure 2.3

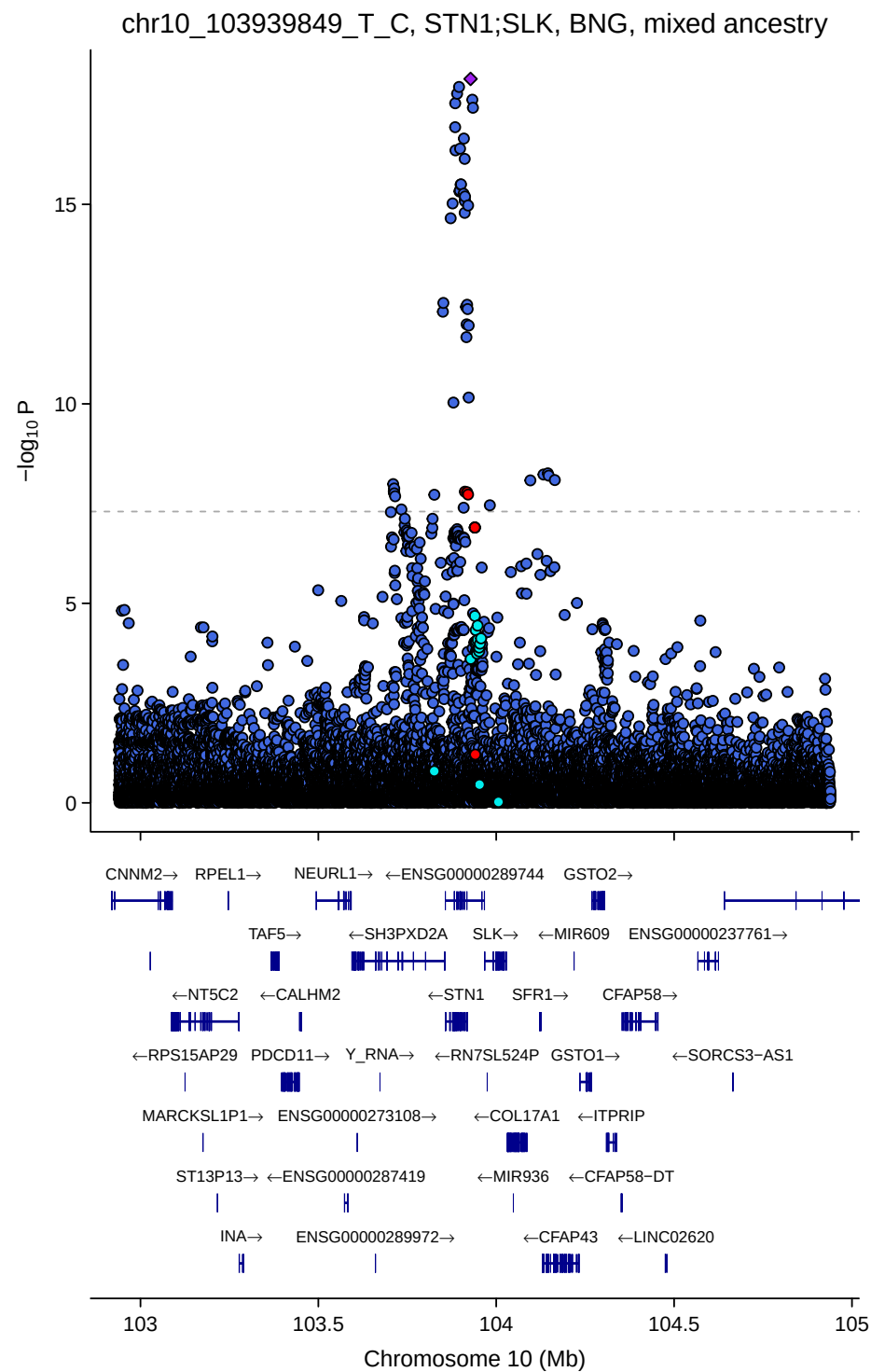
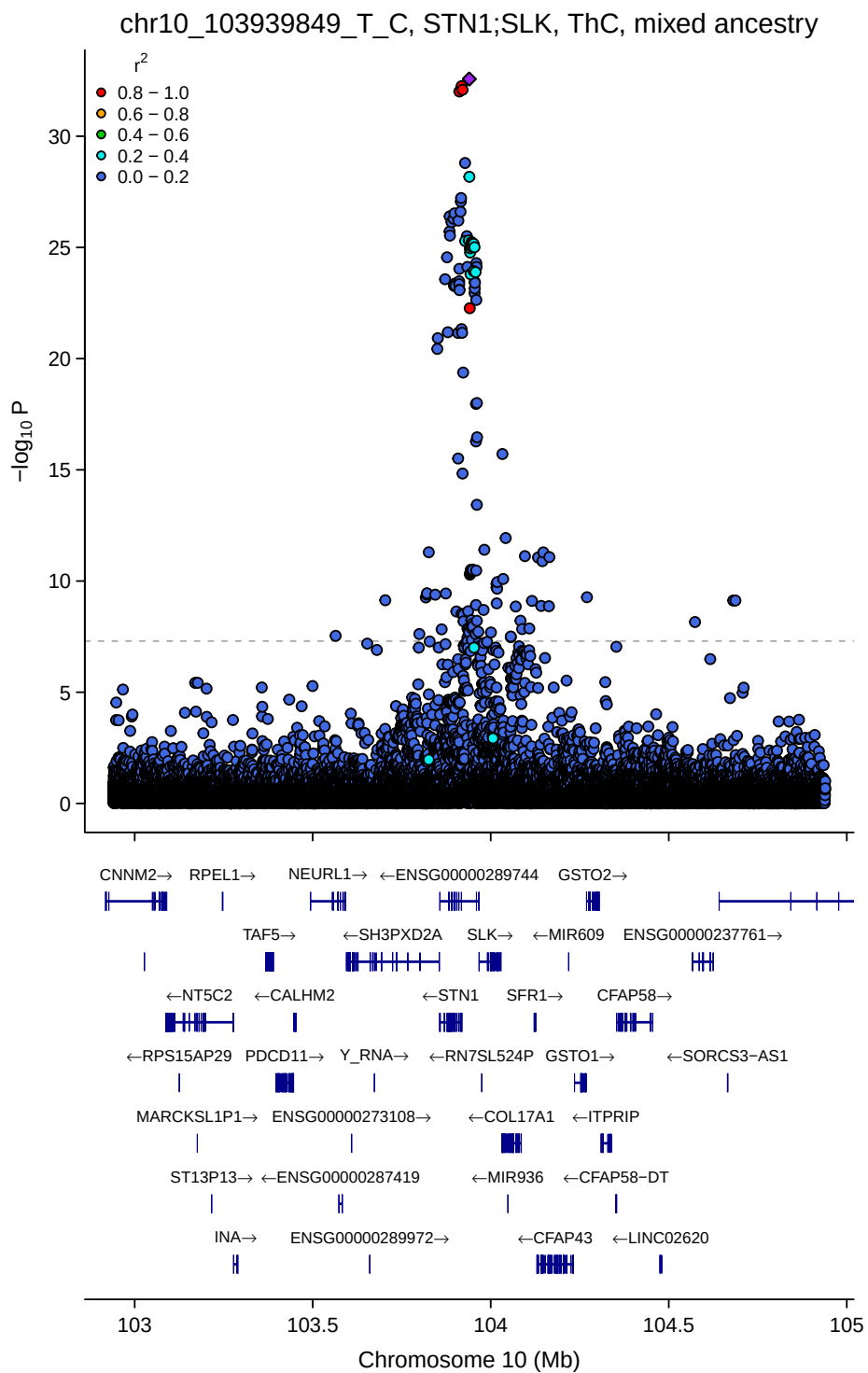
chr15\_67150258\_C\_T, SMAD3, ThC, mixed ancestry



chr15\_67150258\_C\_T, SMAD3, BNG, mixed ancestry

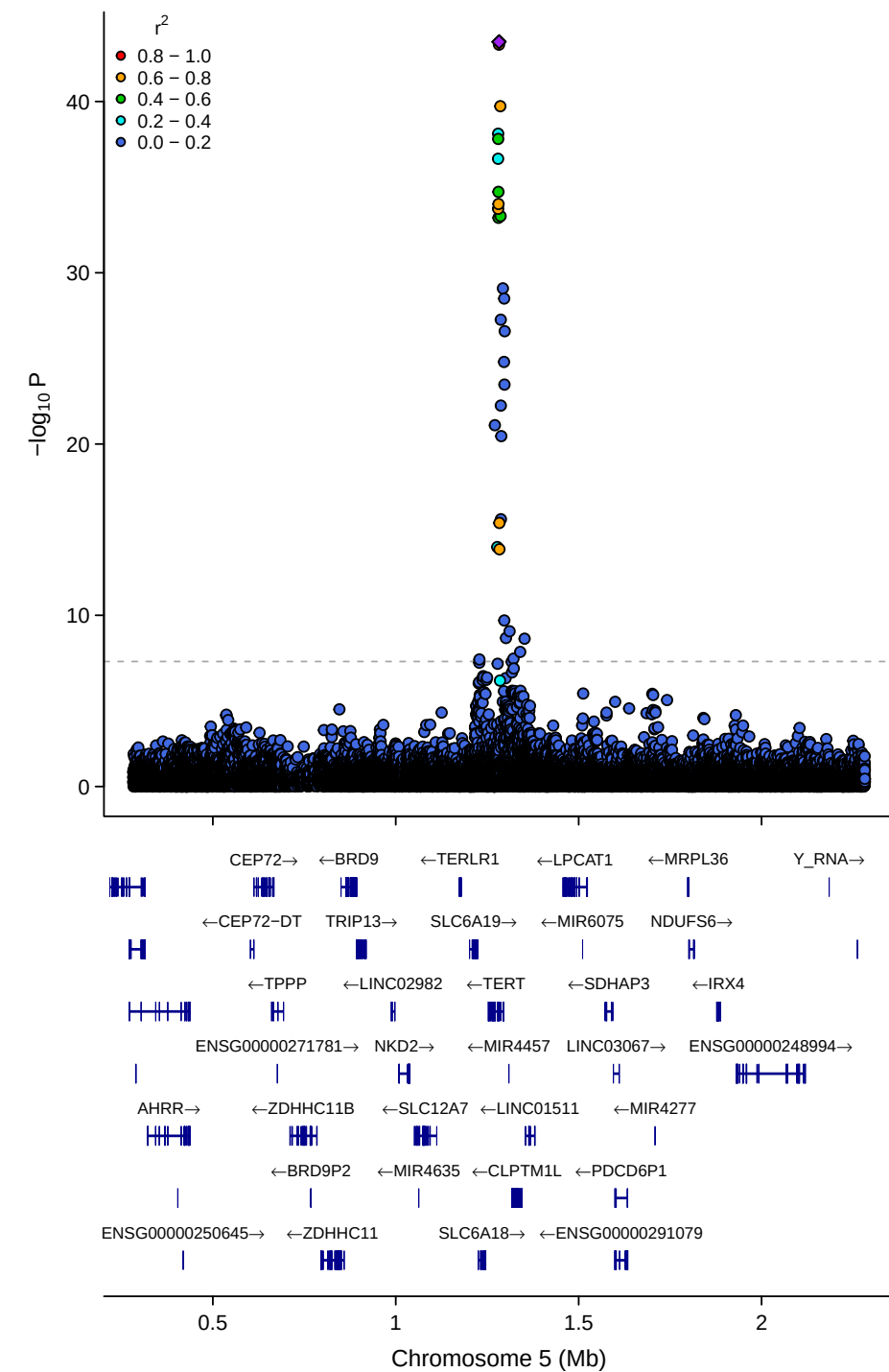


# Supplementary Figure 2.3

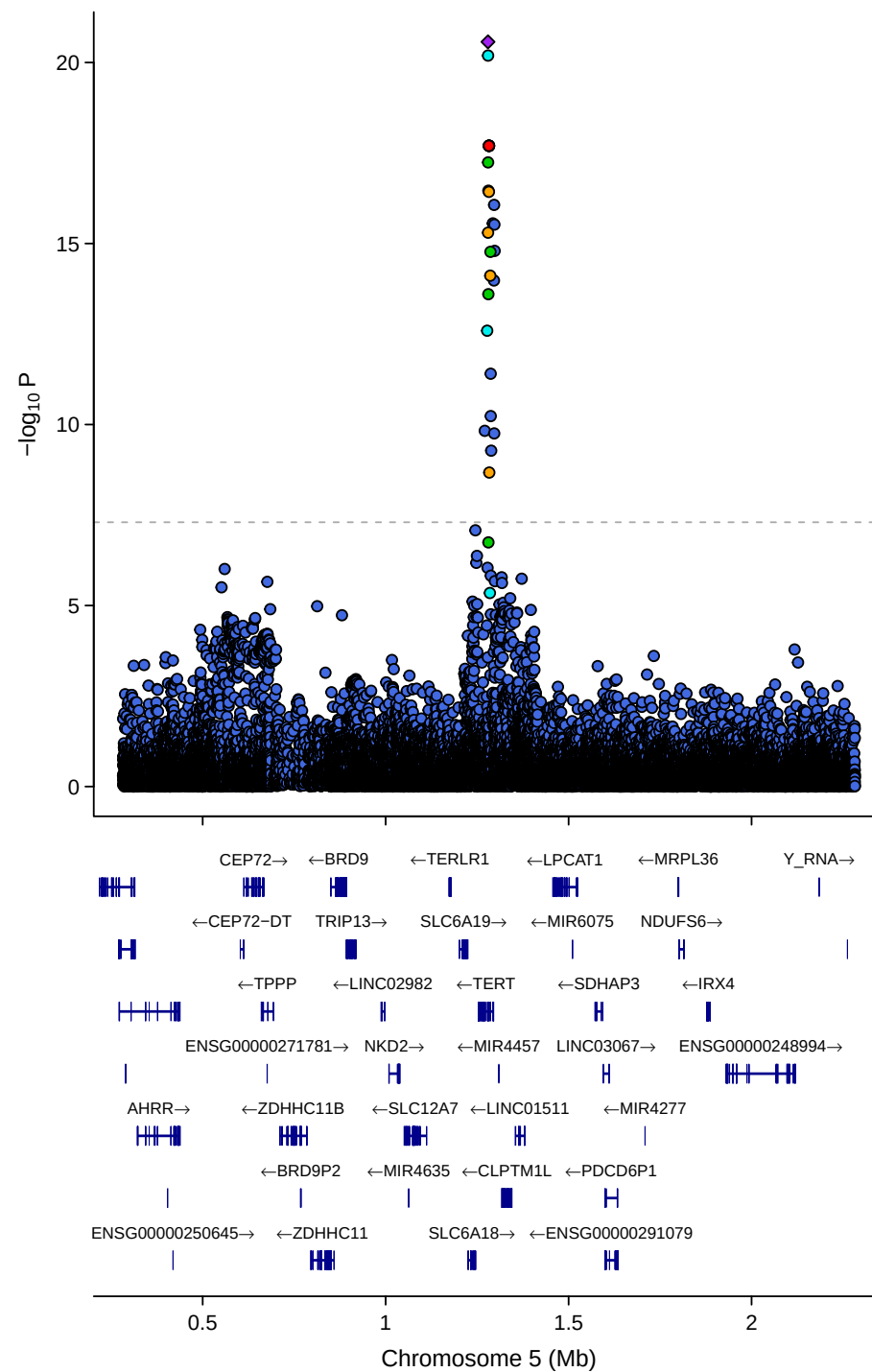


# Supplementary Figure 2.3

chr5\_1282299\_G\_A, TERT, ThC, mixed ancestry

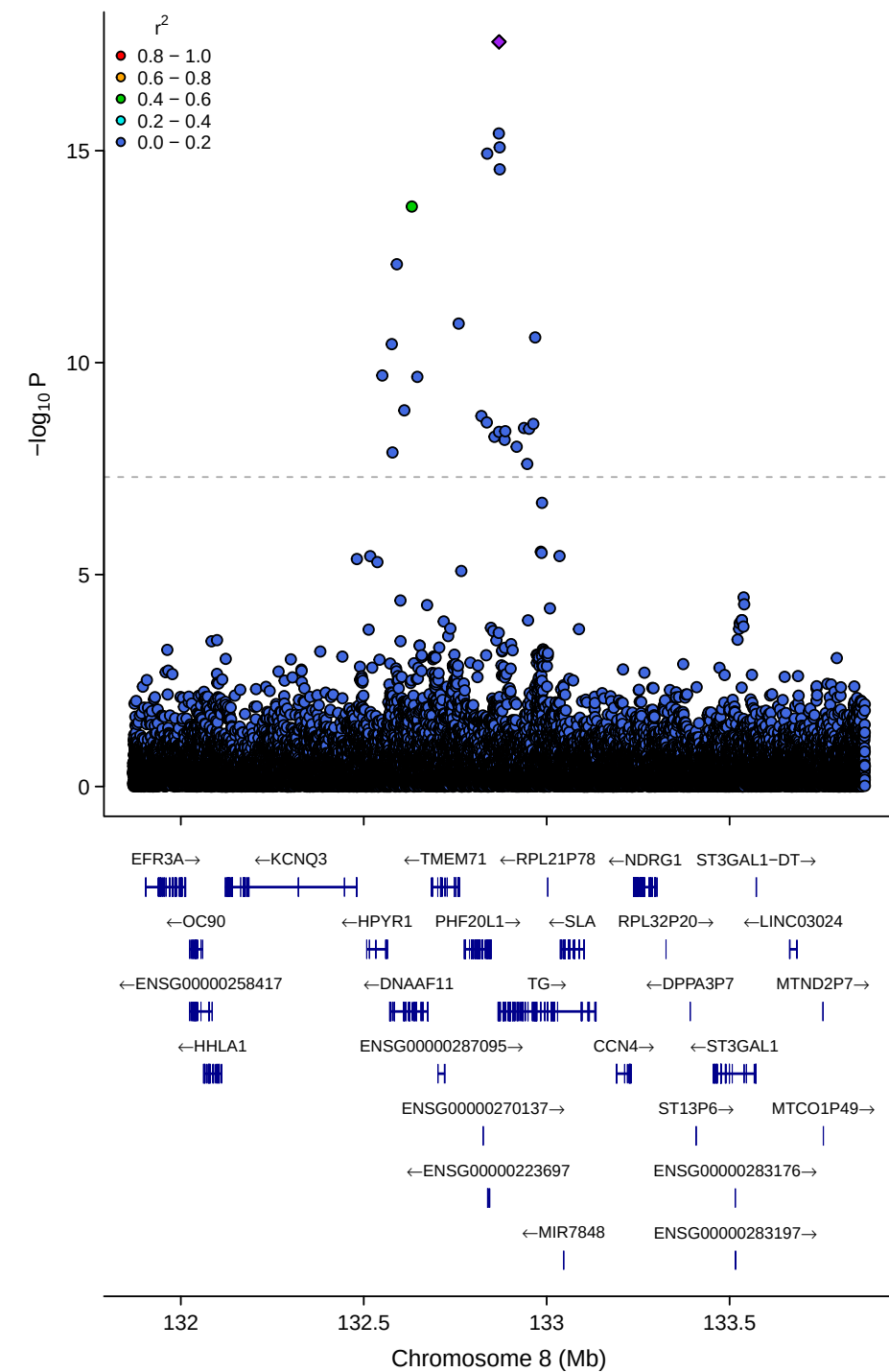


chr5\_1282299\_G\_A, TERT, BNG, mixed ancestry

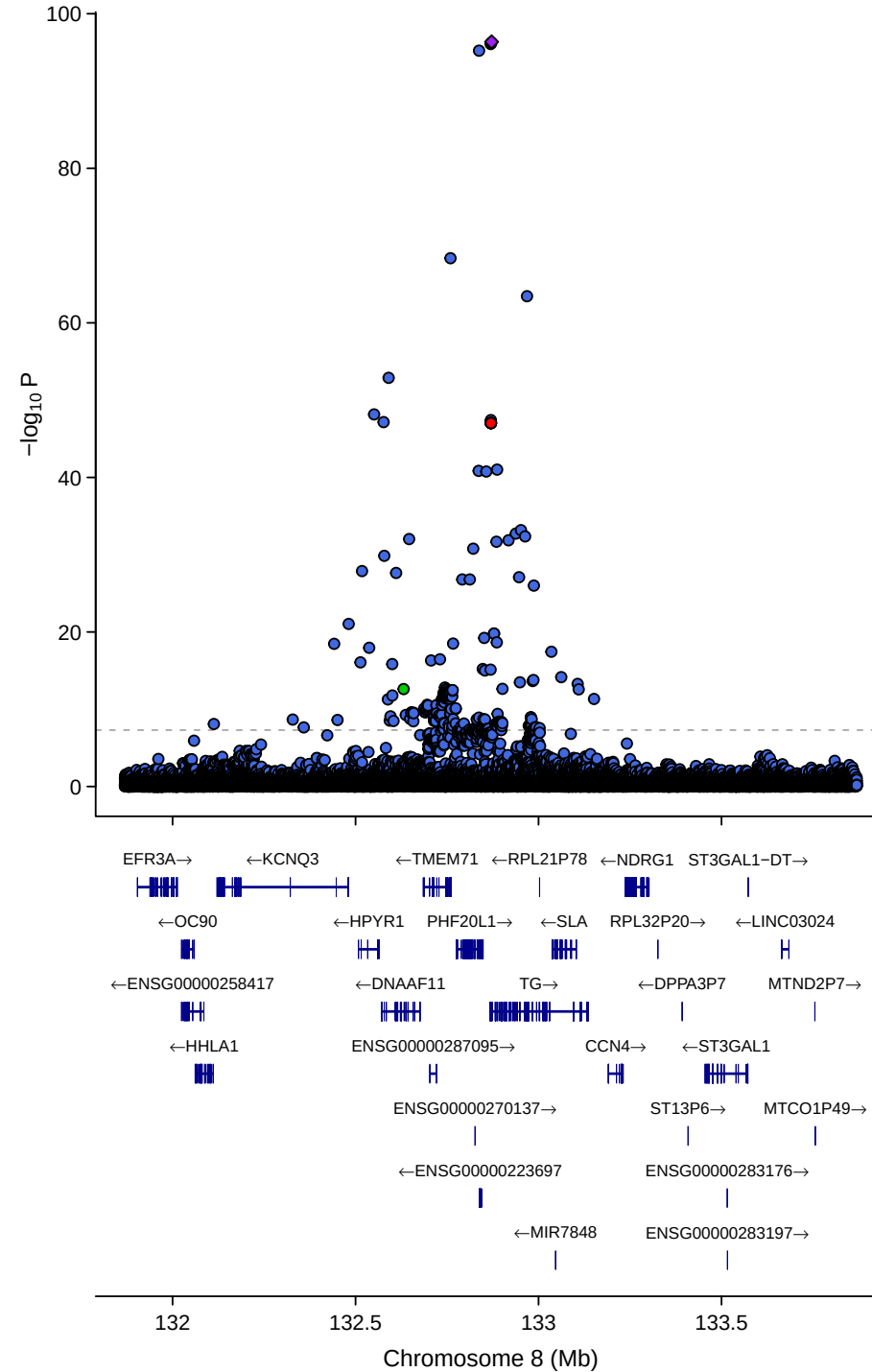


Supplementary Figure 2.3

chr8\_132869781\_G\_A, TG, ThC, mixed ancestry

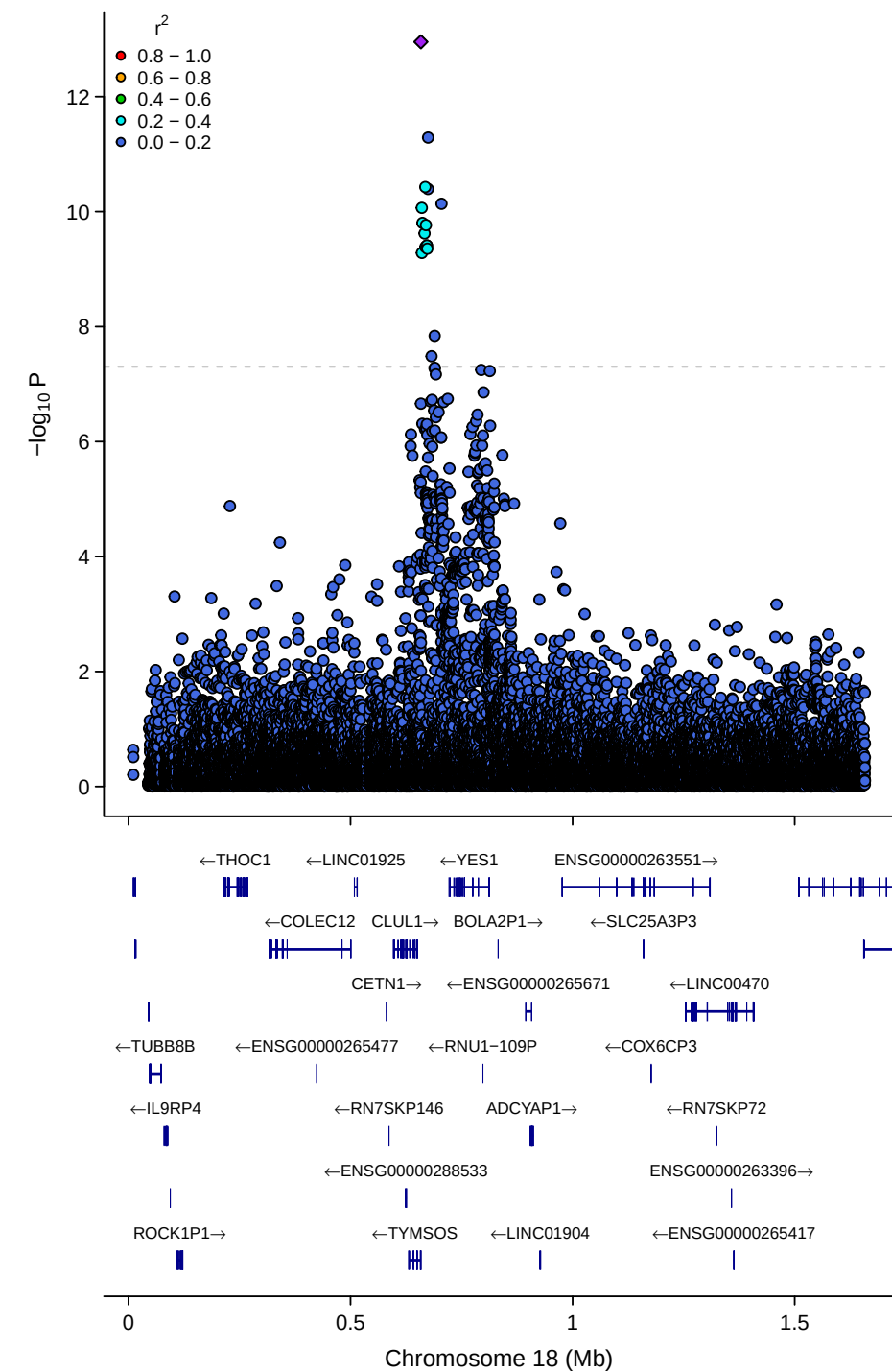


chr8\_132869781\_G\_A, TG, BNG, mixed ancestry

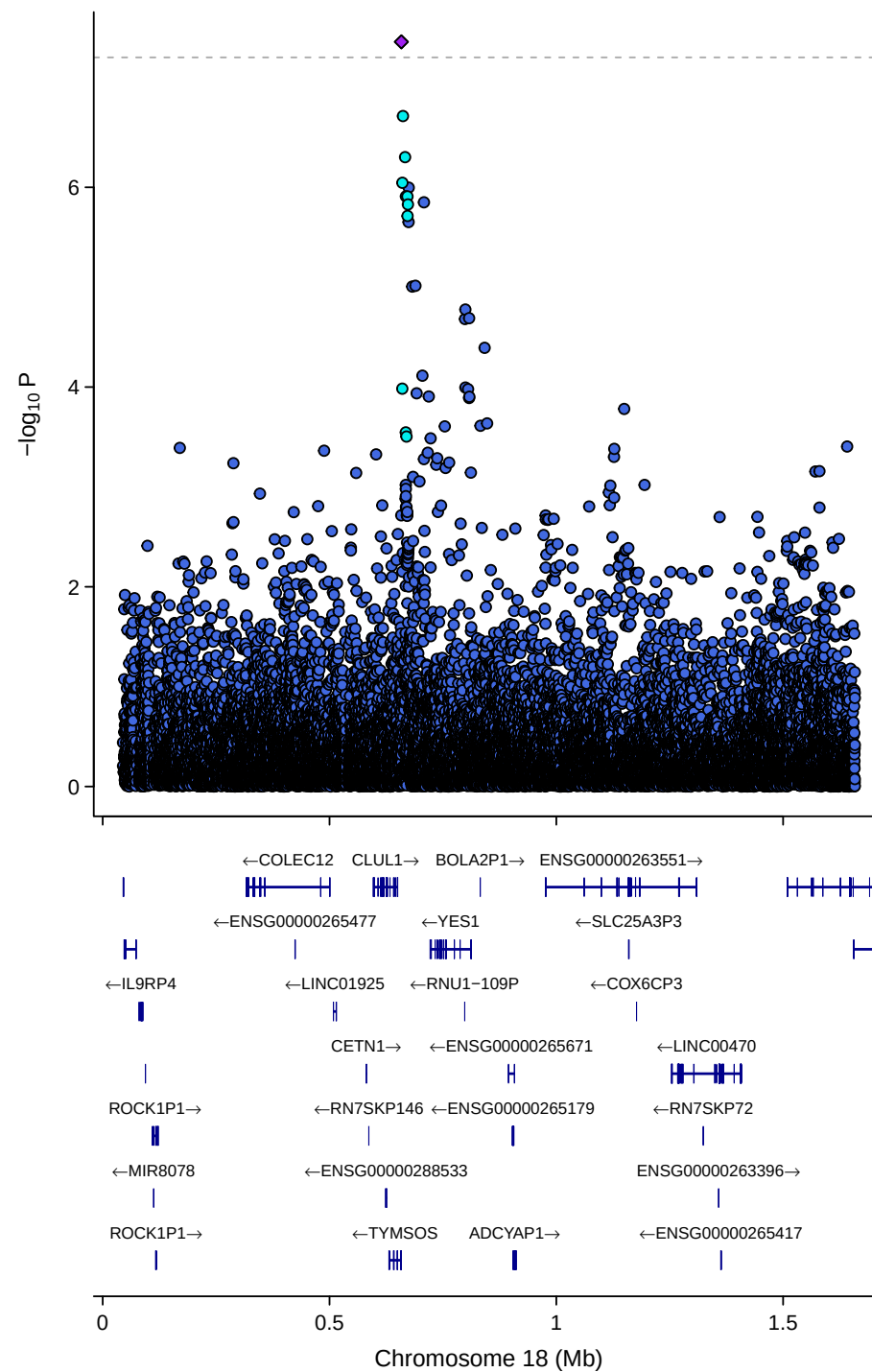


Supplementary Figure 2.3

chr18\_658423\_A\_G, TYMS, ThC, mixed ancestry

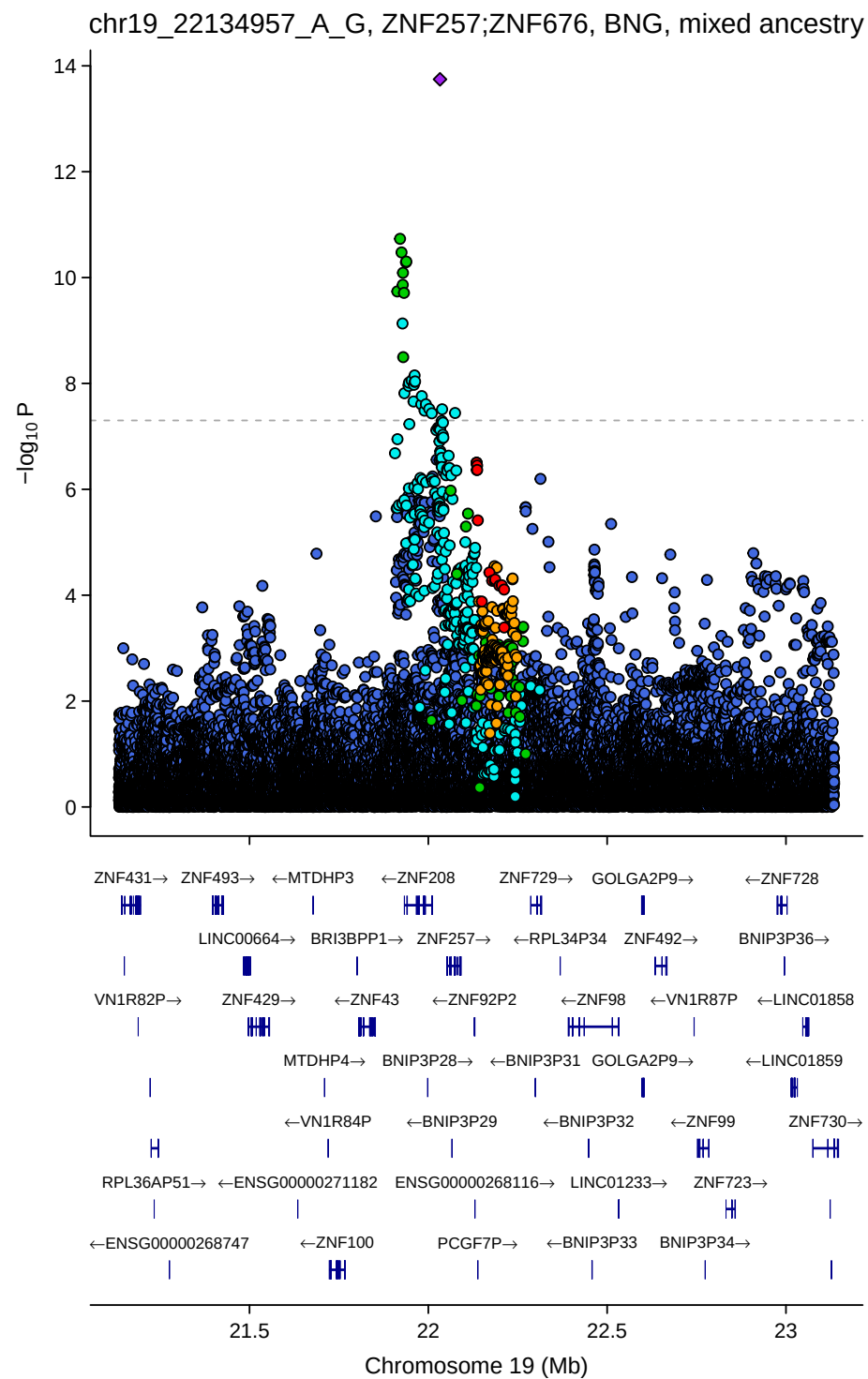
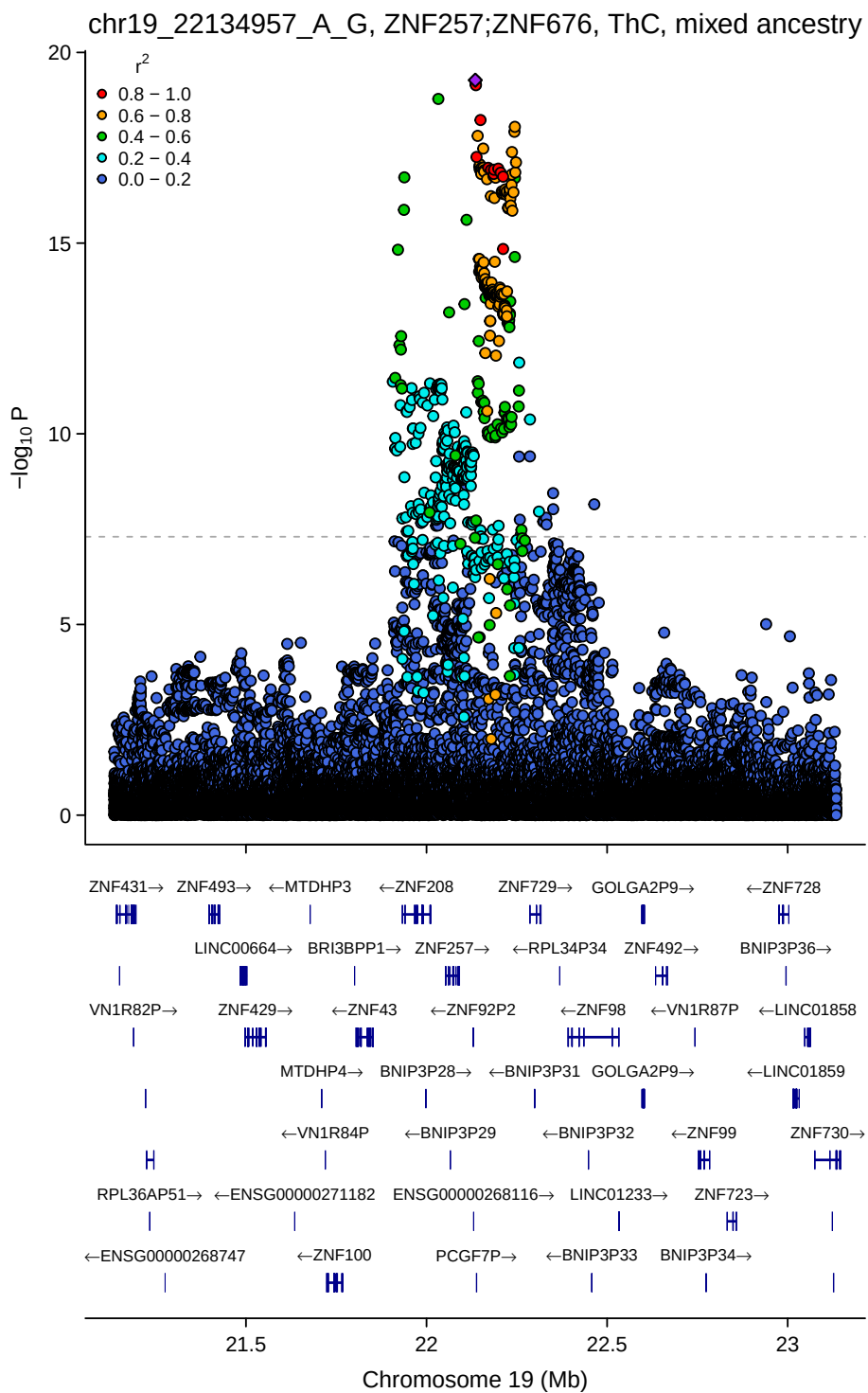


chr18\_658423\_A\_G, TYMS, BNG, mixed ancestry



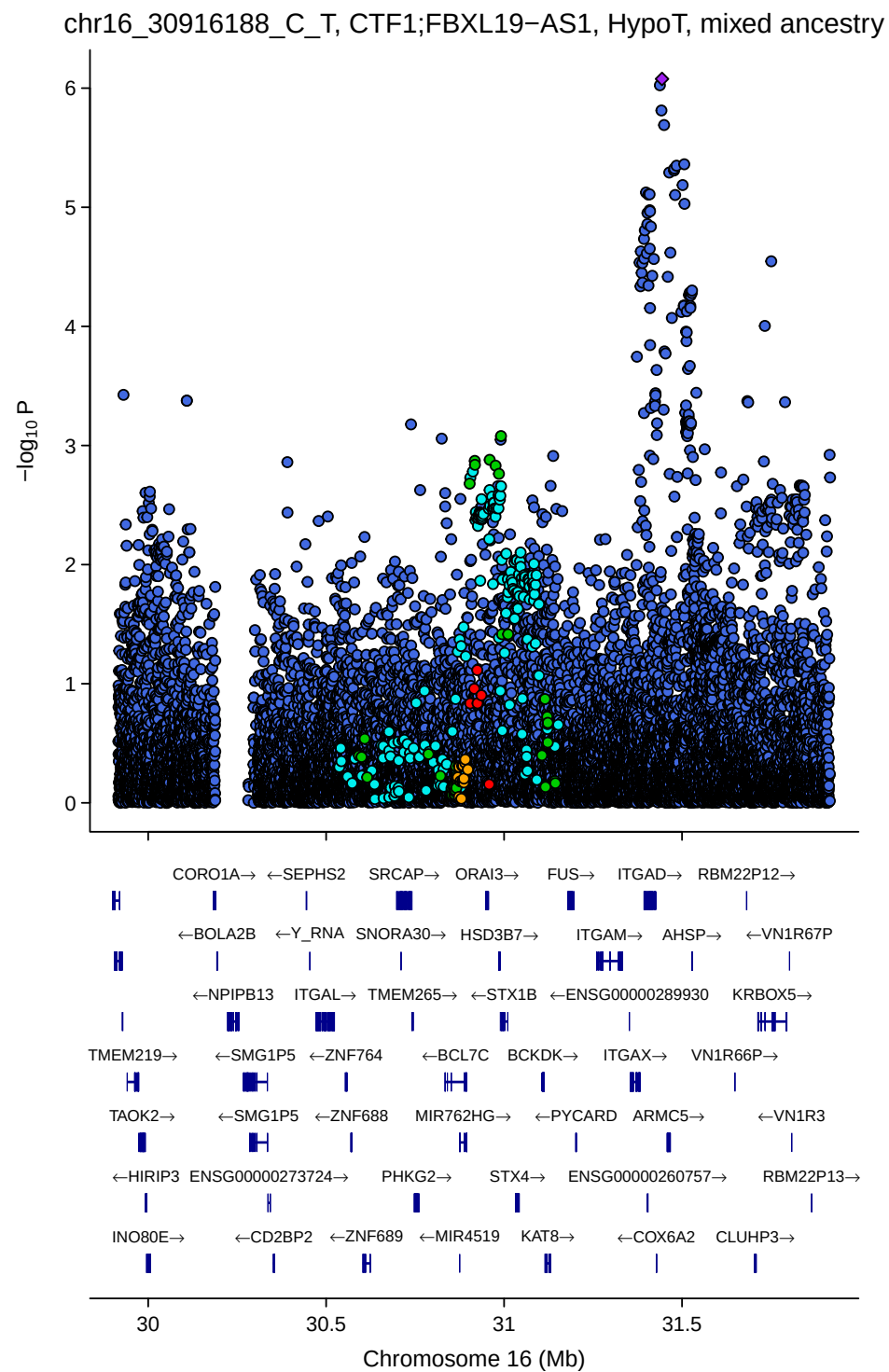
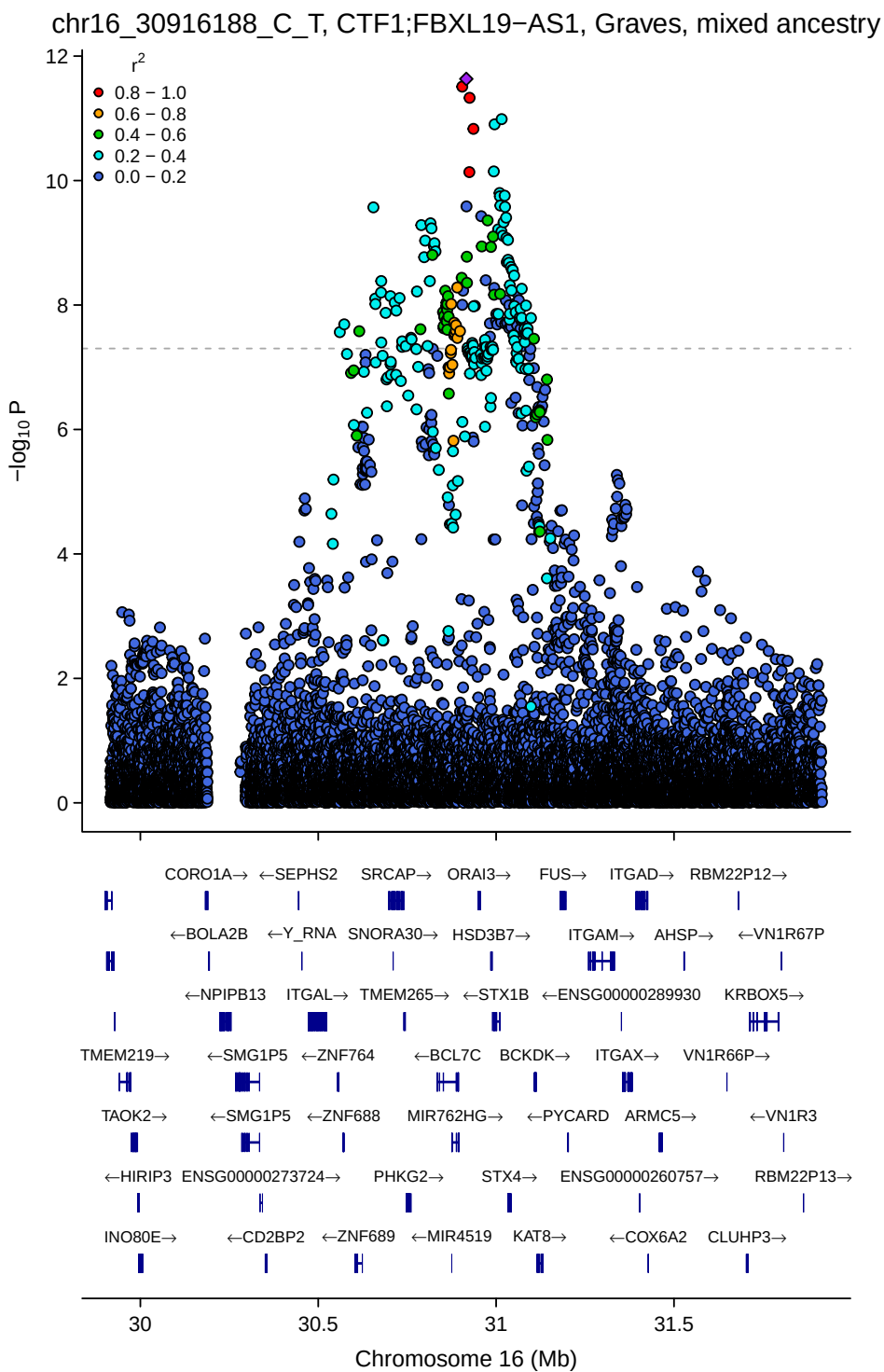


Supplementary Figure 2.3



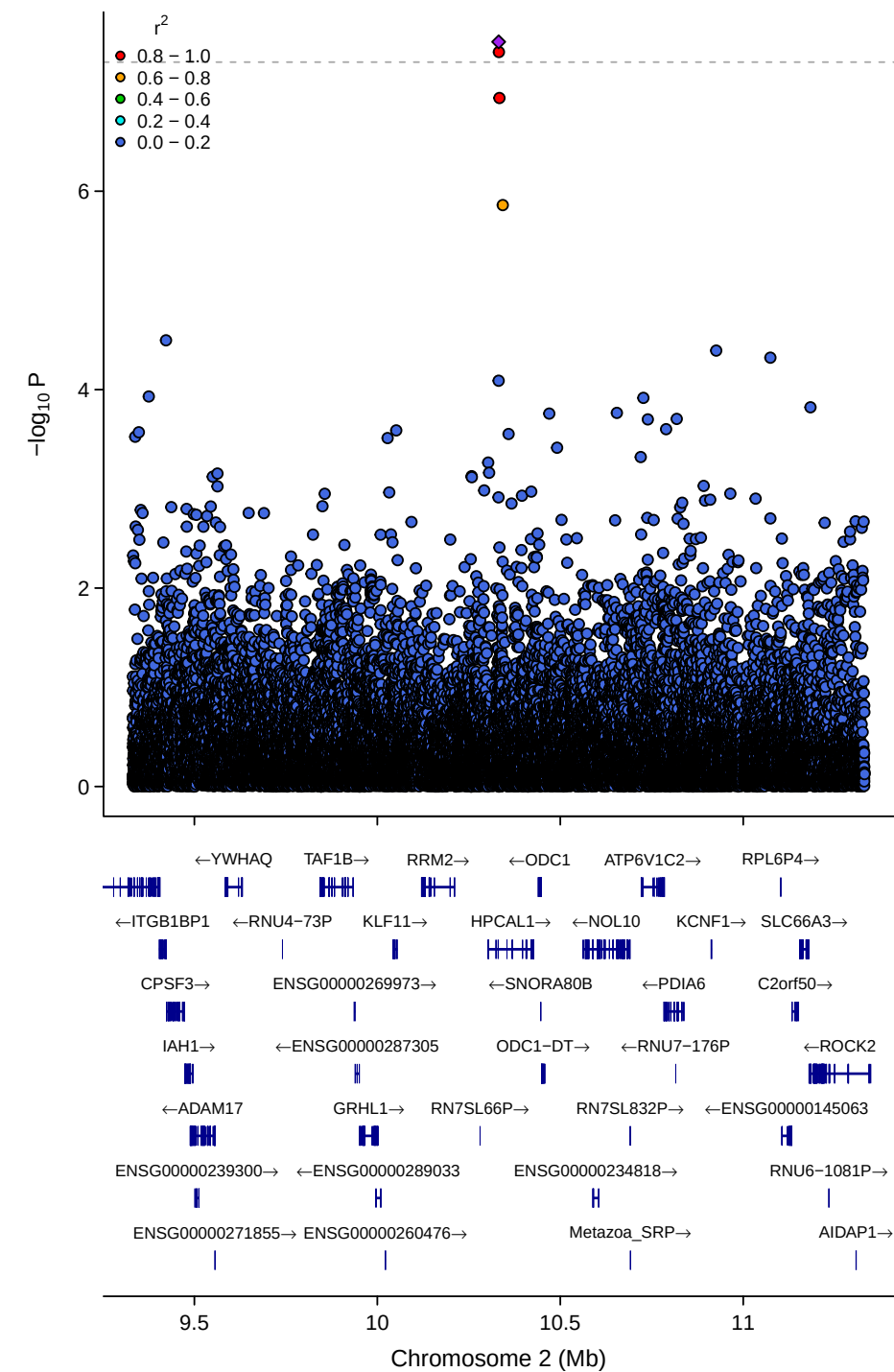
Supplementary Figure 3.1. Locus plots for loci significantly associated with Graves' disease but not hypothyroidism. The left plot displays  $-\log_{10}(\text{p-values})$  for variants from the Graves' disease meta-analysis, the right plot displays  $-\log_{10}(\text{p-values})$  for variants within the same genomic region from the hypothyroidism meta-analysis. The lead variant is shown with a purple diamond. Genome wide significance is indicated by the dashed horizontal line at  $-\log_{10}(5\text{e-}8)$ .

# Supplementary Figure 3.1

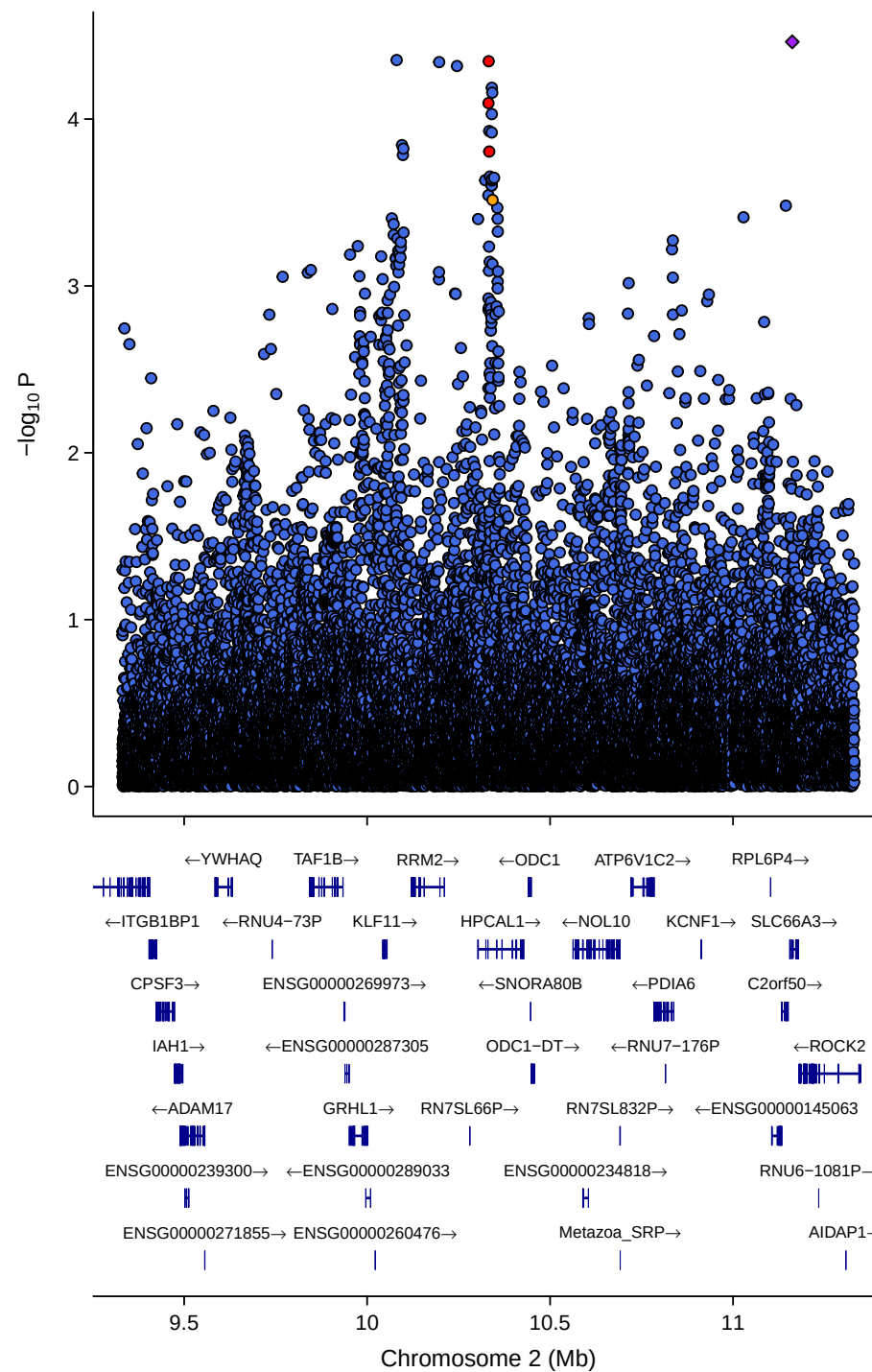


Supplementary Figure 3.1

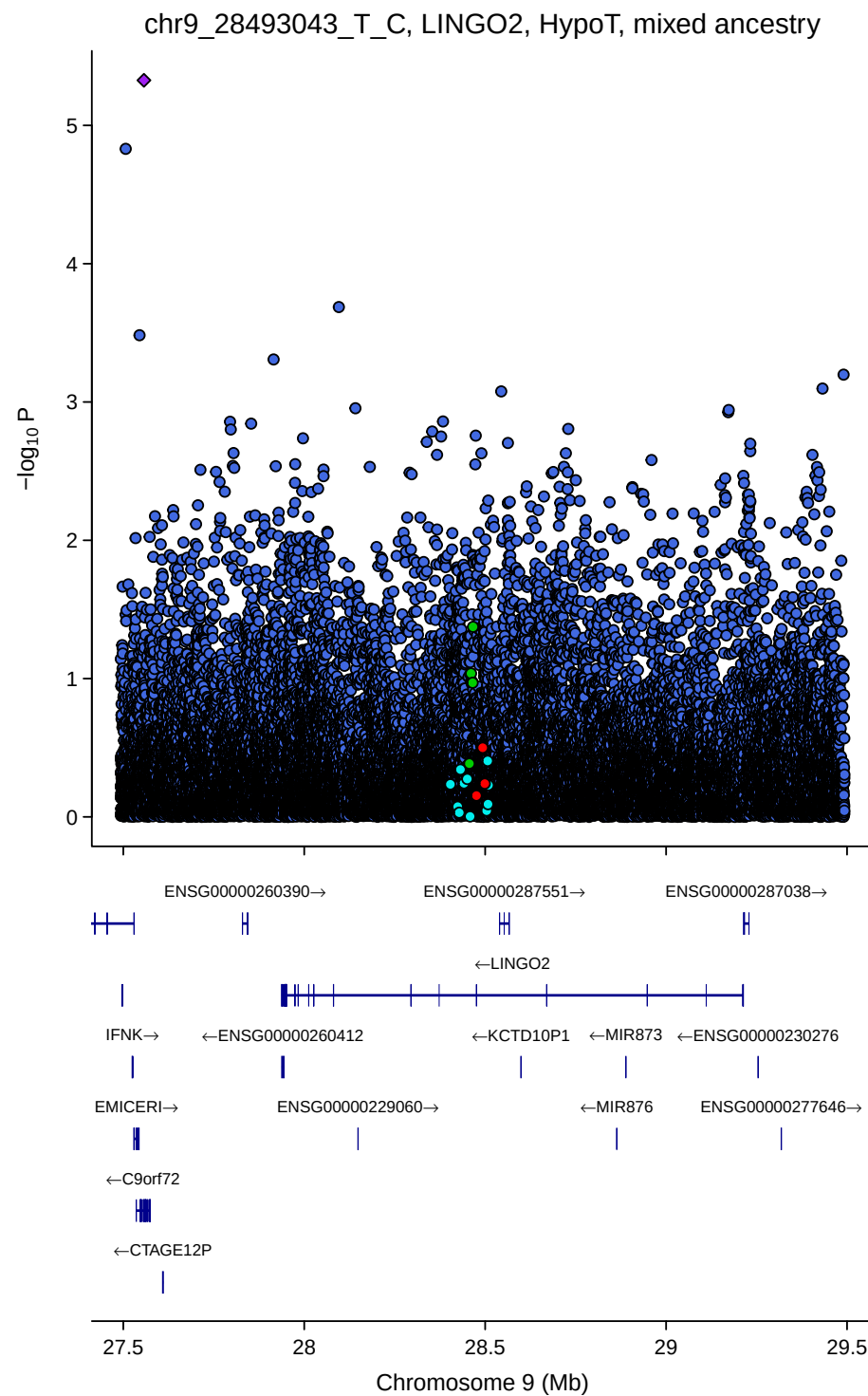
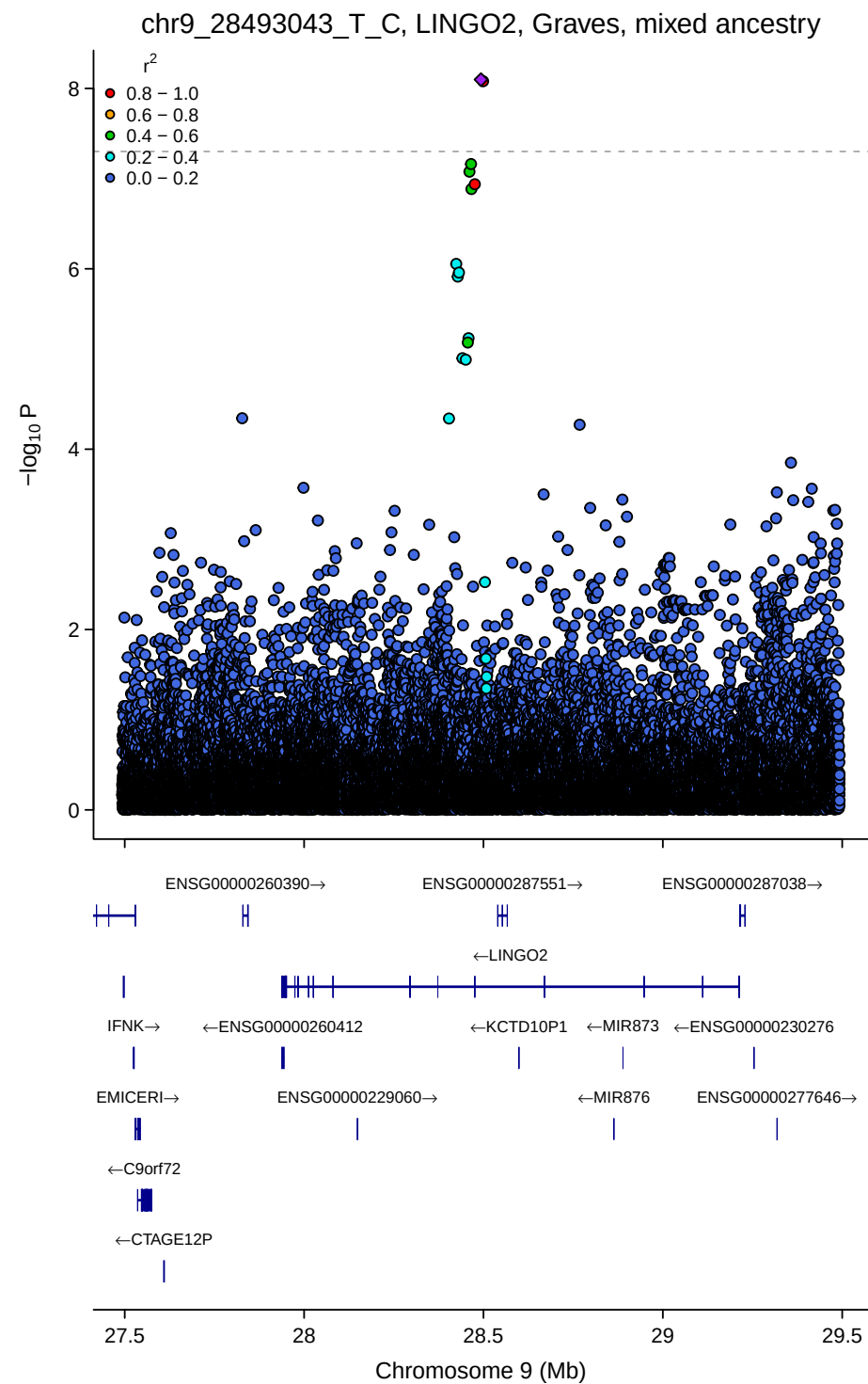
chr2\_10331614\_C\_T, HPCAL1, Graves, mixed ancestry



chr2\_10331614\_C\_T, HPCAL1, HypoT, mixed ancestry

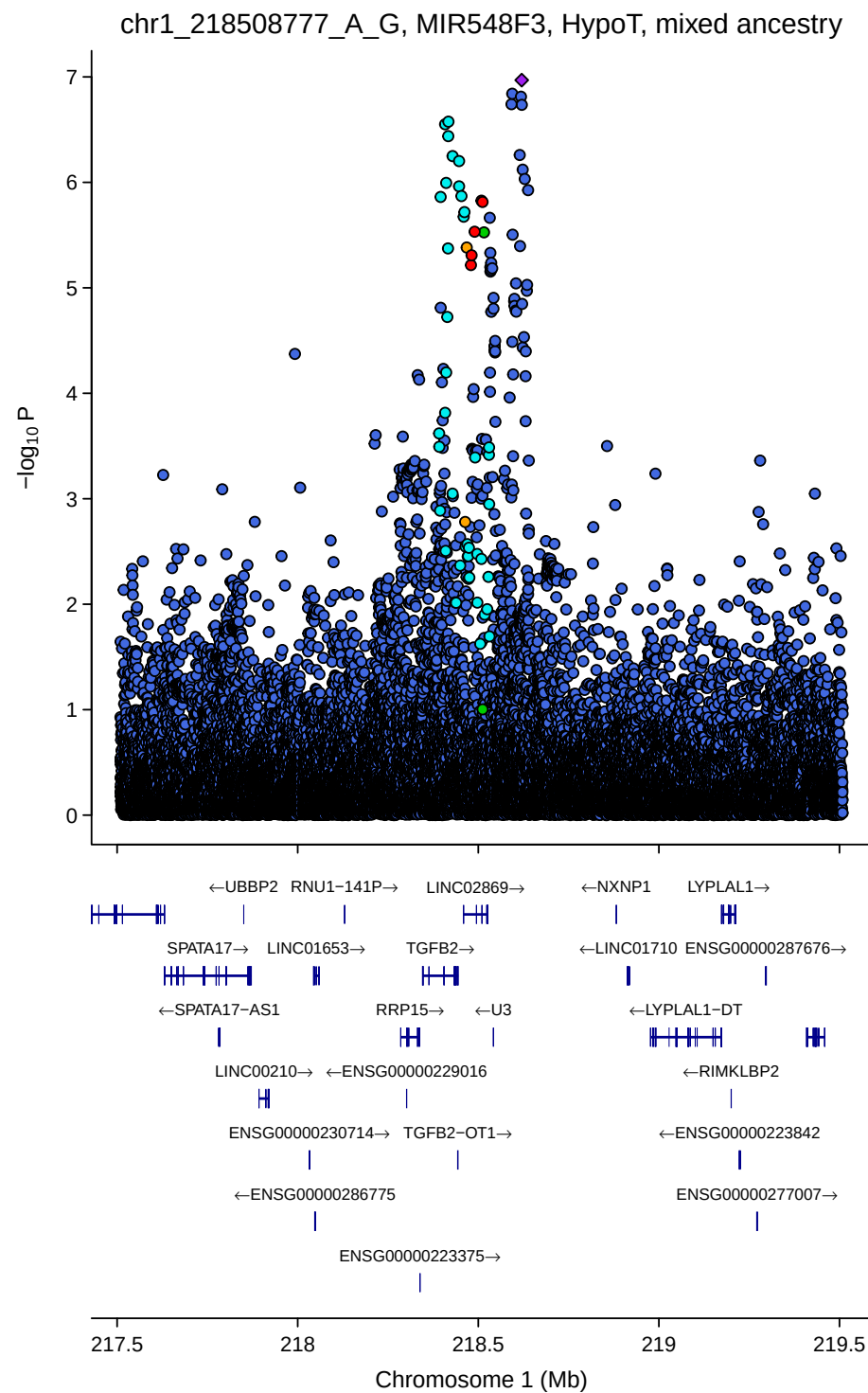
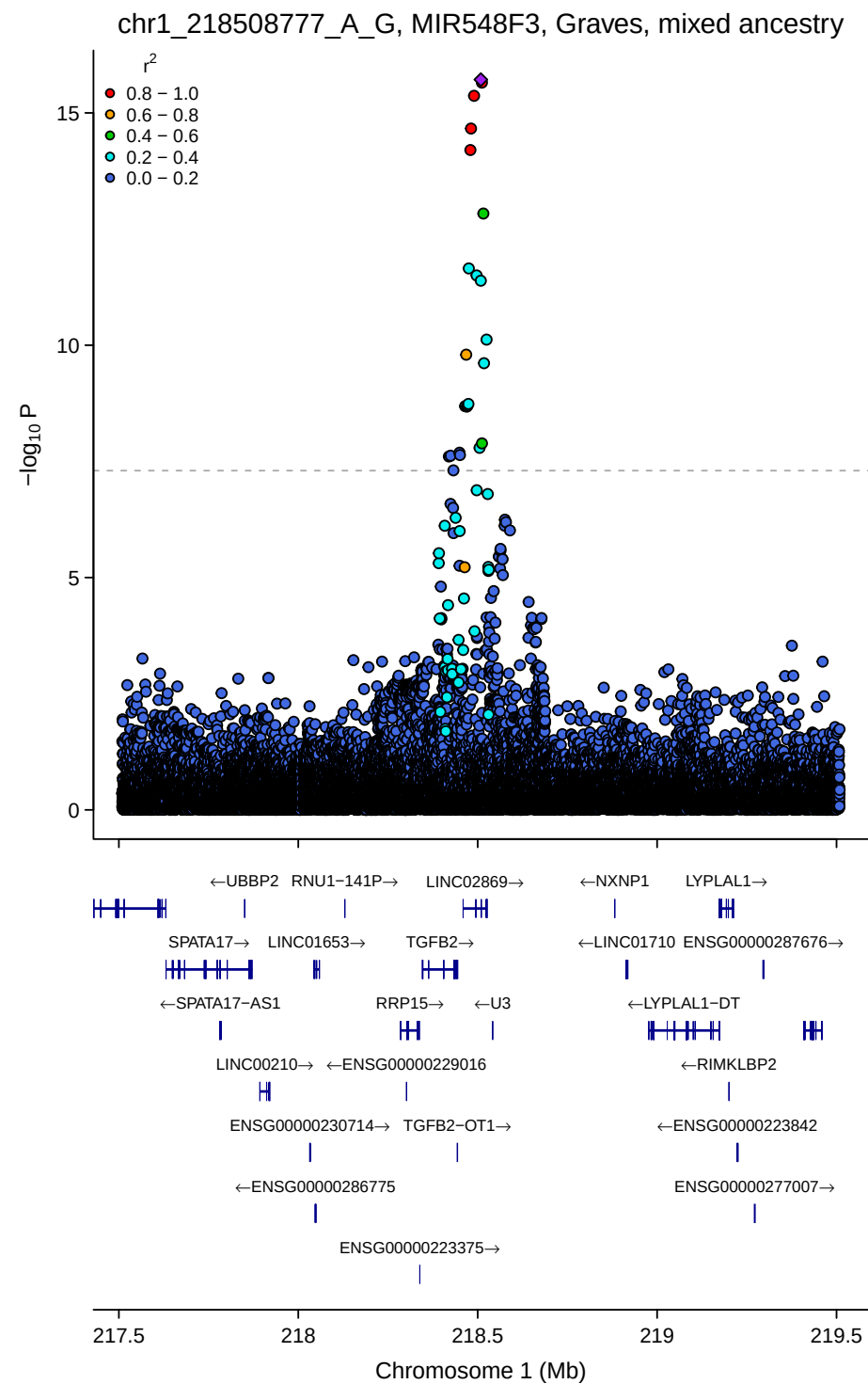


Supplementary Figure 3.1





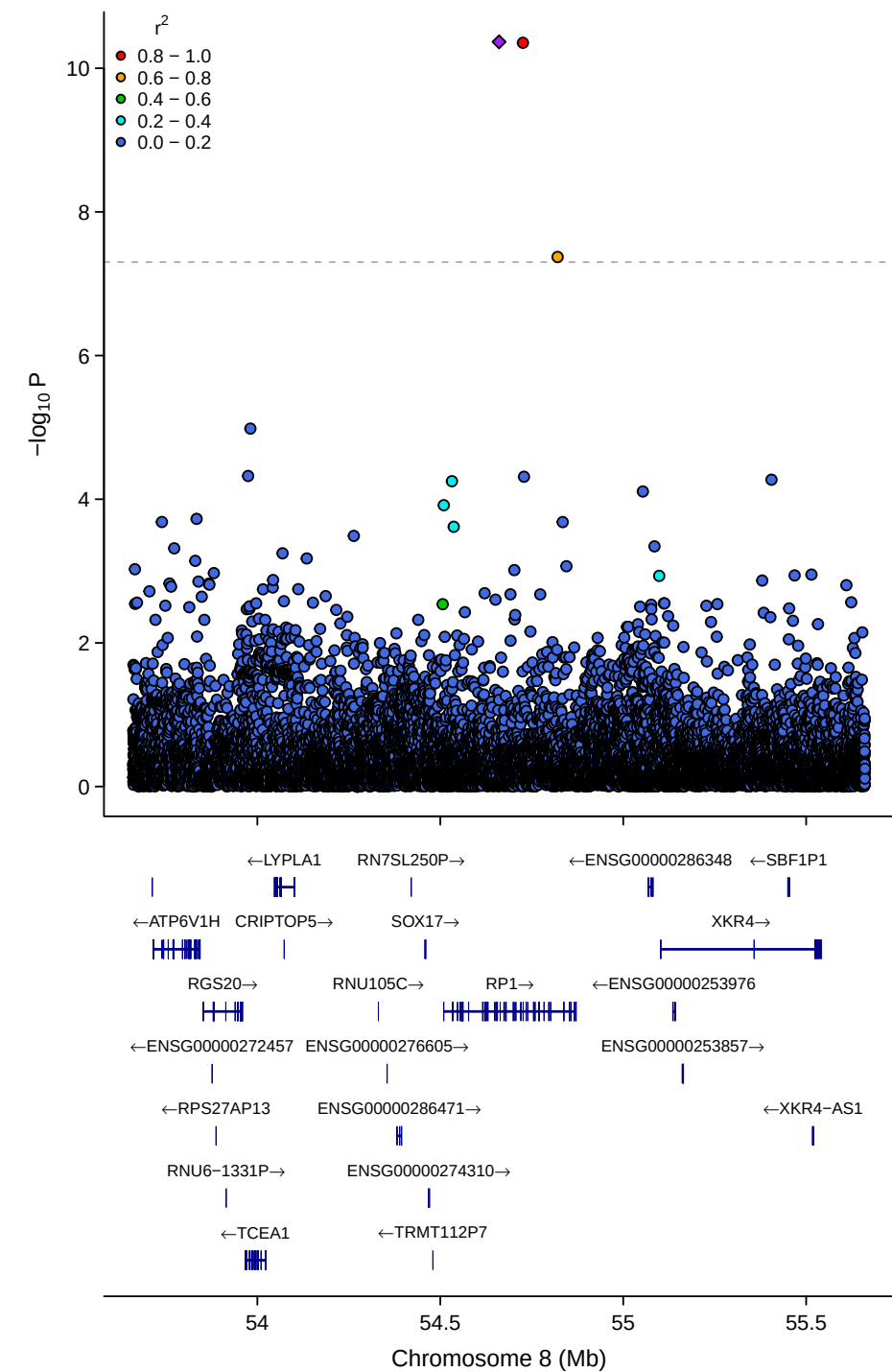
Supplementary Figure 3.1



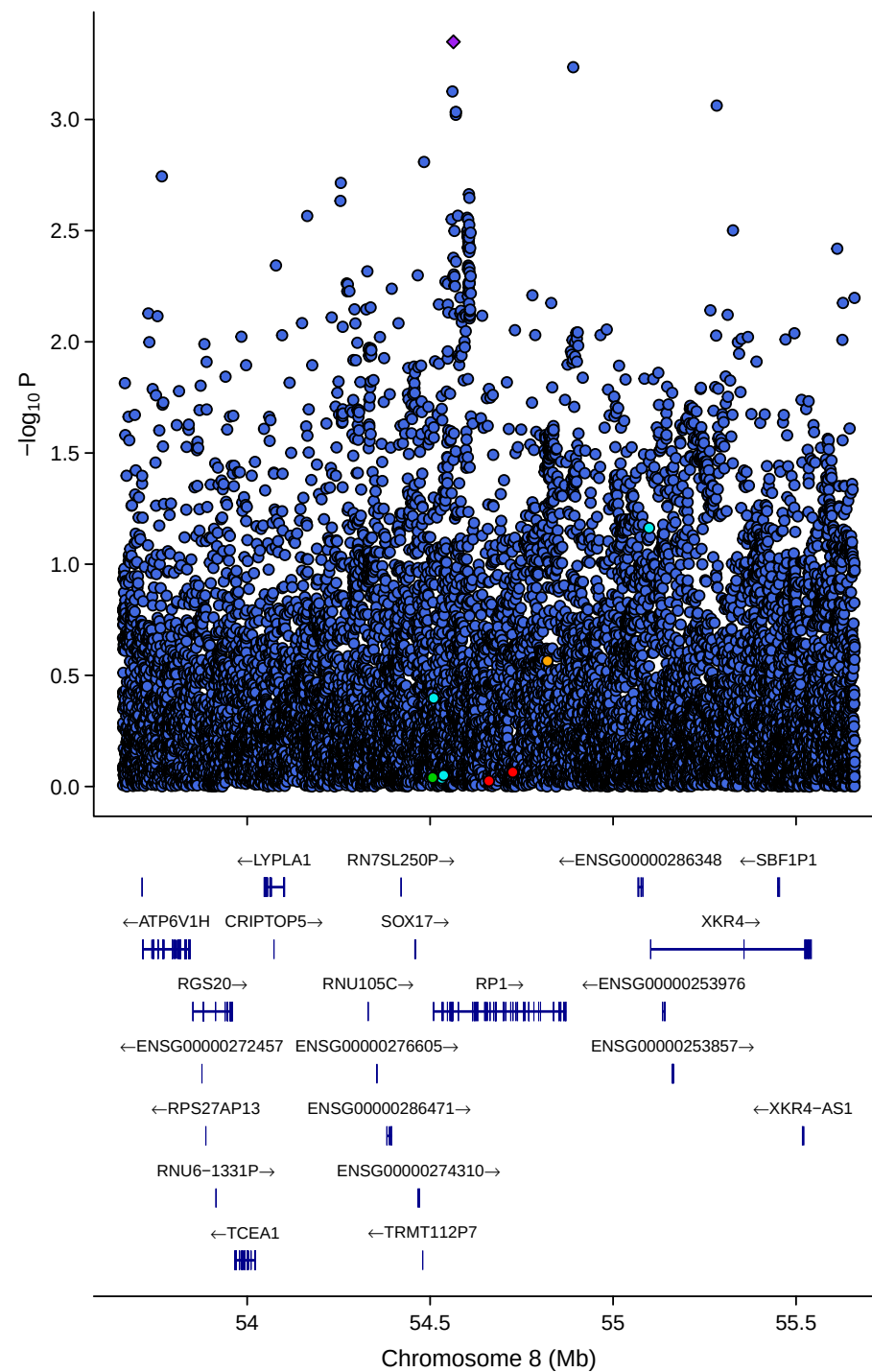


Supplementary Figure 3.1

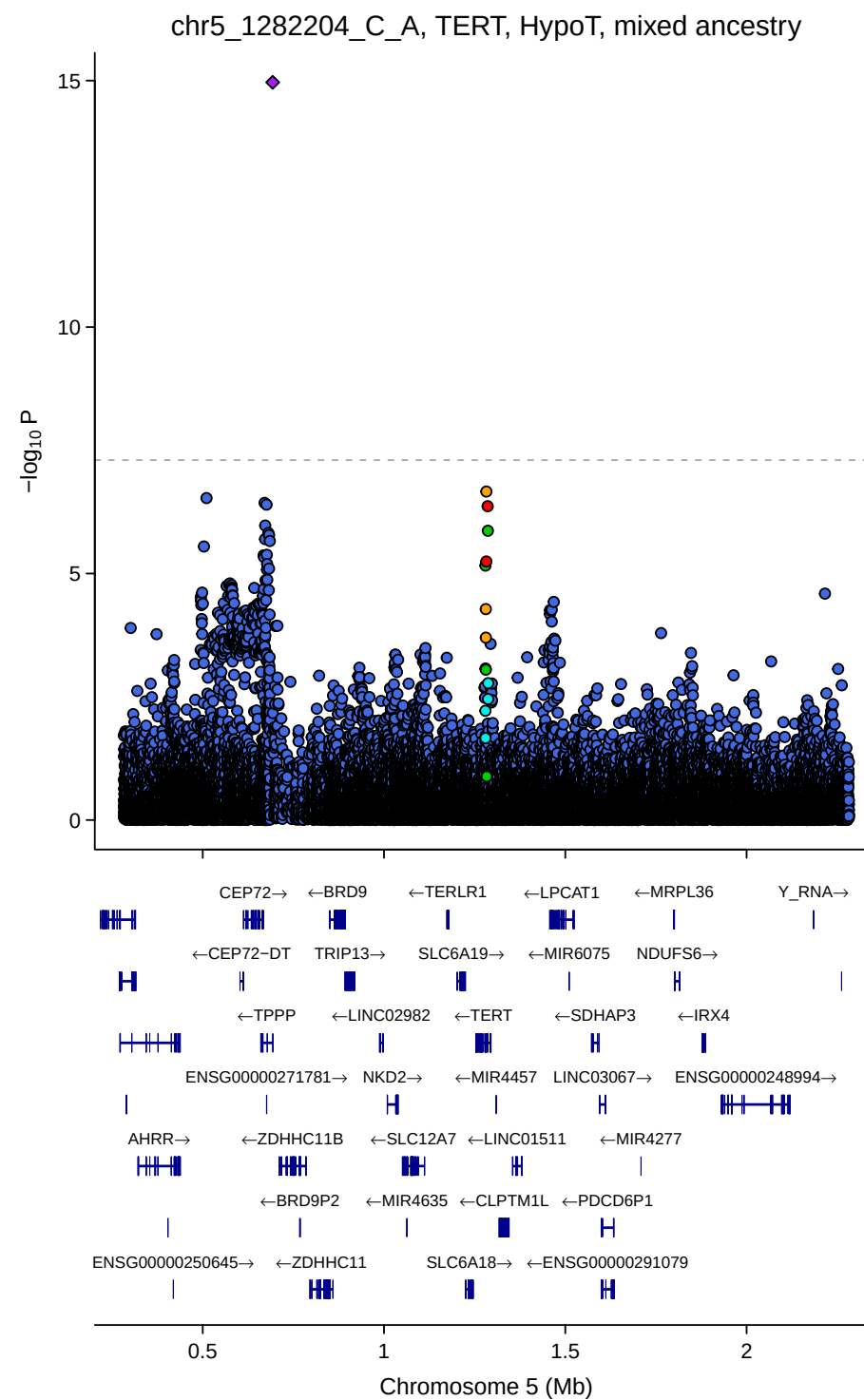
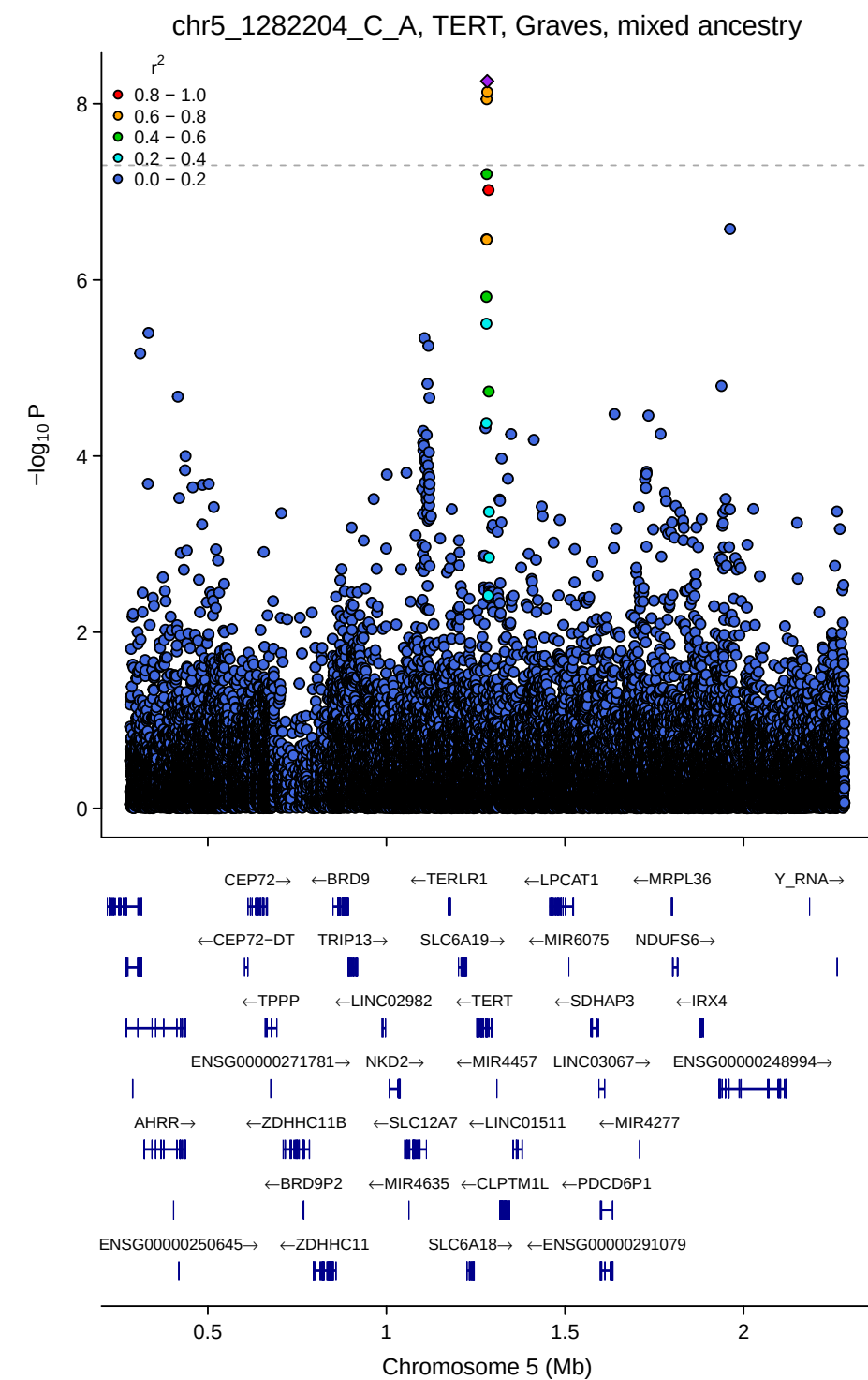
chr8\_54660719\_T\_C, RP1, Graves, EUR ancestry



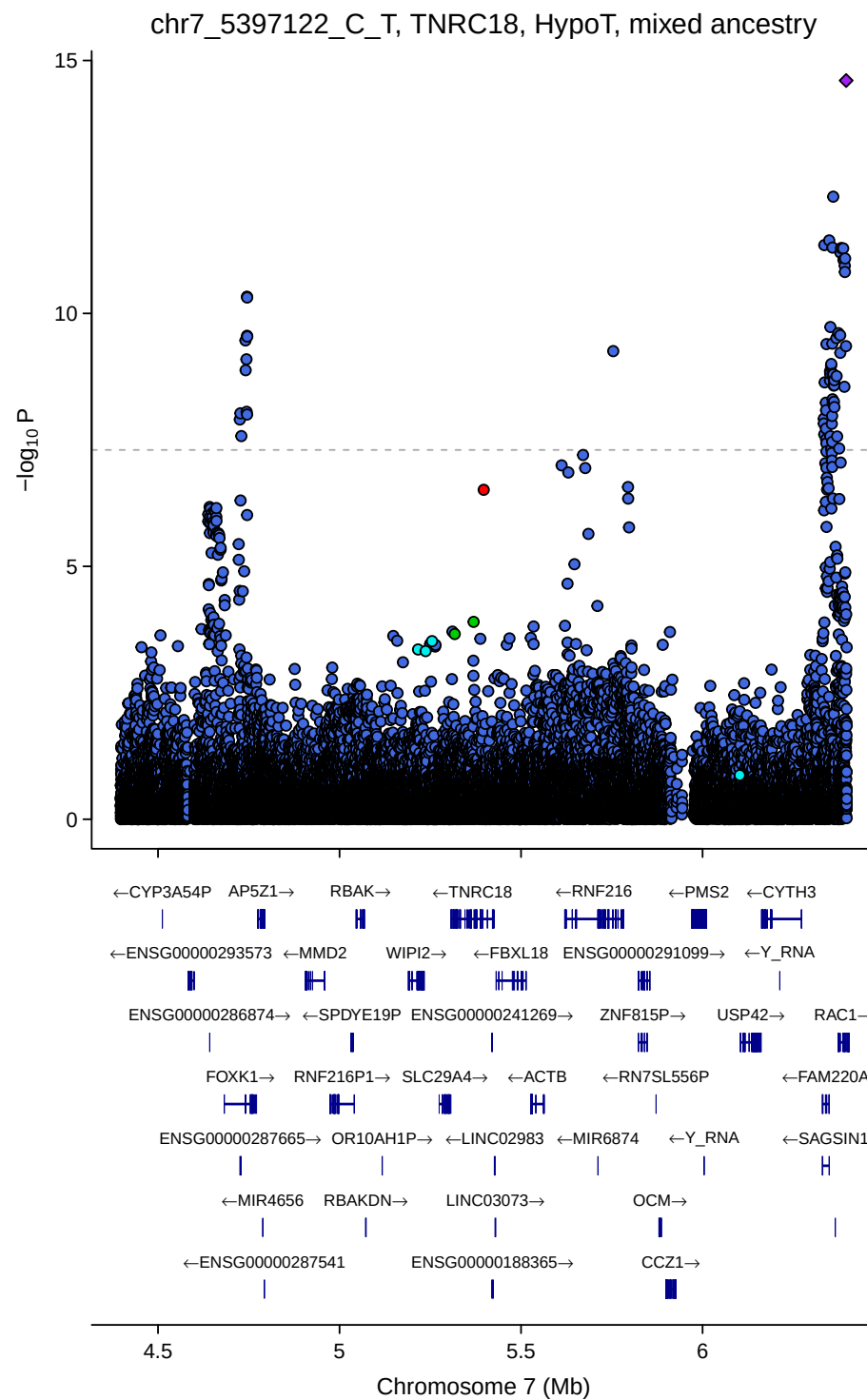
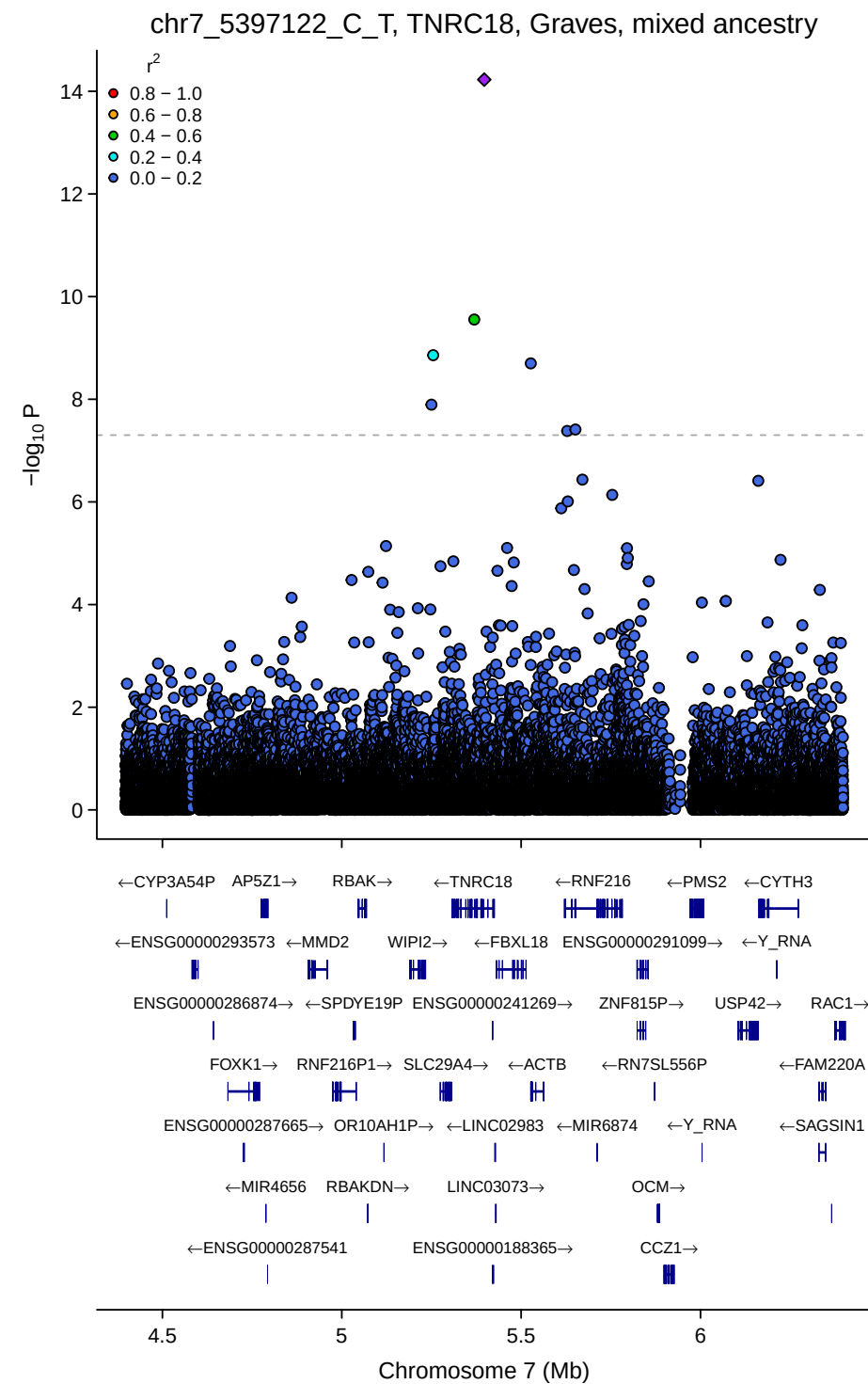
chr8\_54660719\_T\_C, RP1, HypoT, EUR ancestry



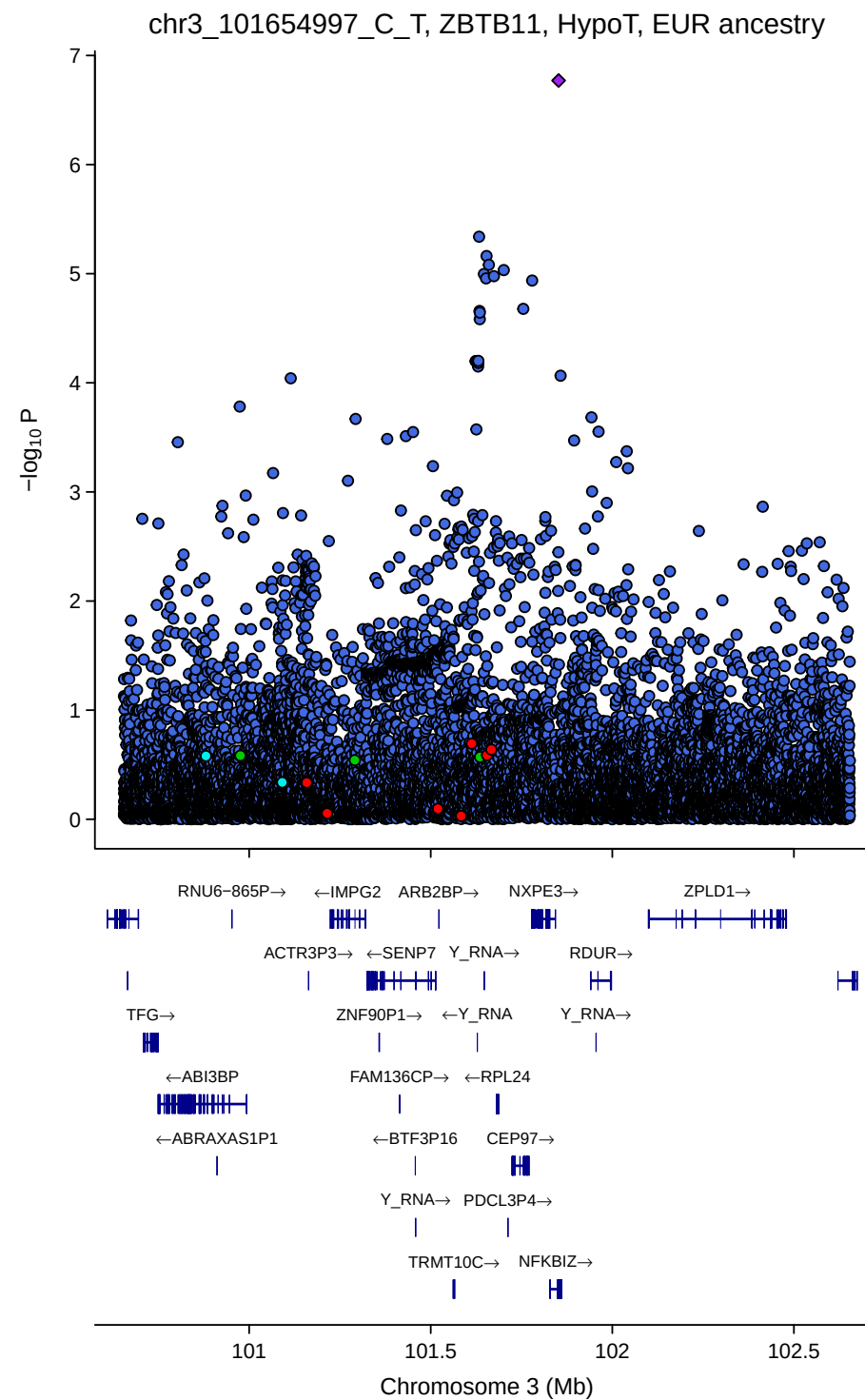
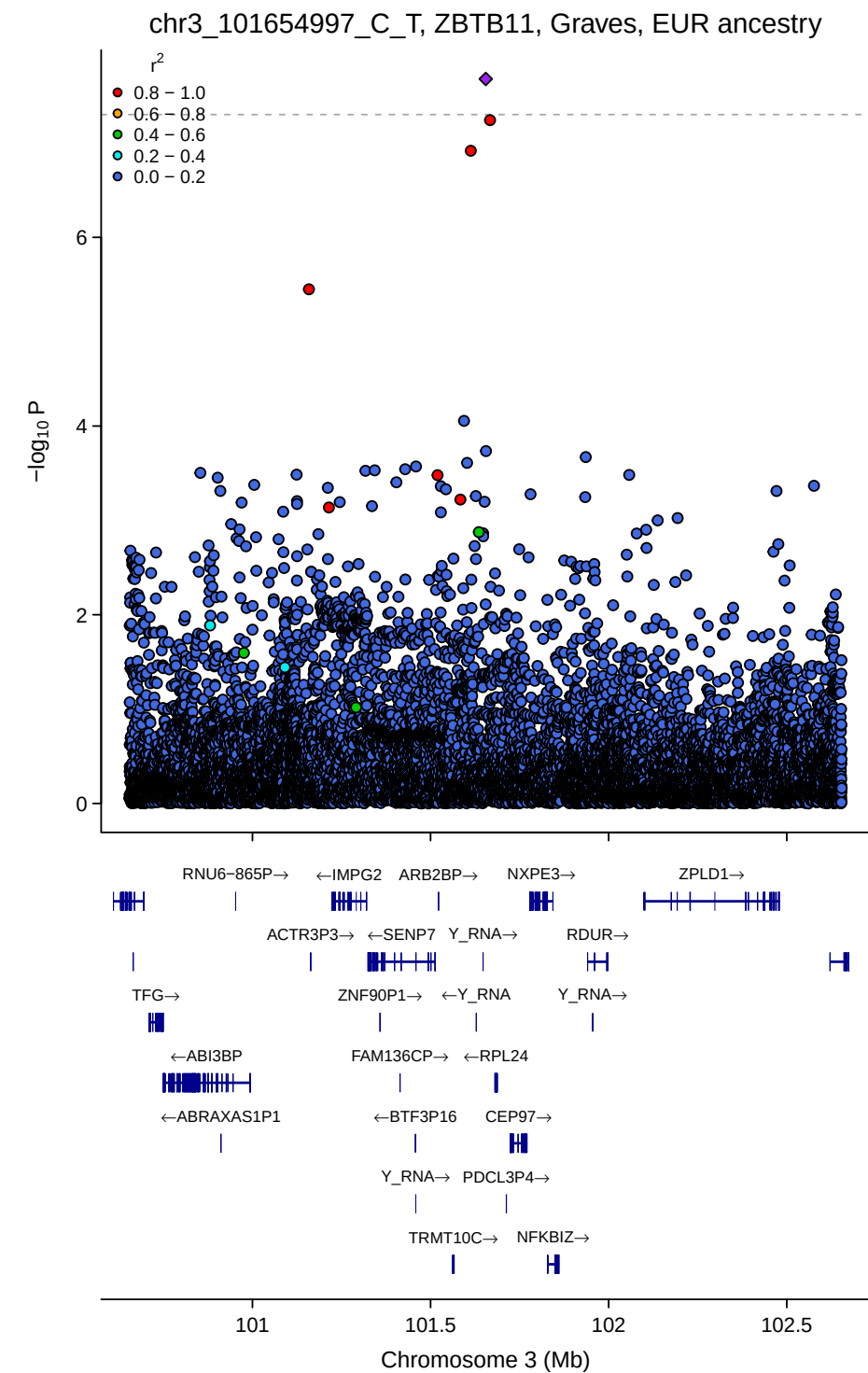
Supplementary Figure 3.1



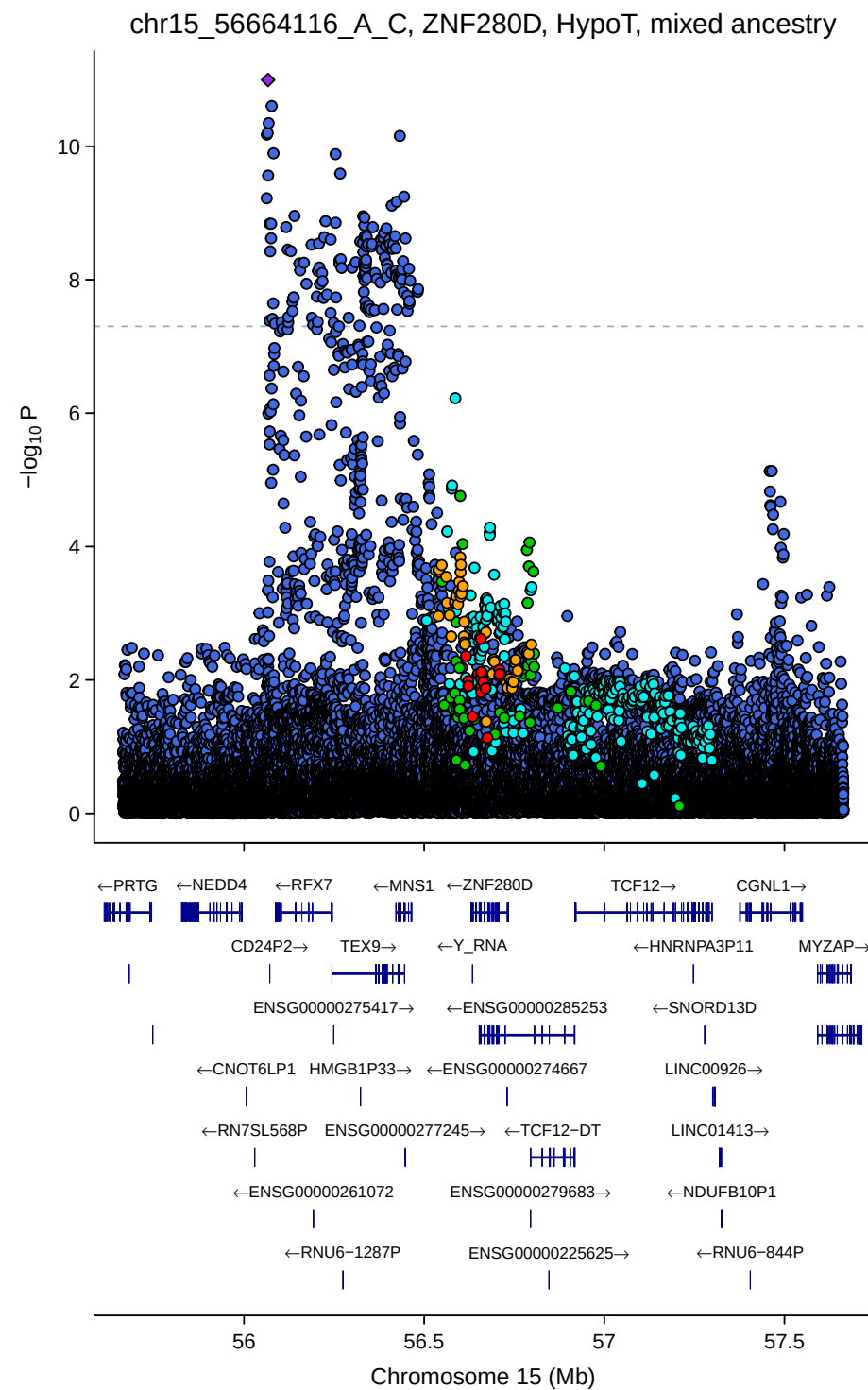
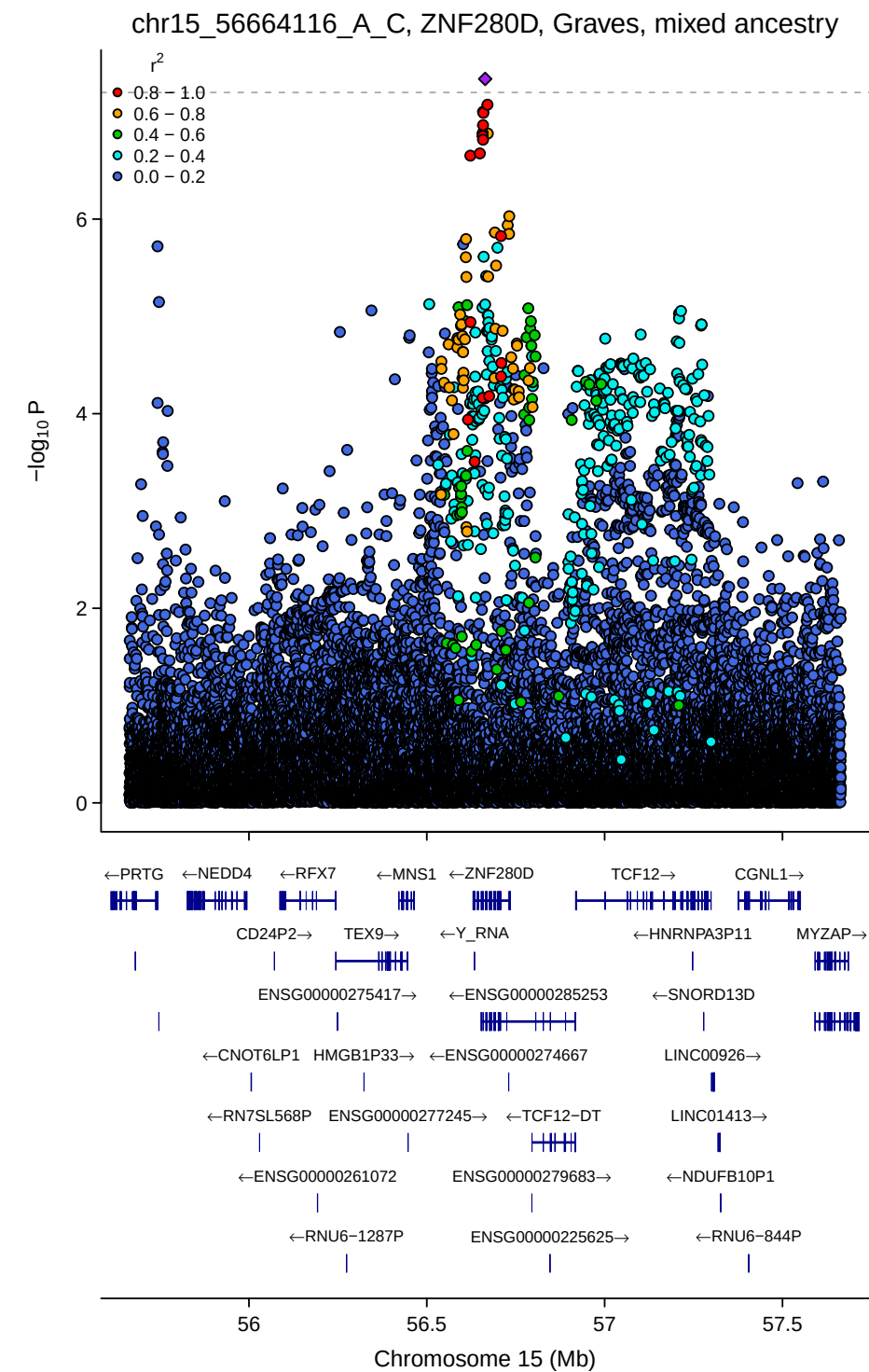
Supplementary Figure 3.1



Supplementary Figure 3.1



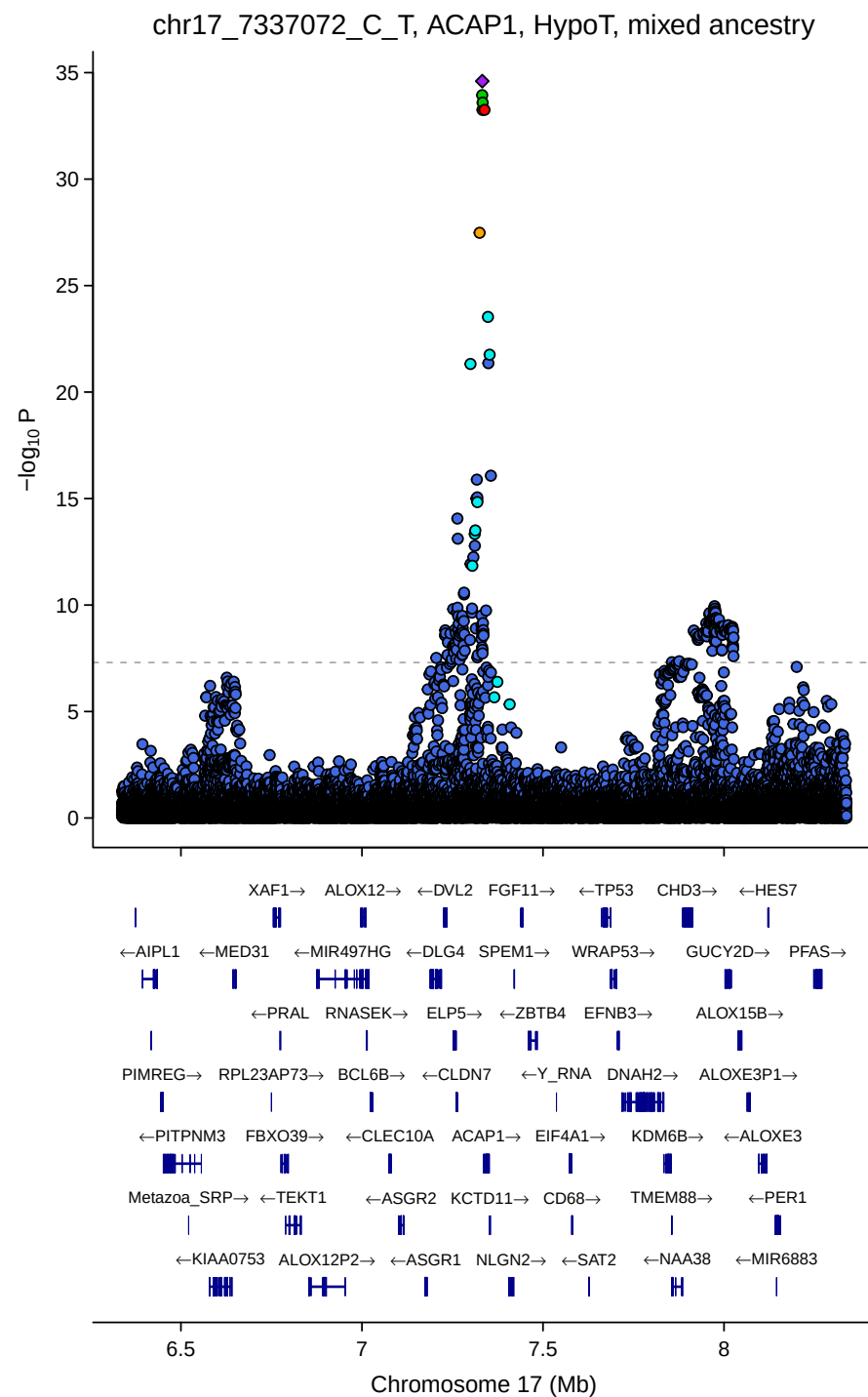
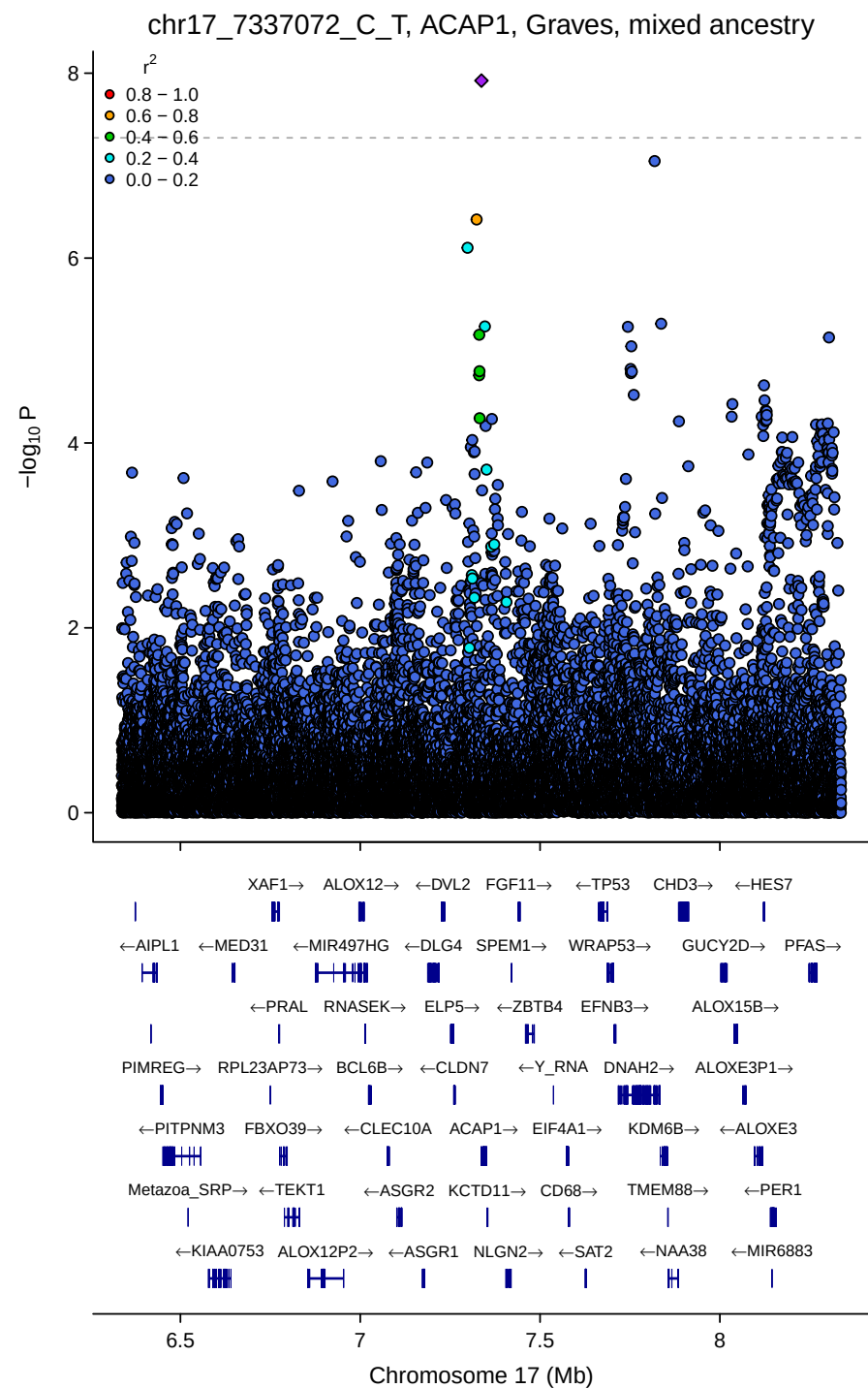
Supplementary Figure 3.1



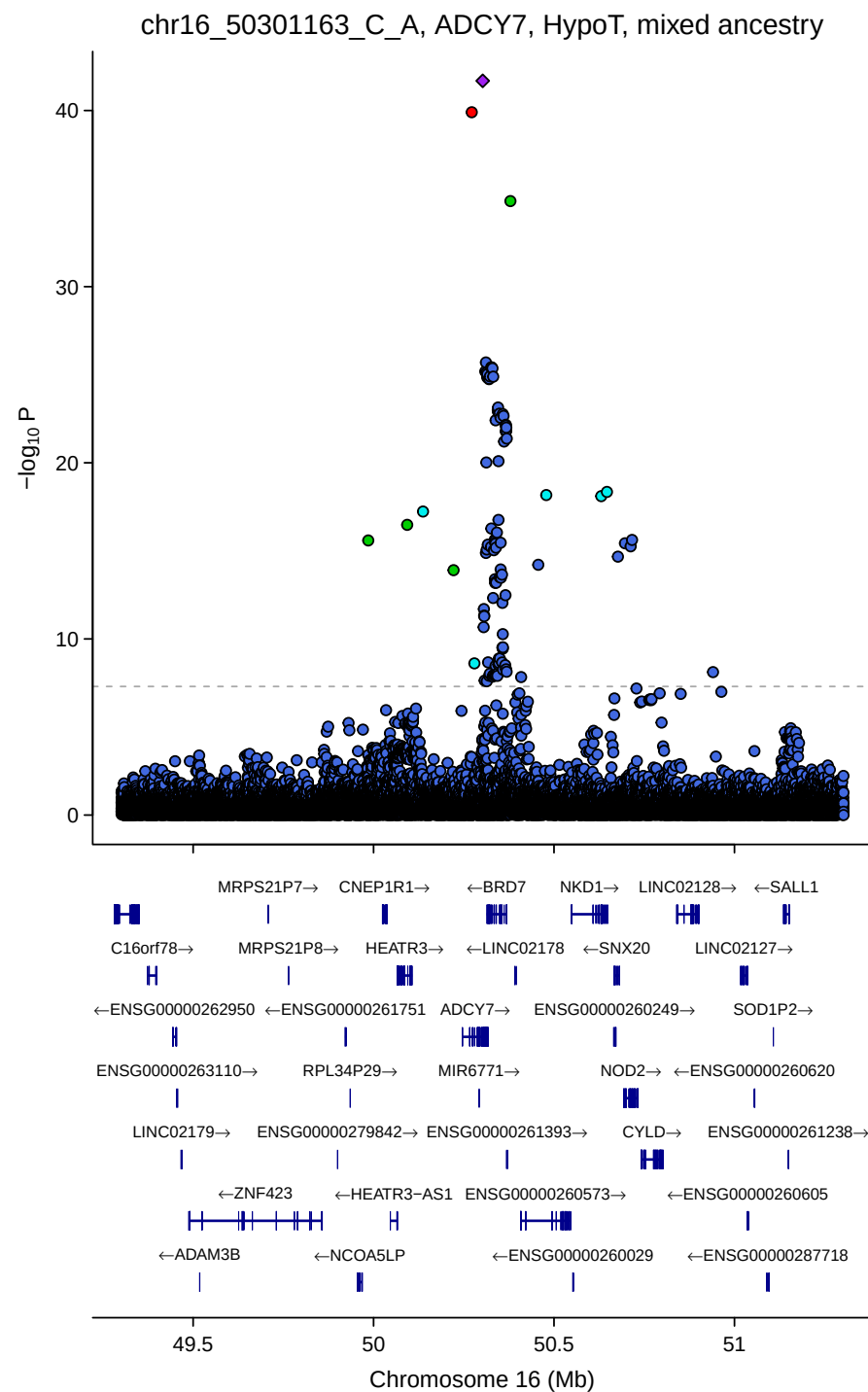
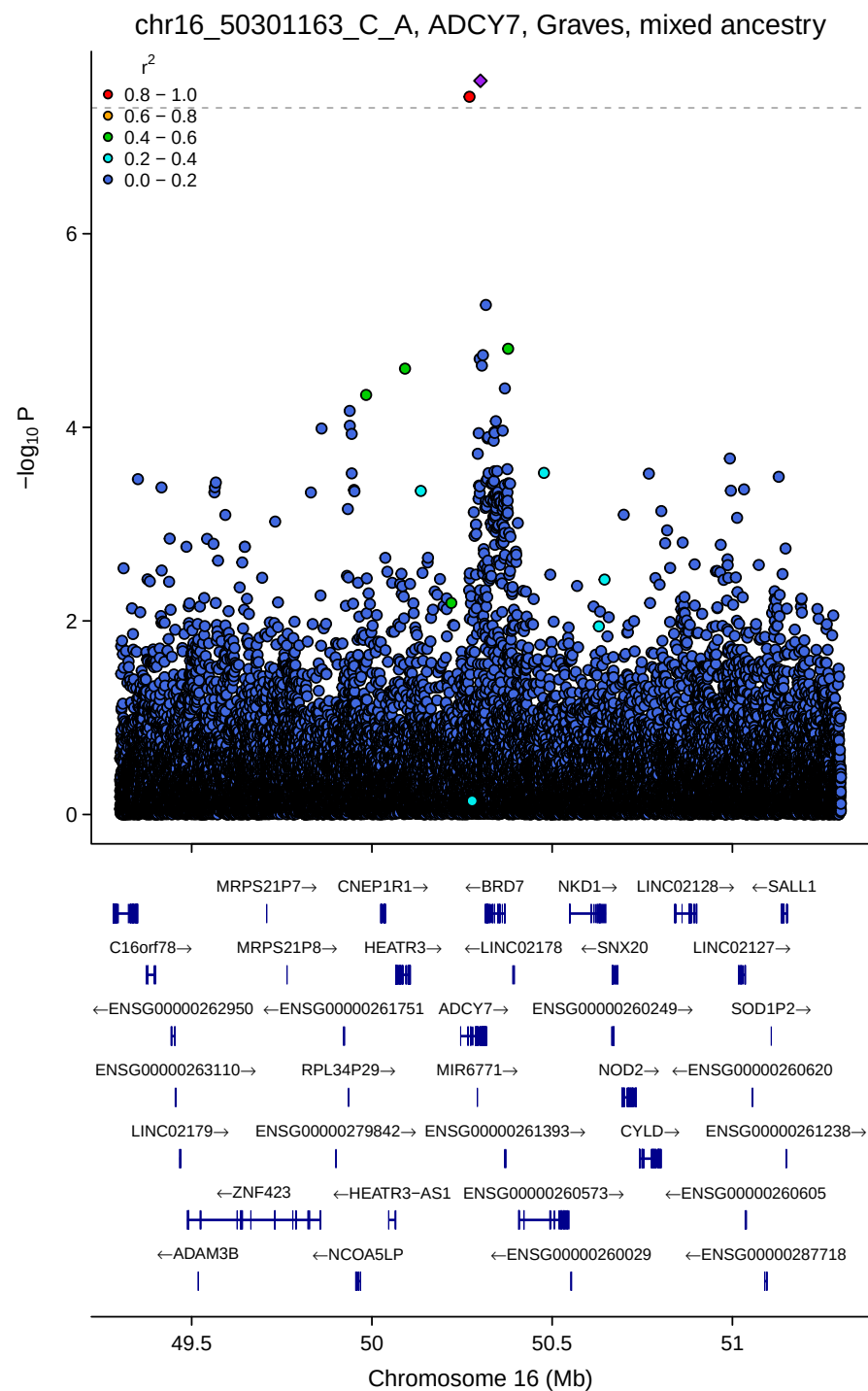
Supplementary Figure 3.2. Locus plots for loci significantly associated with both Graves' disease and hypothyroidism. The left plot displays  $-\log_{10}(\text{p-values})$  for variants from the Graves' disease meta-analysis, the right plot displays  $-\log_{10}(\text{p-values})$  for variants within the same genomic region from the hypothyroidism meta-analysis. The lead variant is shown with a purple diamond. Genome wide significance is indicated by the dashed horizontal line at  $-\log_{10}(5\text{e-}8)$ .



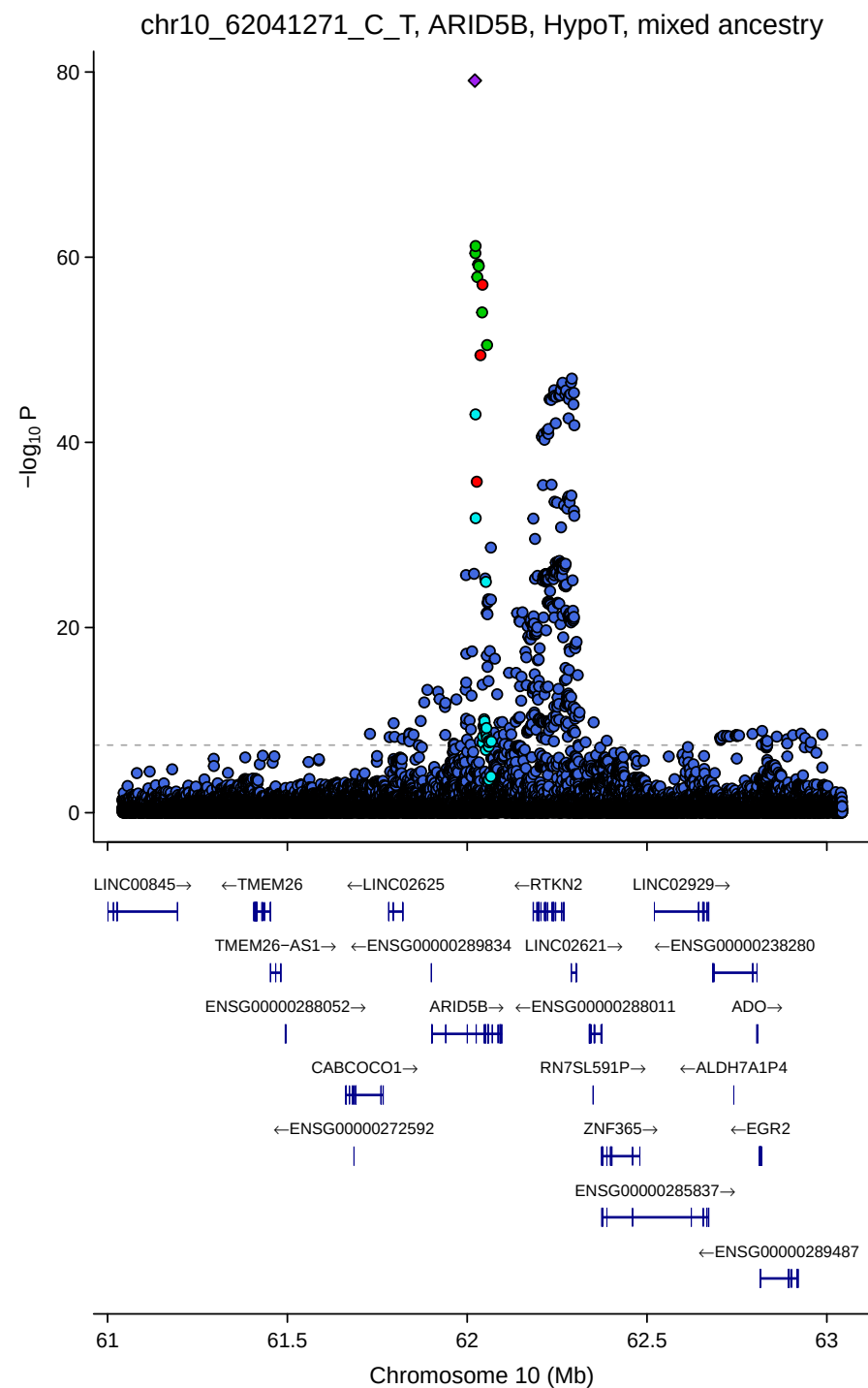
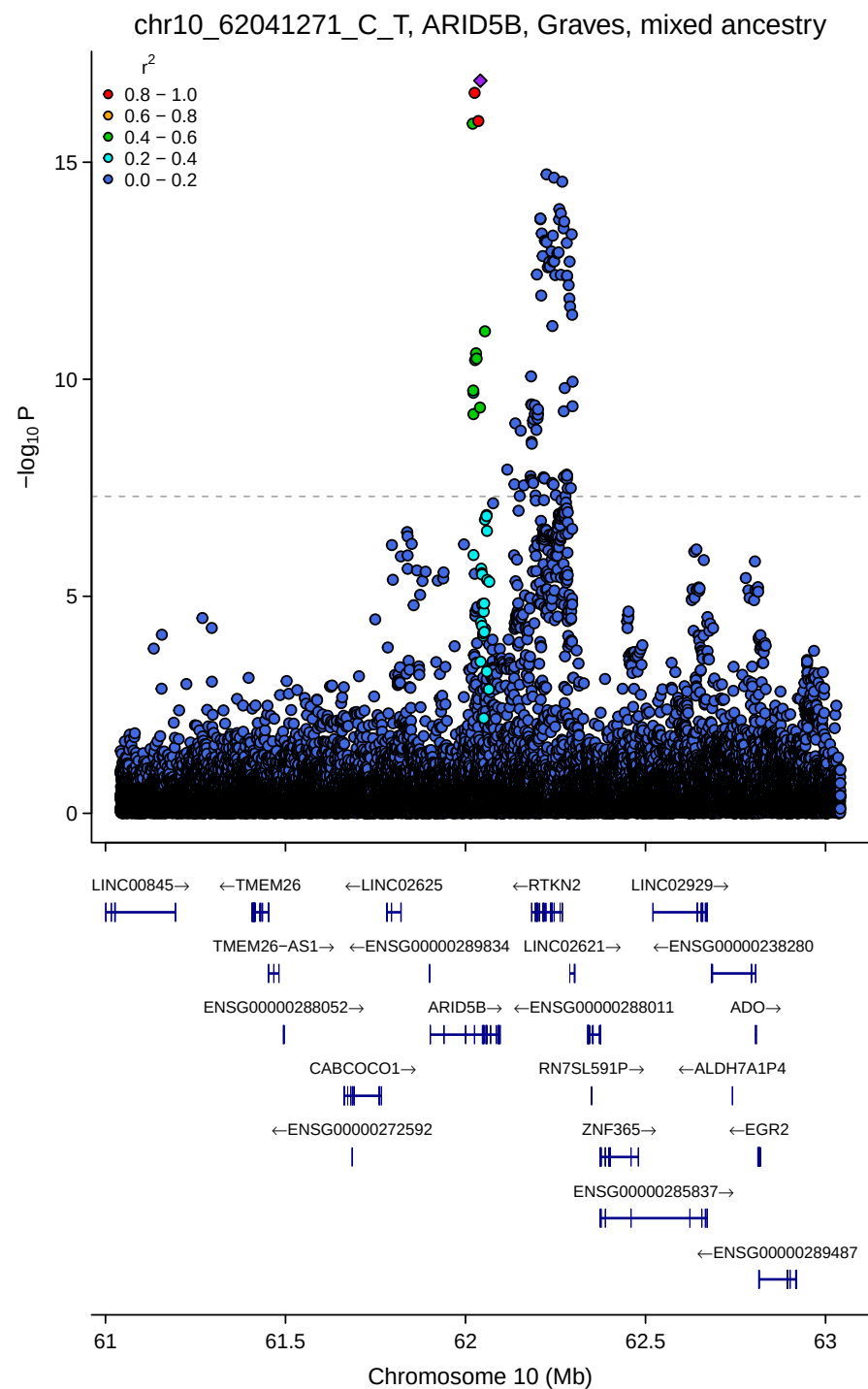
Supplementary Figure 3.2



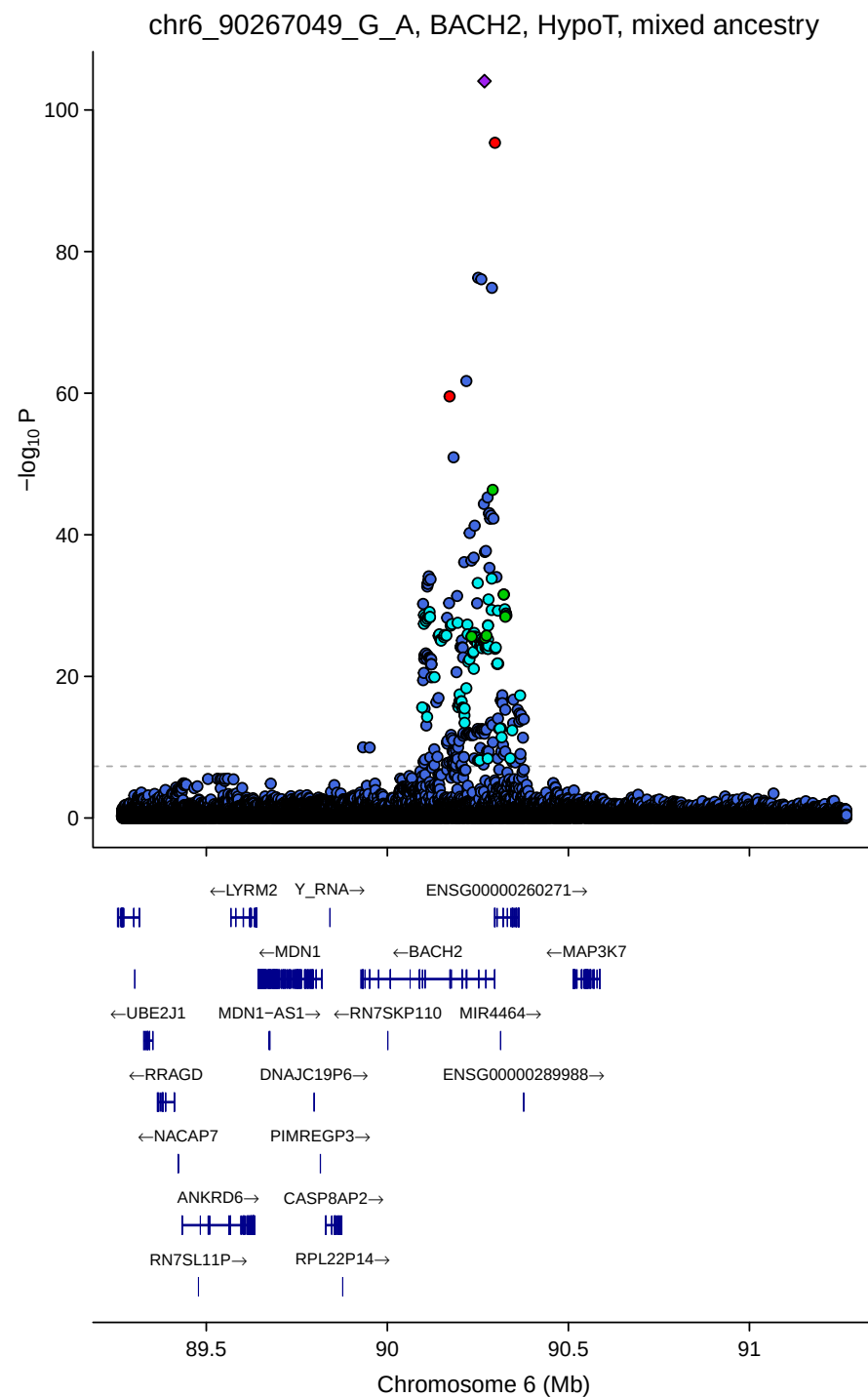
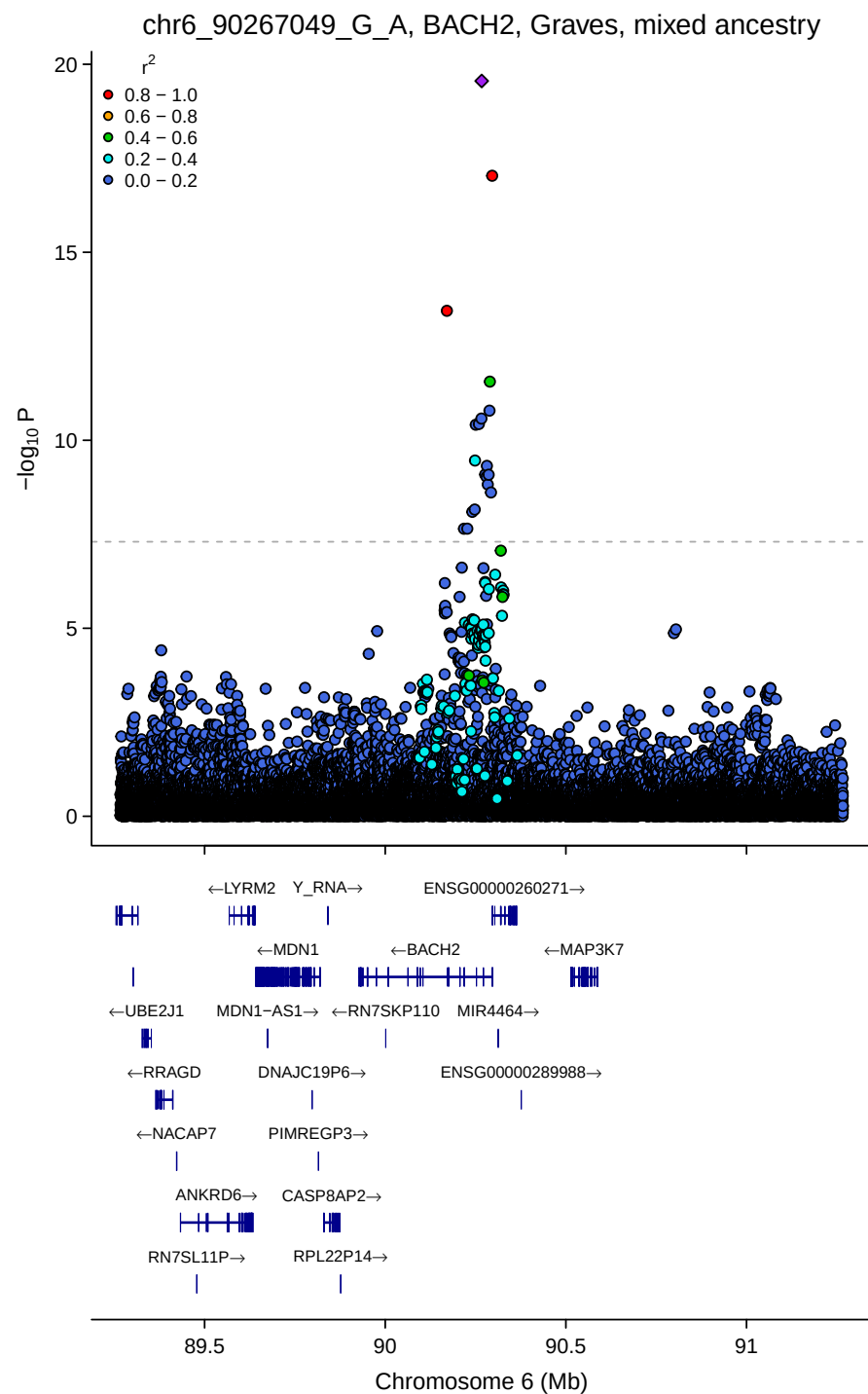
Supplementary Figure 3.2



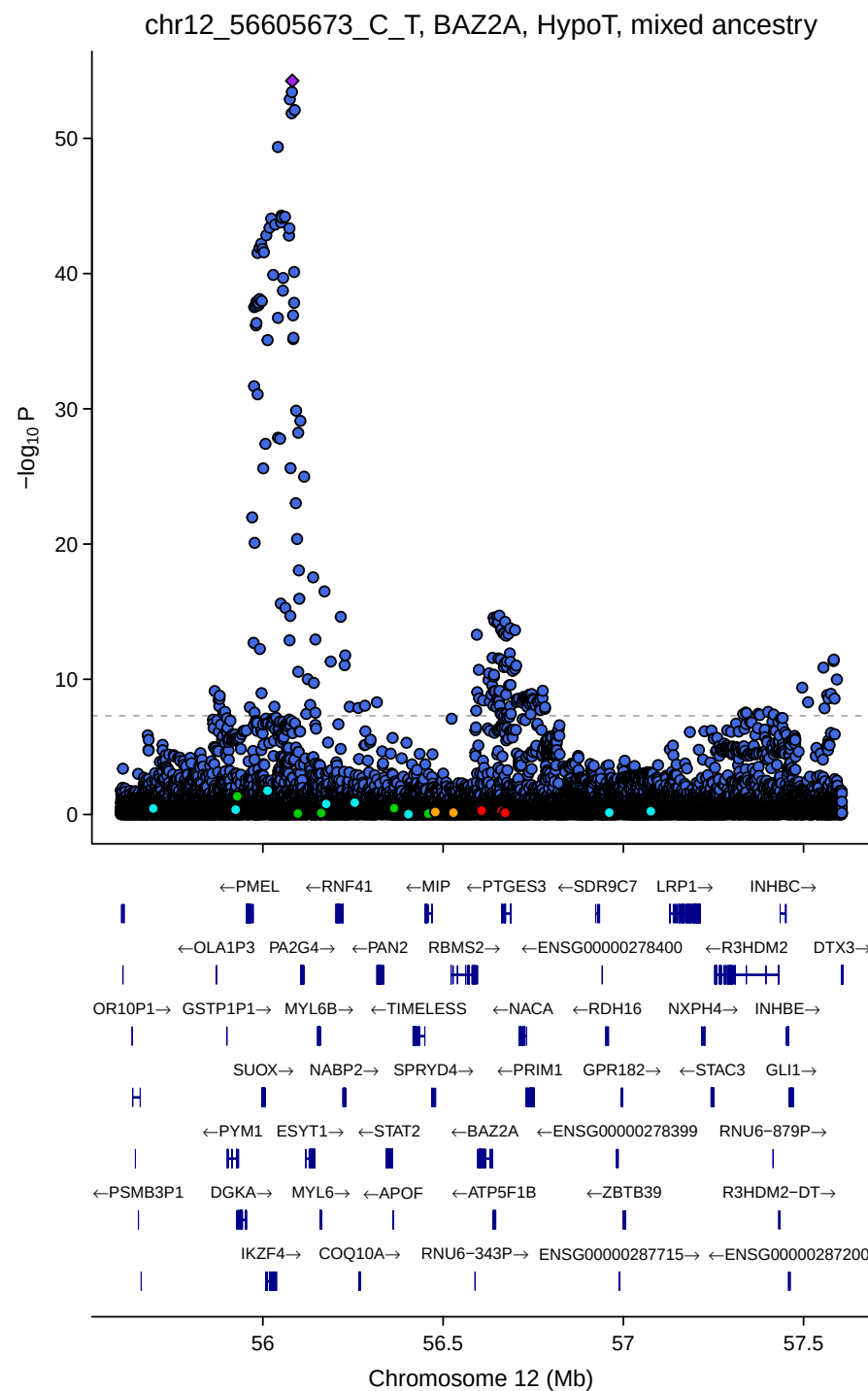
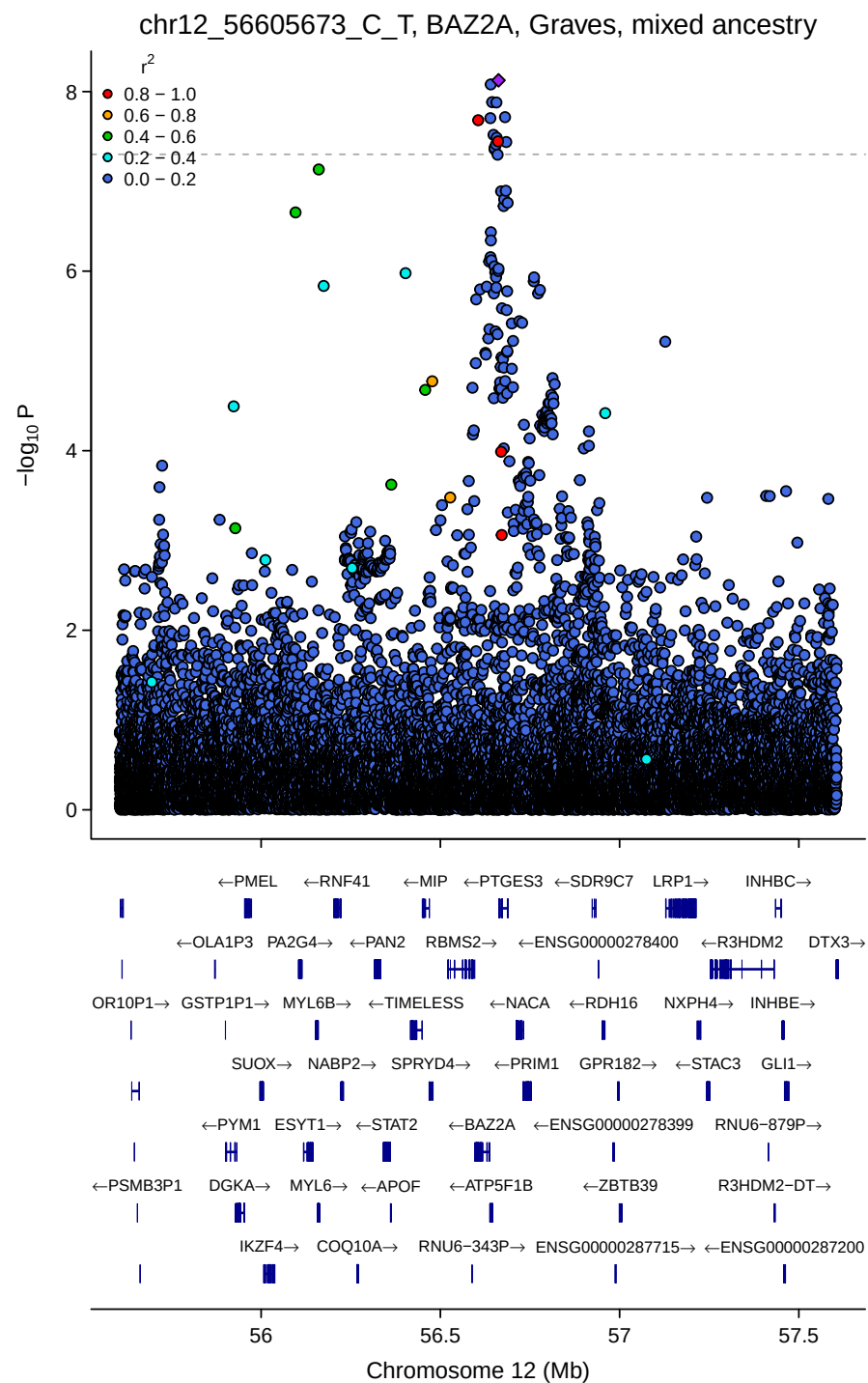
Supplementary Figure 3.2



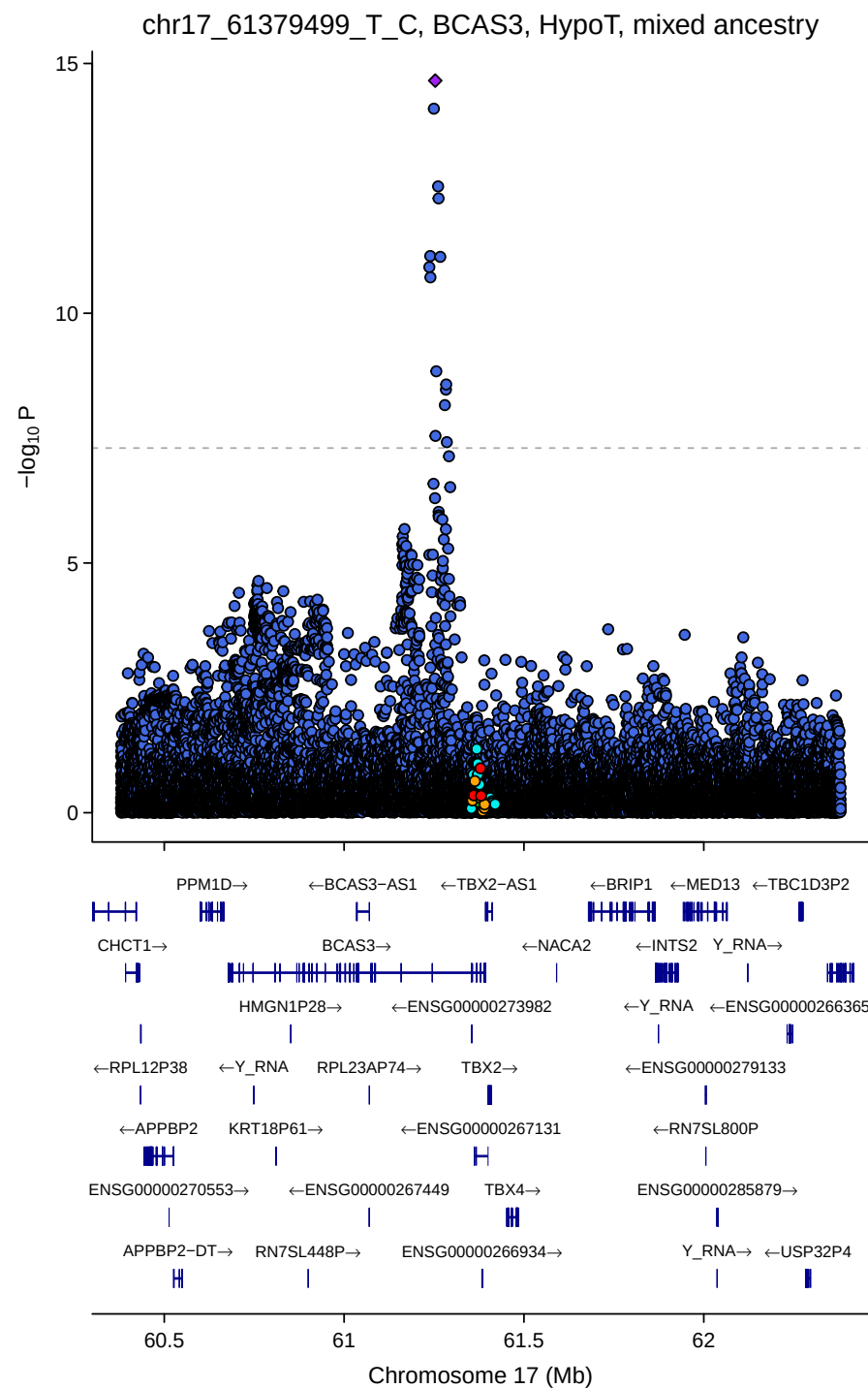
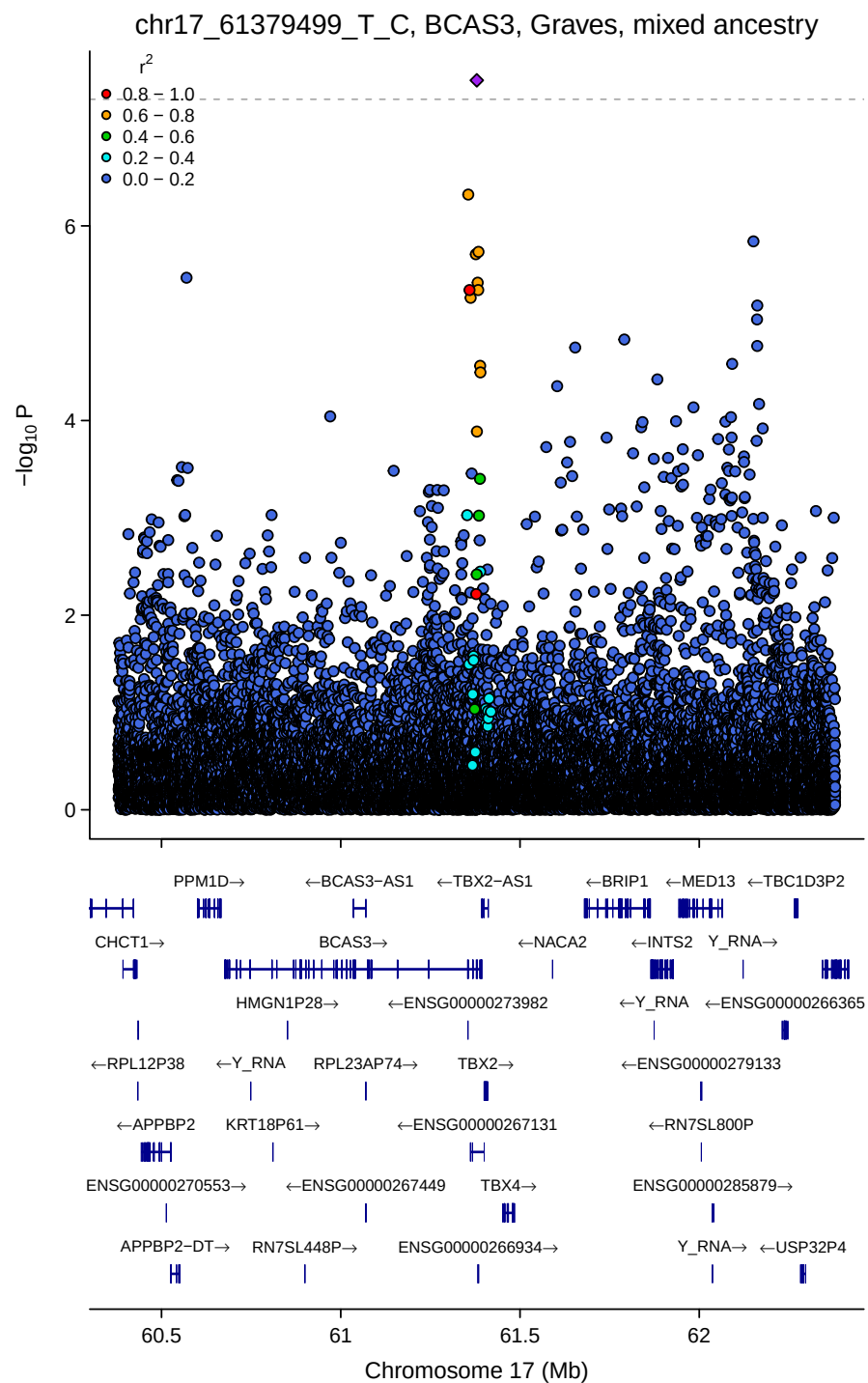
Supplementary Figure 3.2



Supplementary Figure 3.2

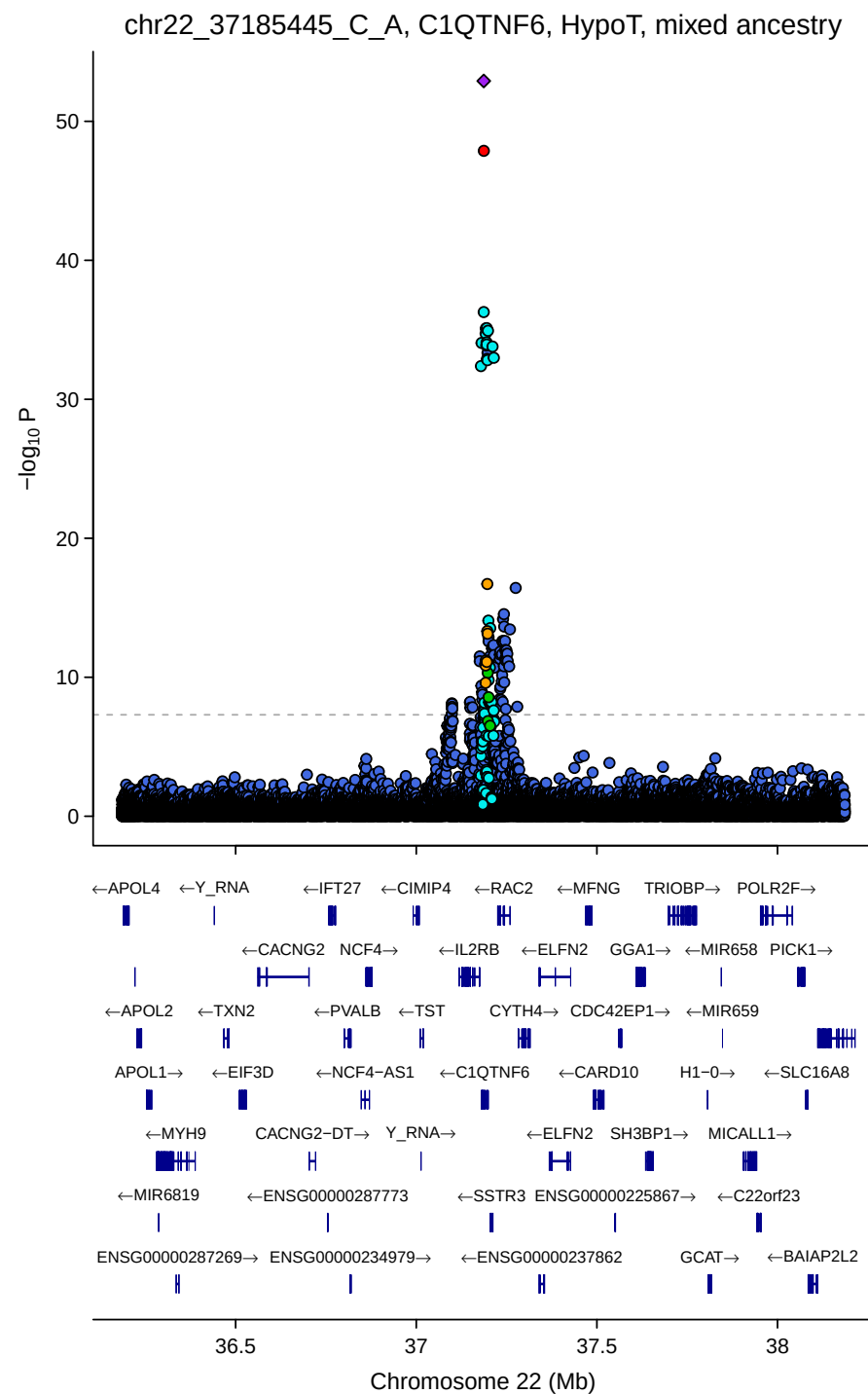
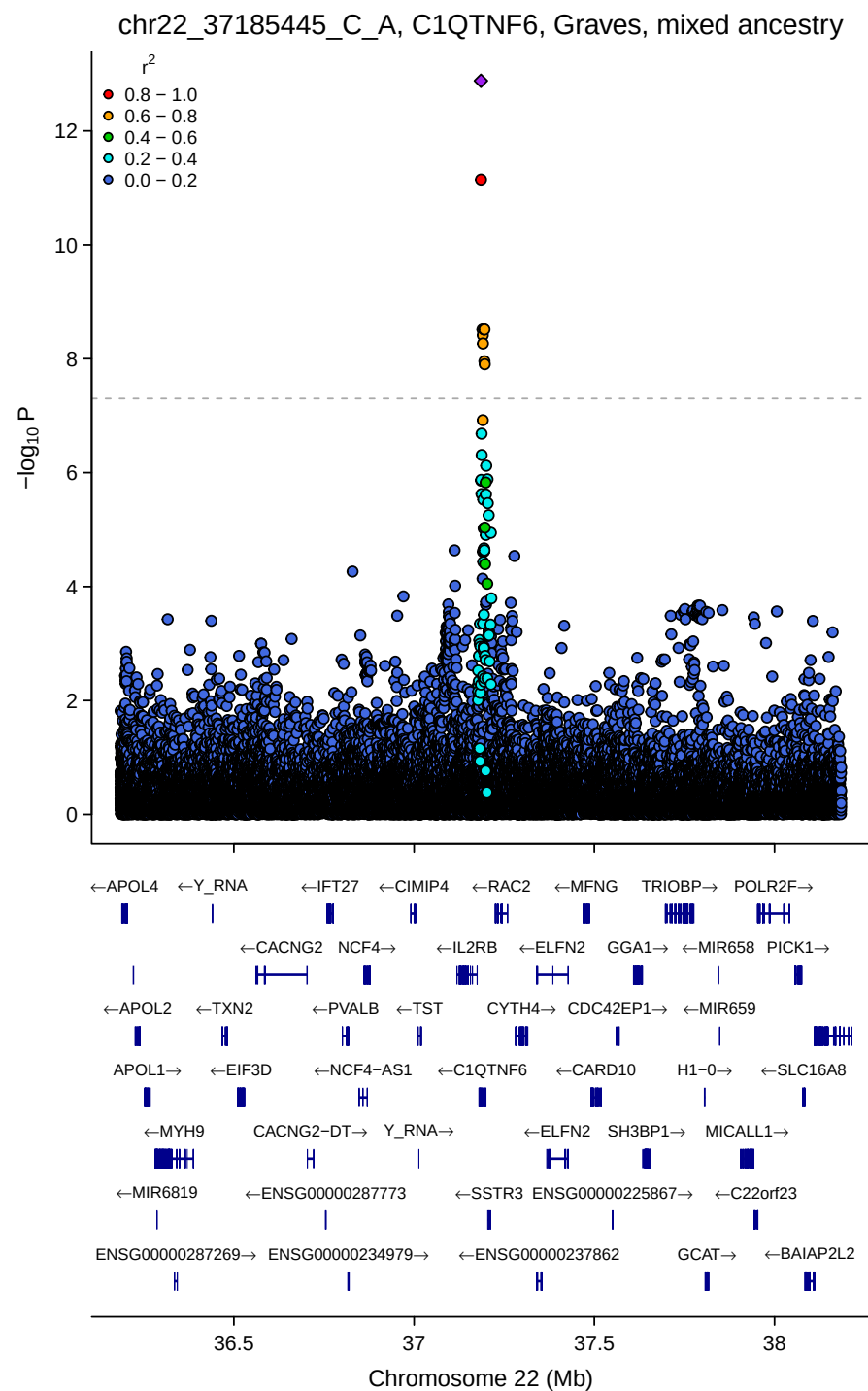


Supplementary Figure 3.2

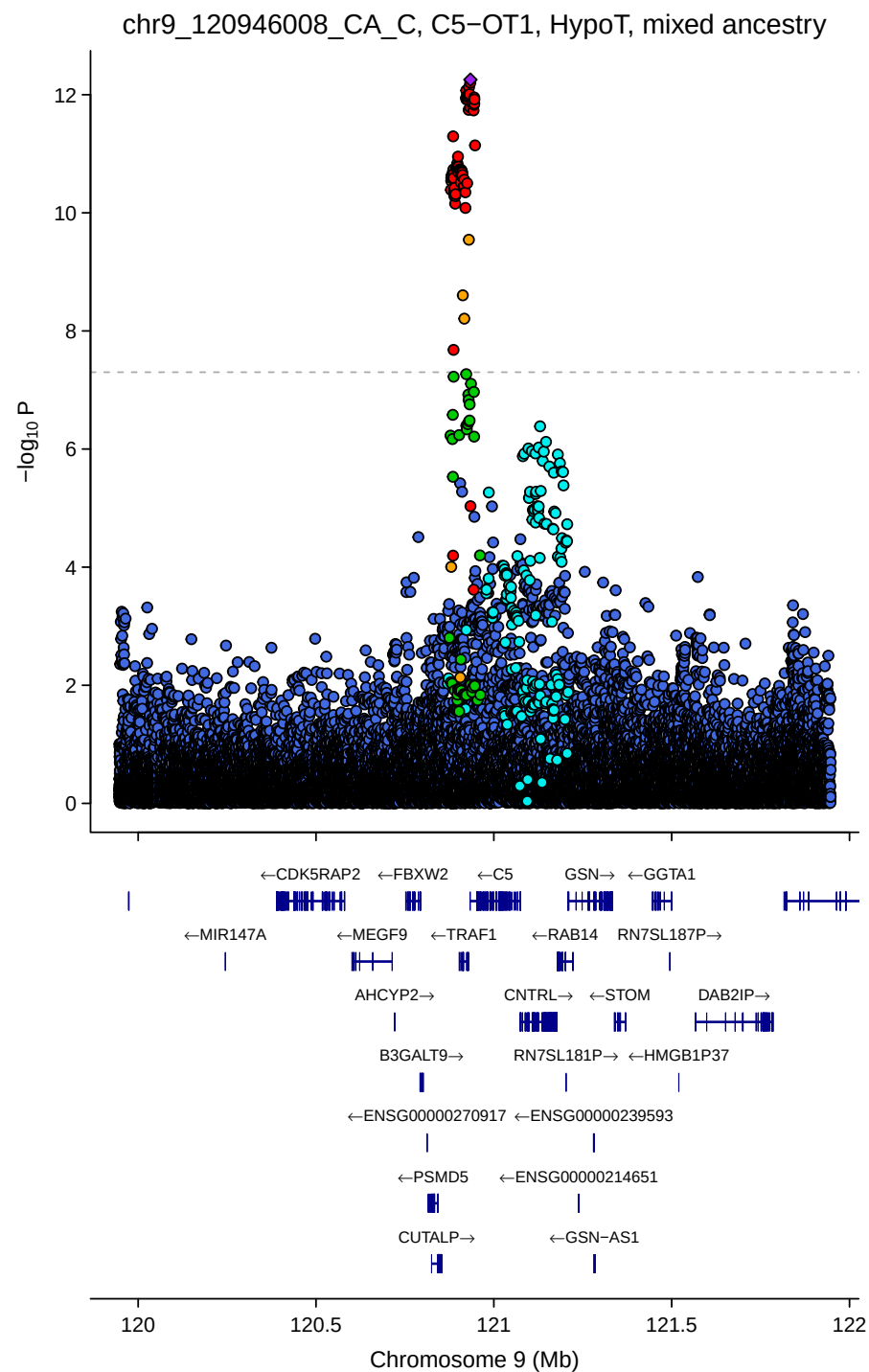
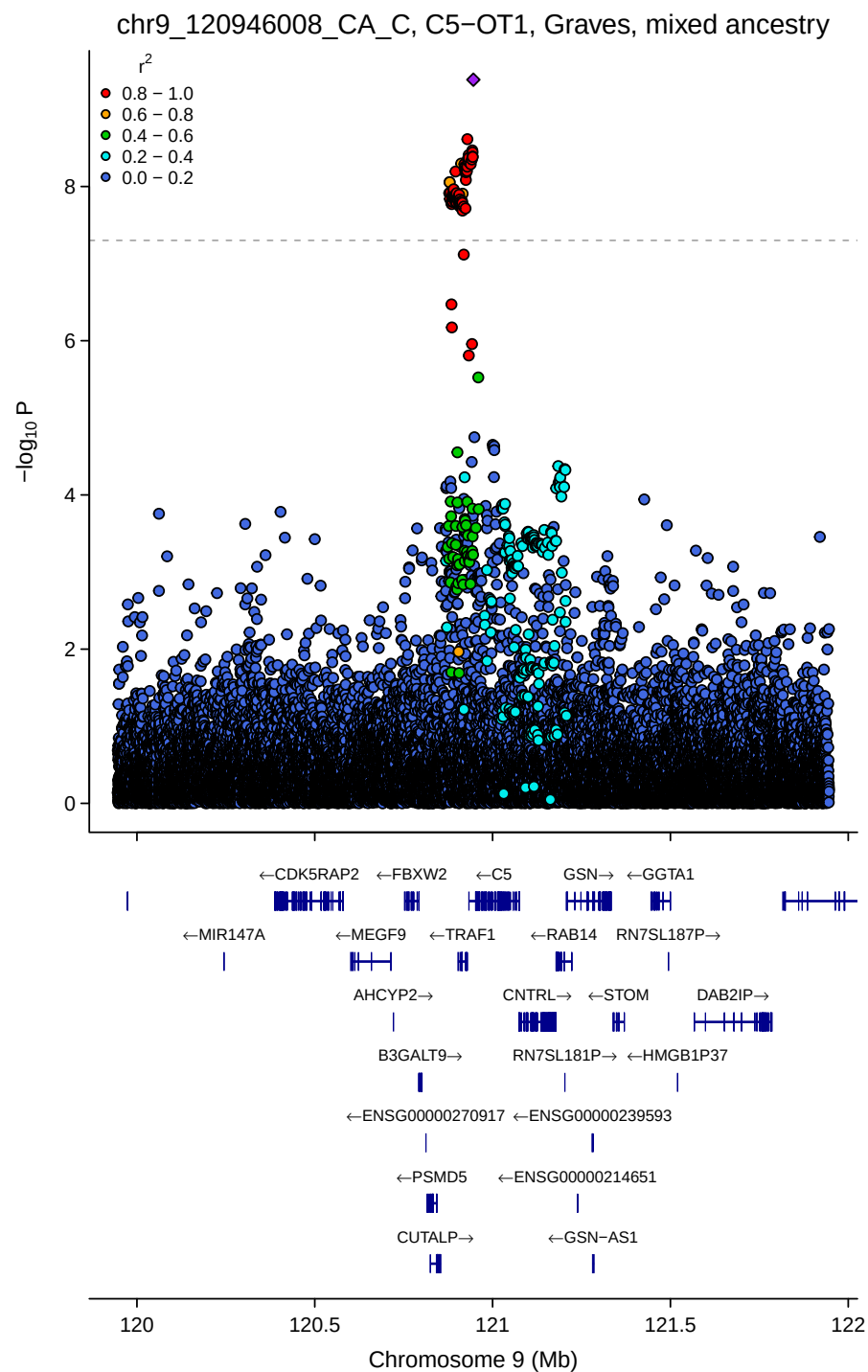




Supplementary Figure 3.2

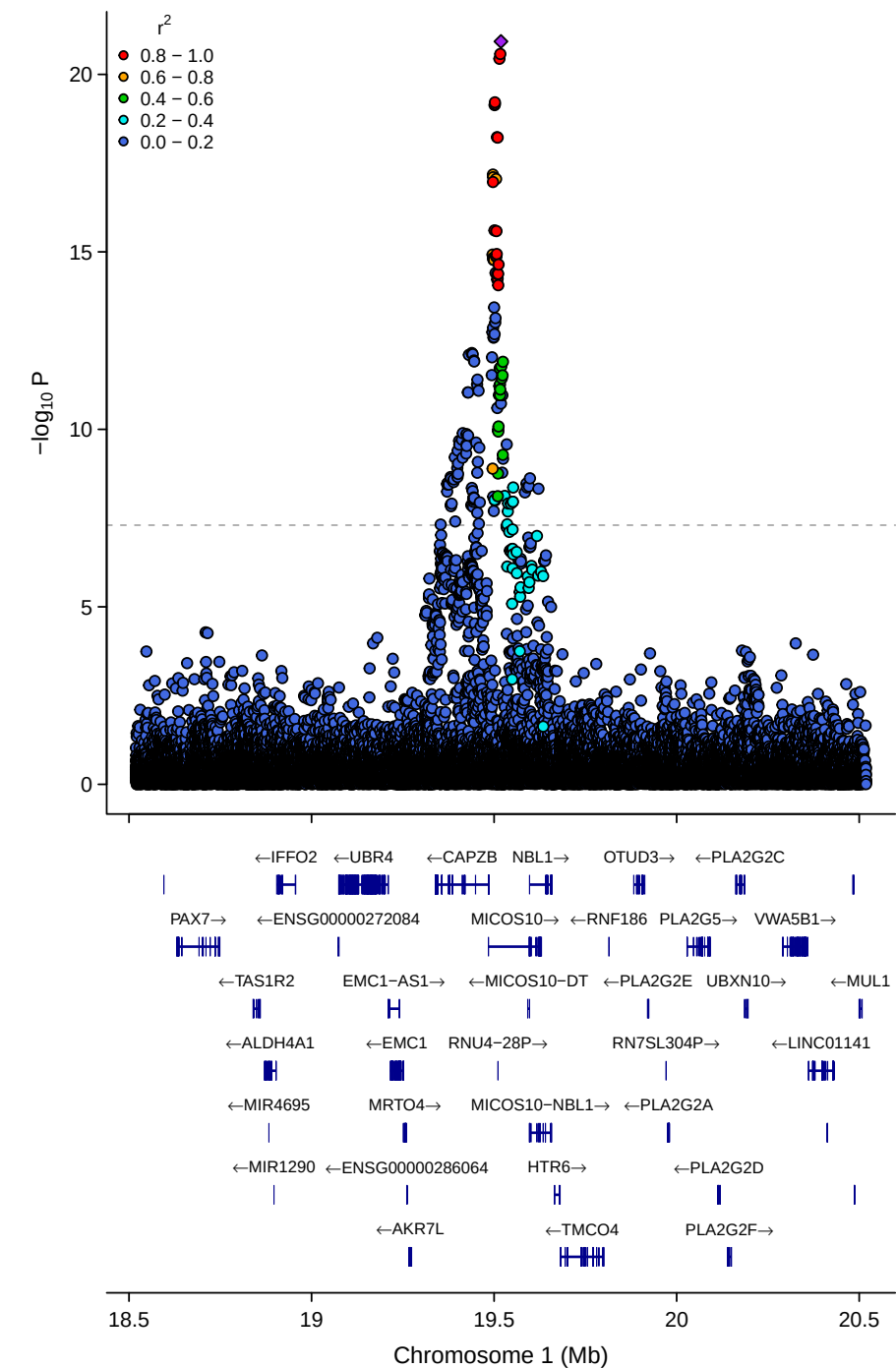


Supplementary Figure 3.2

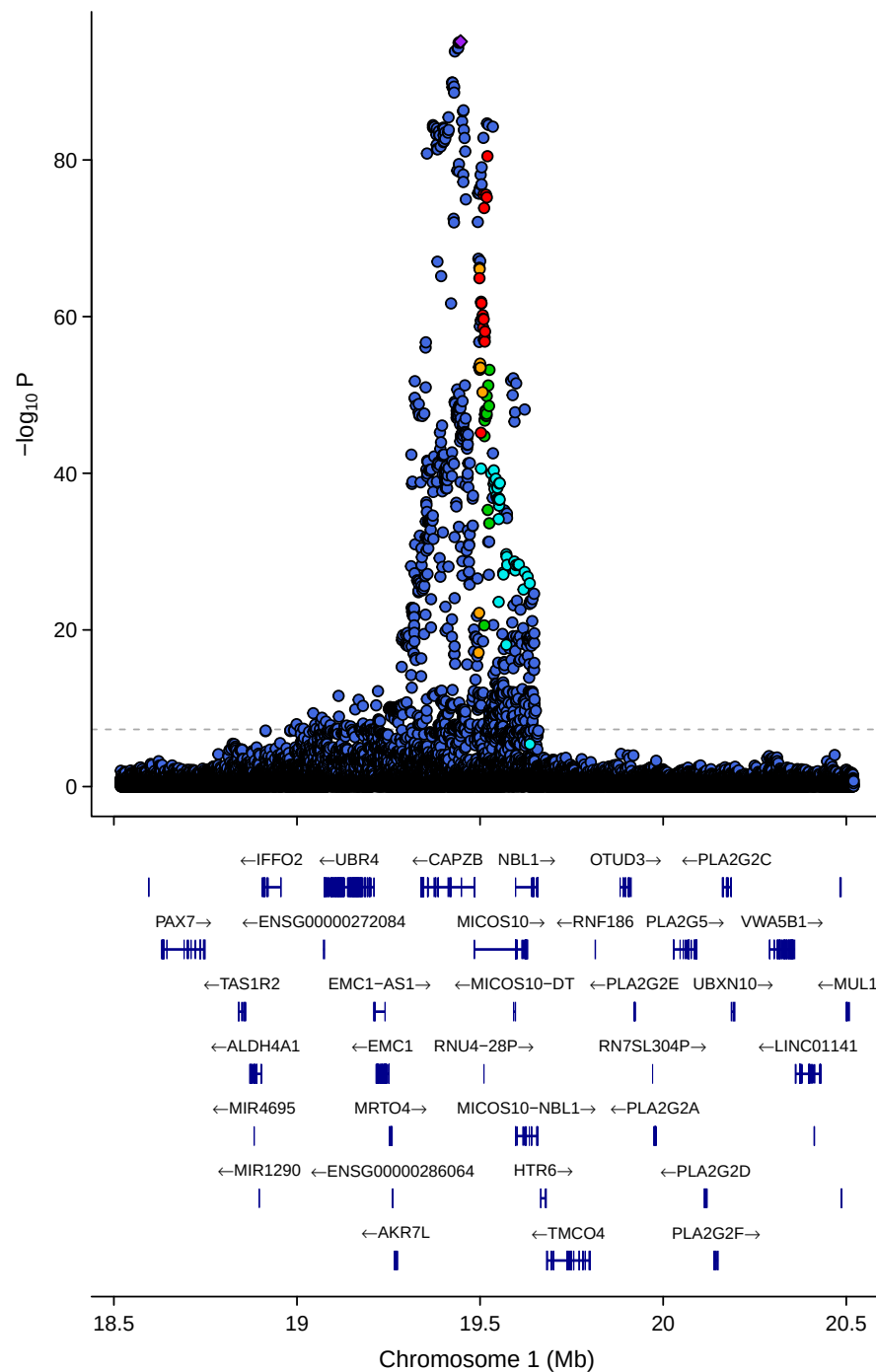


Supplementary Figure 3.2

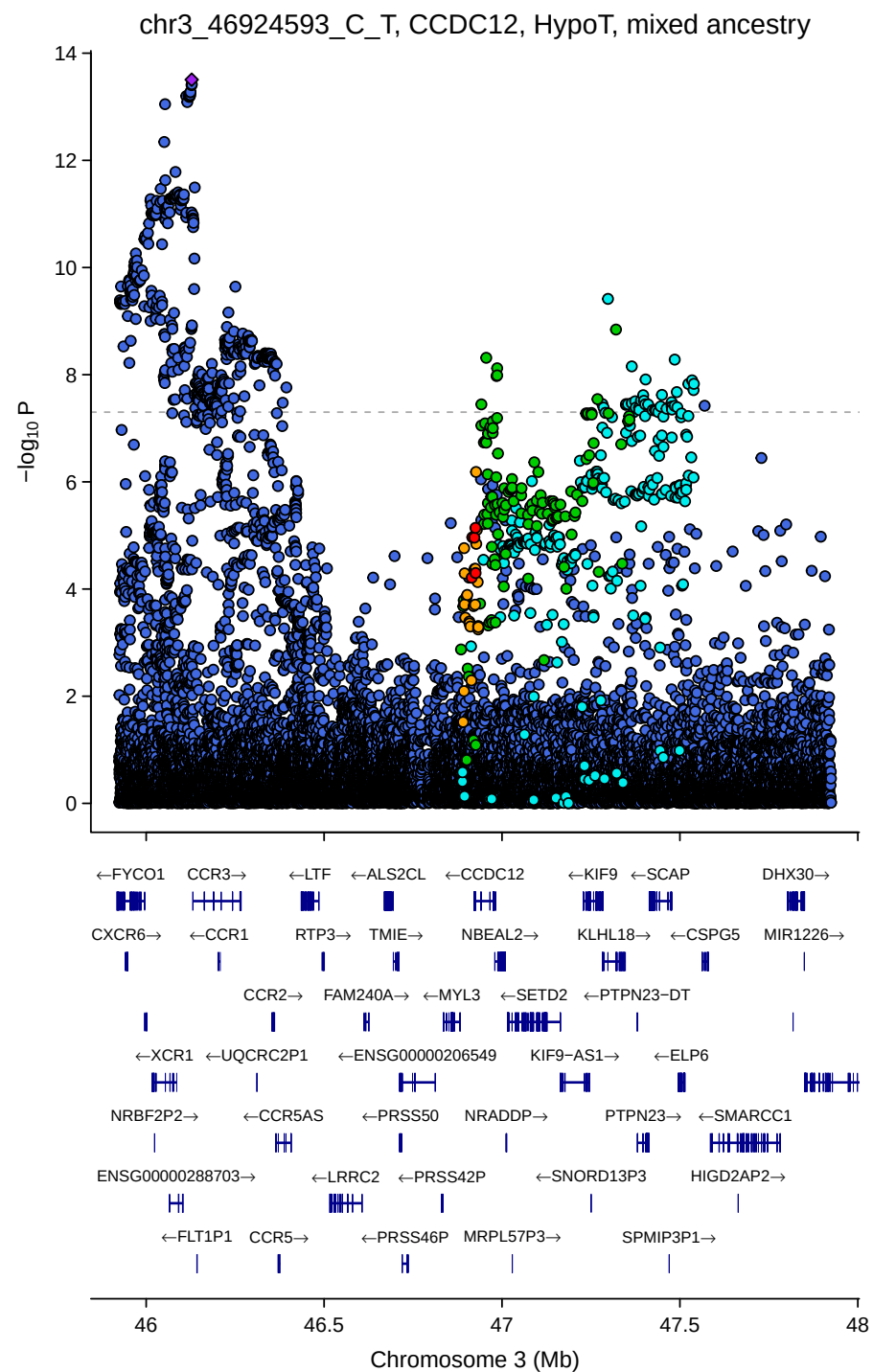
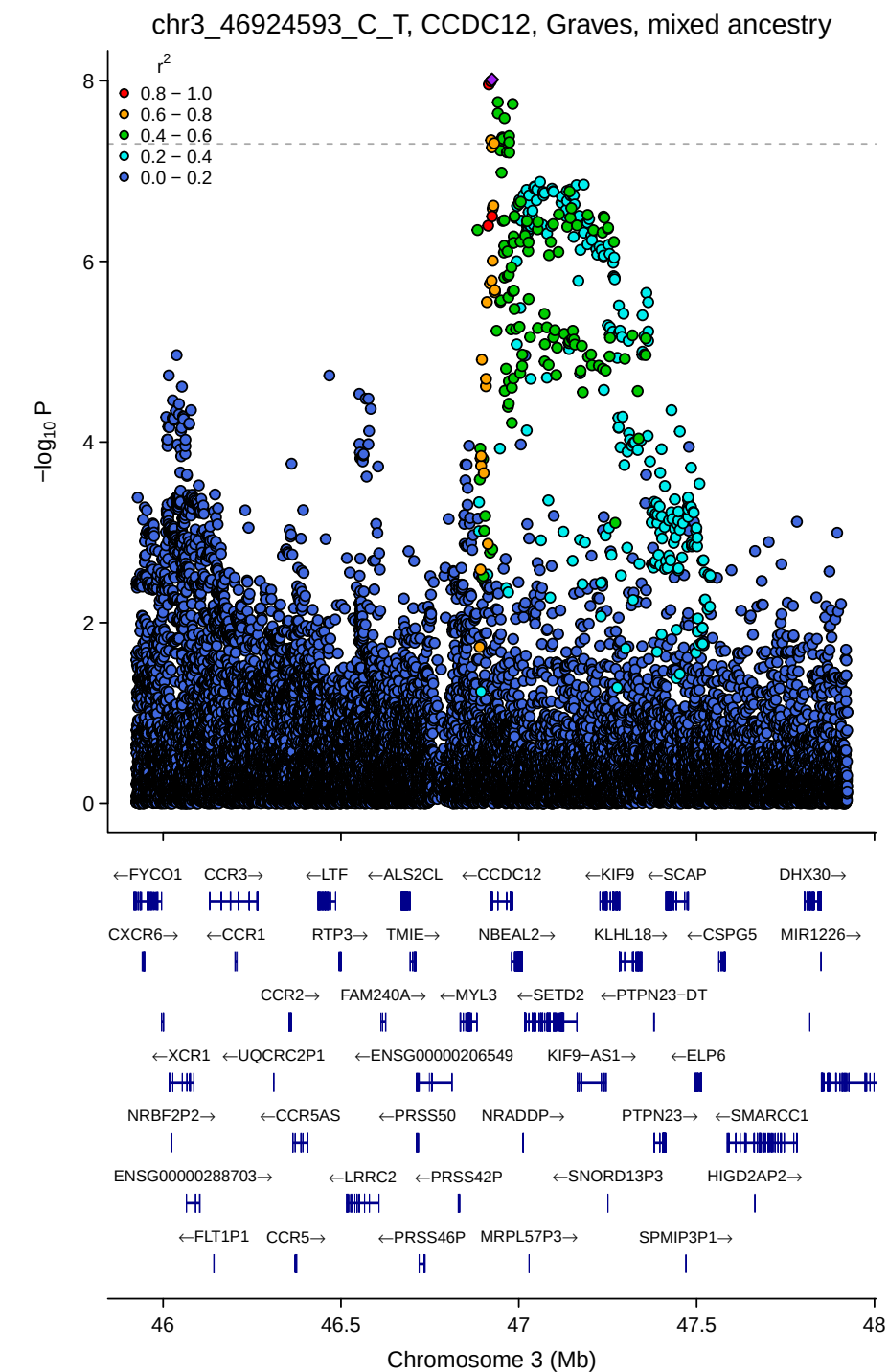
chr1\_19518785\_C\_T, CAPZB;LOC105378614, Graves, mixed ancestry



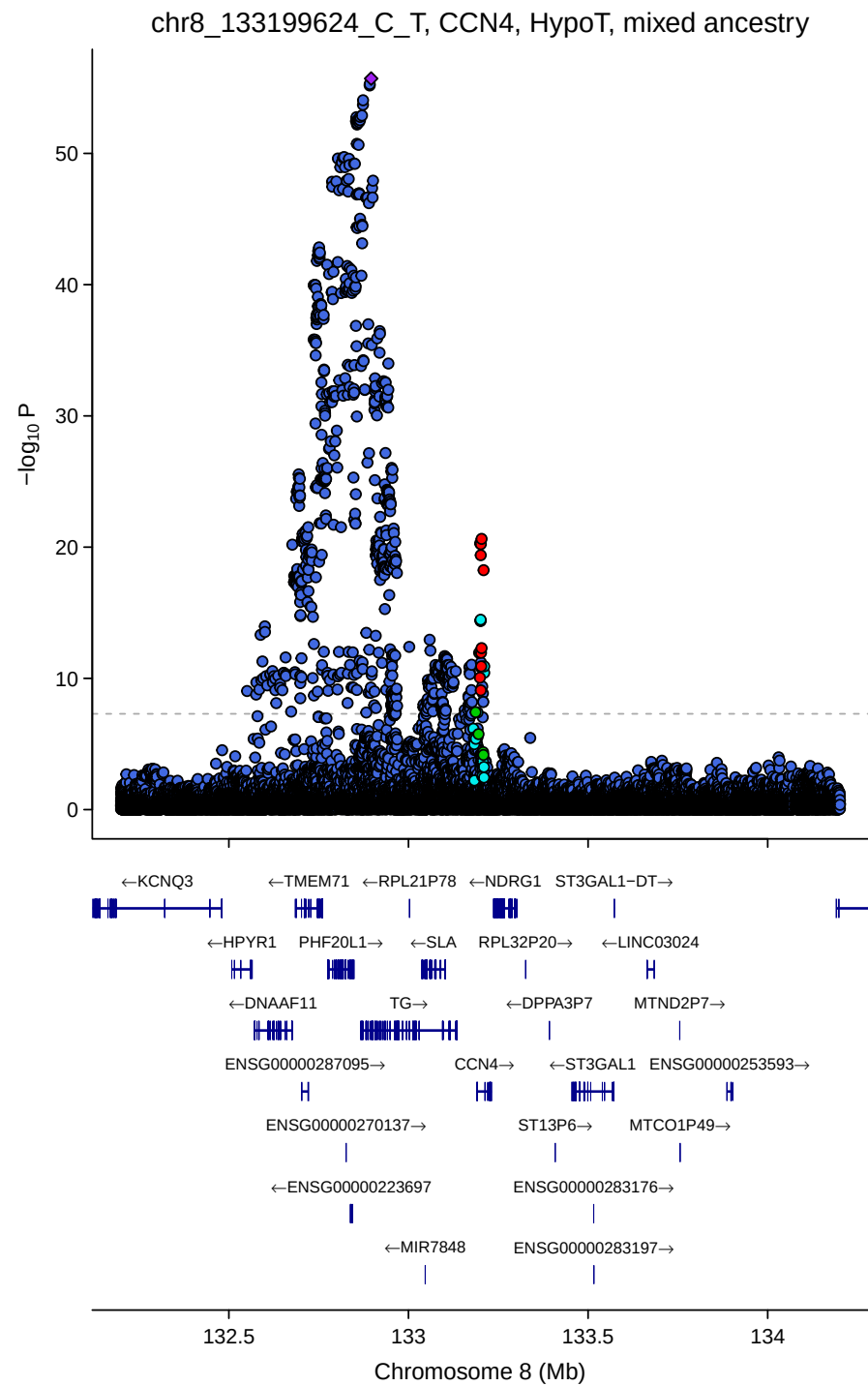
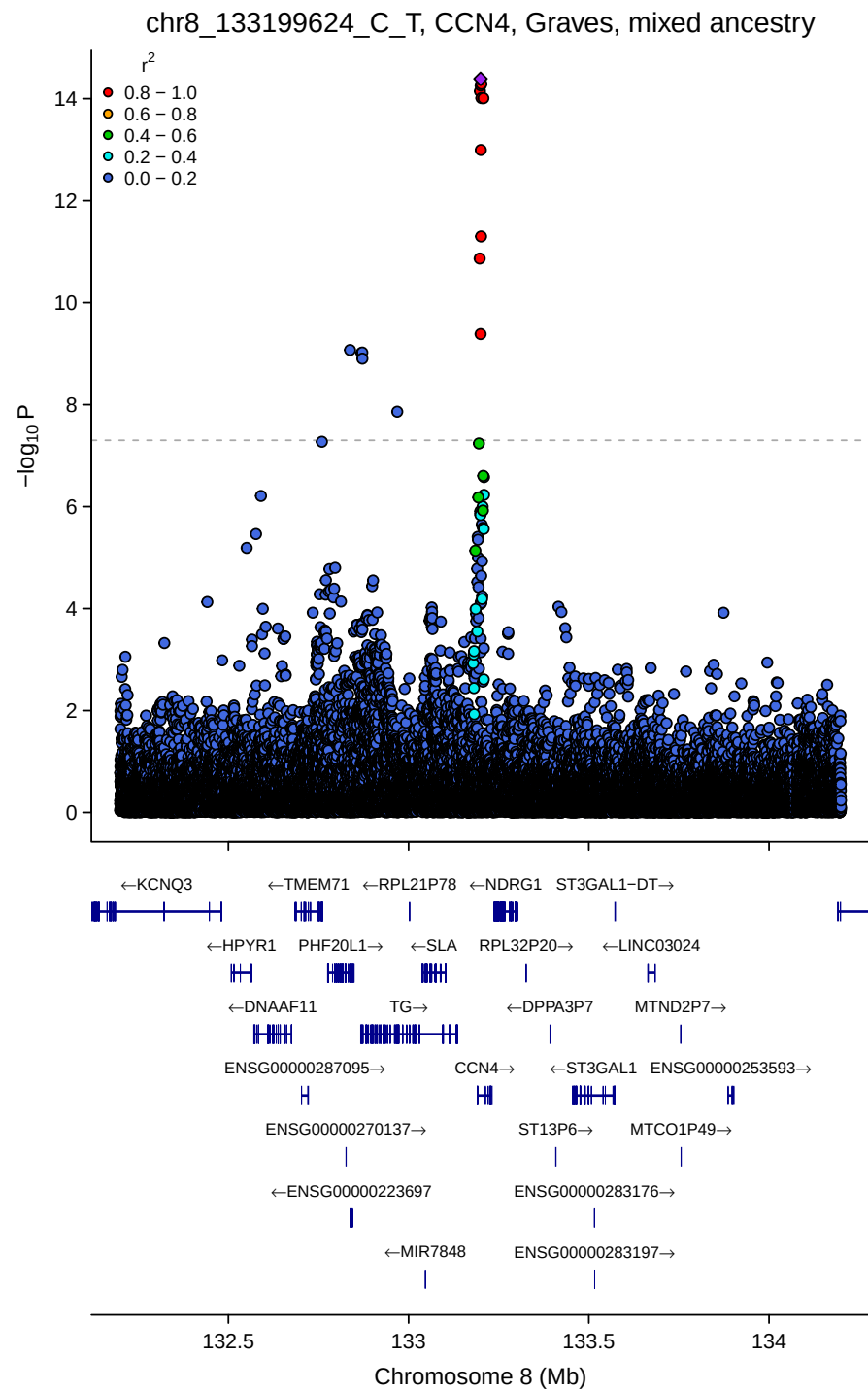
chr1\_19518785\_C\_T, CAPZB;LOC105378614, HypoT, mixed ancestry



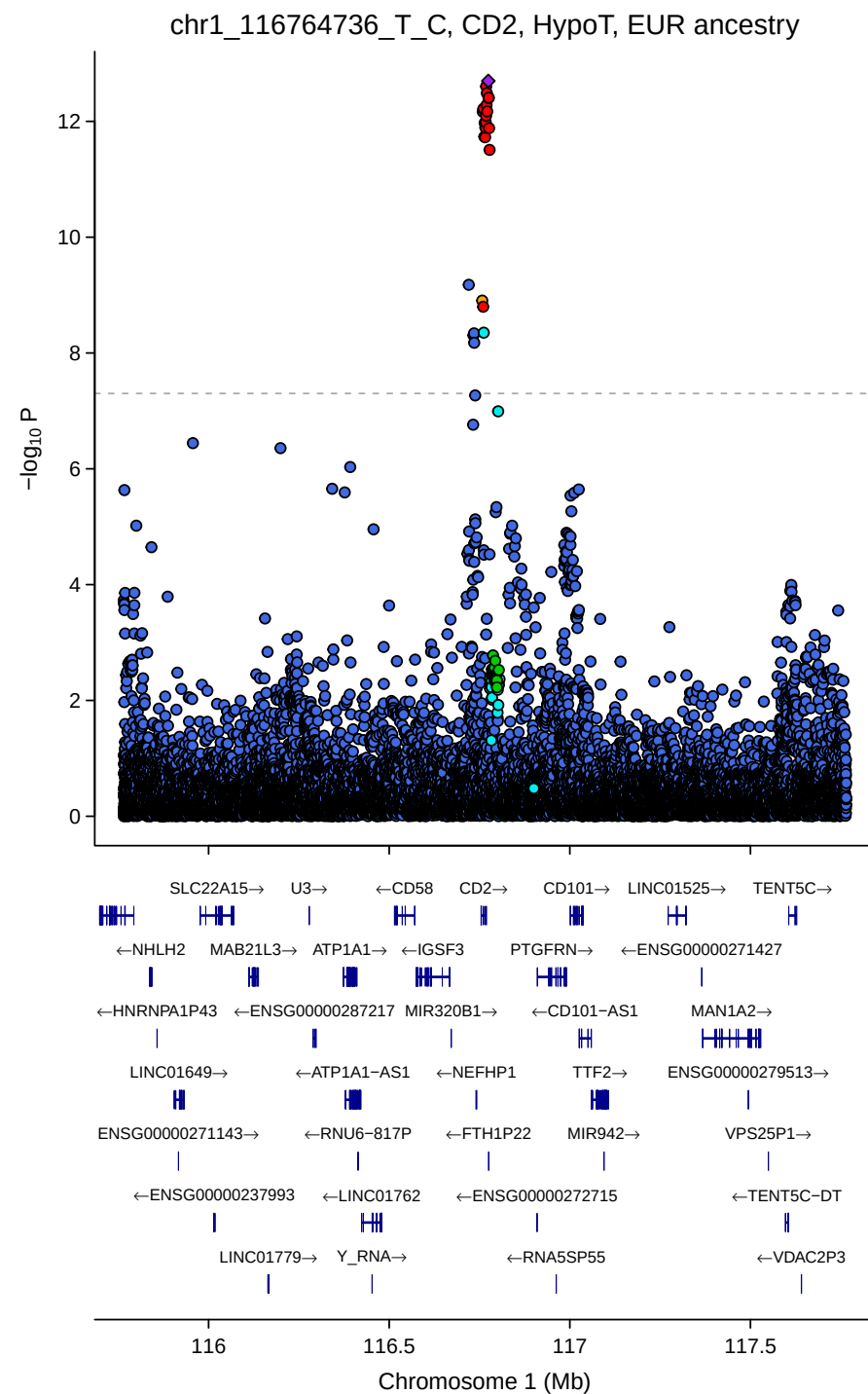
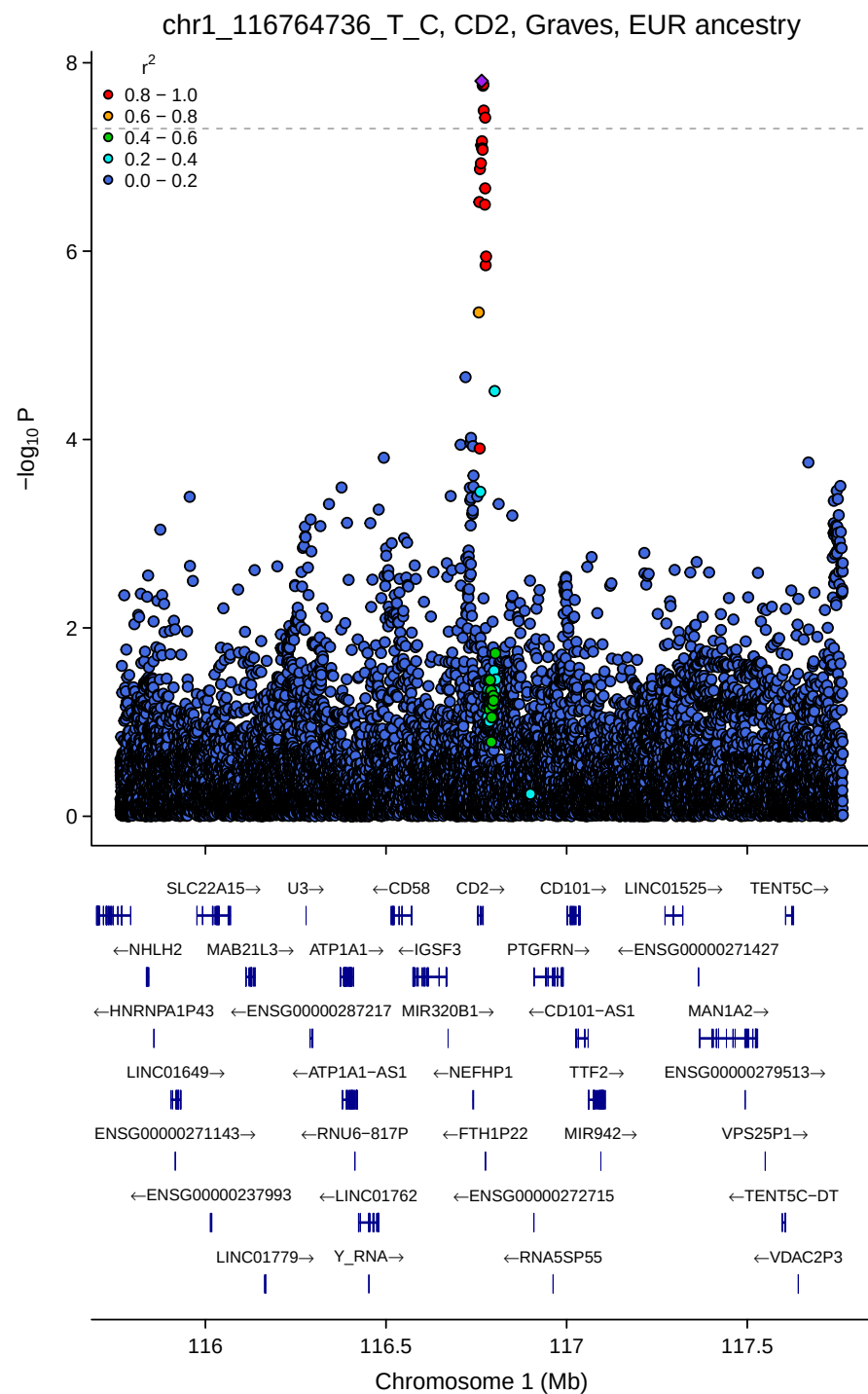
Supplementary Figure 3.2



Supplementary Figure 3.2

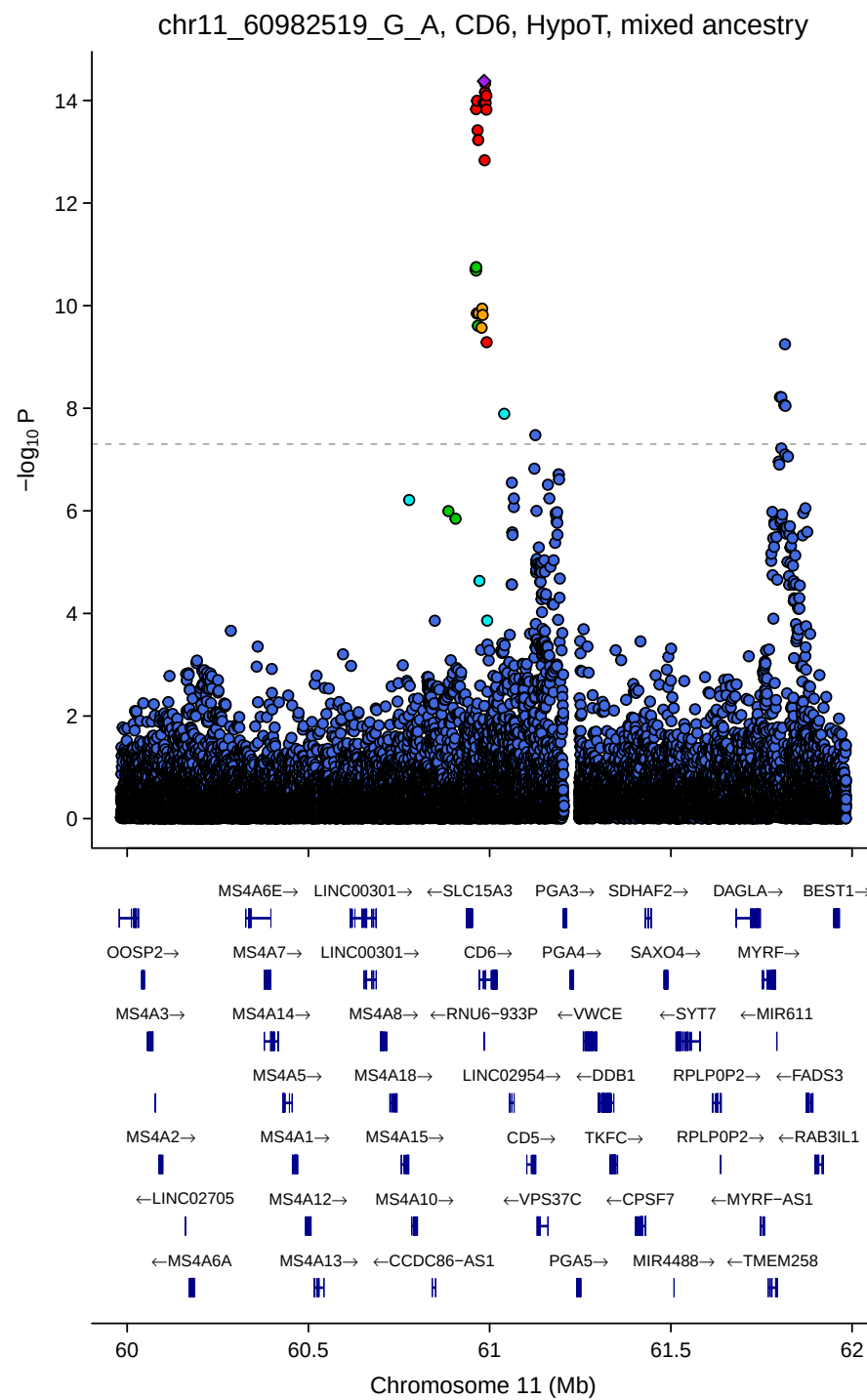
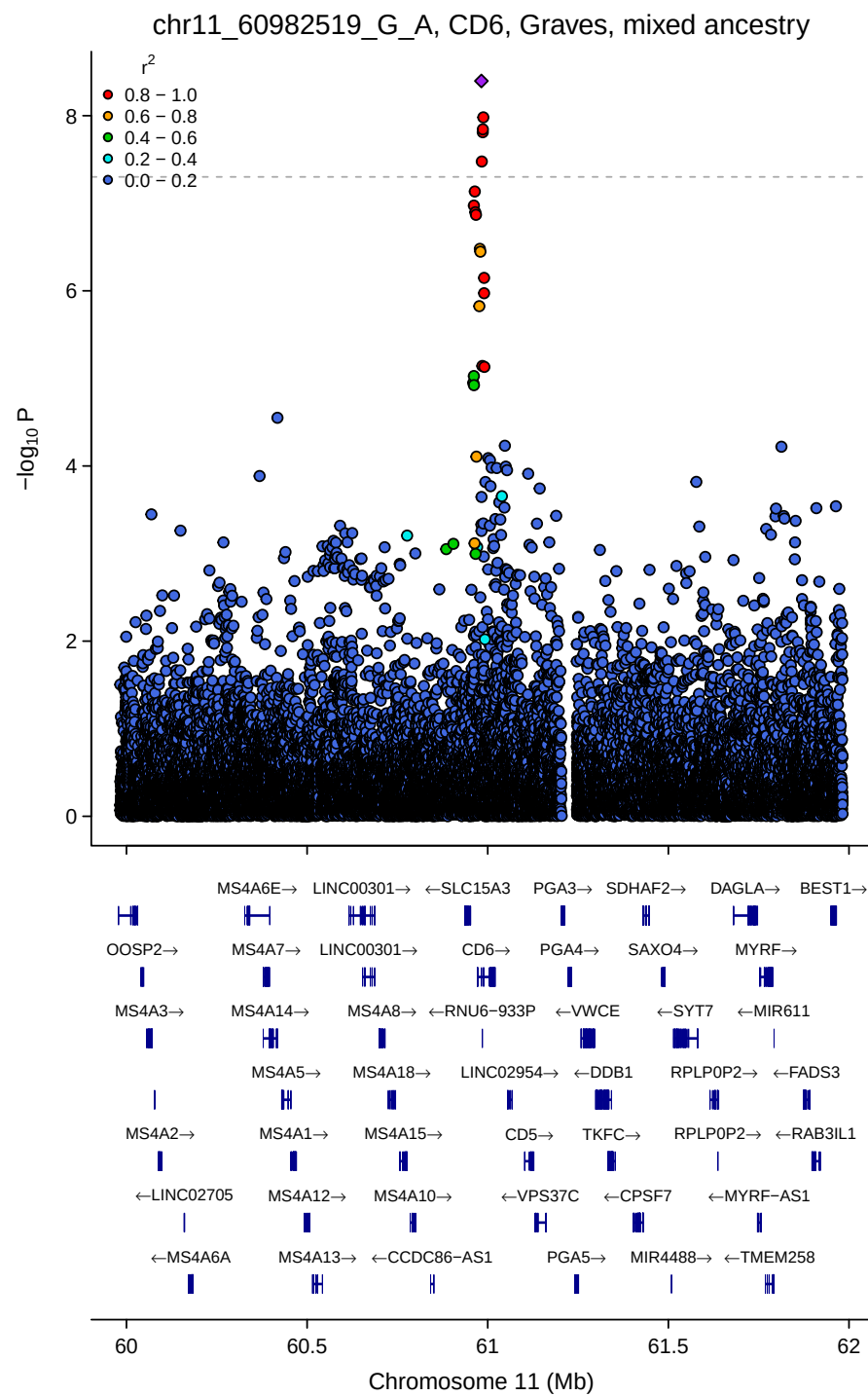


Supplementary Figure 3.2

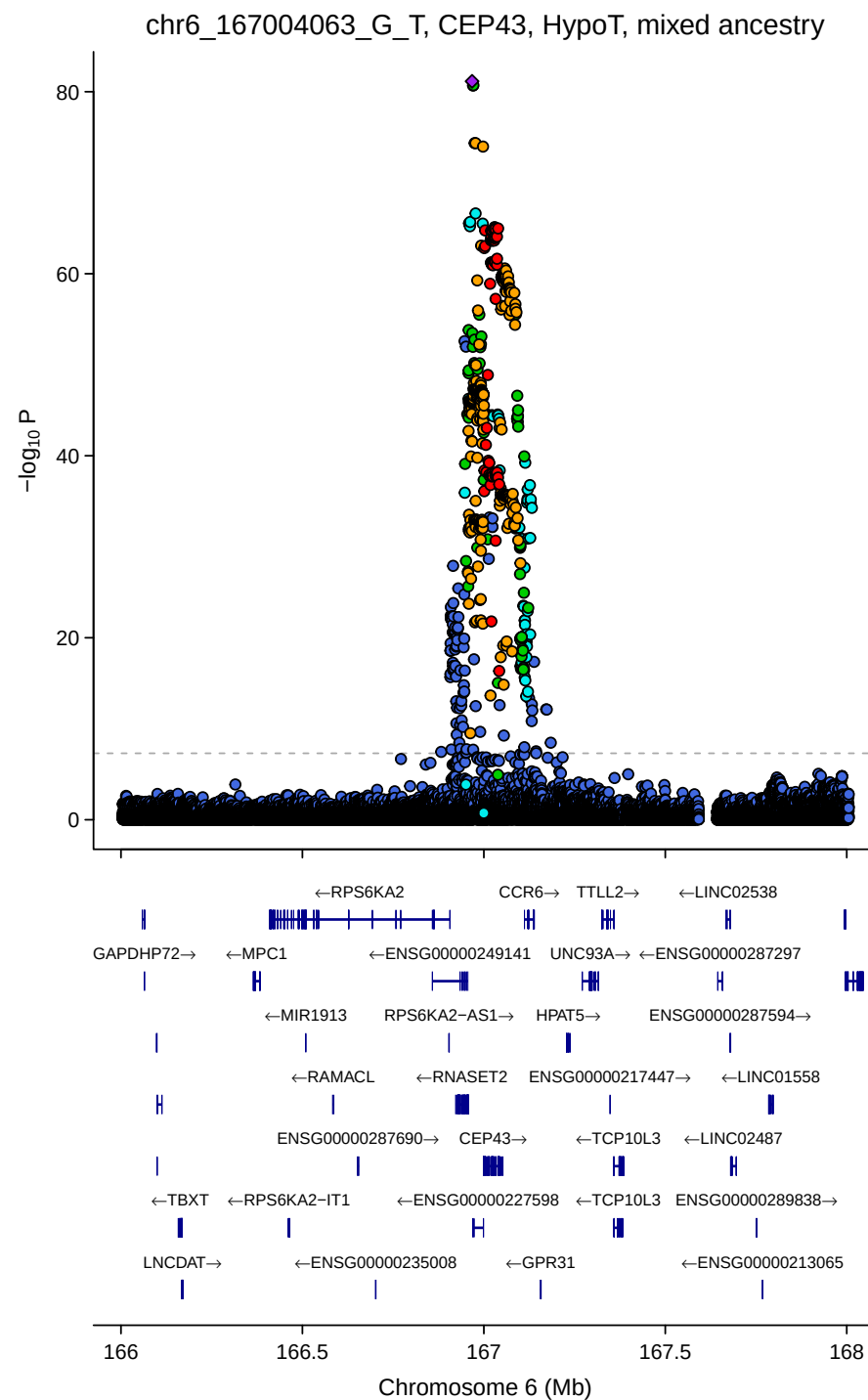
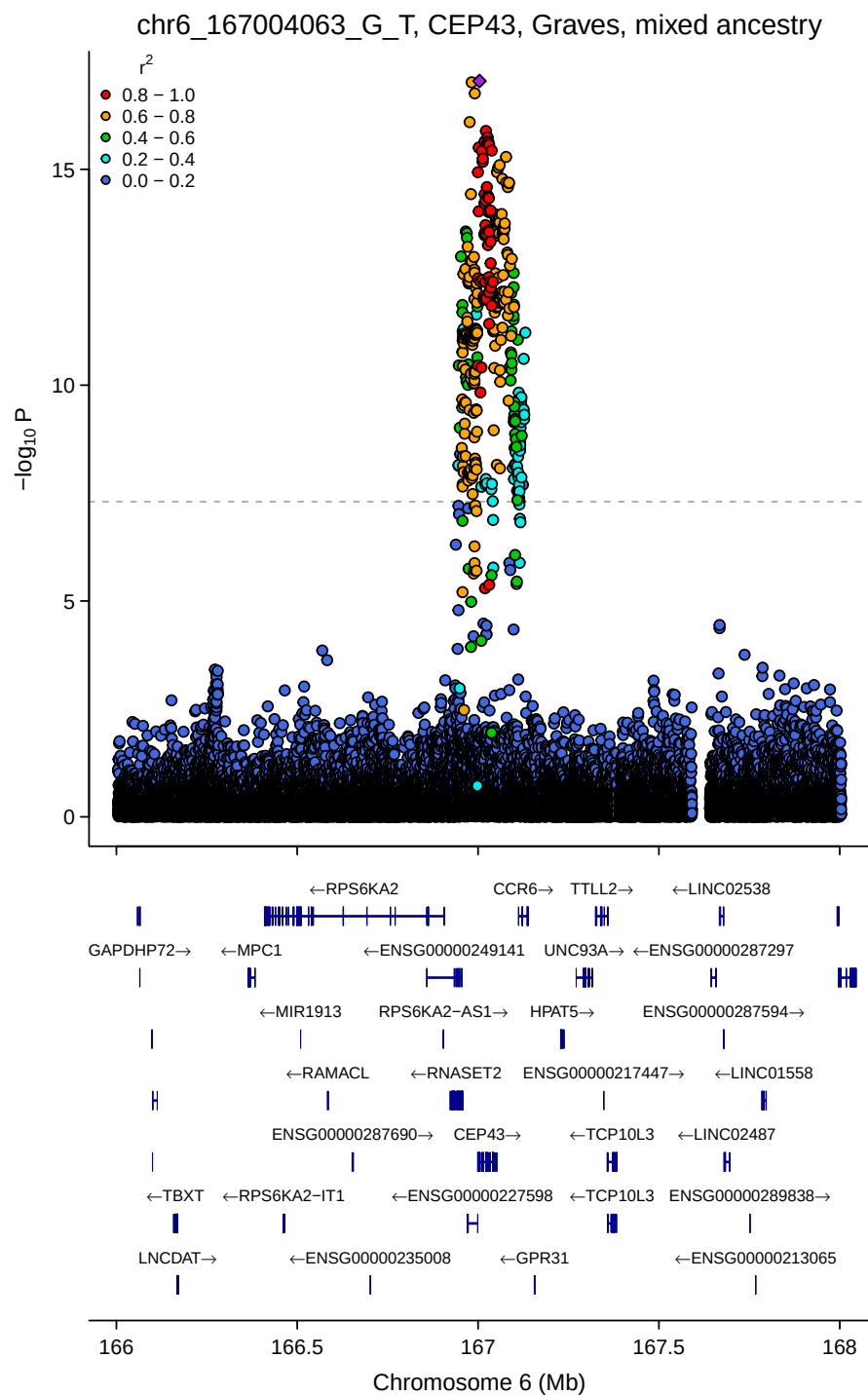




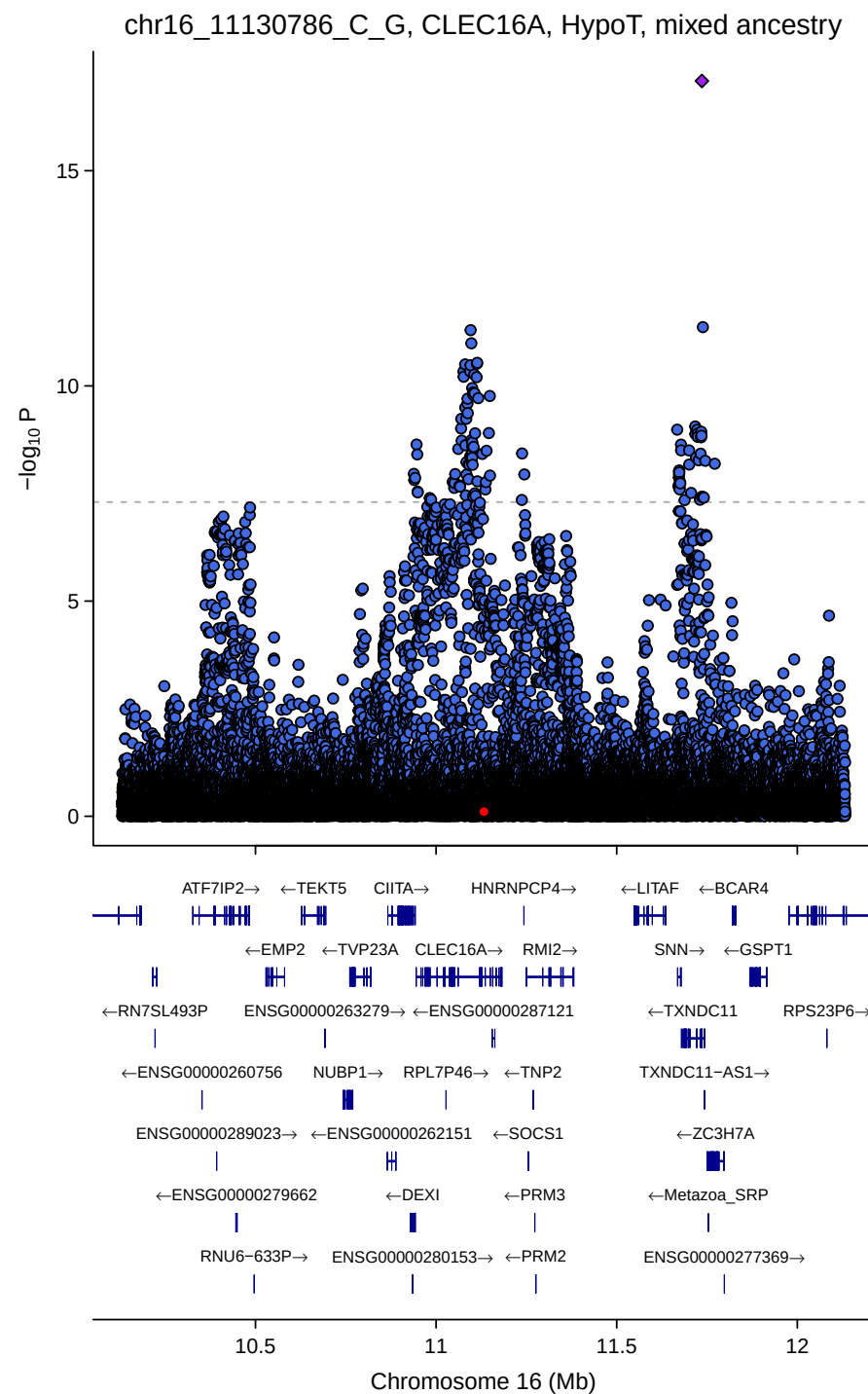
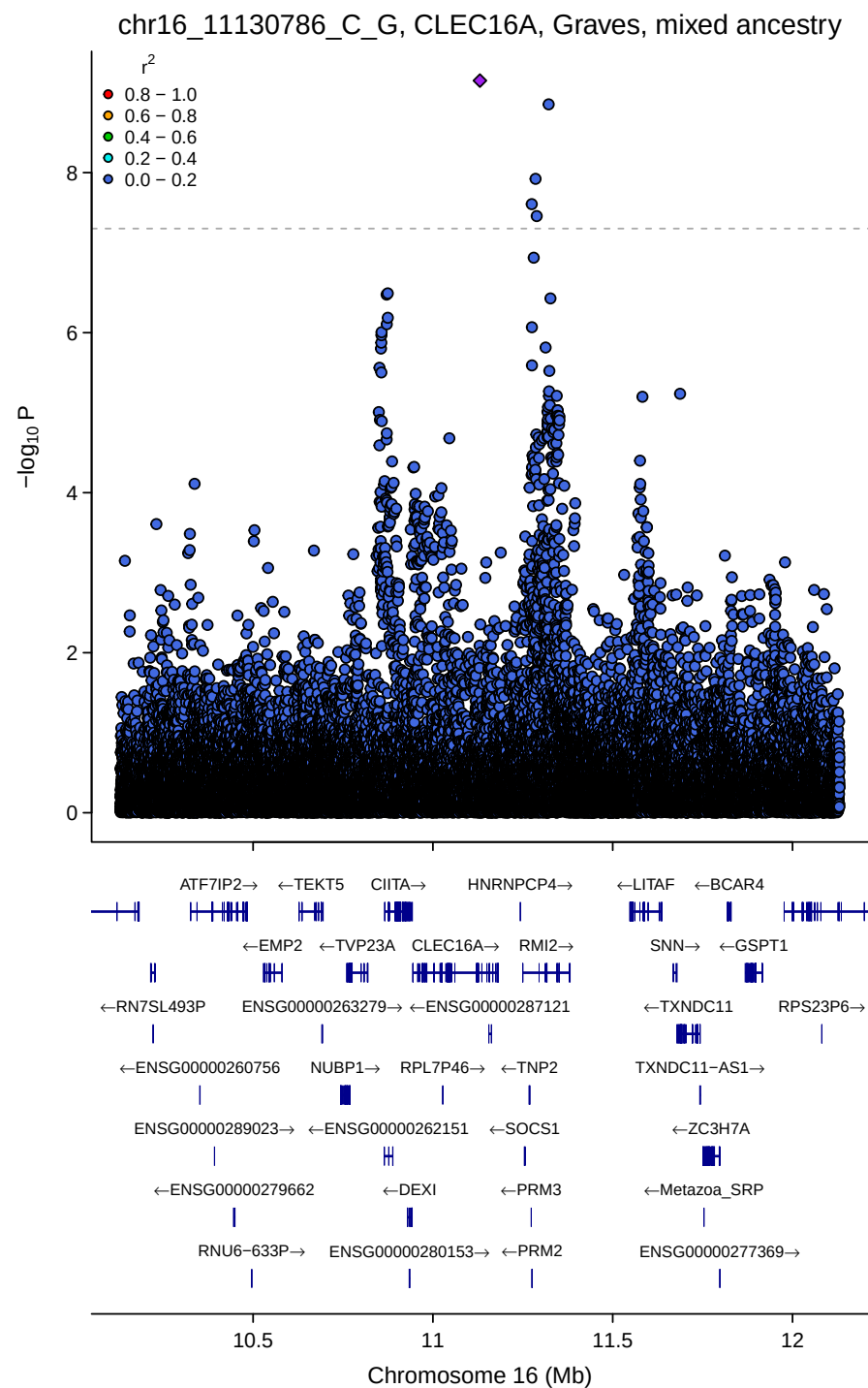
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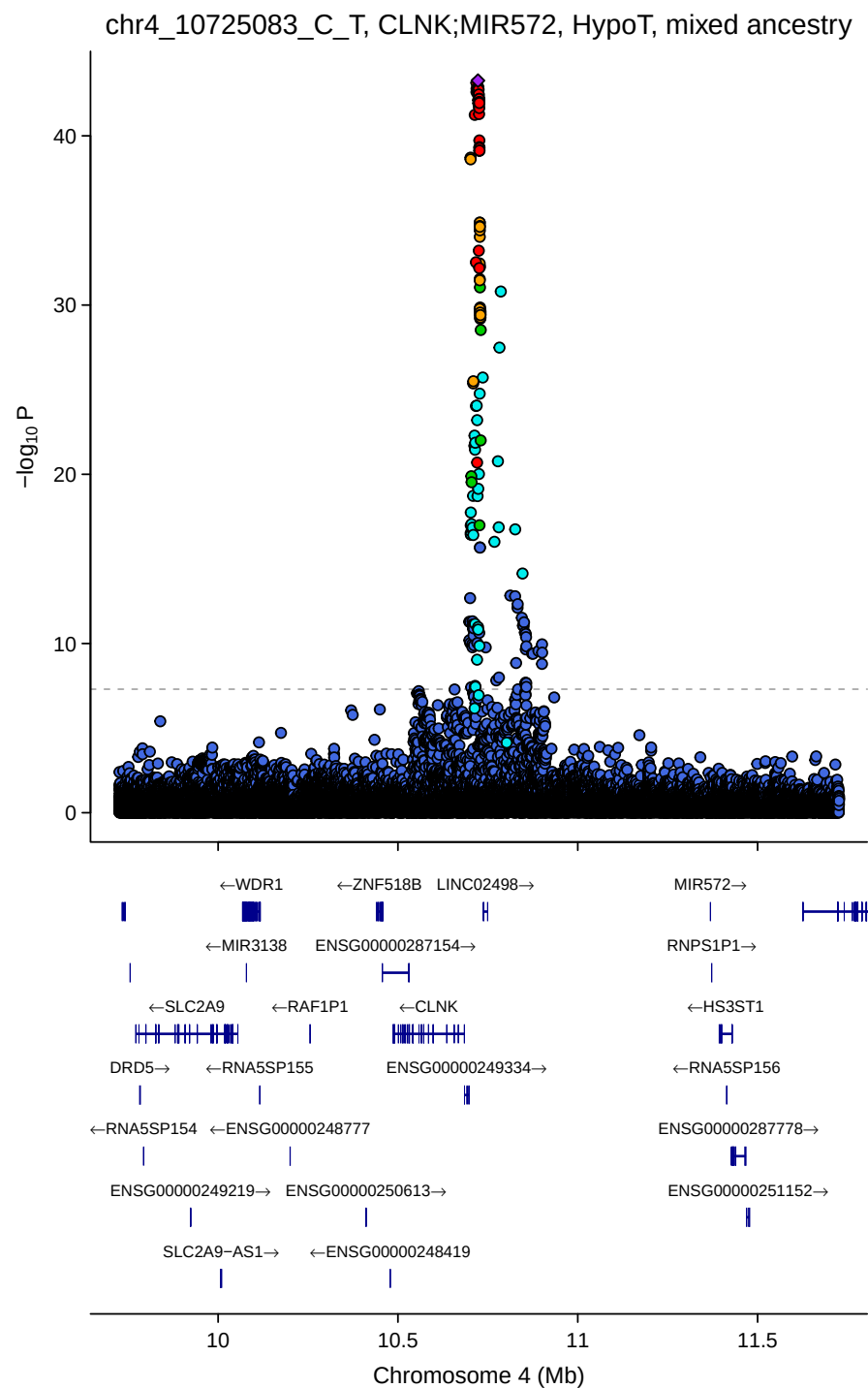
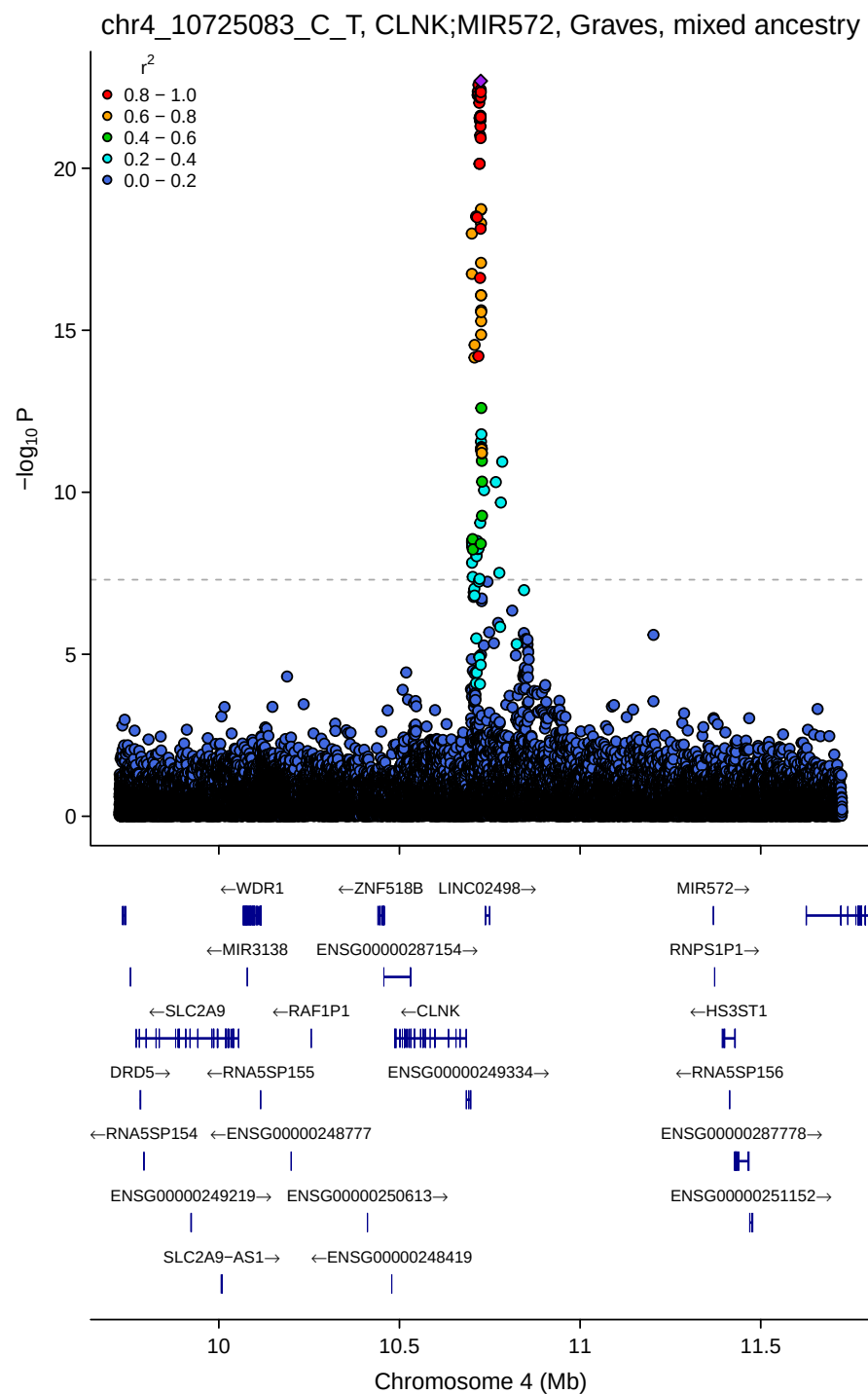
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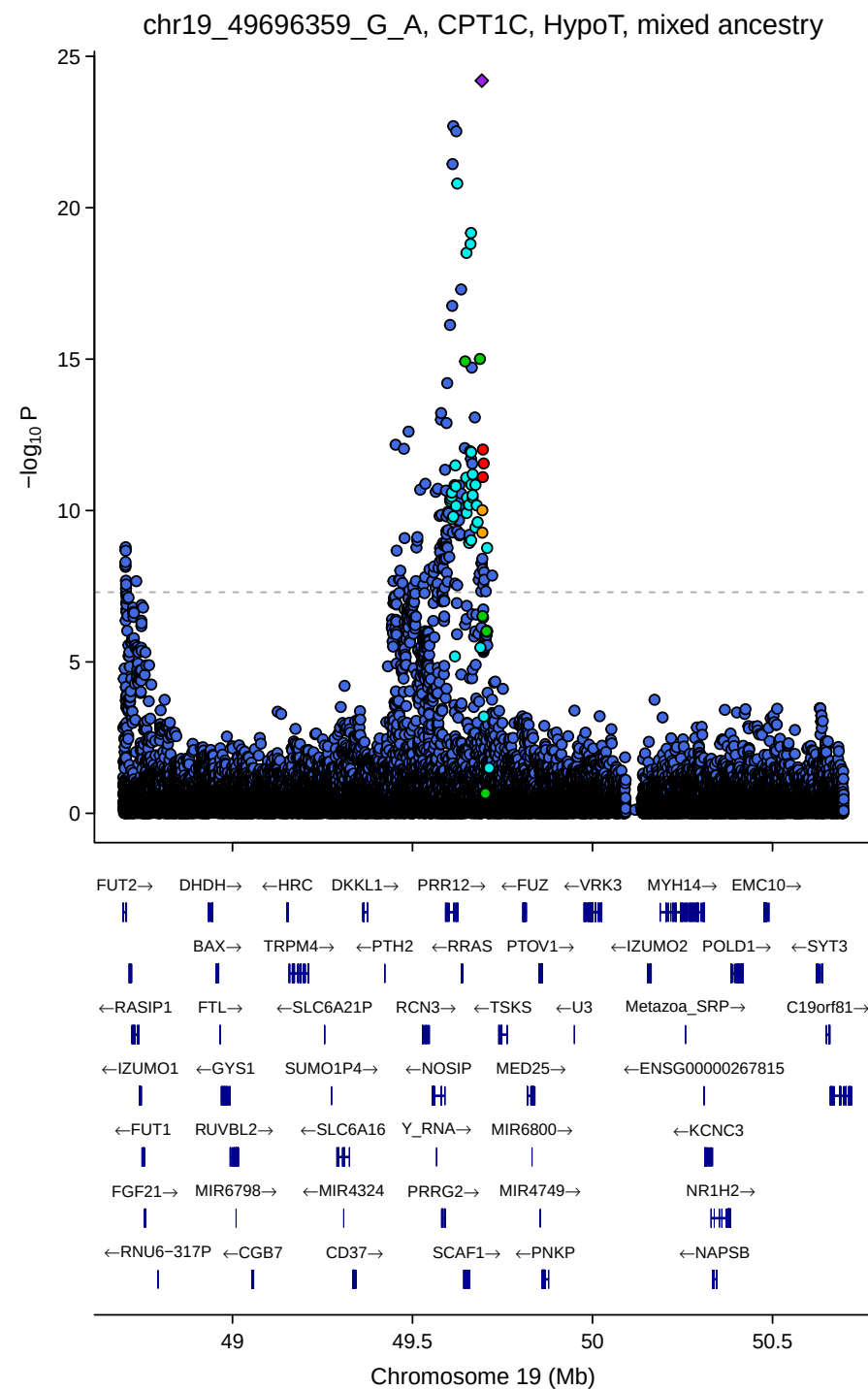
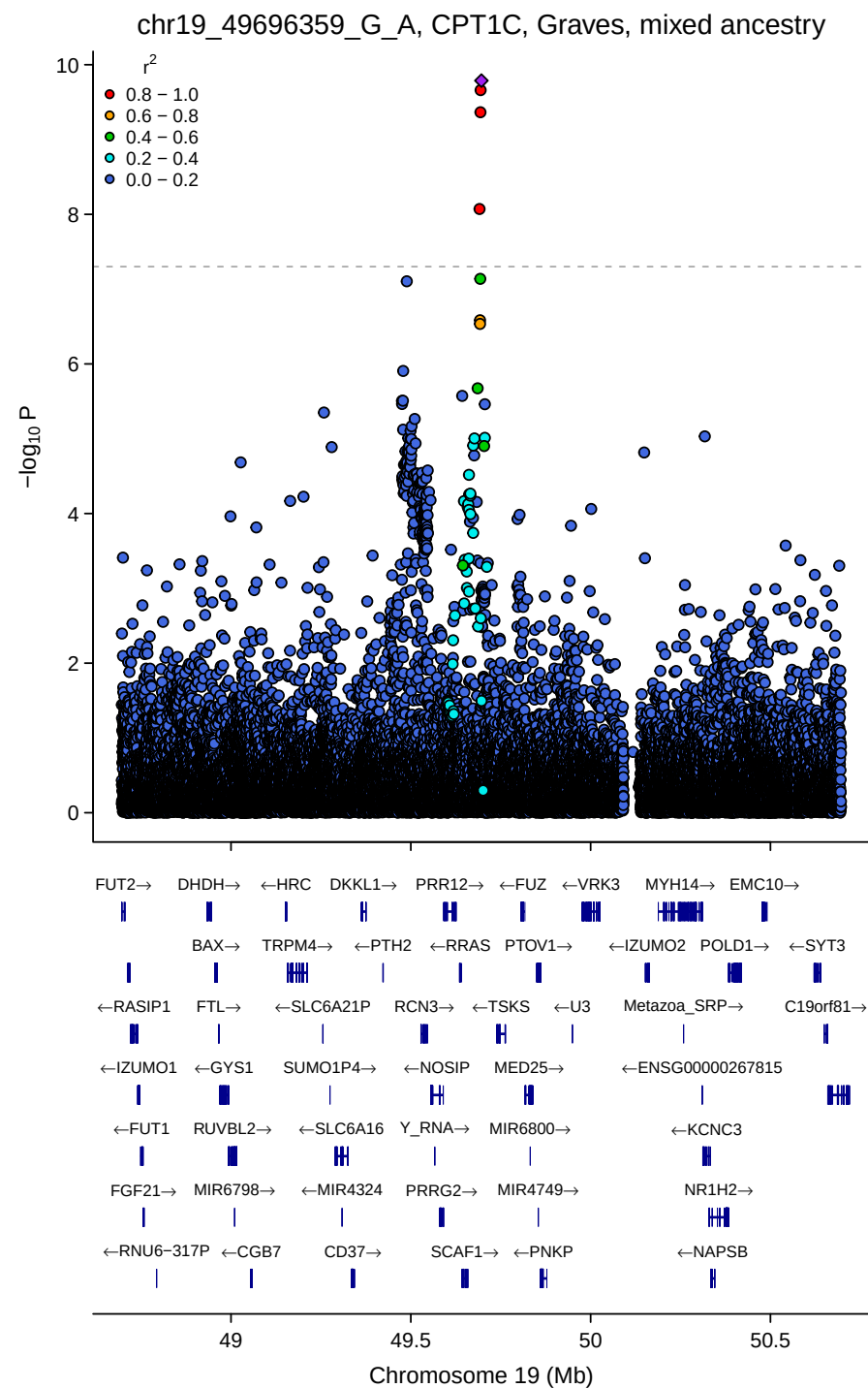
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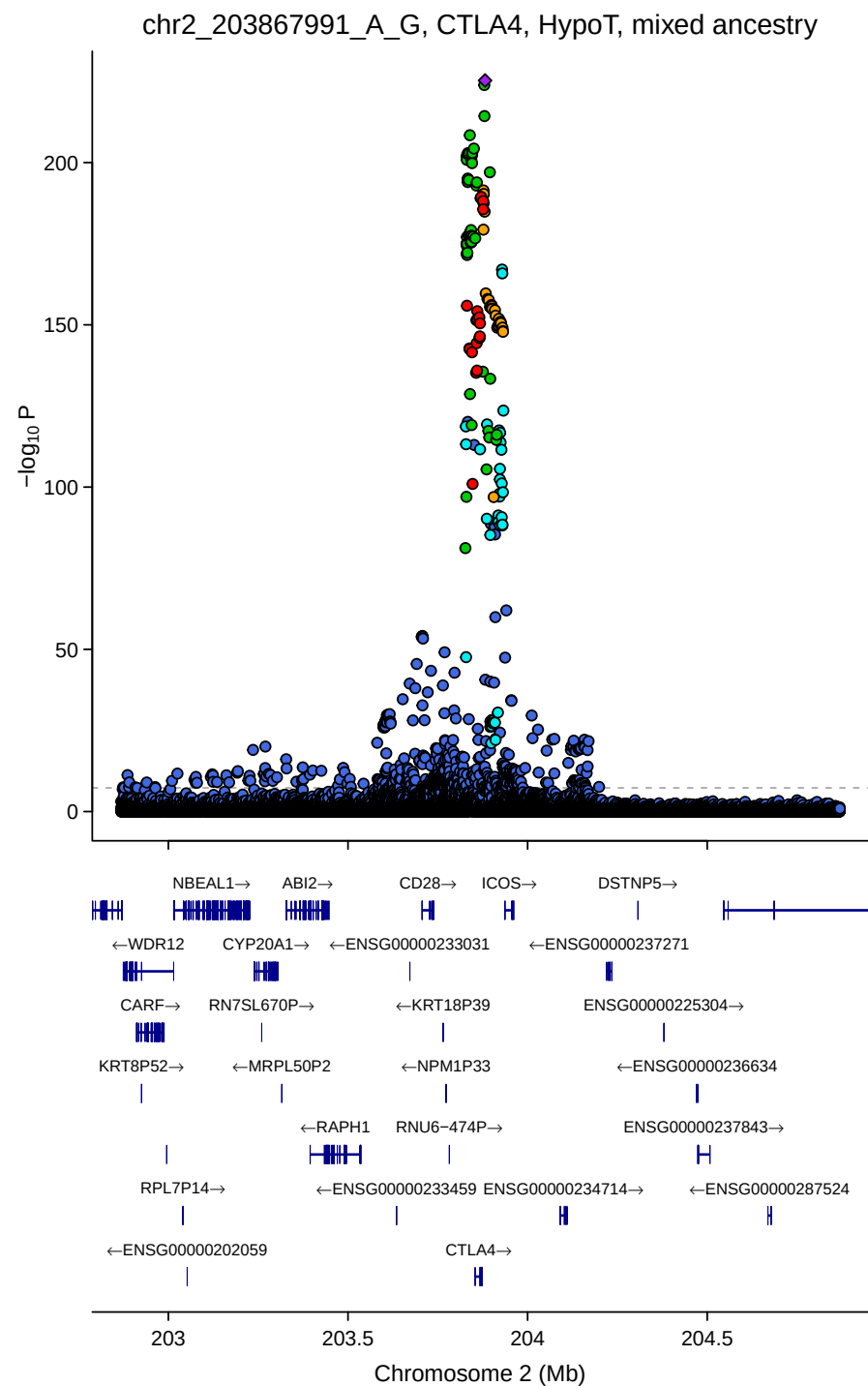
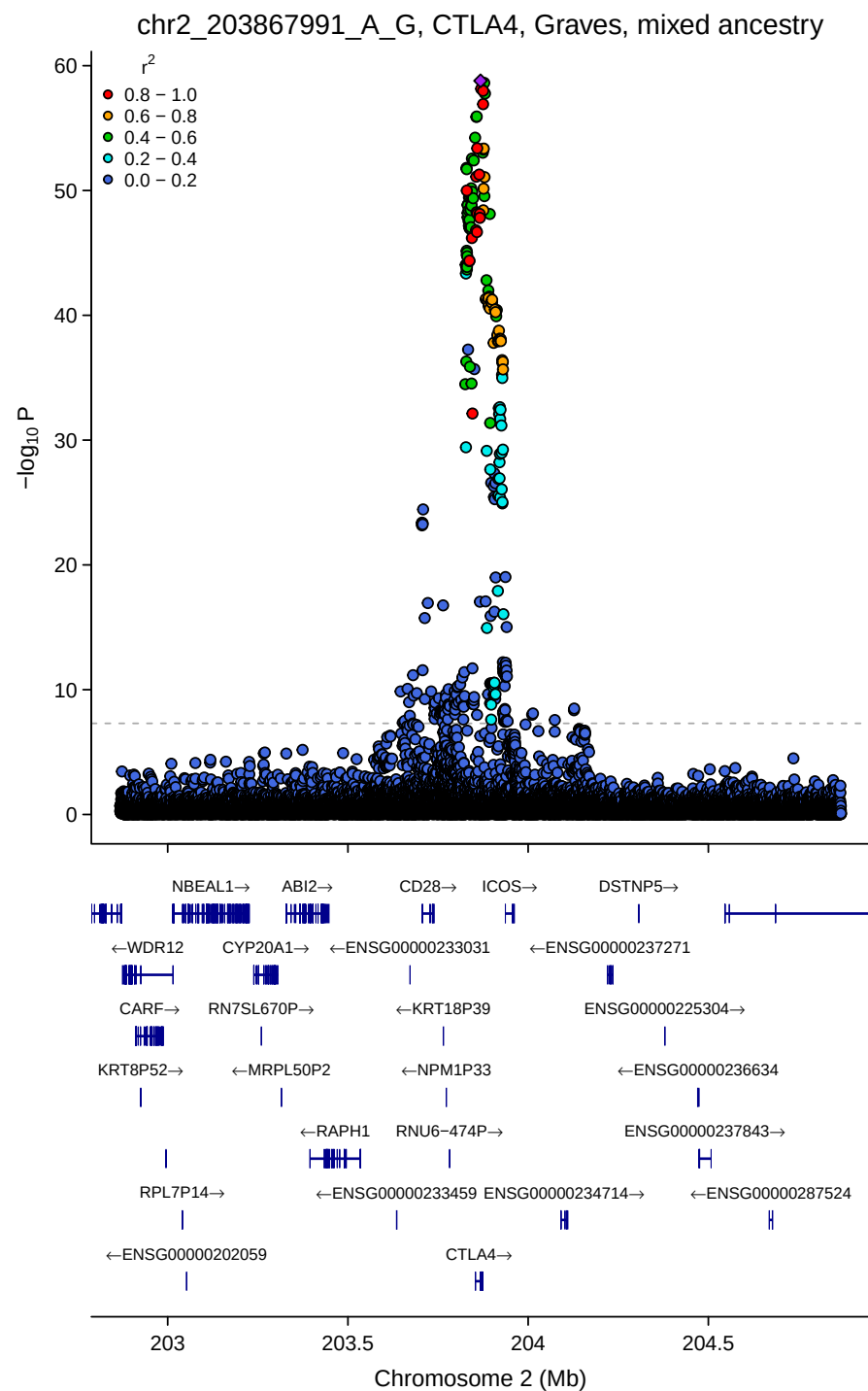
Supplementary Figure 3.2



Supplementary Figure 3.2

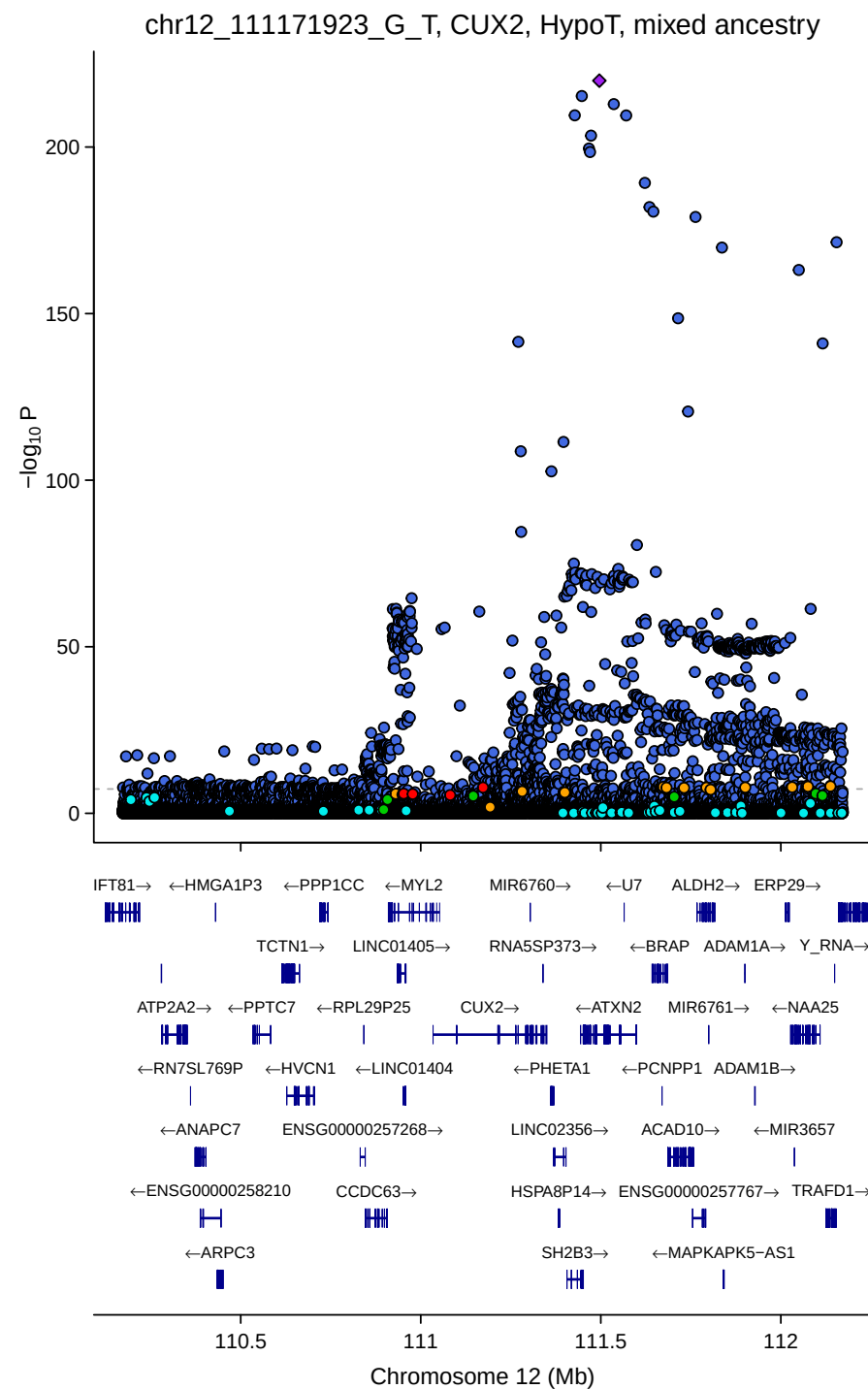
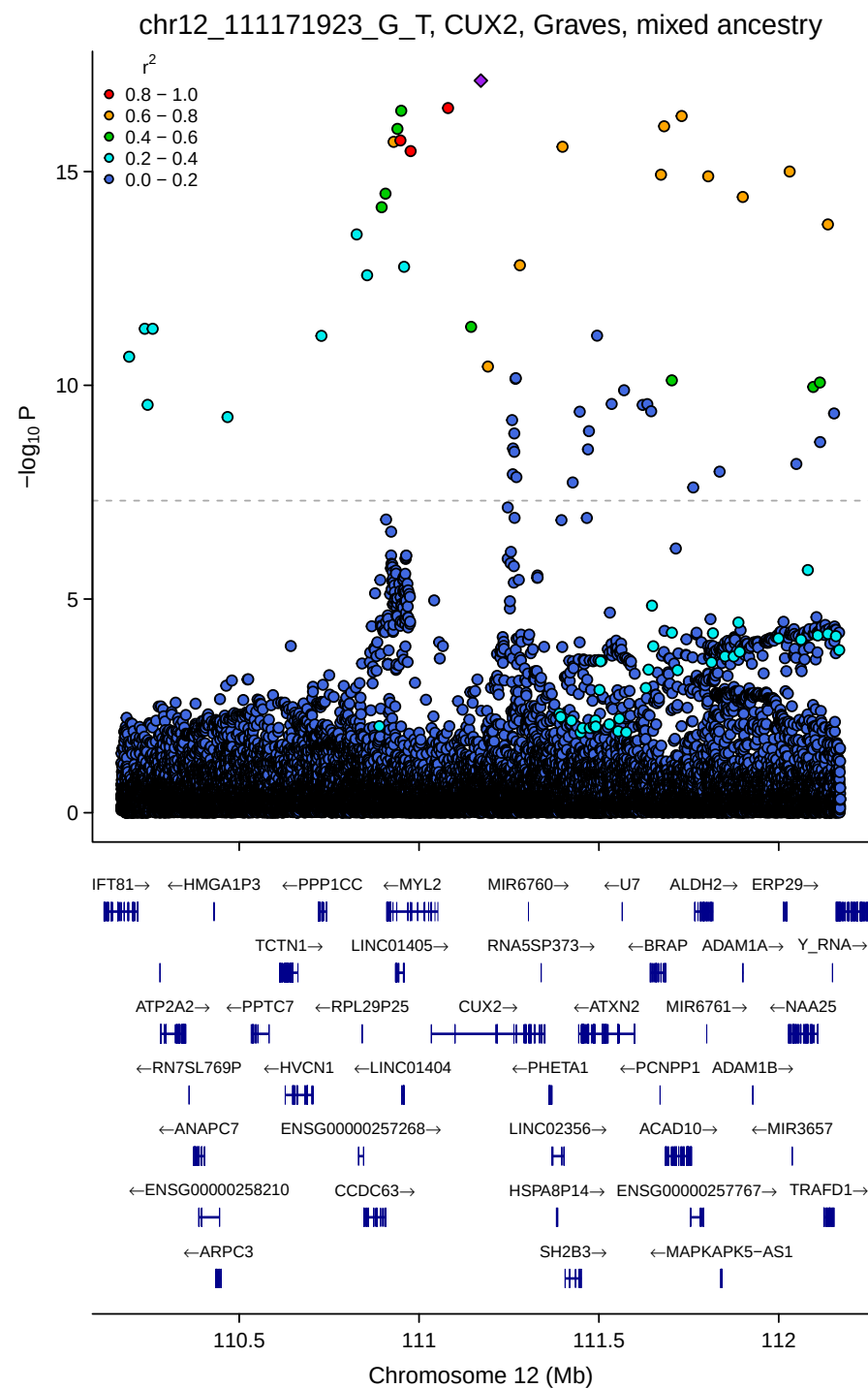


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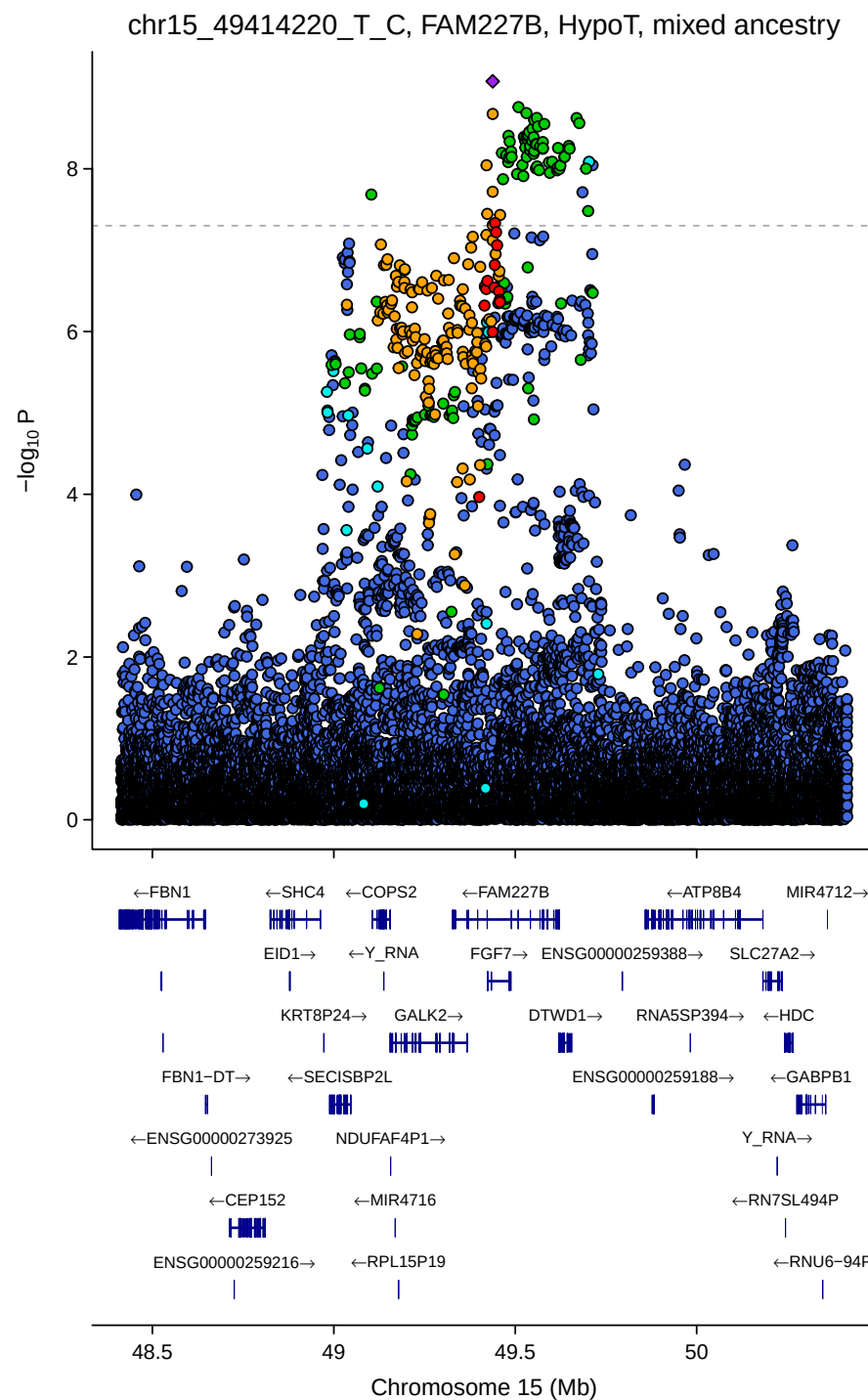
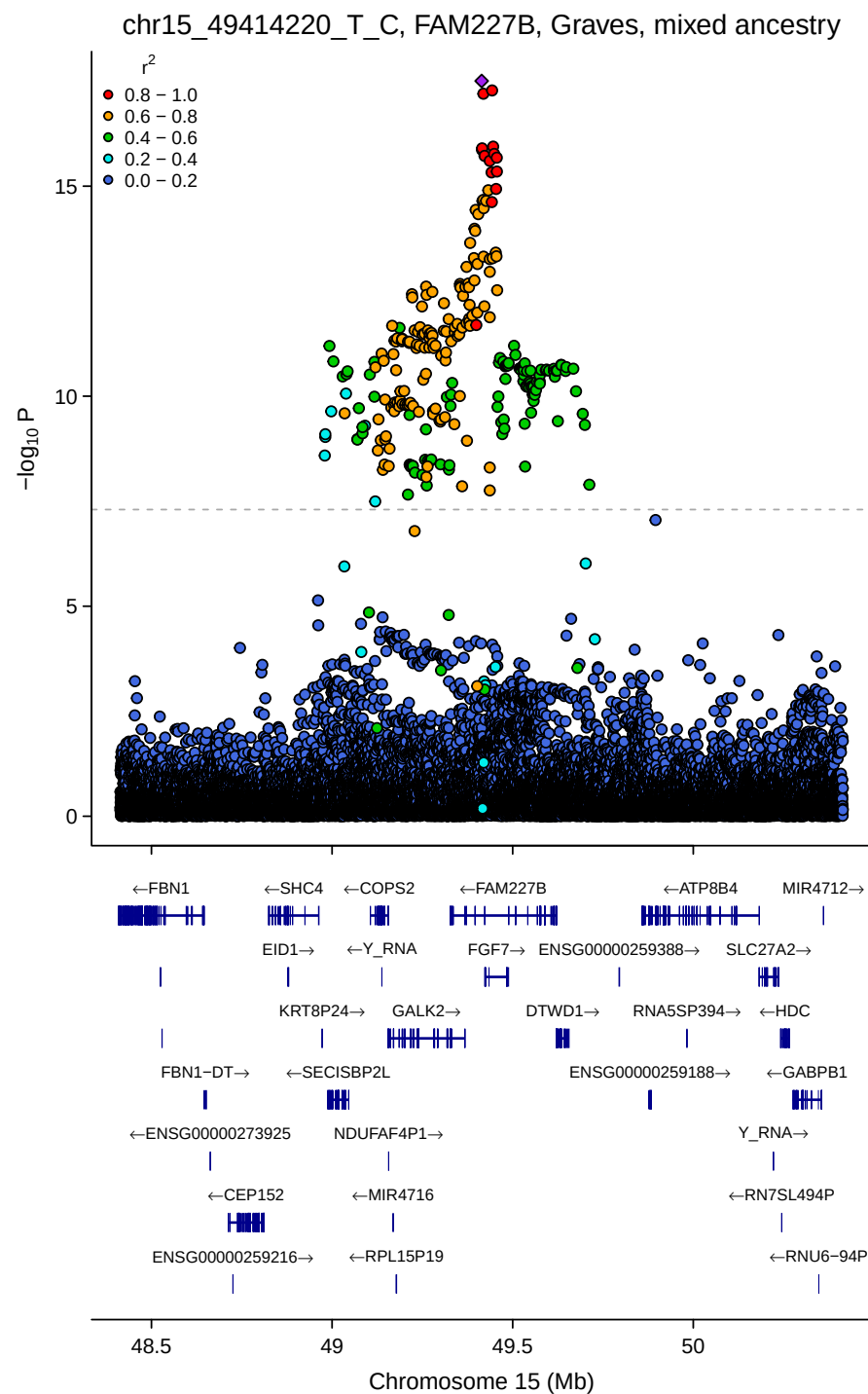




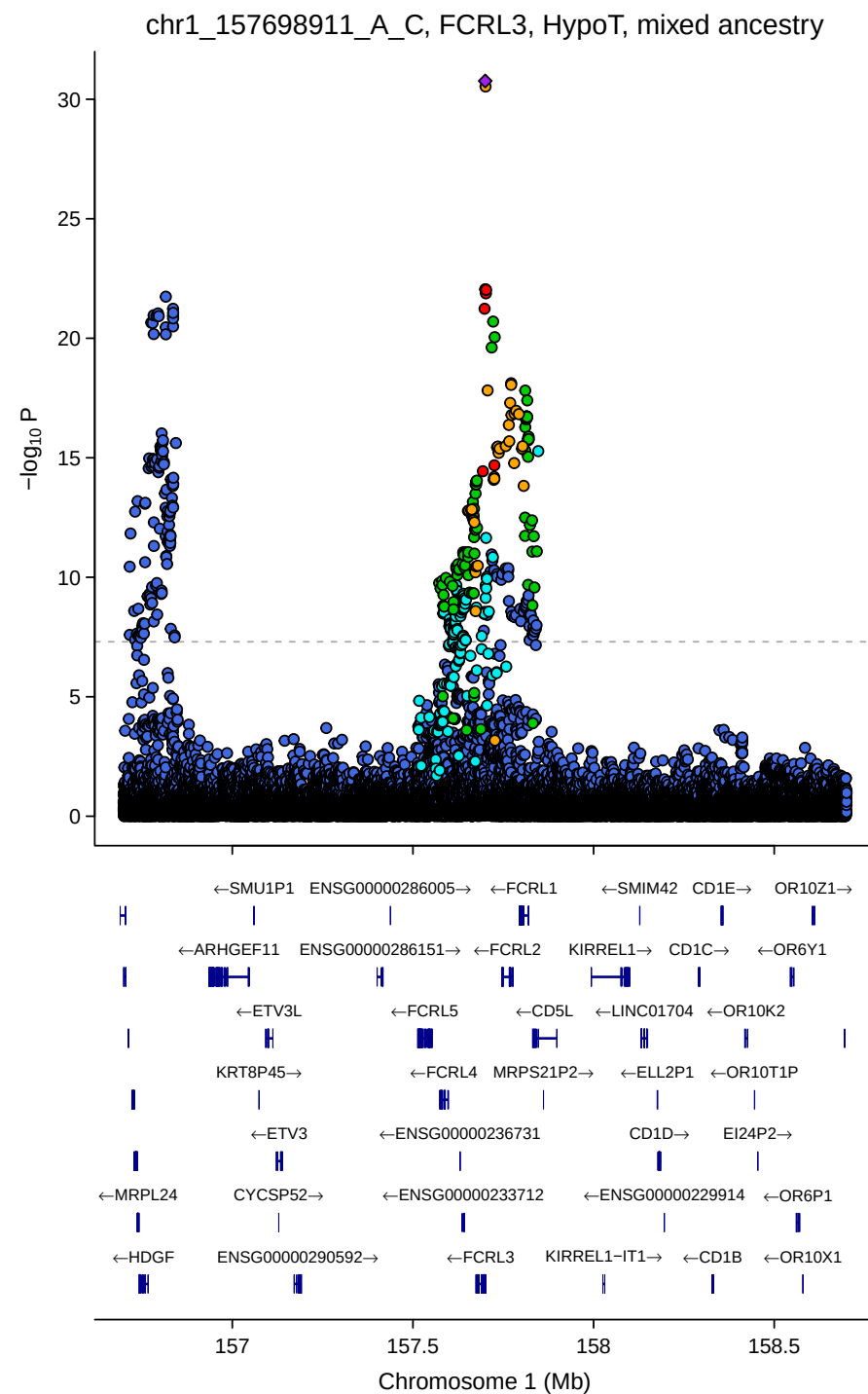
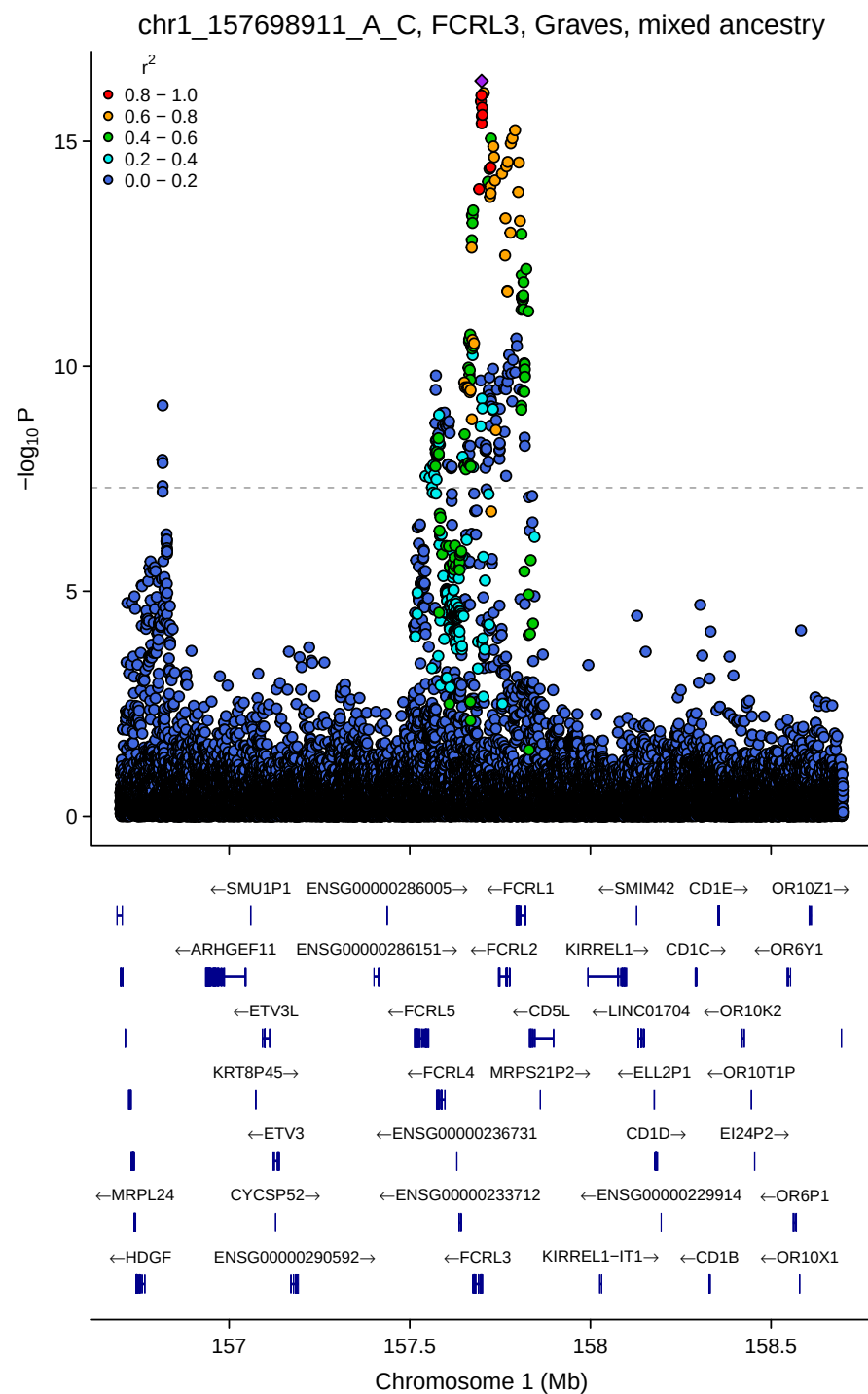
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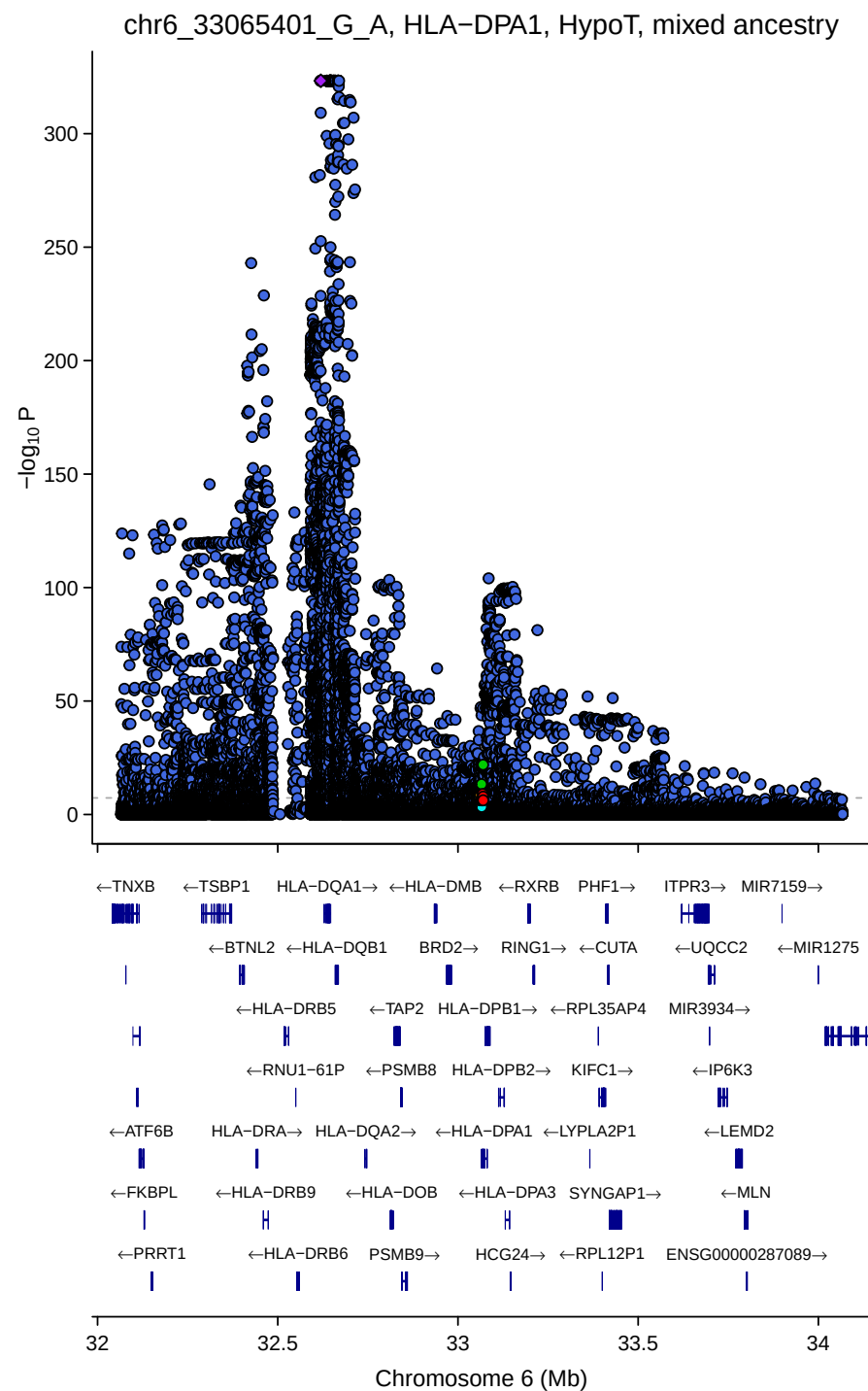
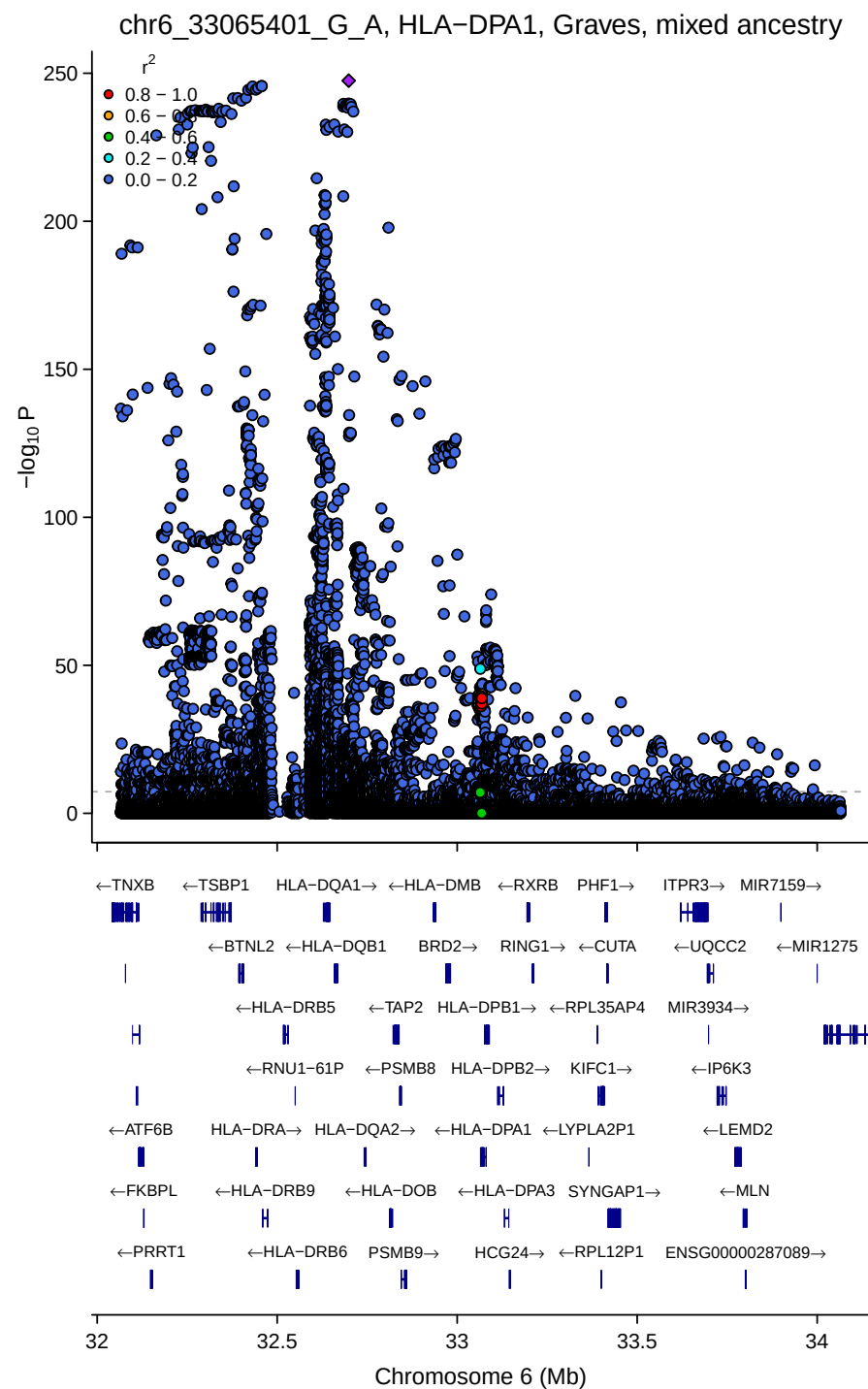
Supplementary Figure 3.2



Supplementary Figure 3.2

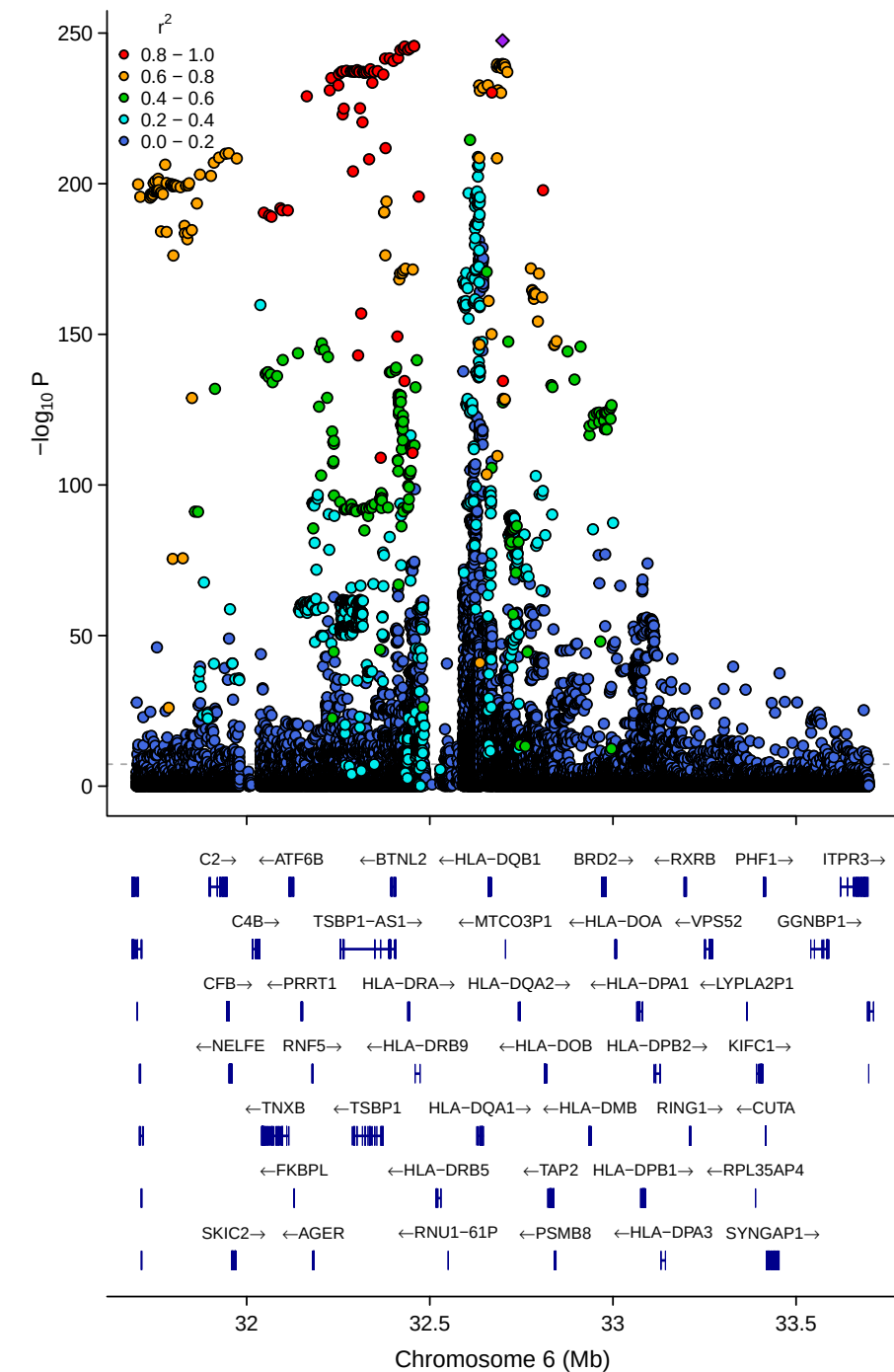


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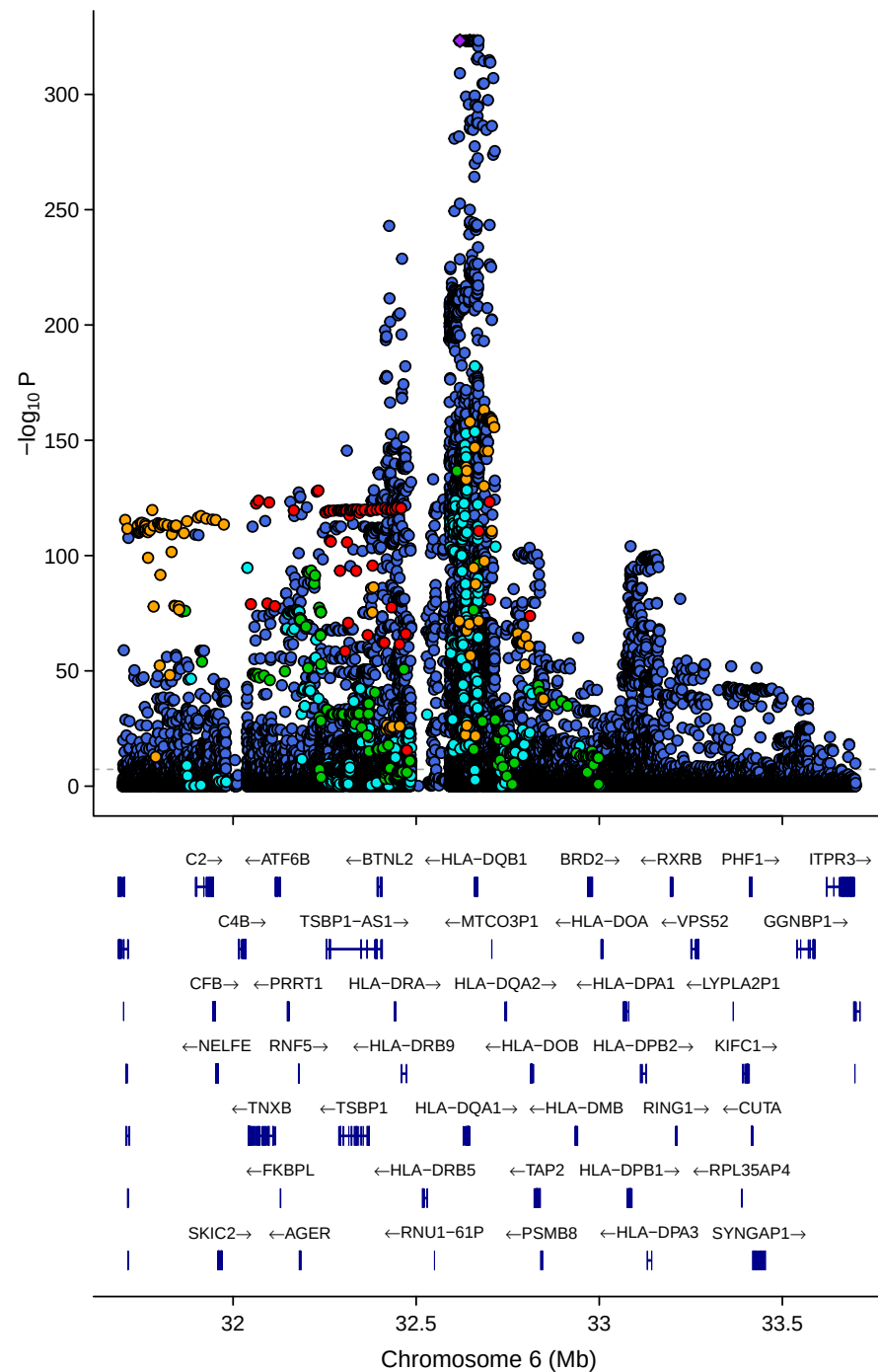


Supplementary Figure 3.2

chr6\_32698749\_C\_T, HLA-DQB1;HLA-DQA2, Graves, mixed ancestry

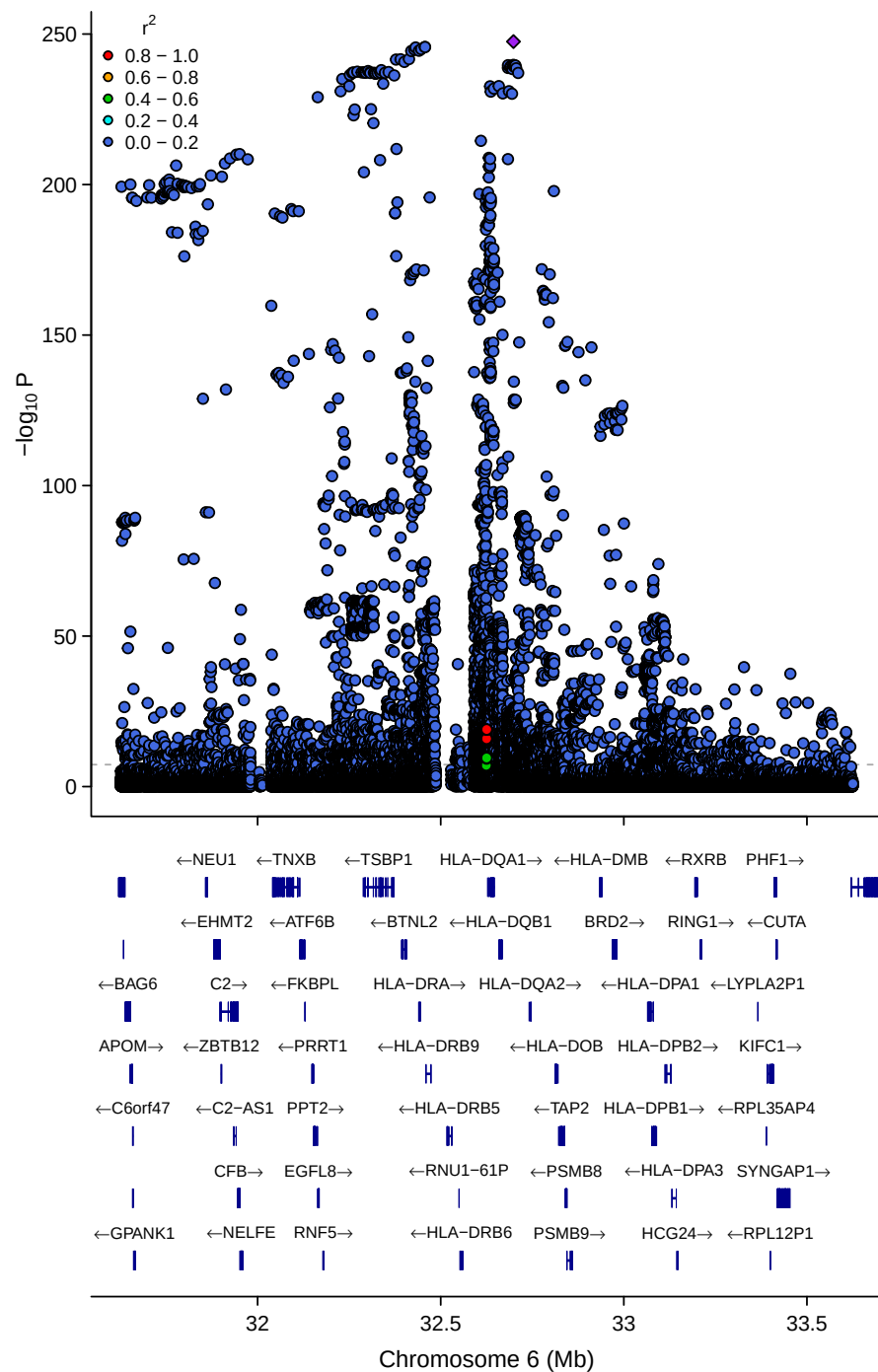


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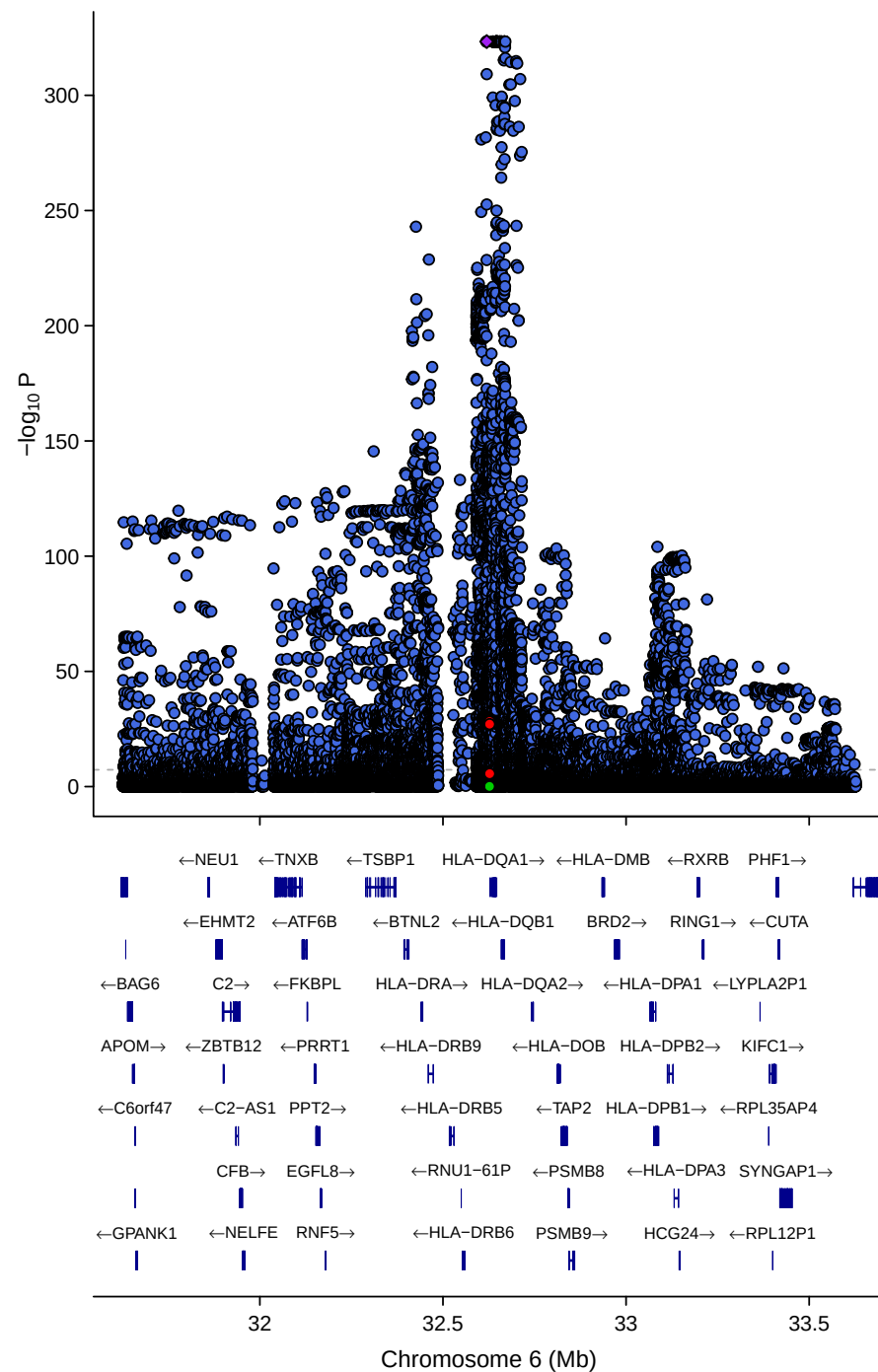


Supplementary Figure 3.2

chr6\_32625591\_G\_A, HLA-DRB1;HLA-DQA1, Graves, mixed ancestry

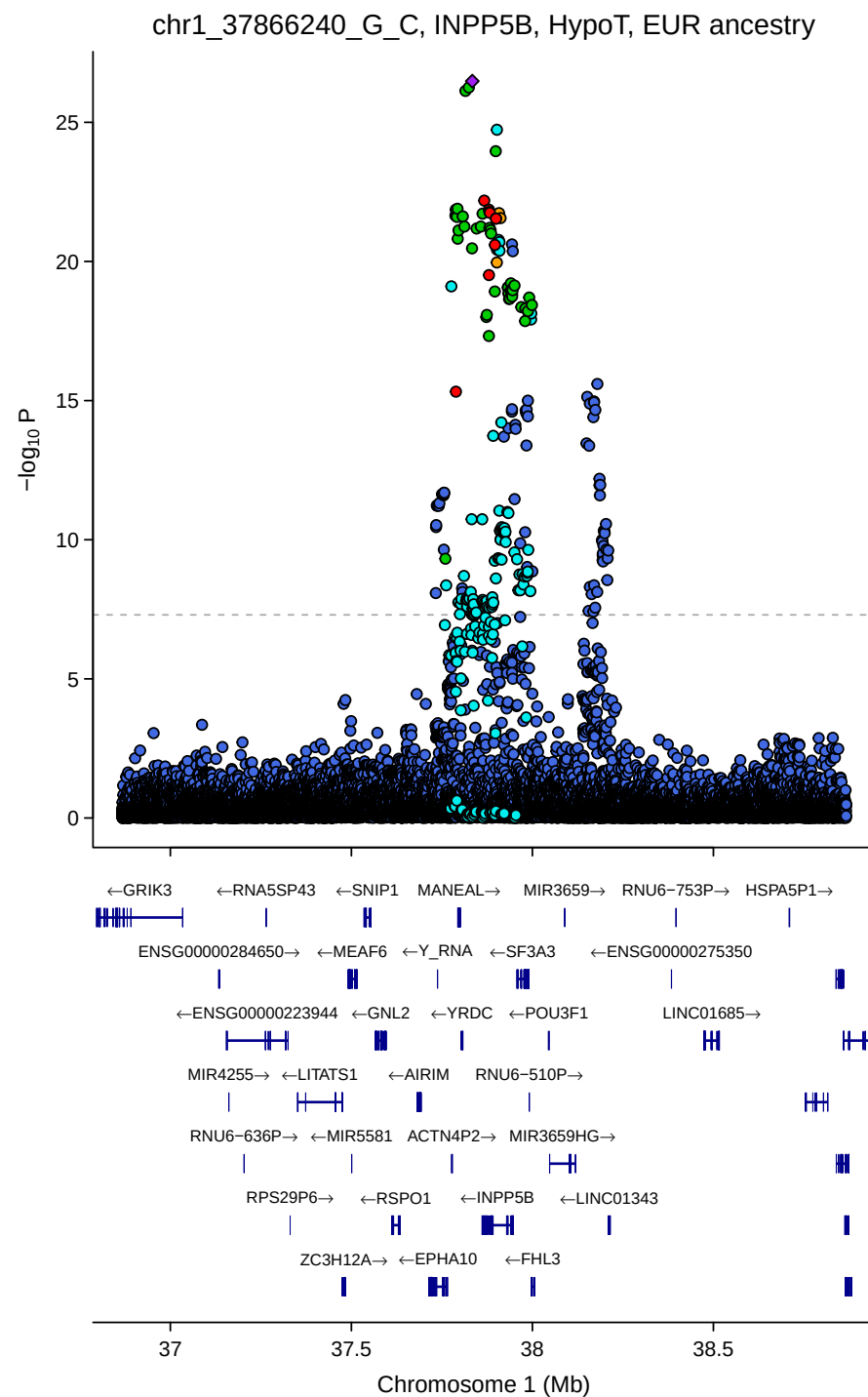
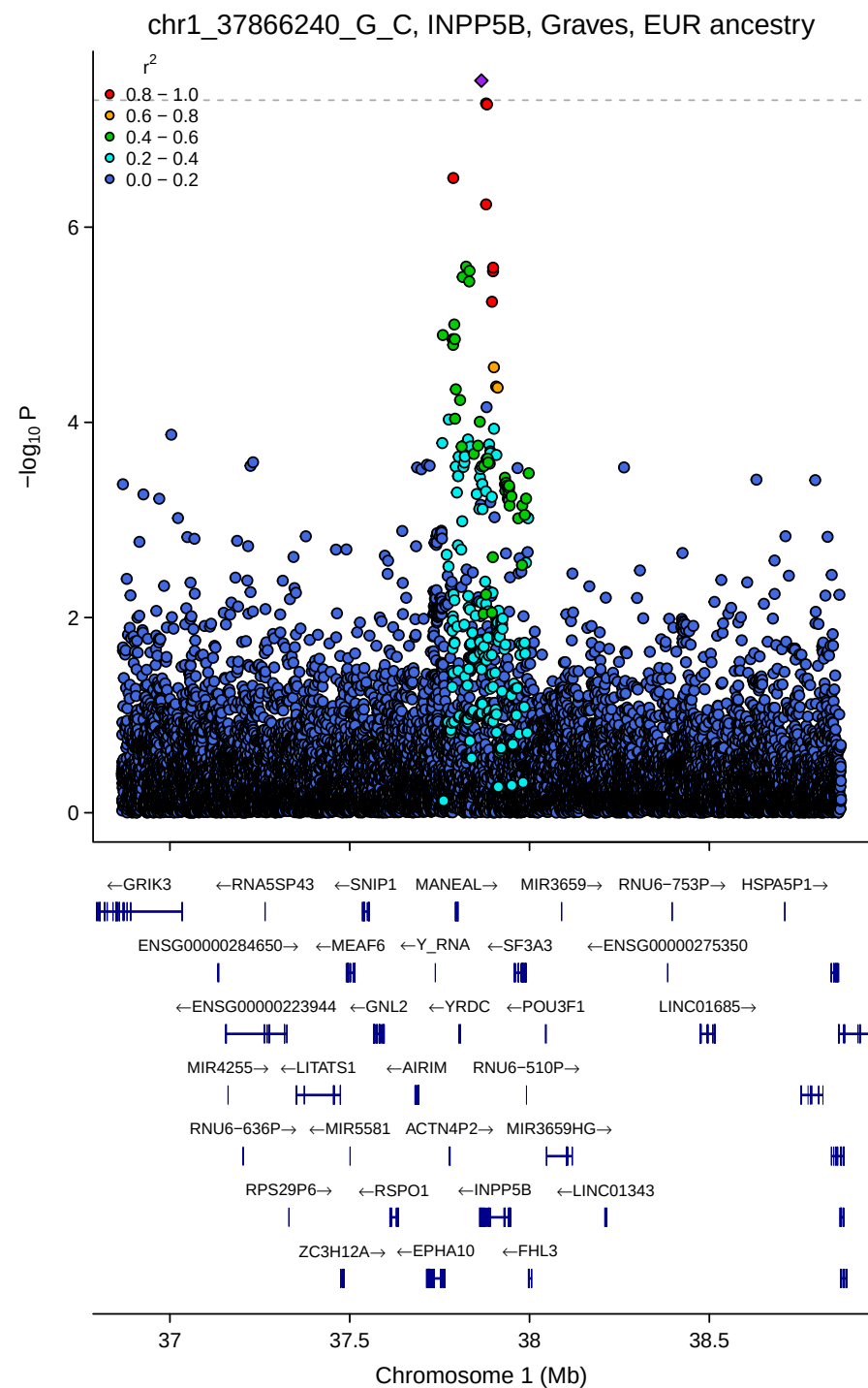


chr6\_32625591\_G\_A, HLA-DRB1;HLA-DQA1, HypoT, mixed ancestry

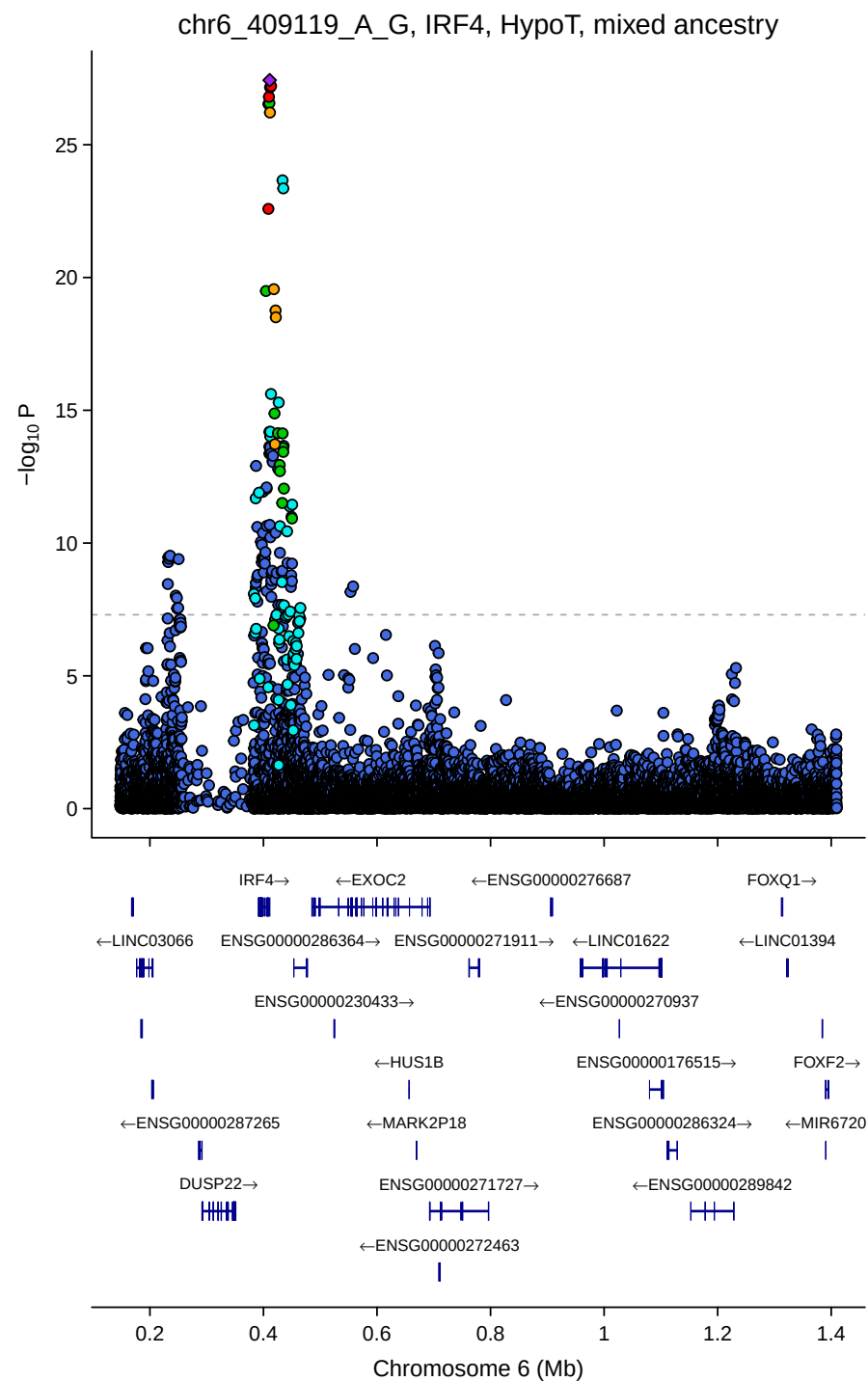
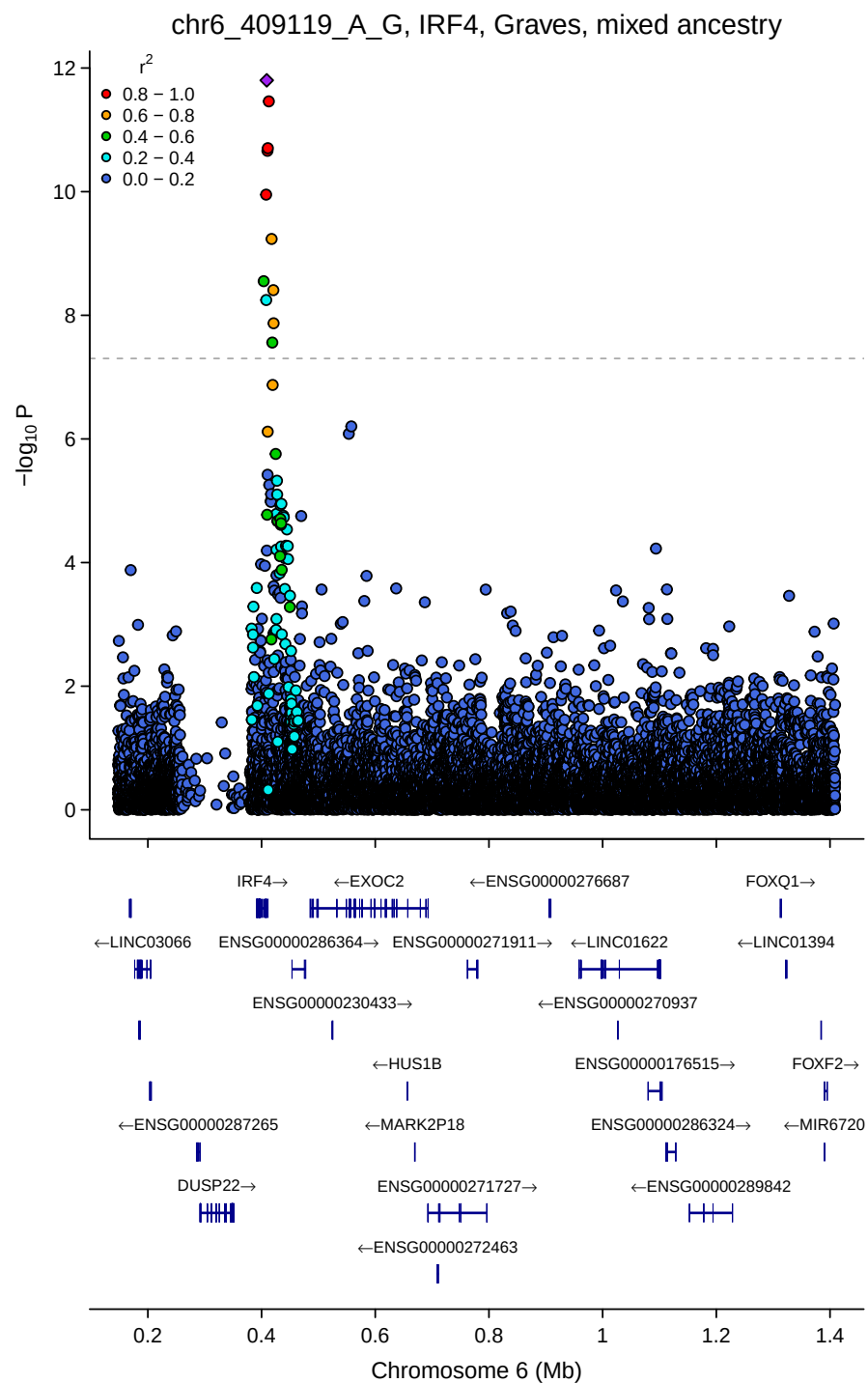




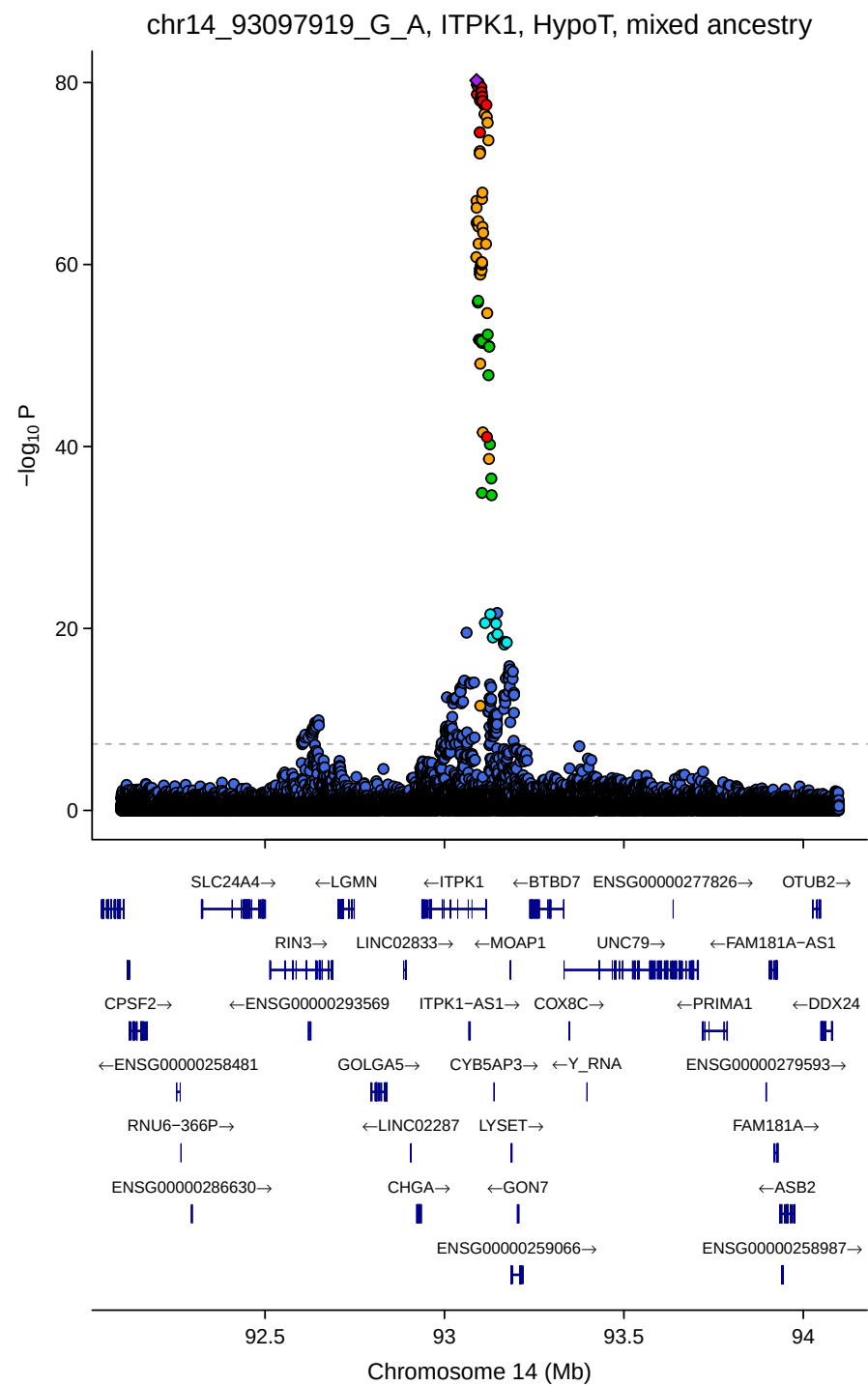
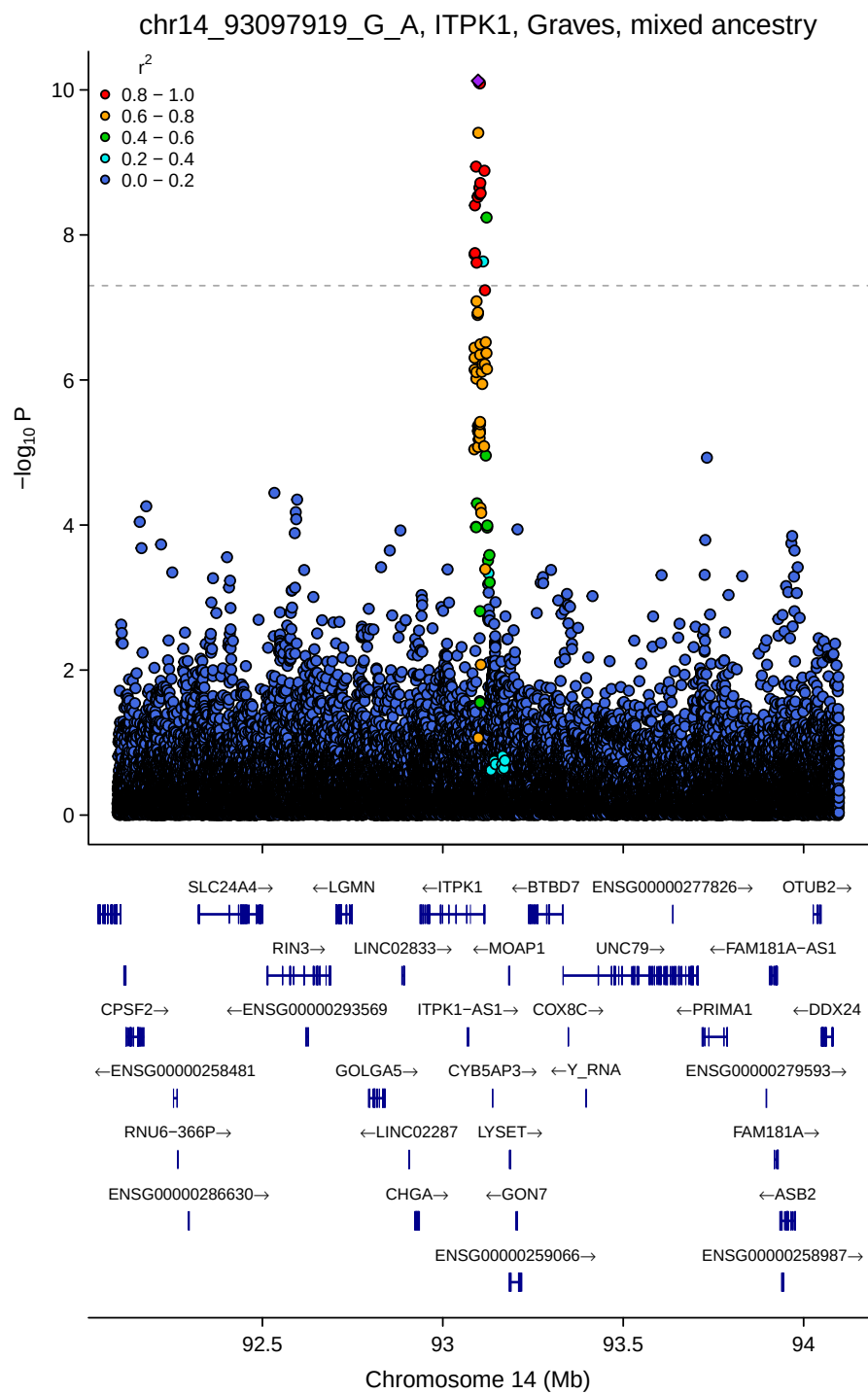
Supplementary Figure 3.2



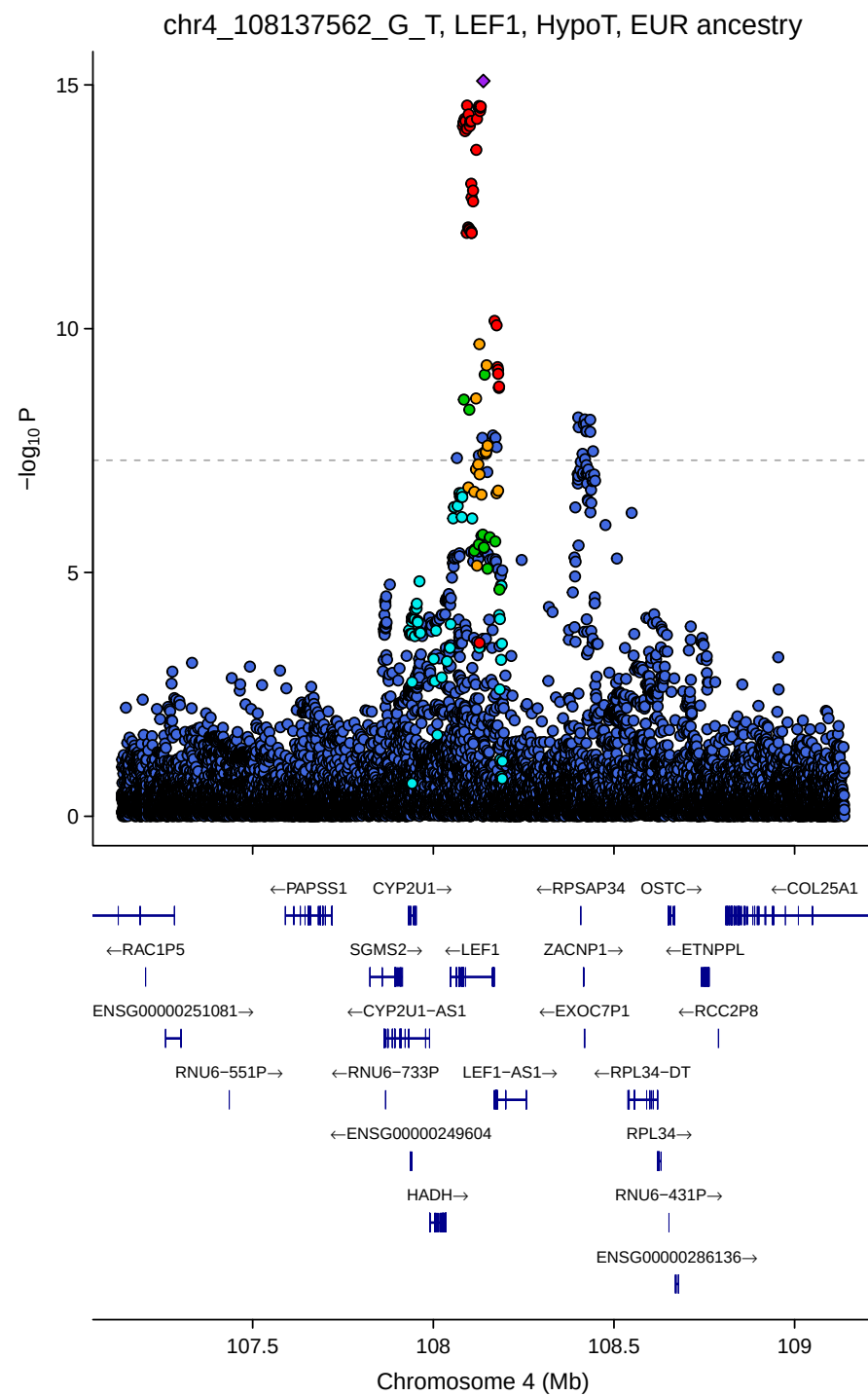
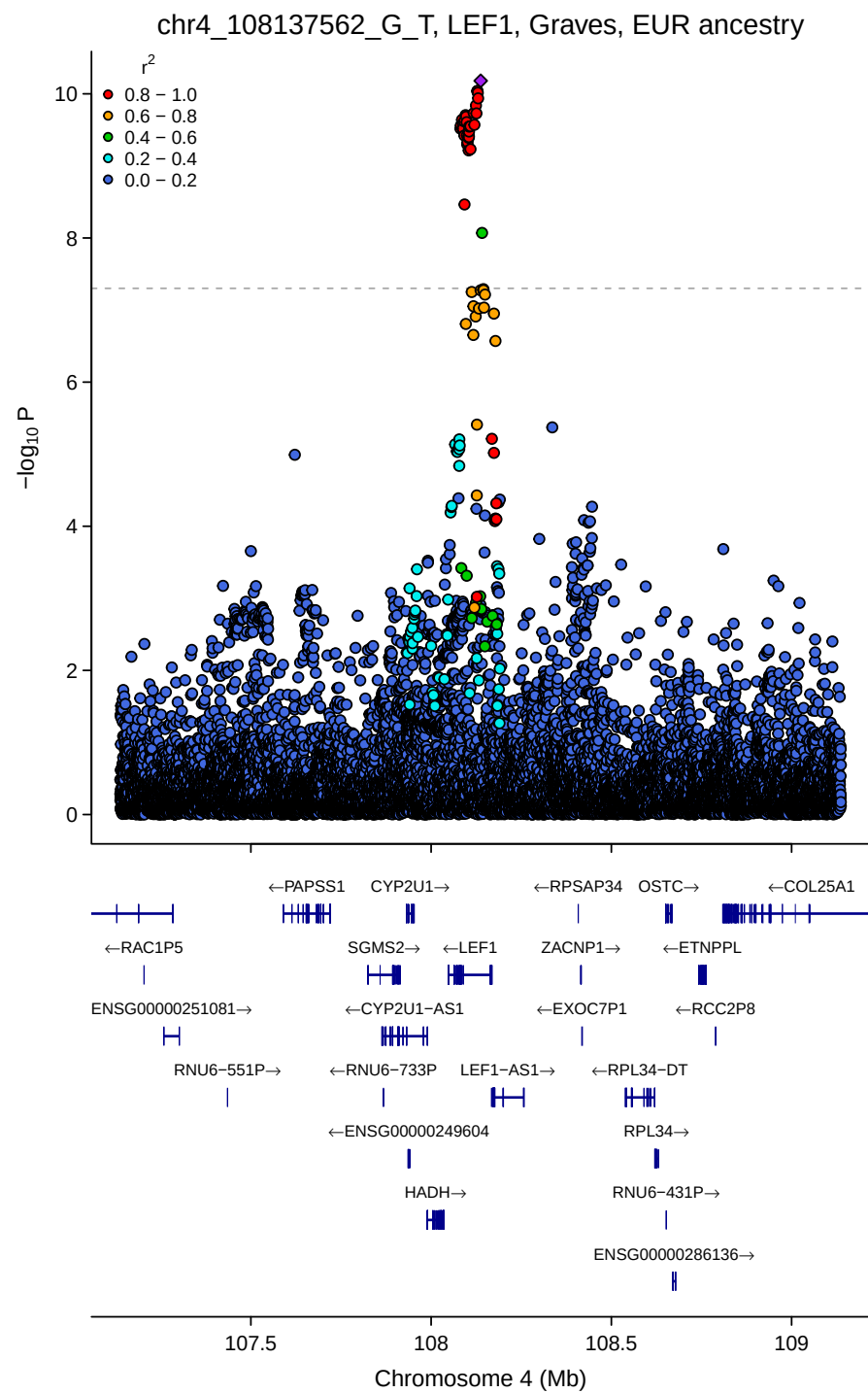
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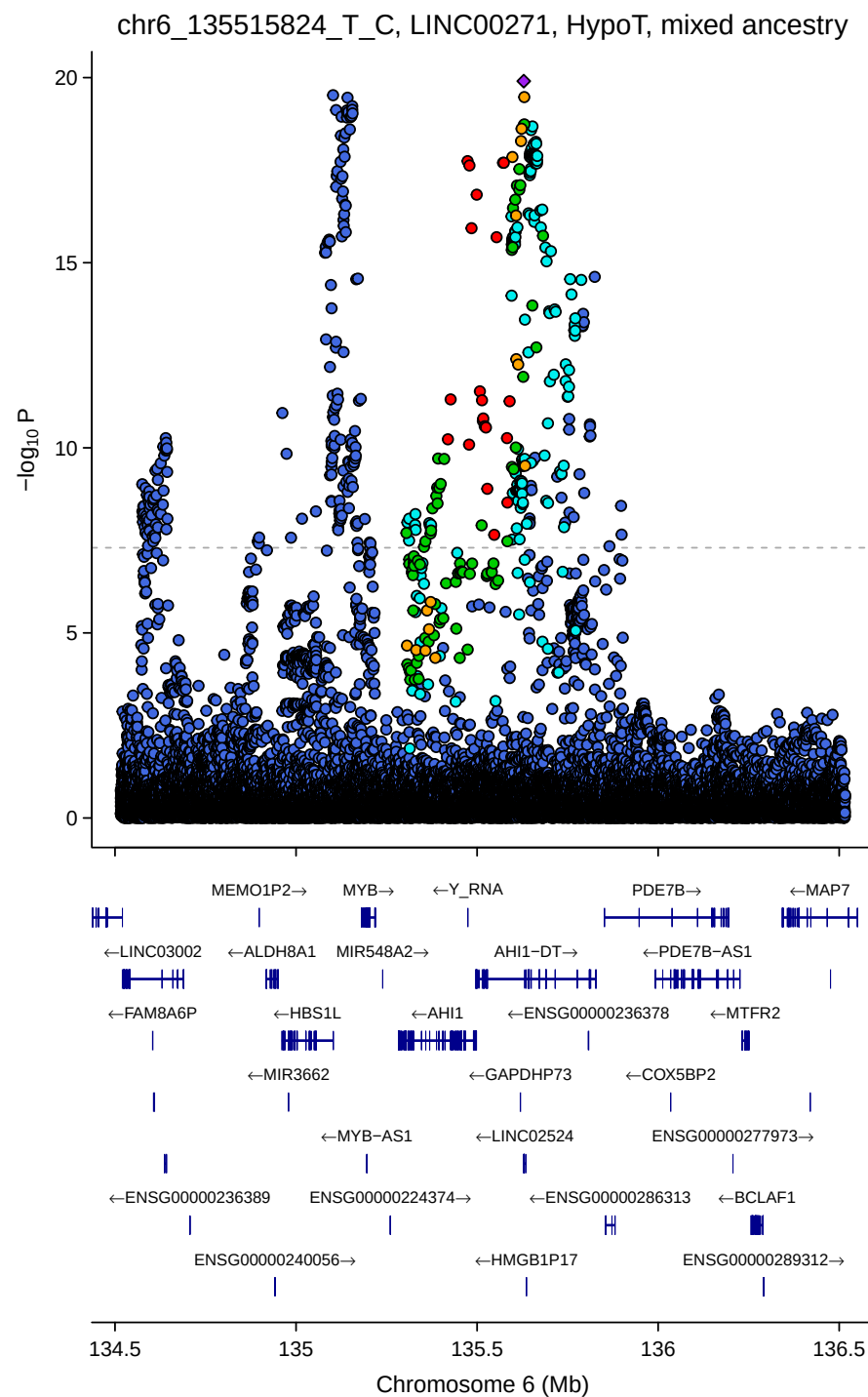
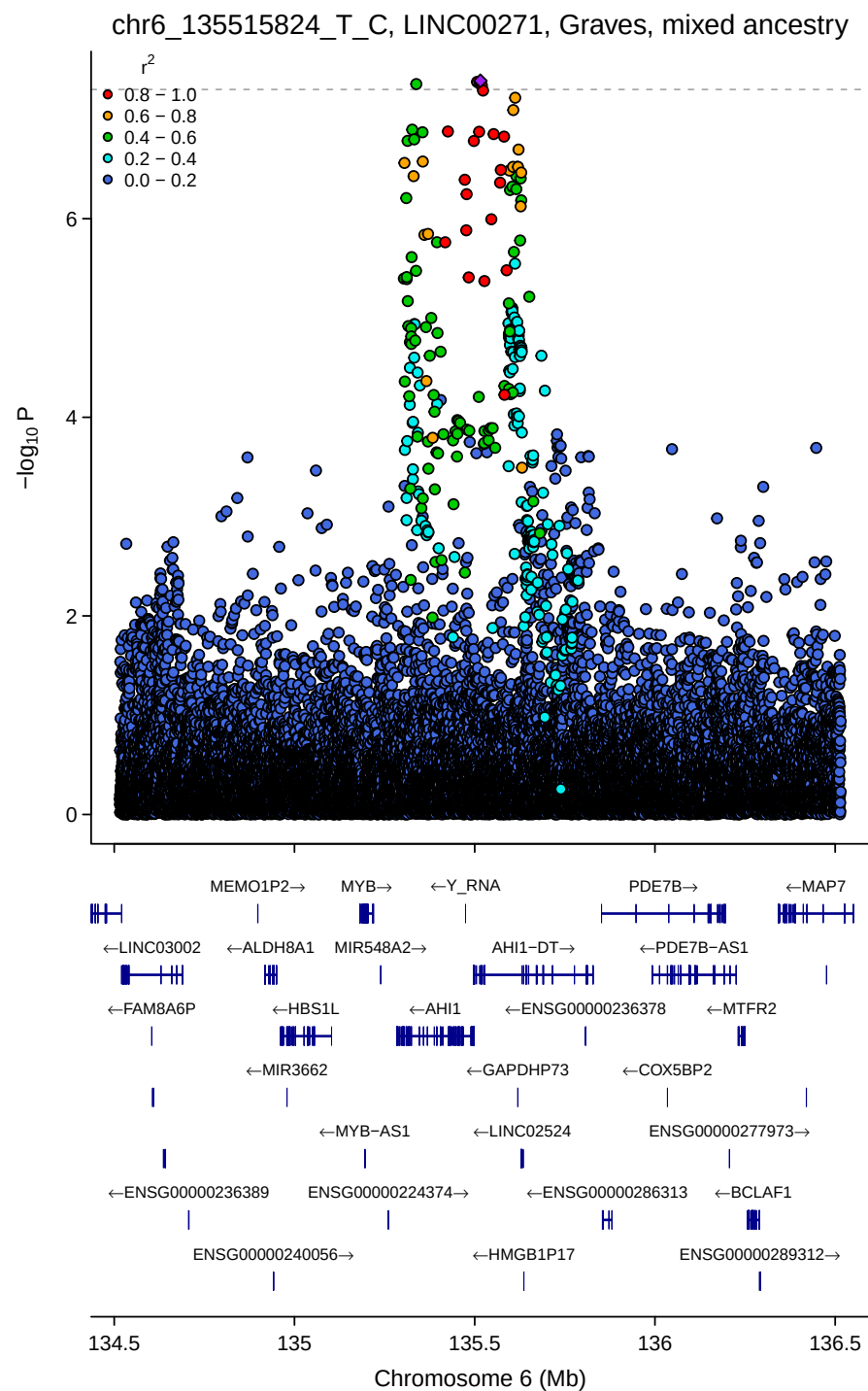
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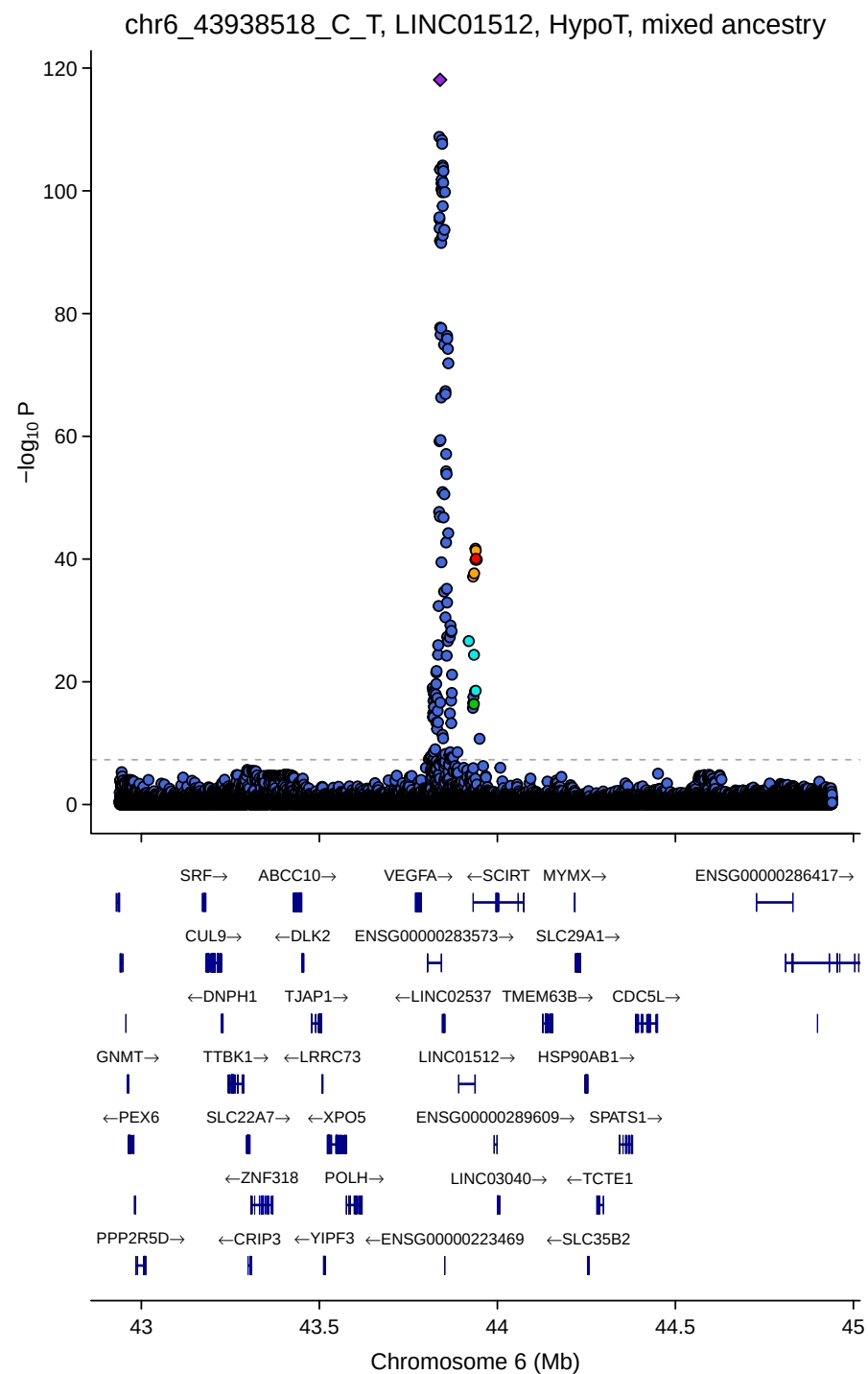
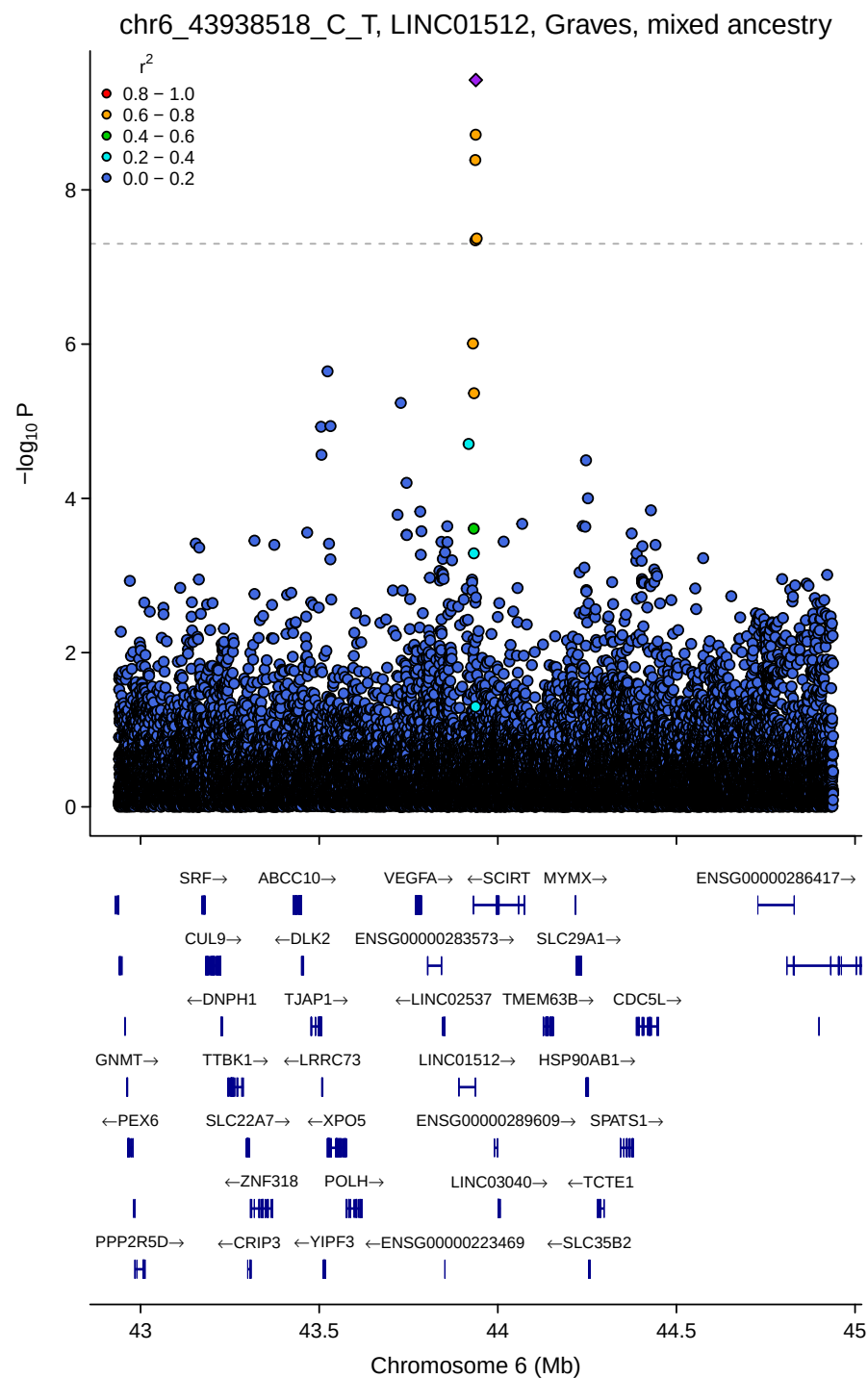
Supplementary Figure 3.2



Supplementary Figure 3.2



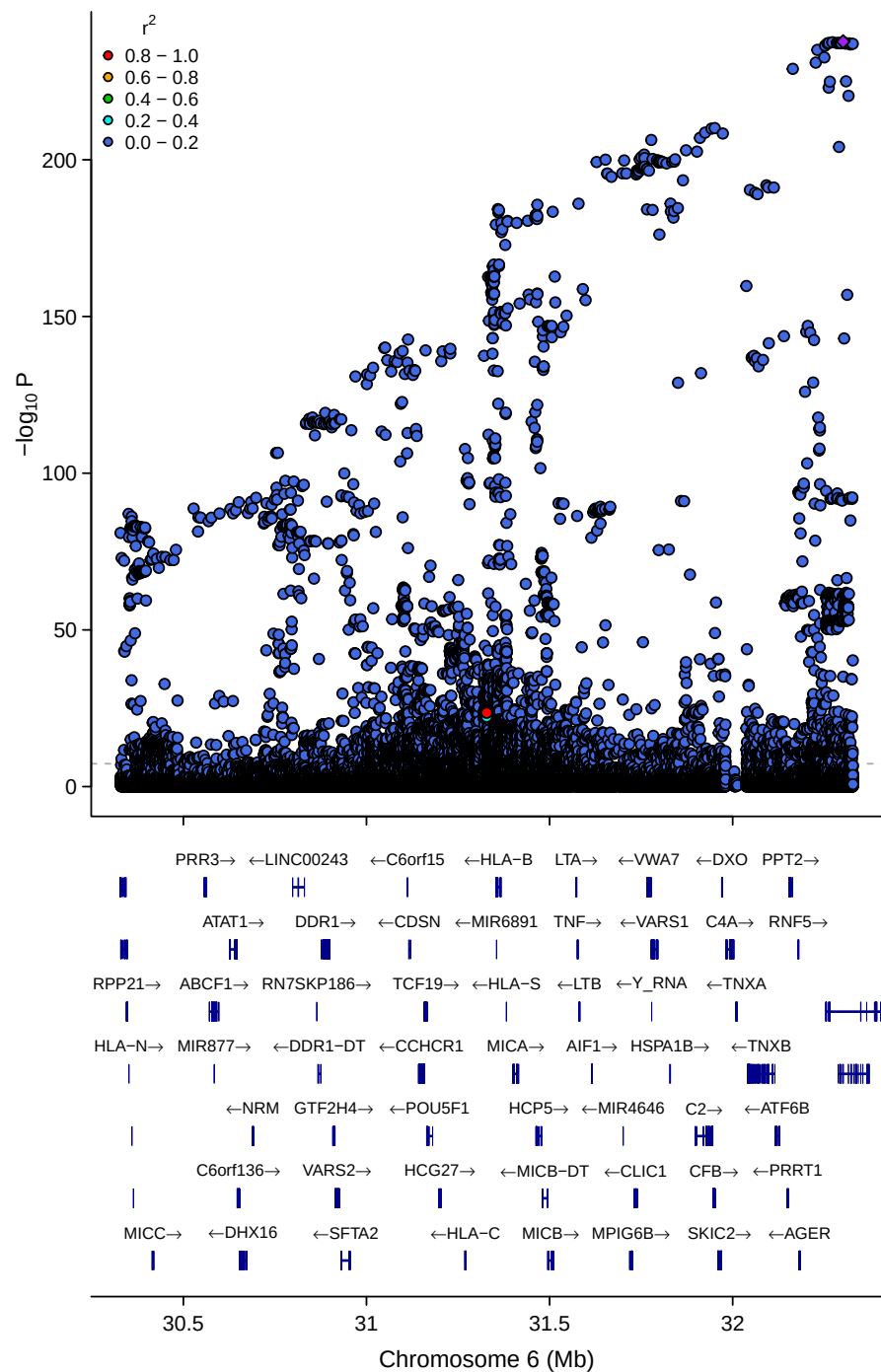
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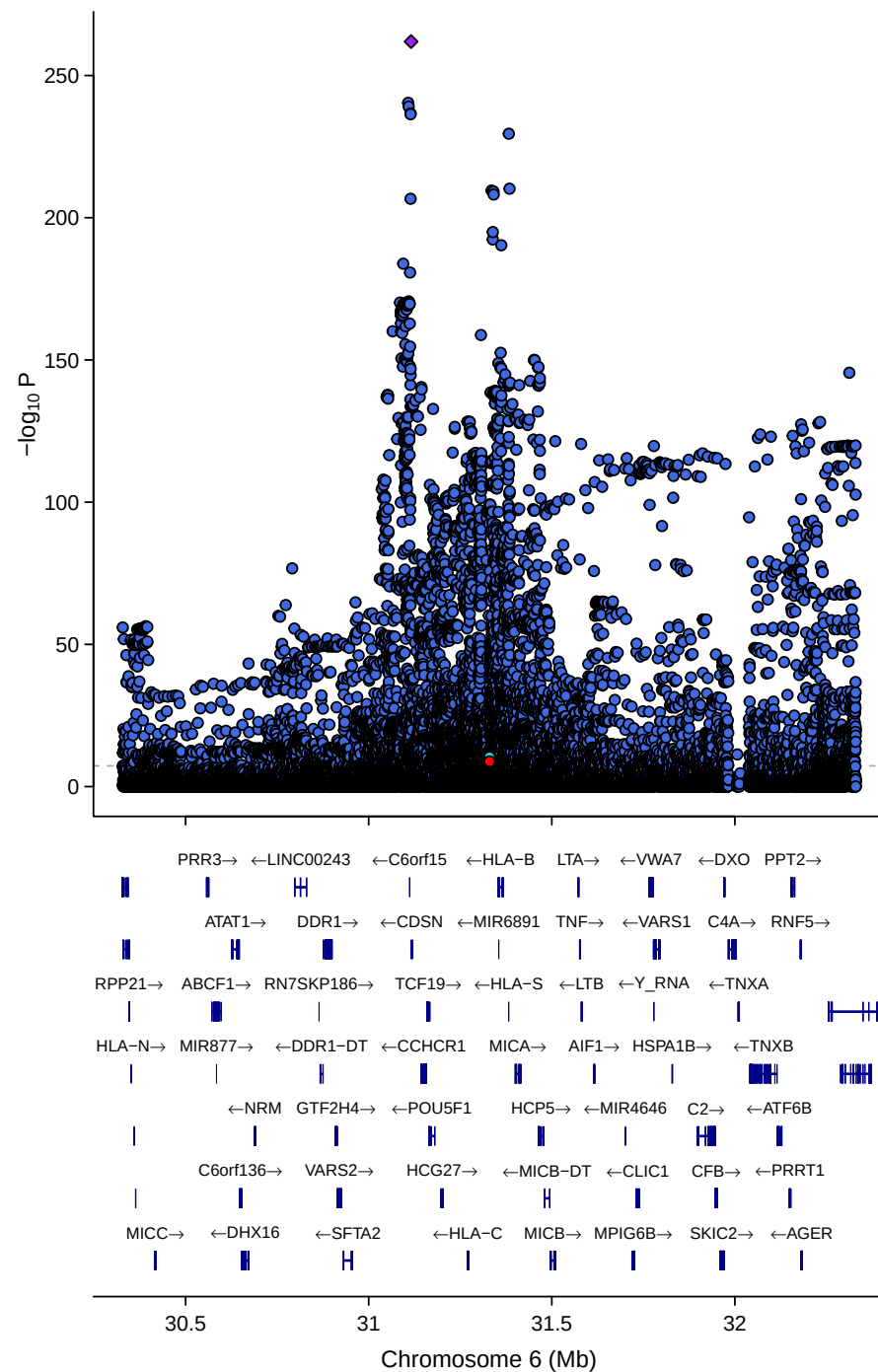


Supplementary Figure 3.2

chr6\_31328394\_C\_T, LINC02571;HLA-B, Graves, mixed ancestry

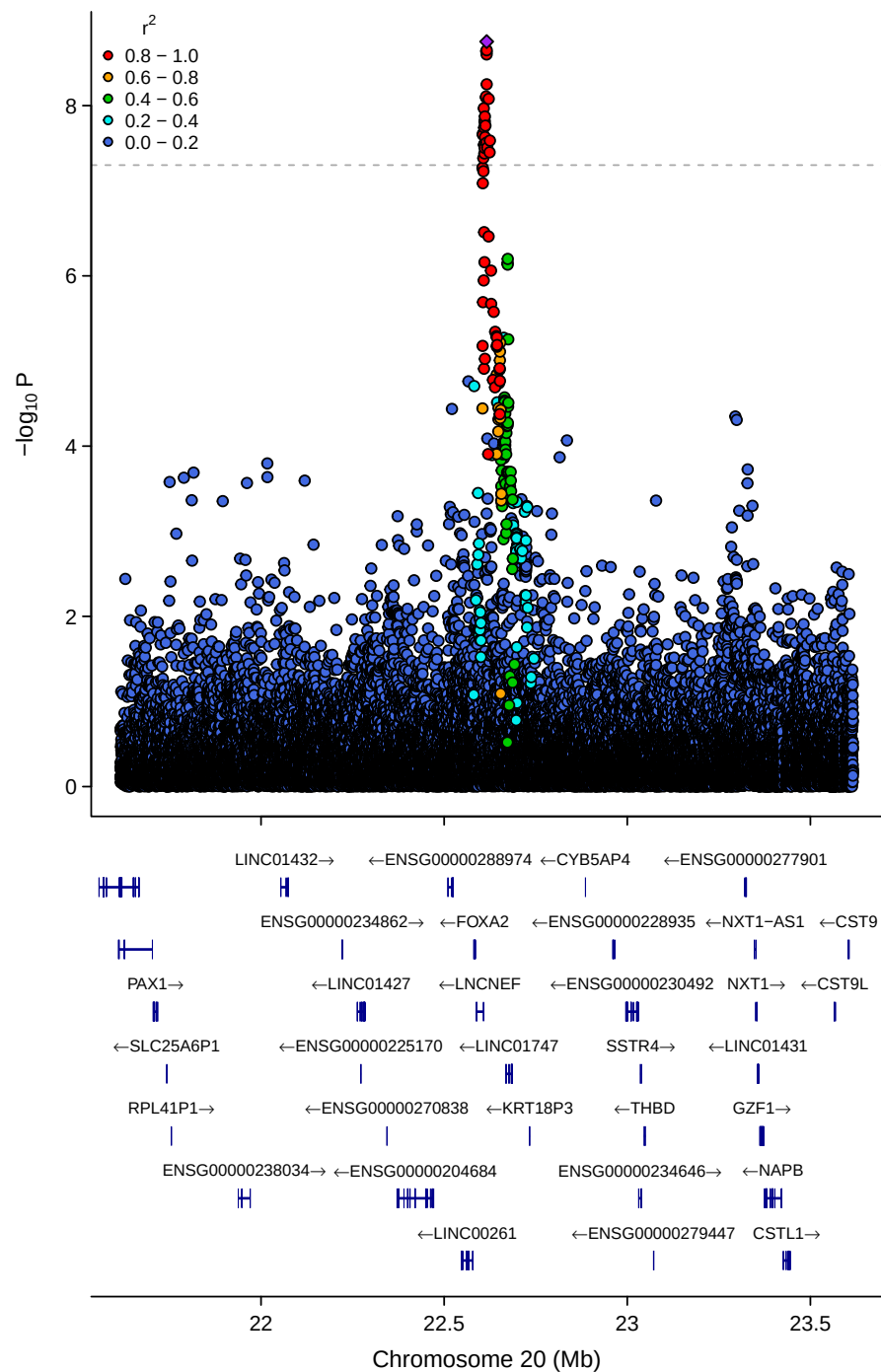


chr6\_31328394\_C\_T, LINC02571;HLA-B, HypoT, mixed ancestry

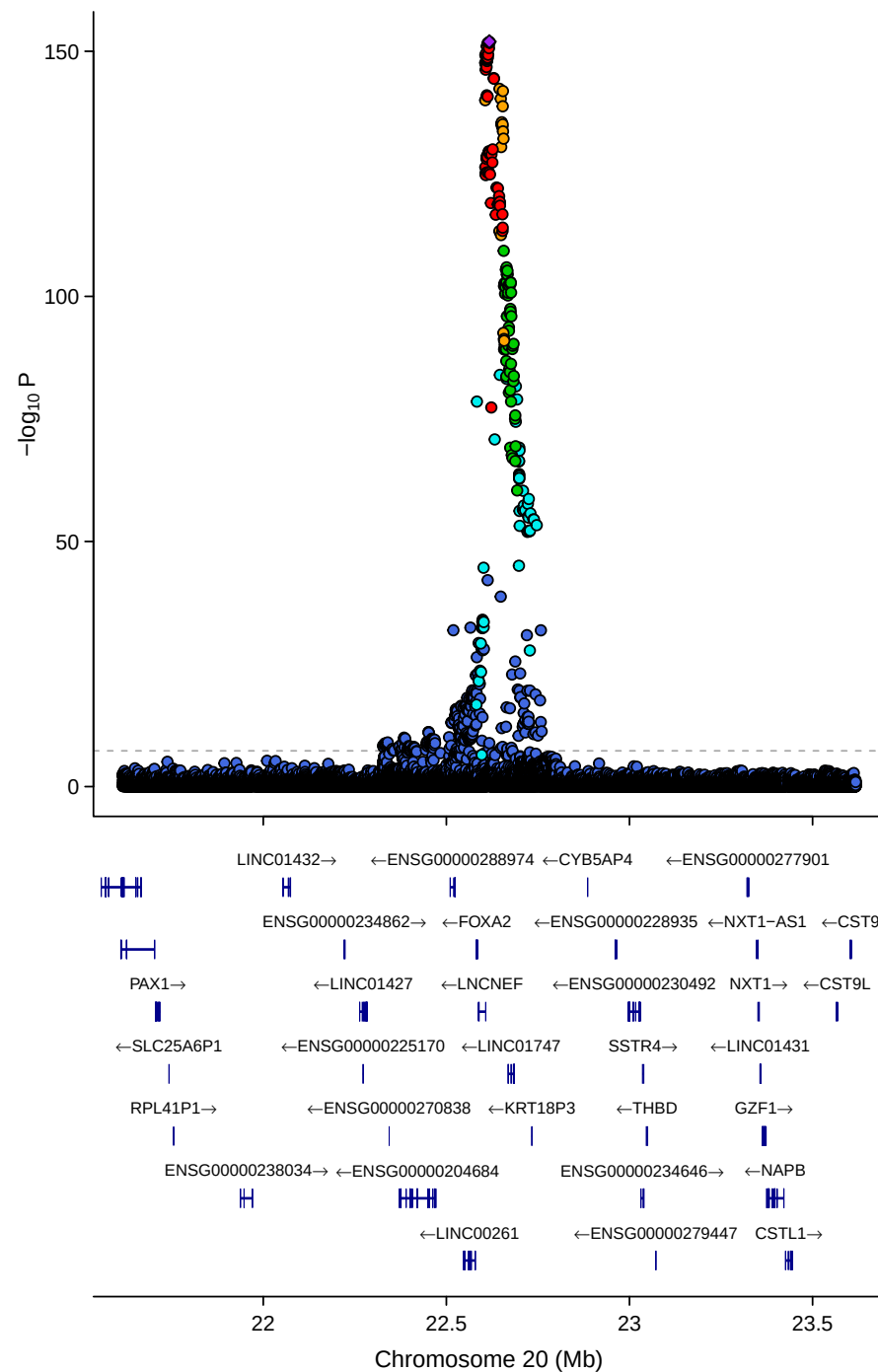


Supplementary Figure 3.2

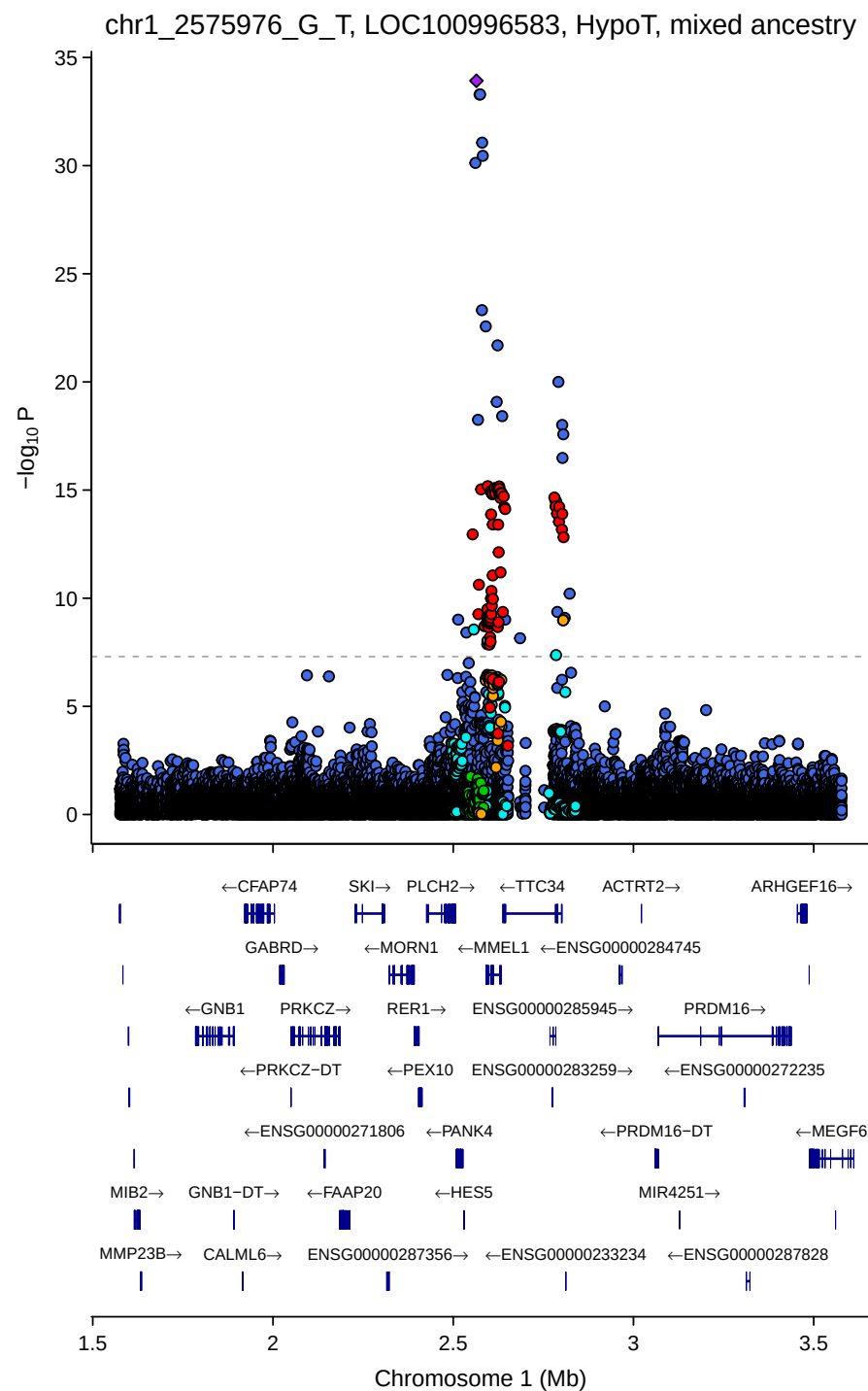
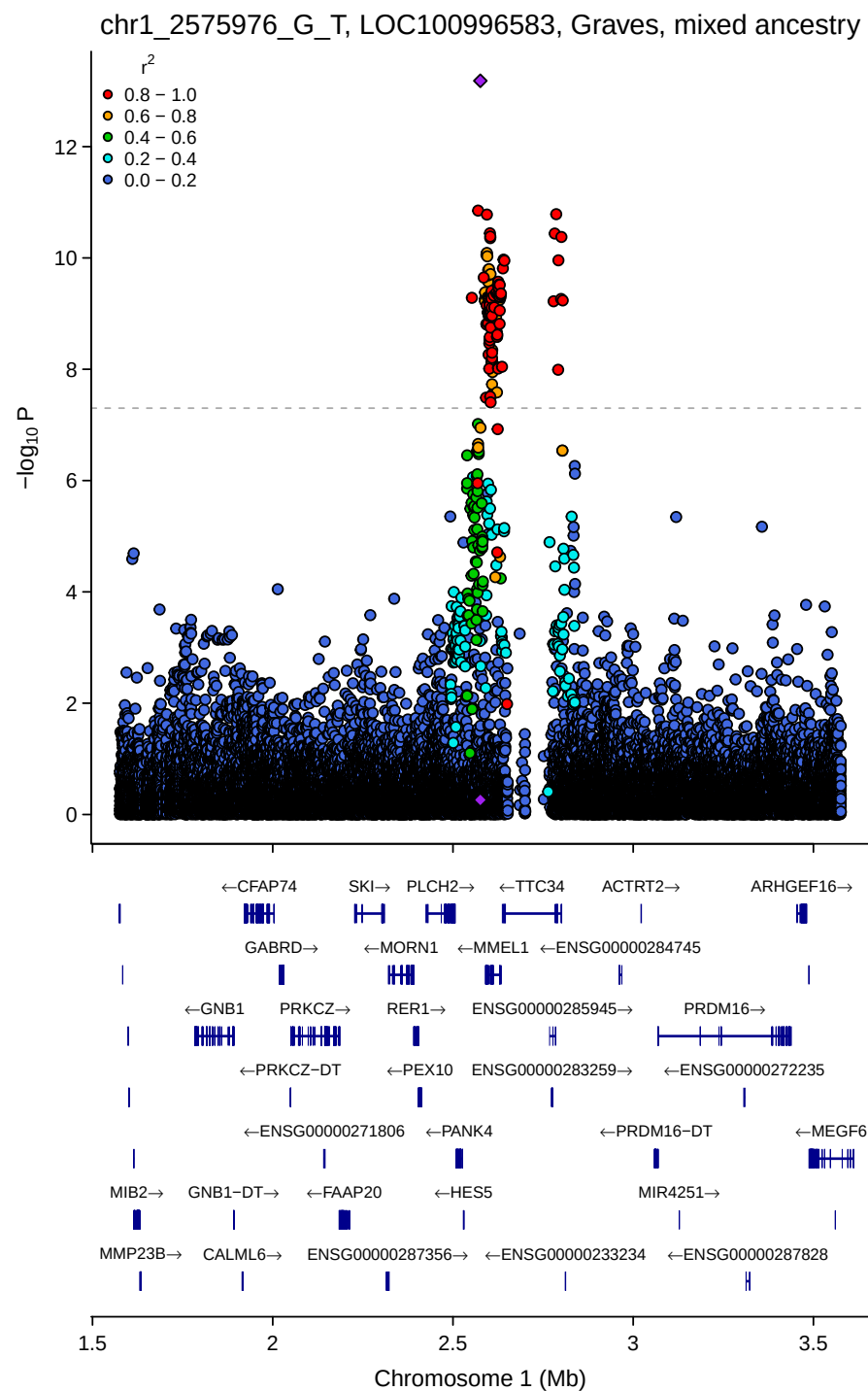
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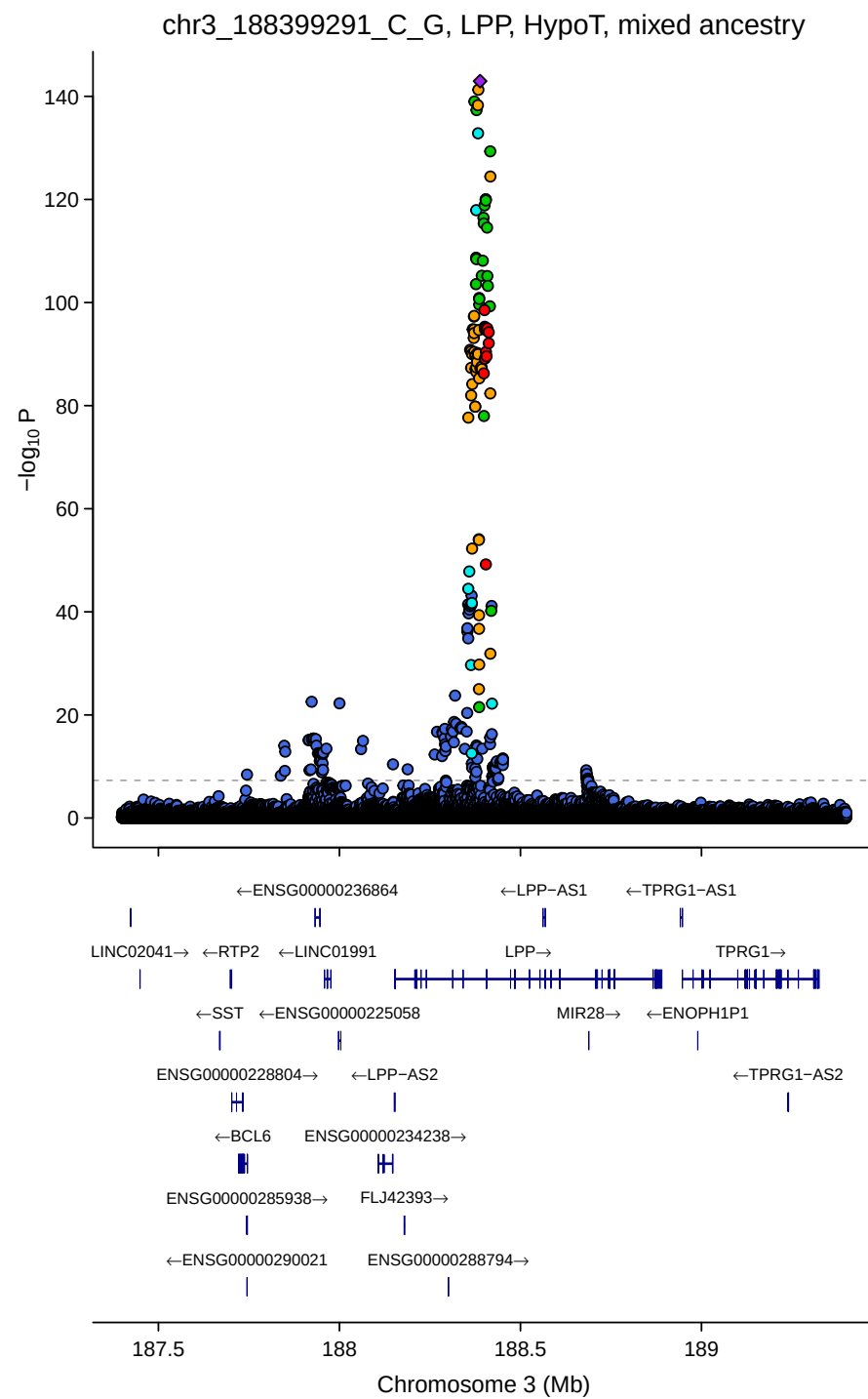
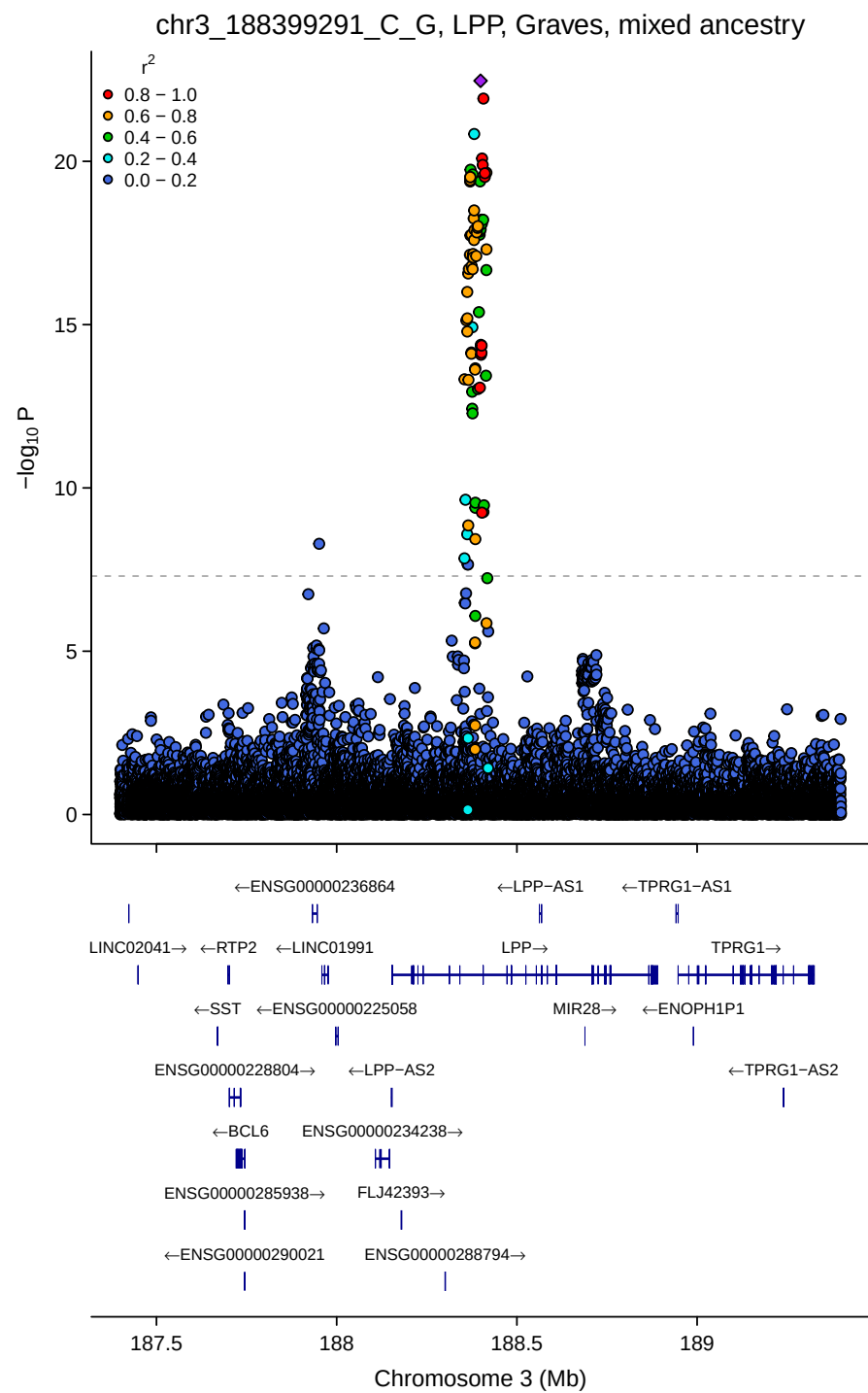
chr20\_22616187\_T\_C, LINCNEF;LINC01747, HypoT, mixed ancestry



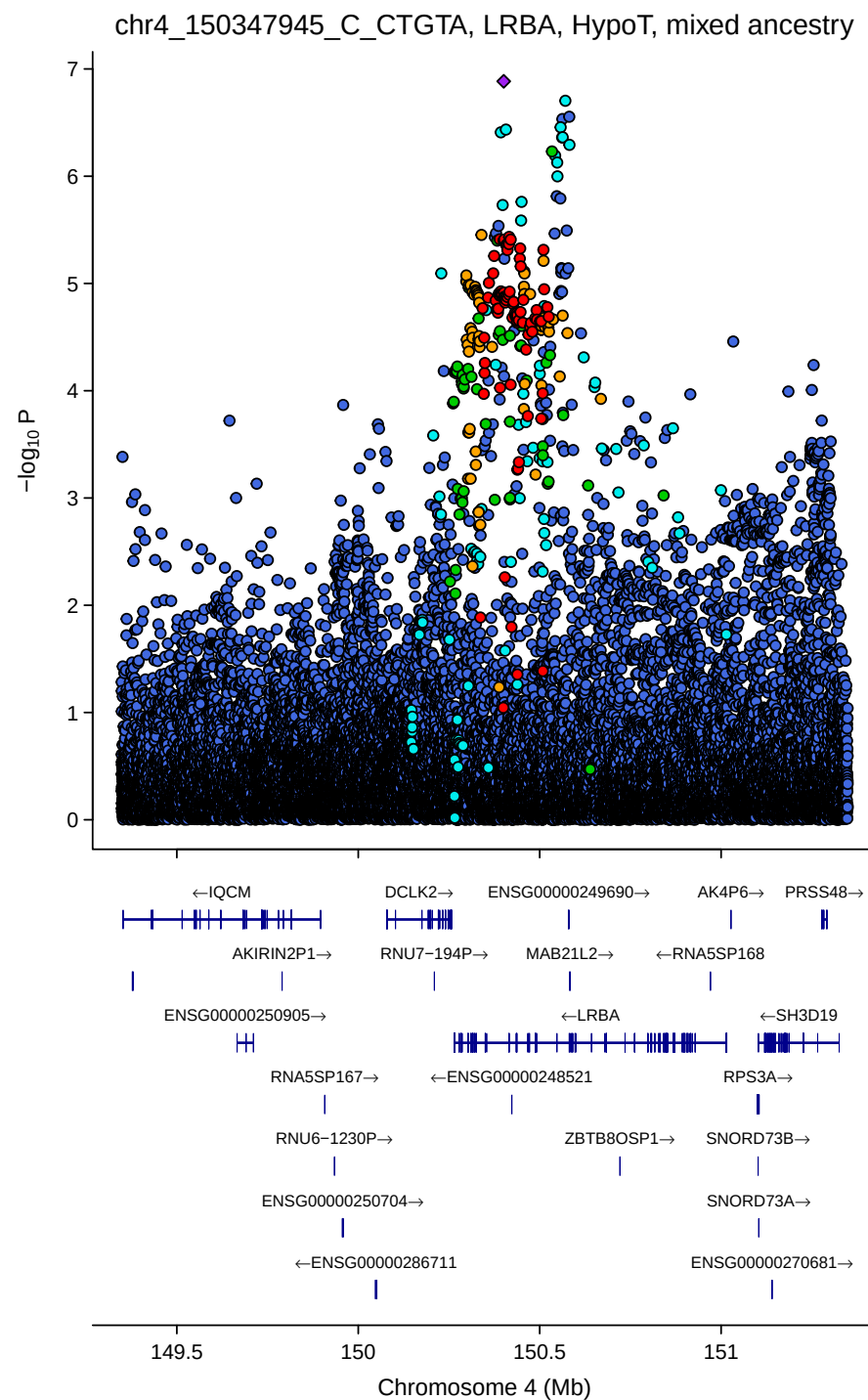
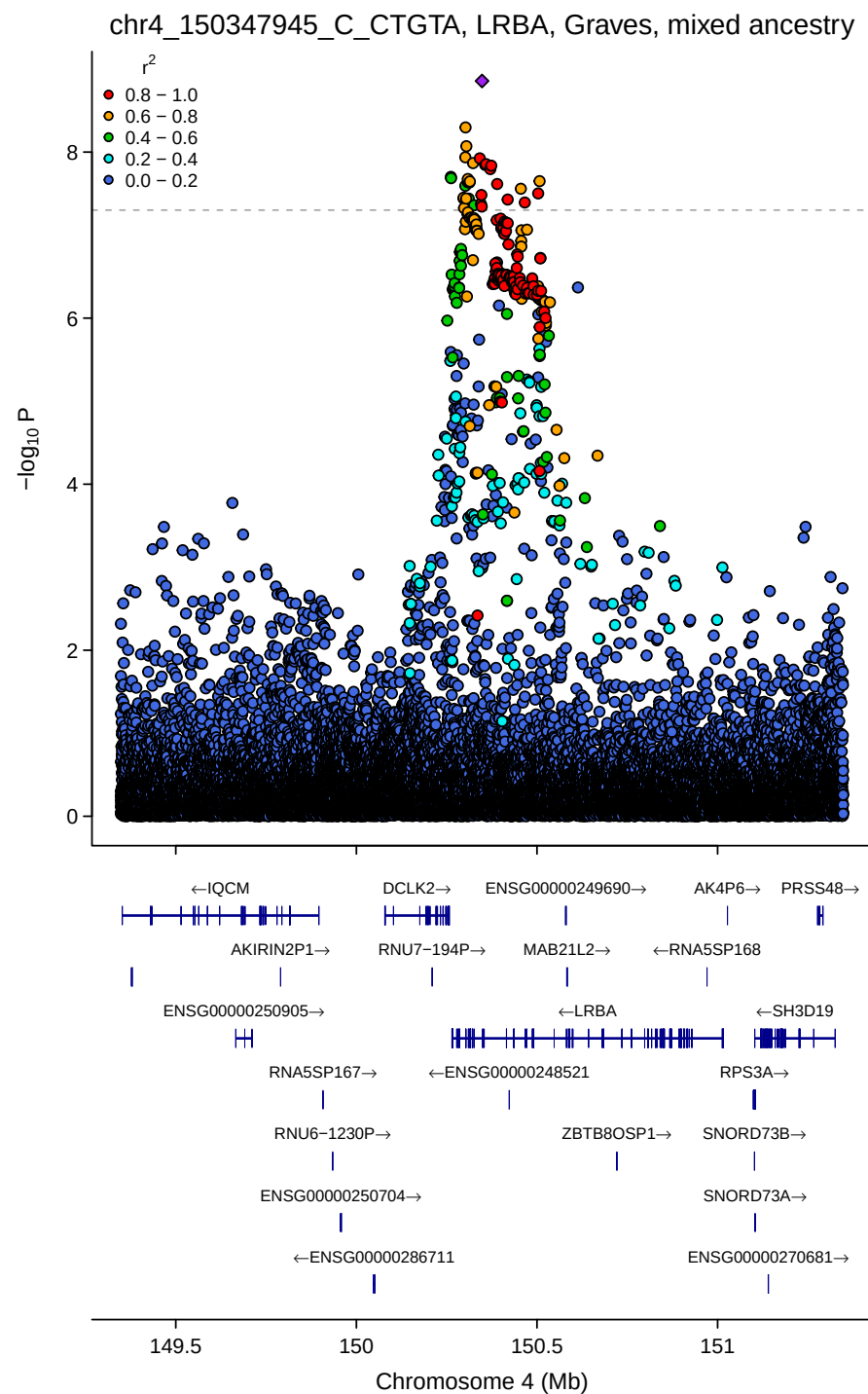
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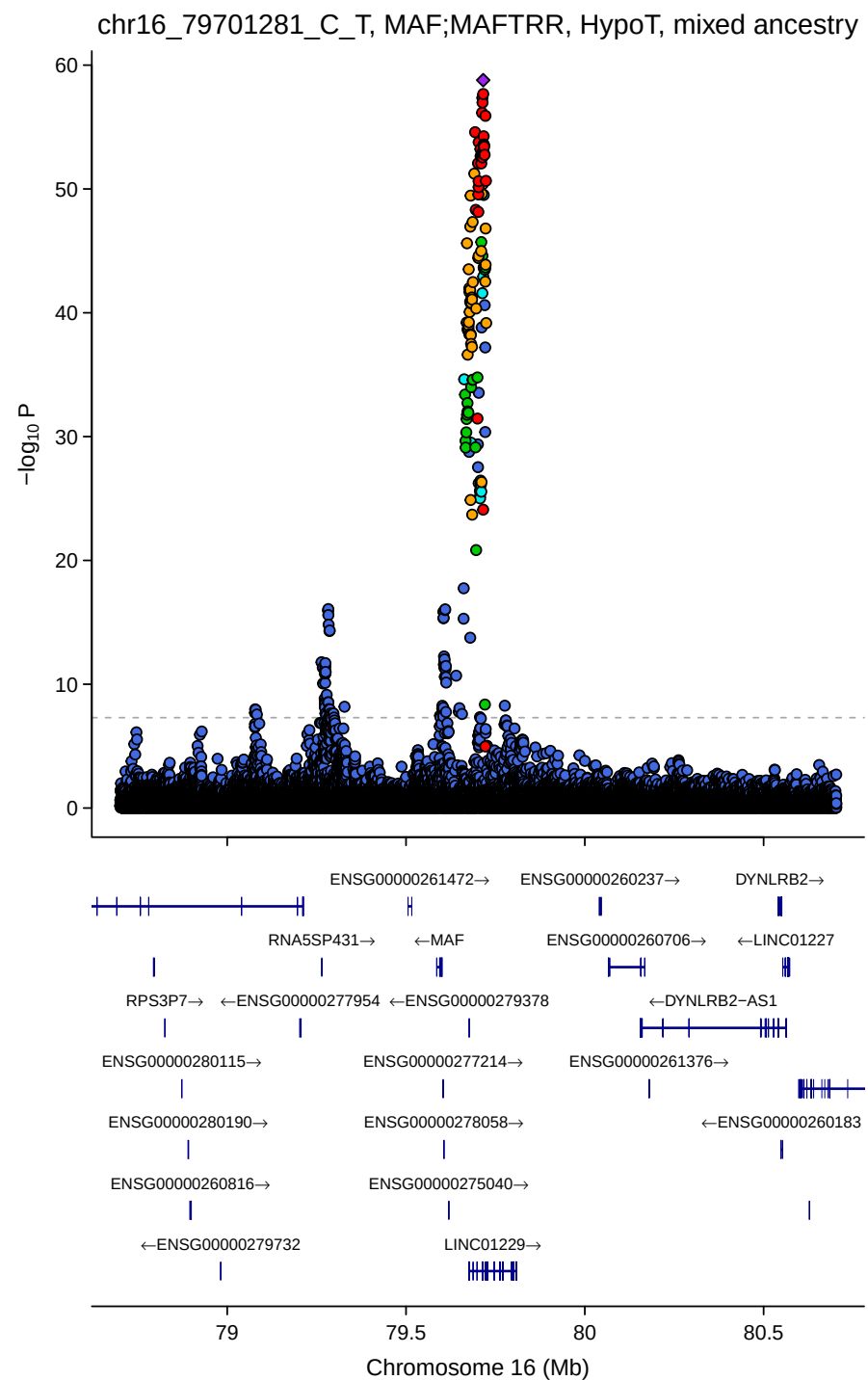
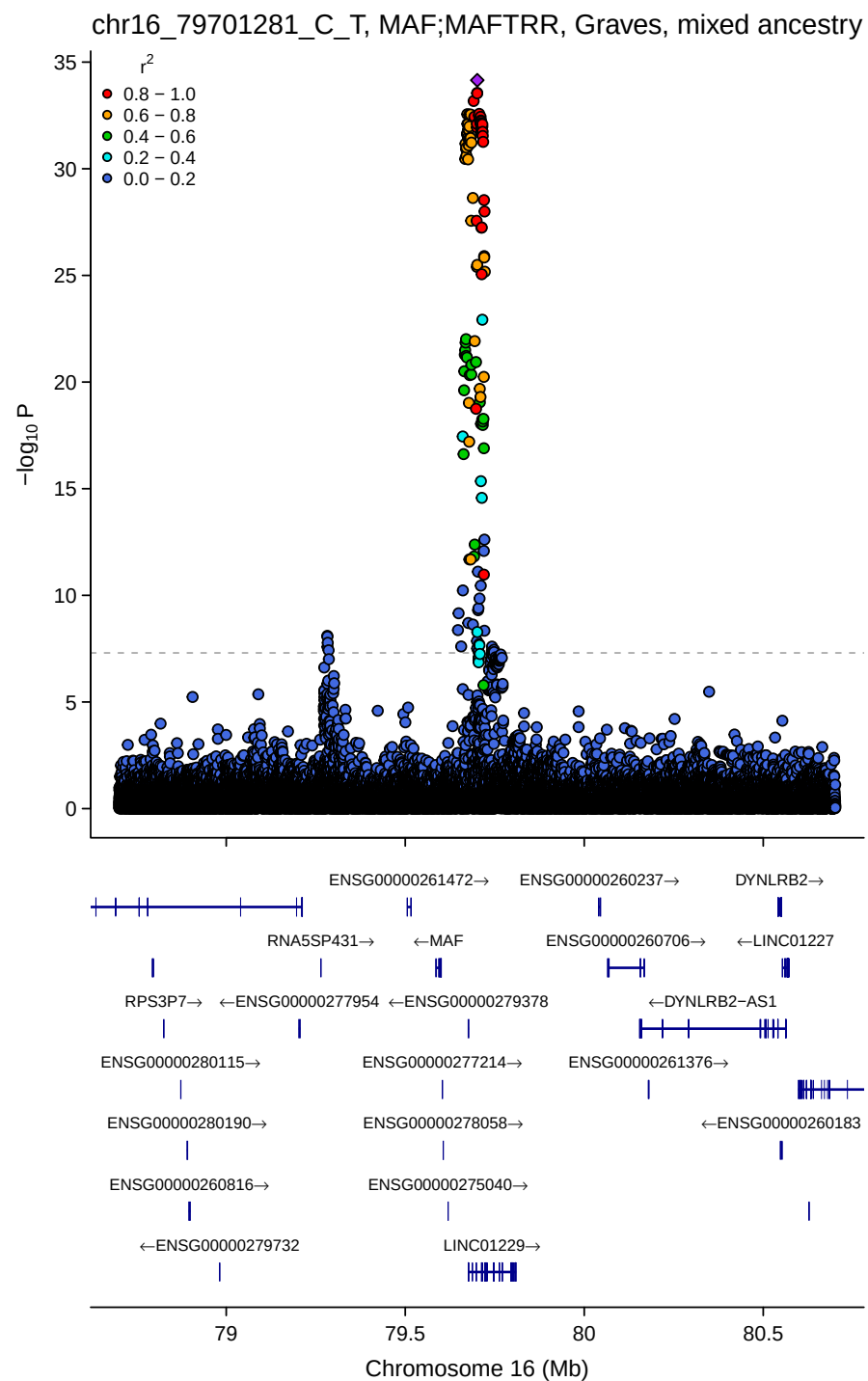
Supplementary Figure 3.2



Supplementary Figure 3.2

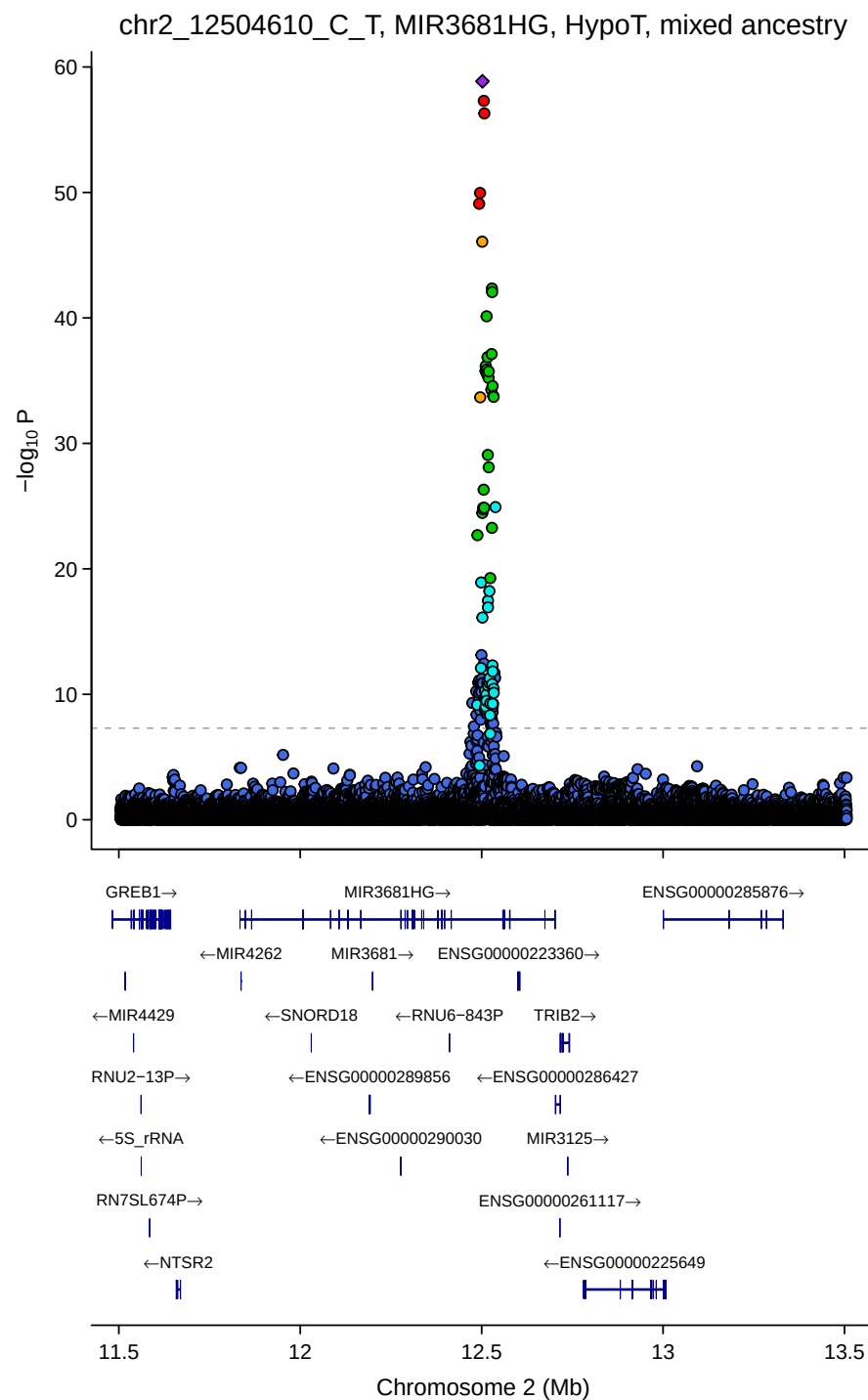
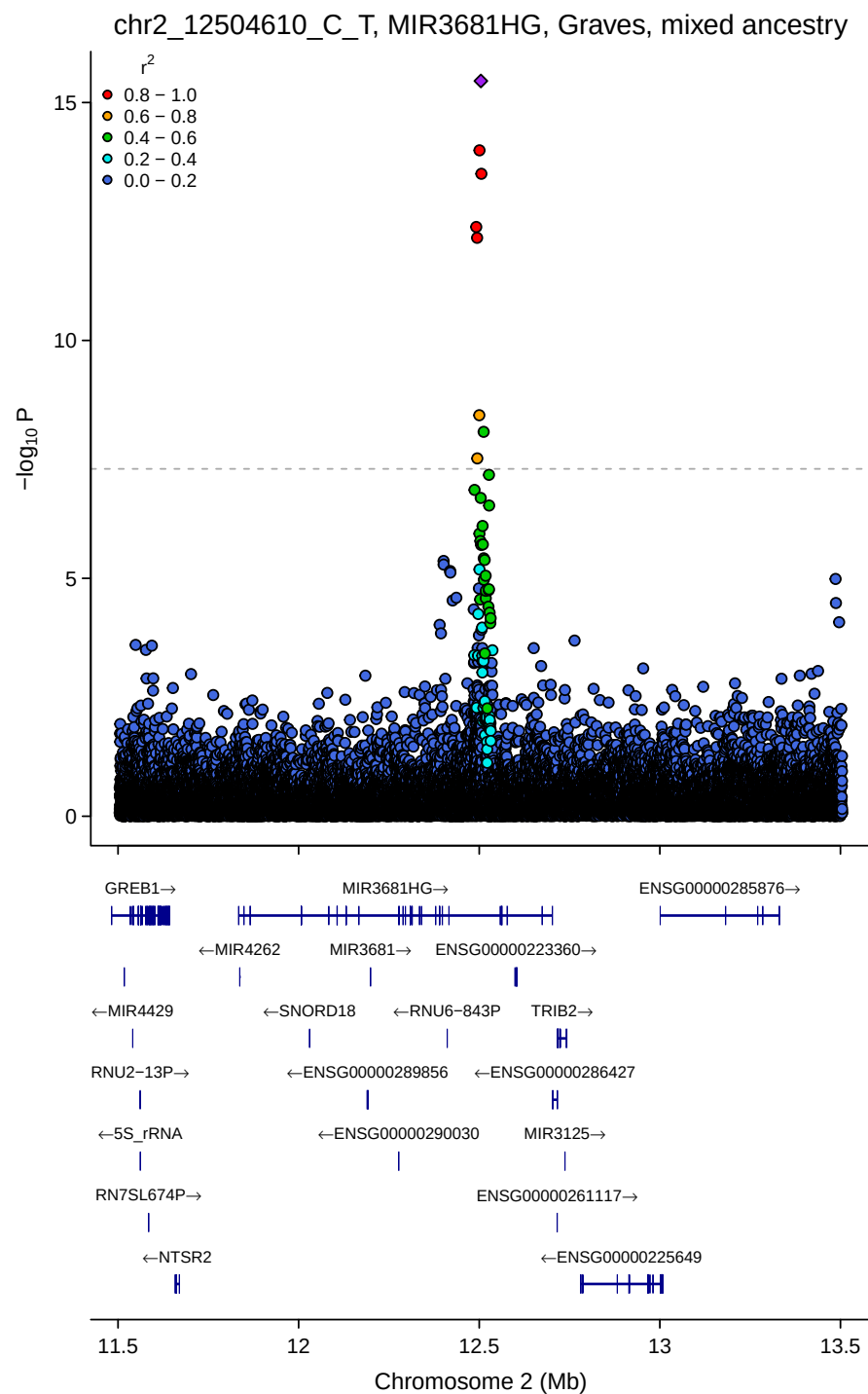


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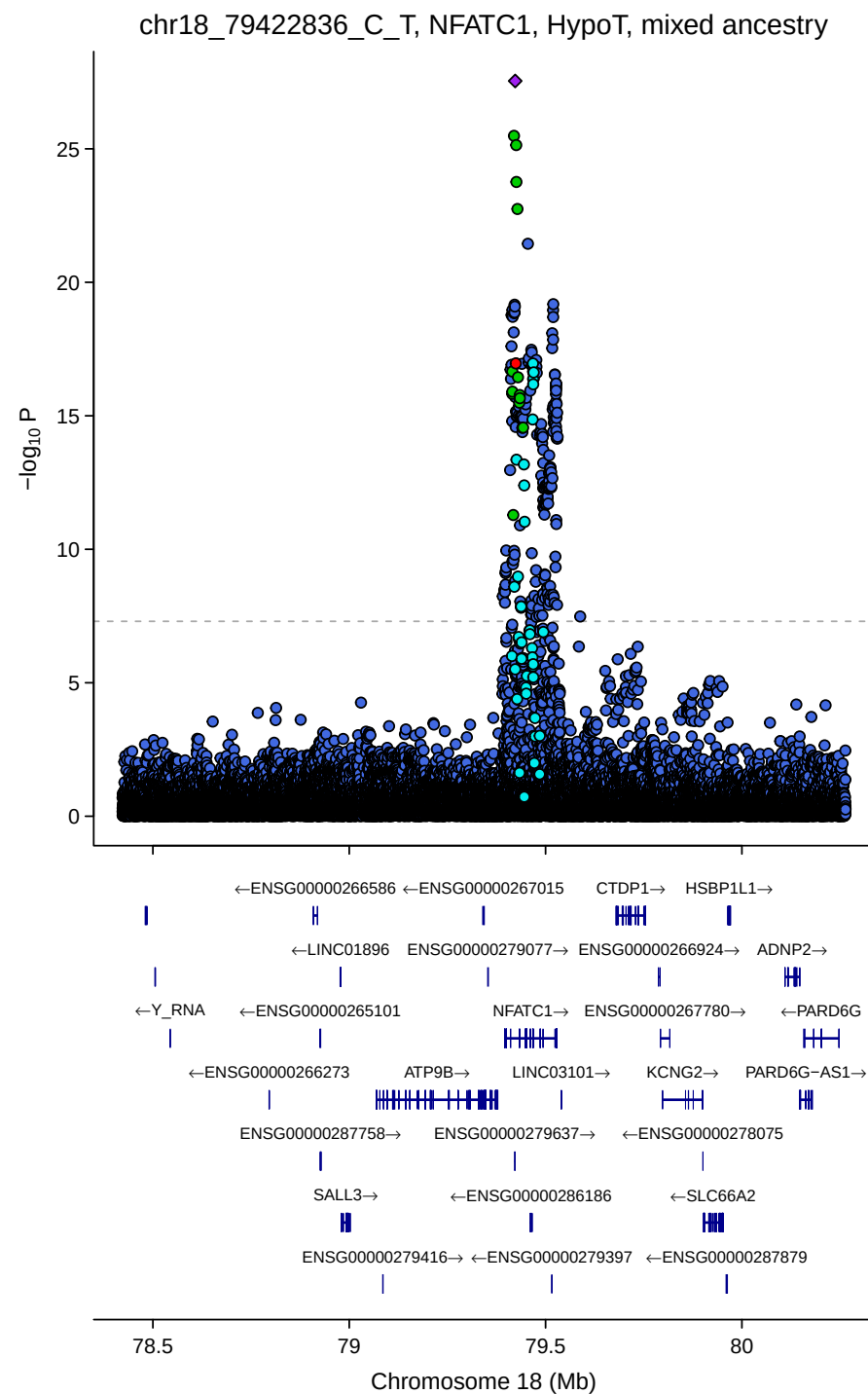
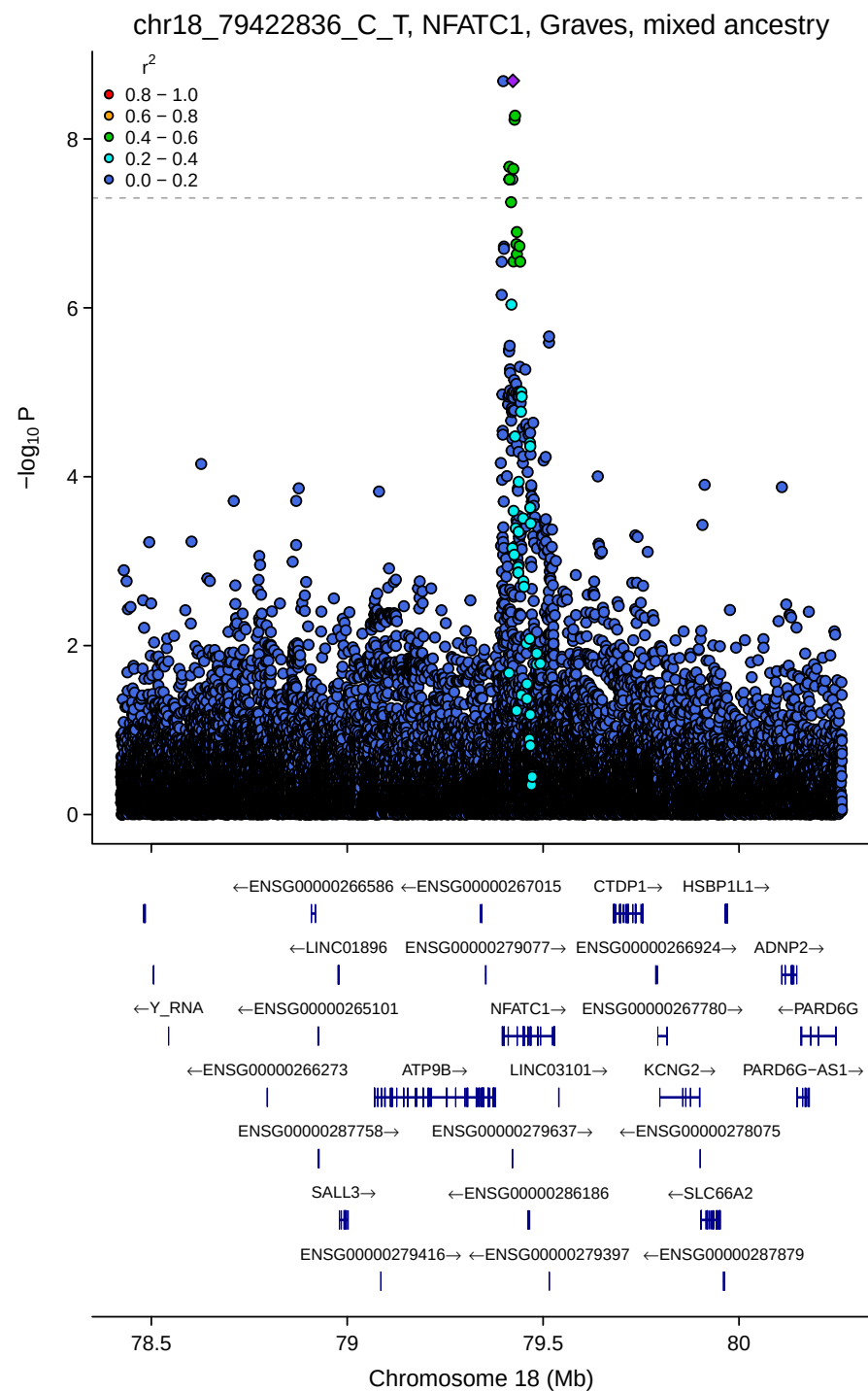




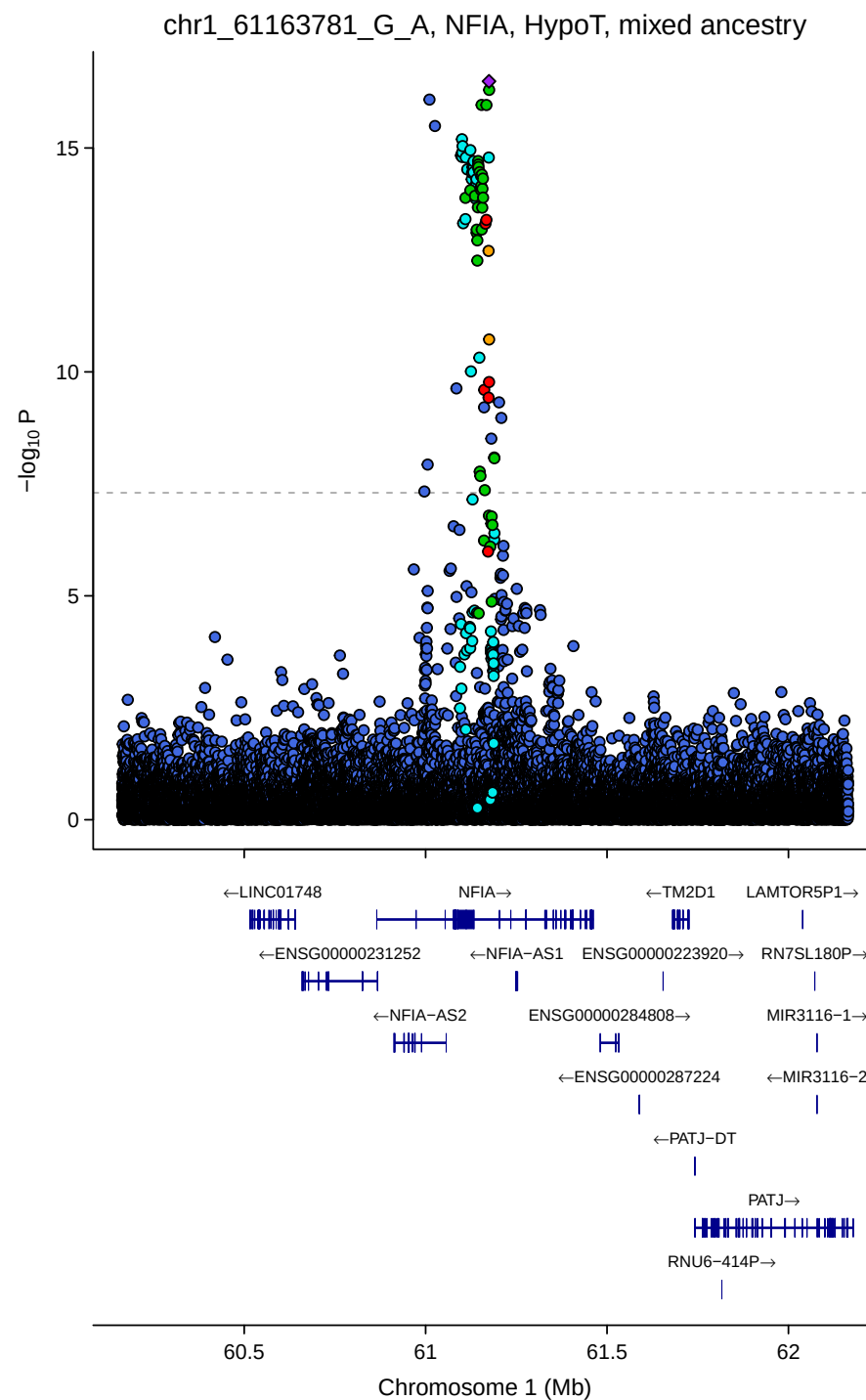
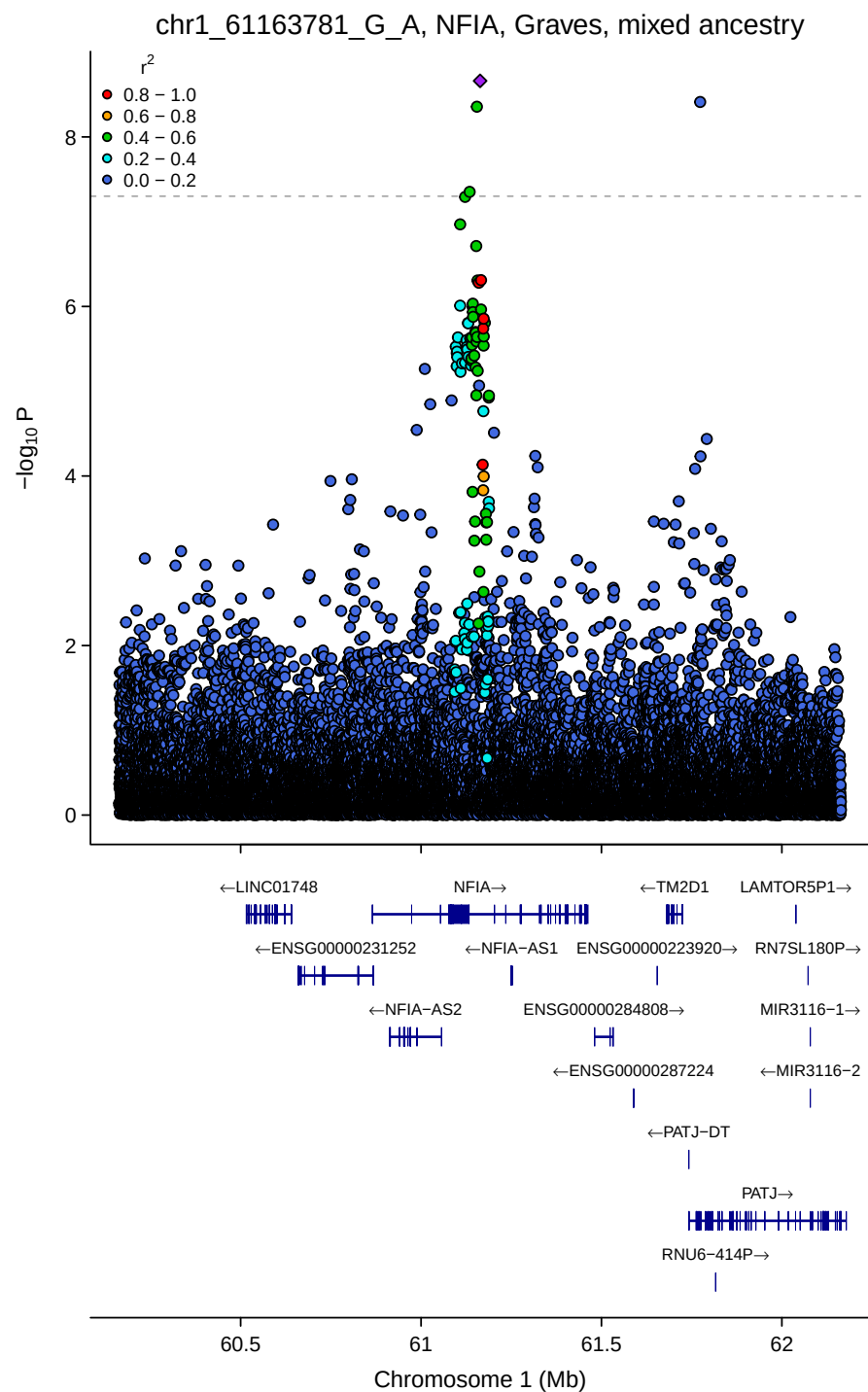
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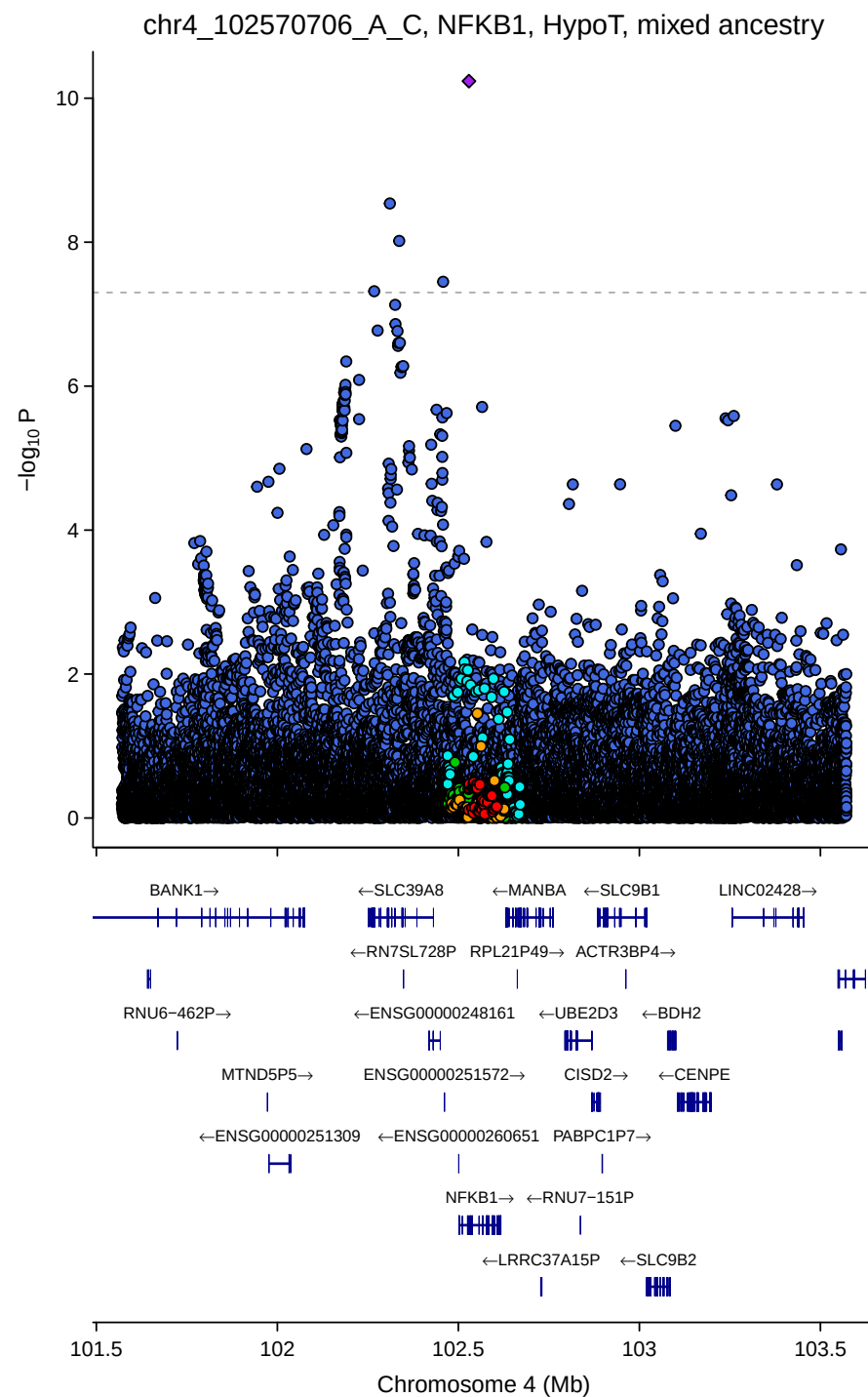
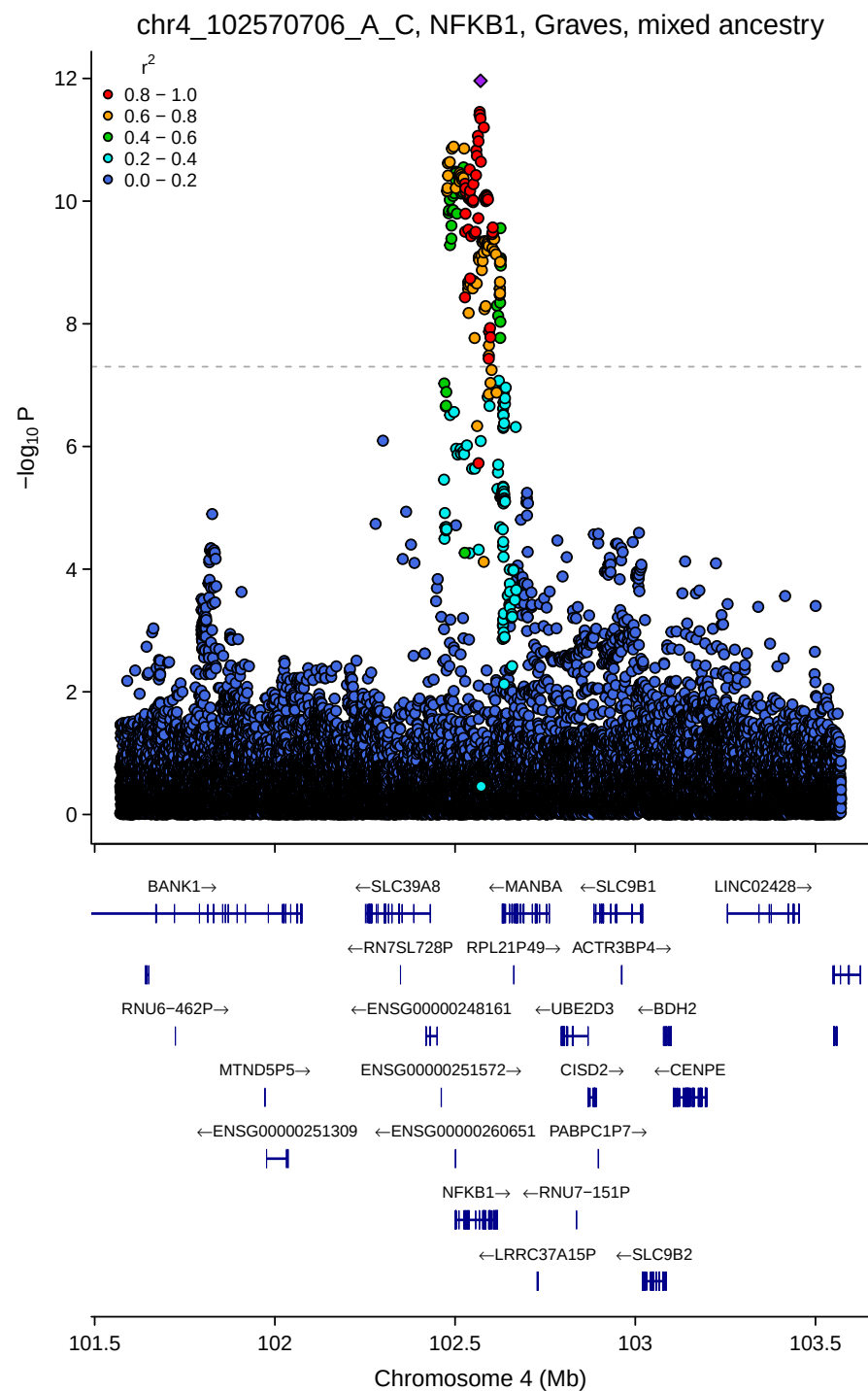
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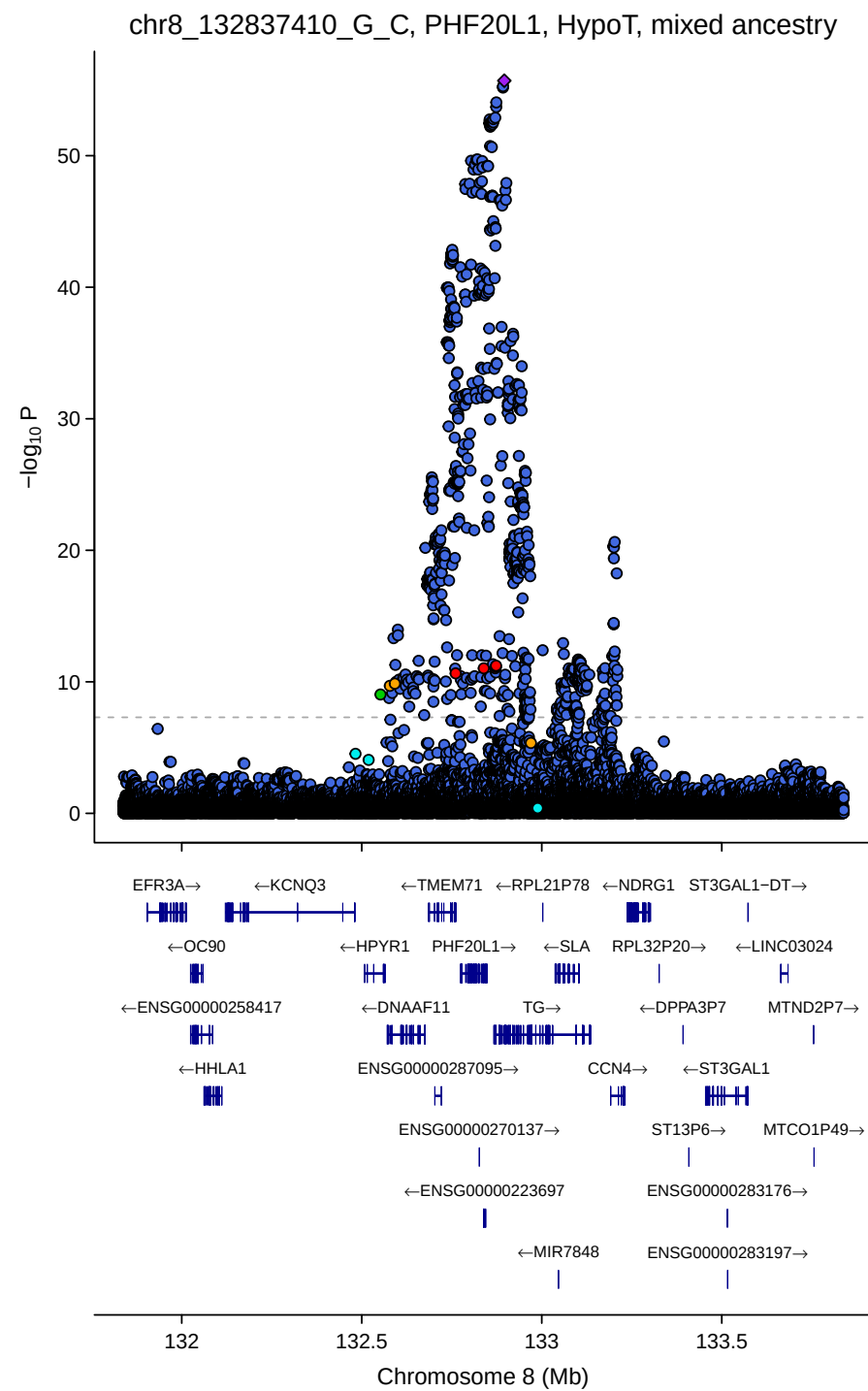
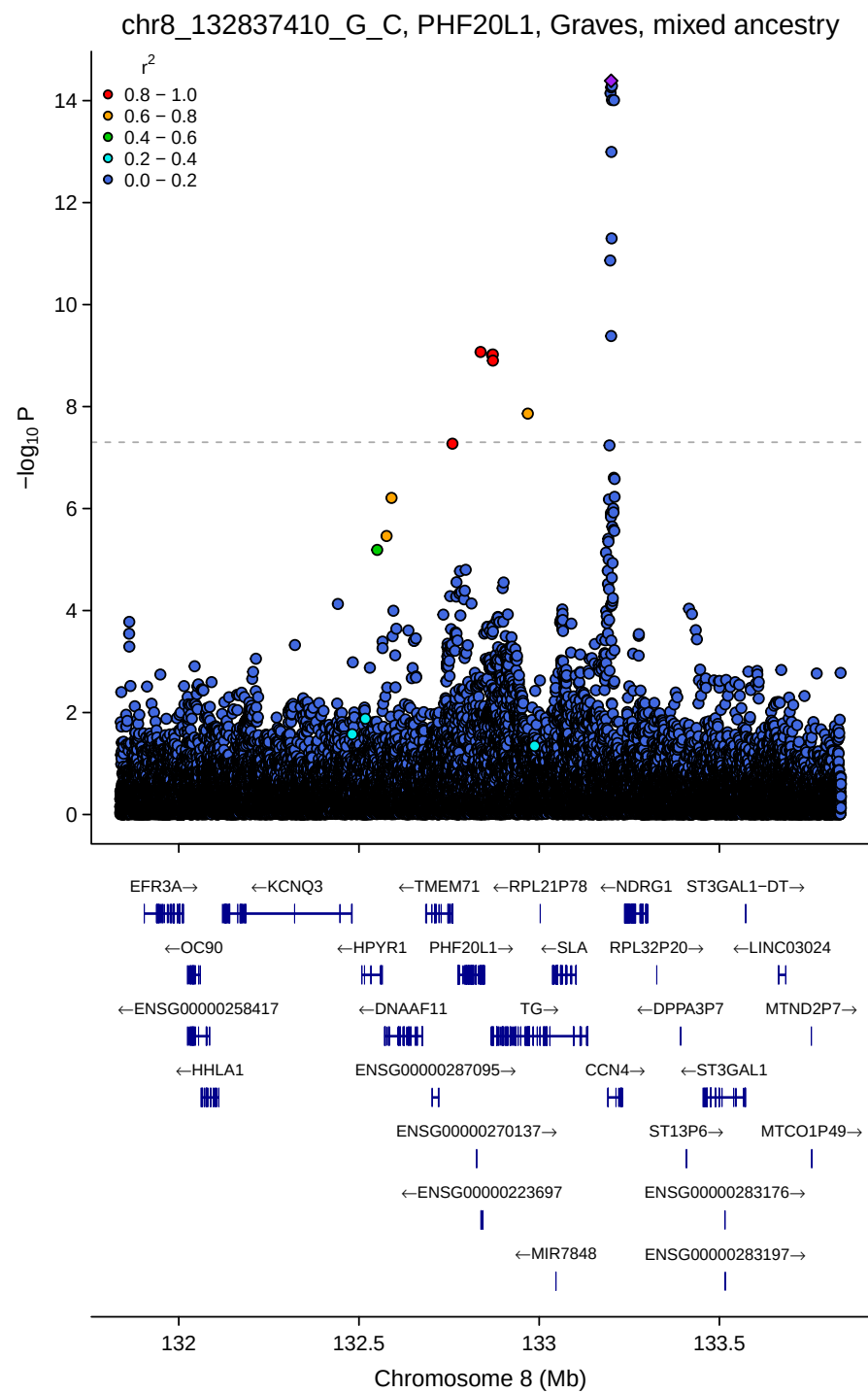
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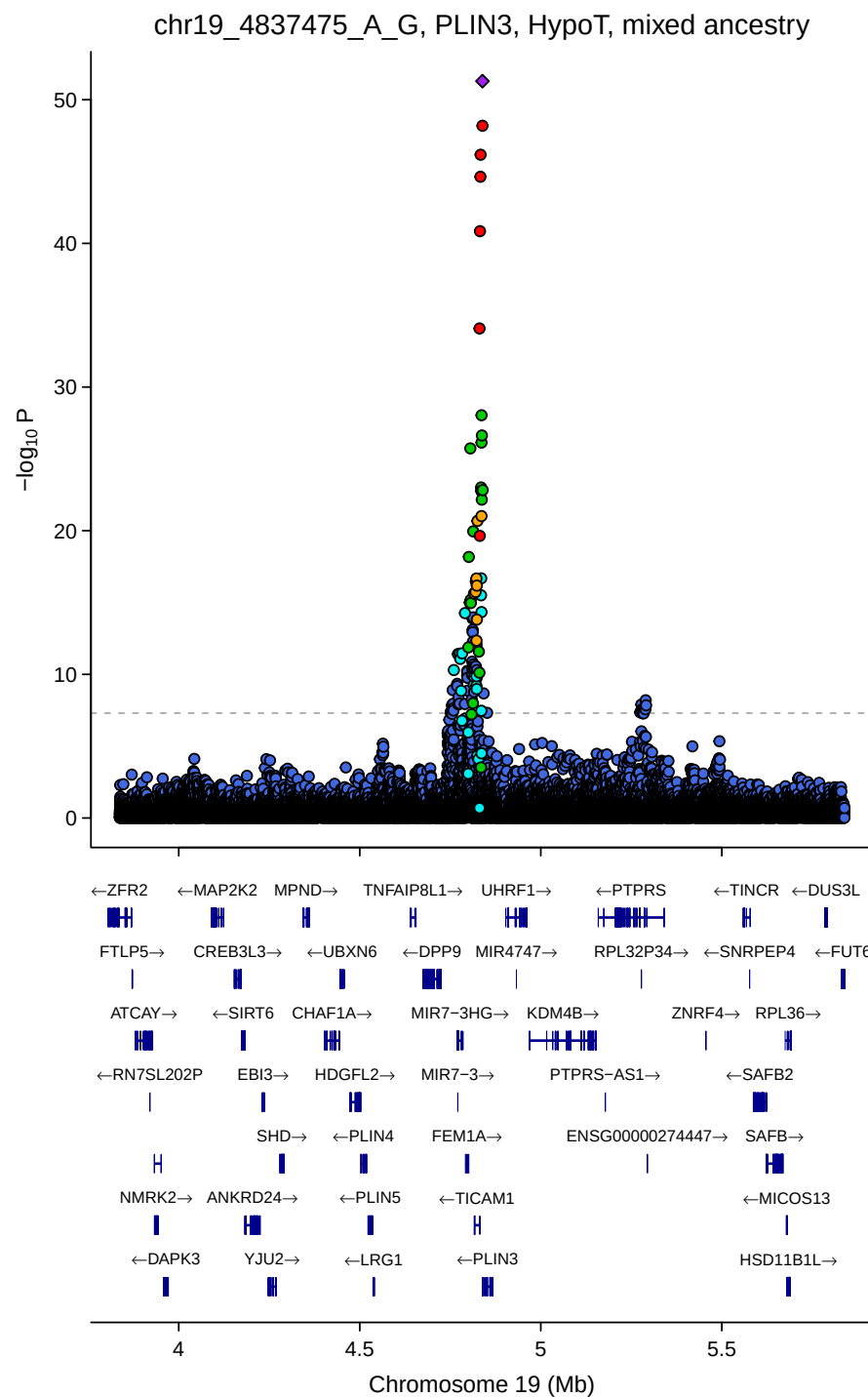
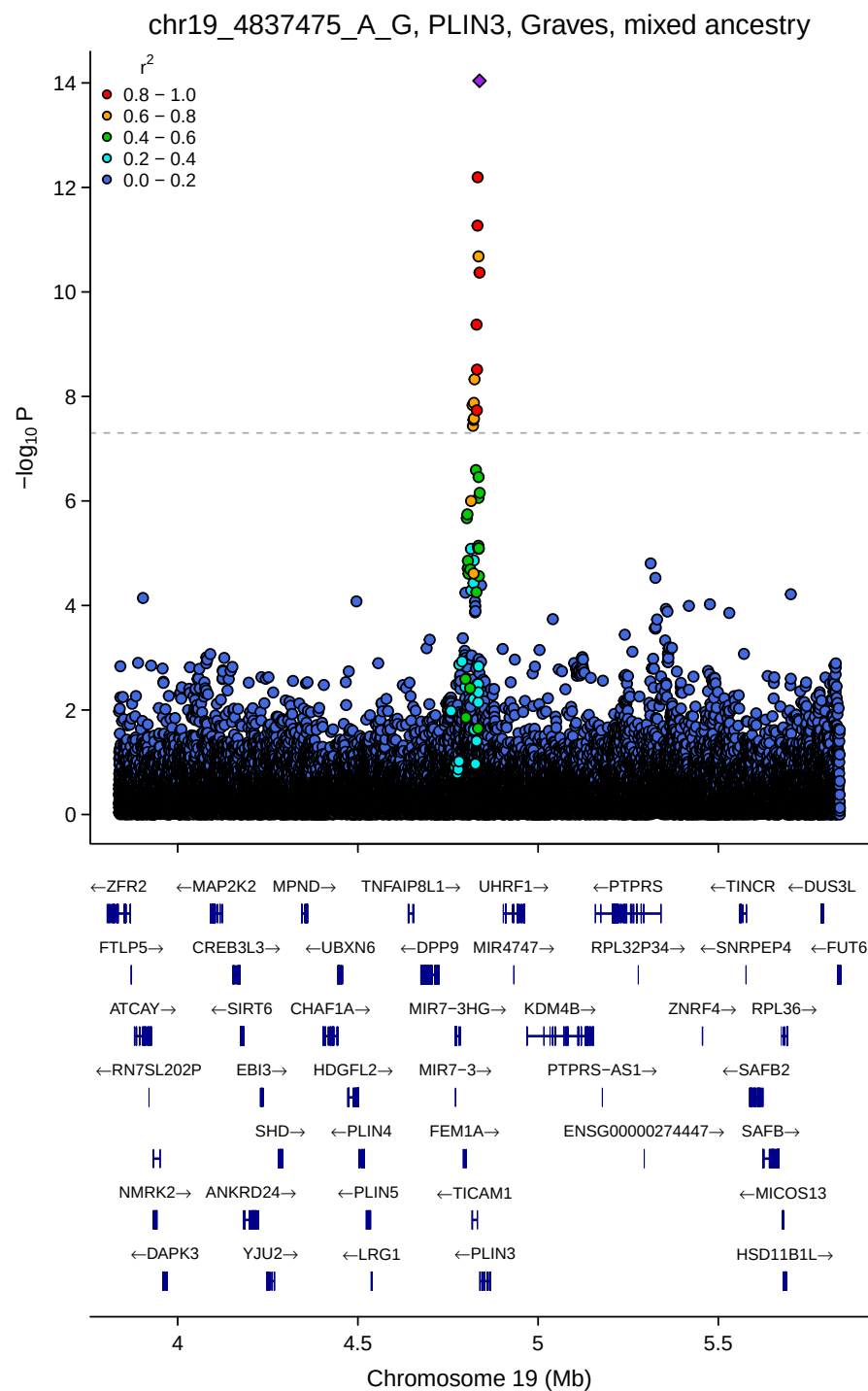
Supplementary Figure 3.2



Supplementary Figure 3.2

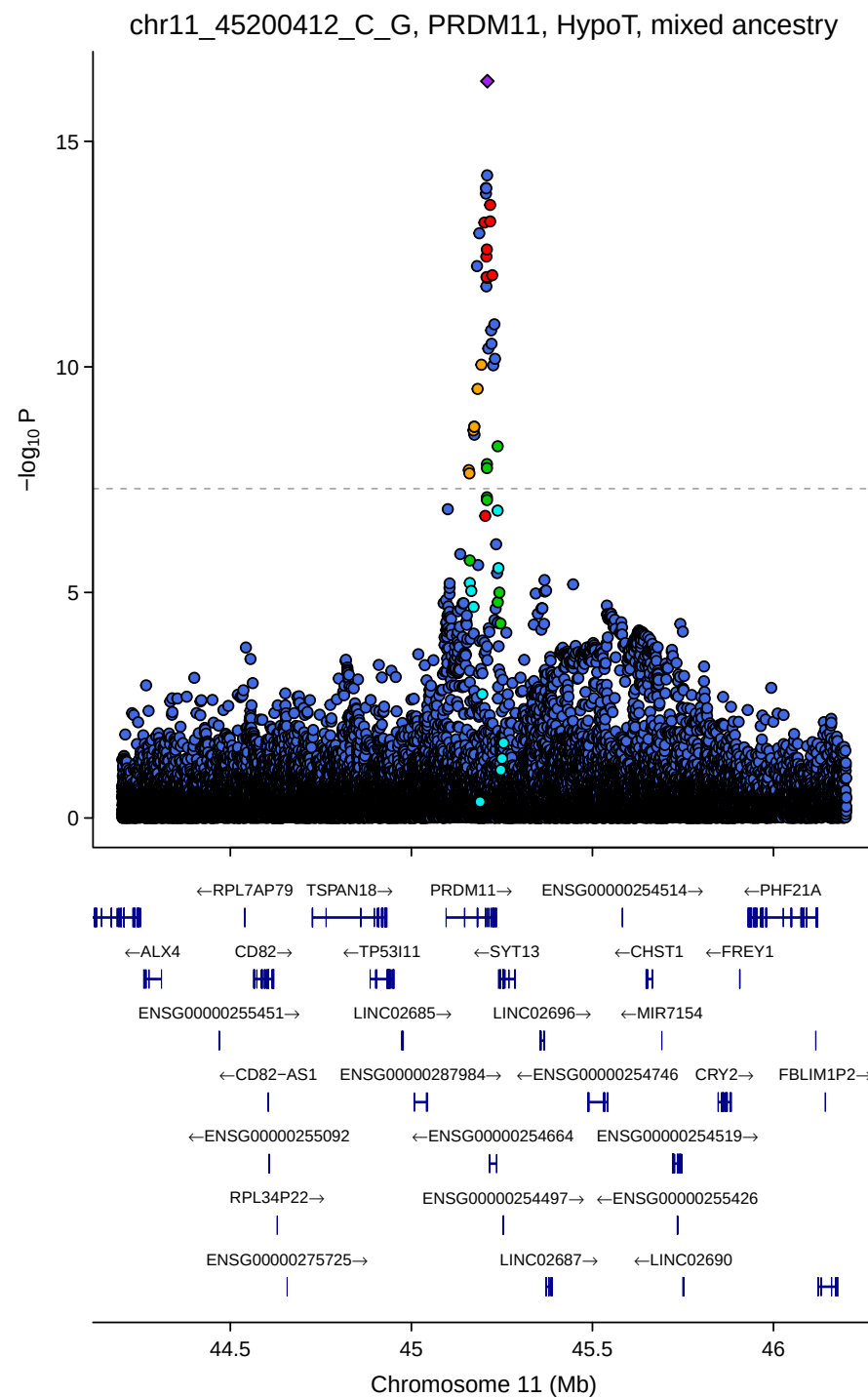
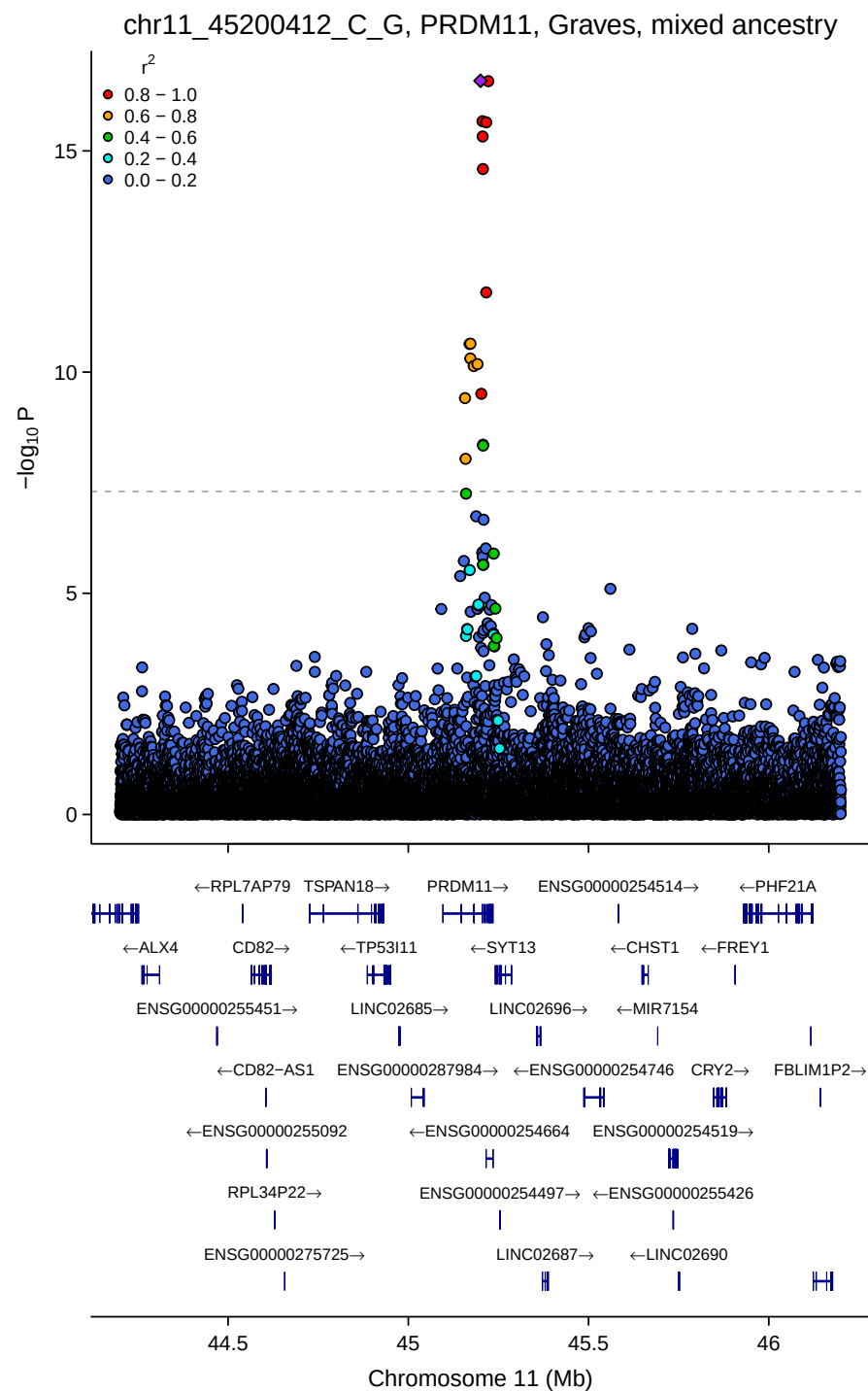


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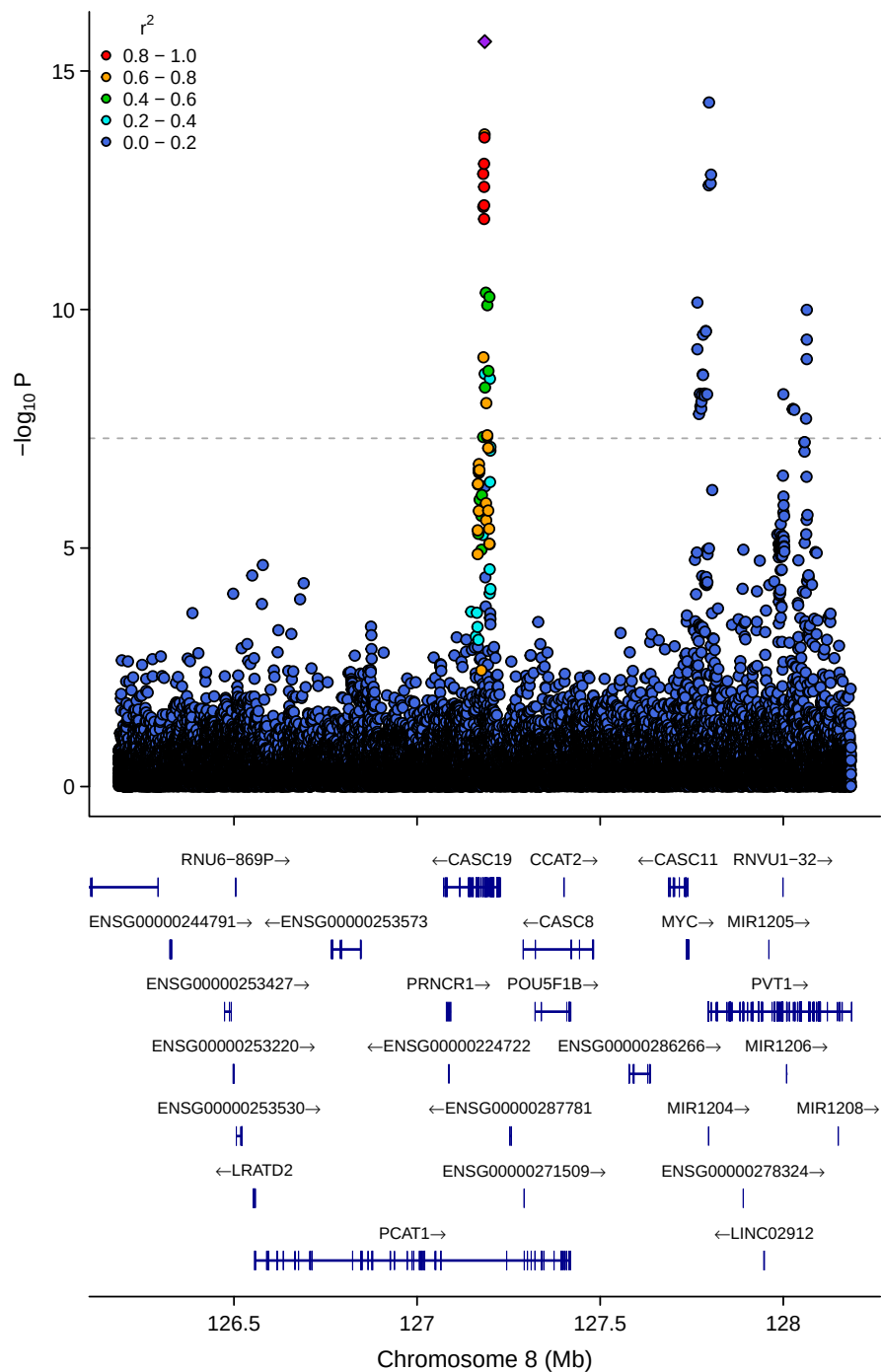


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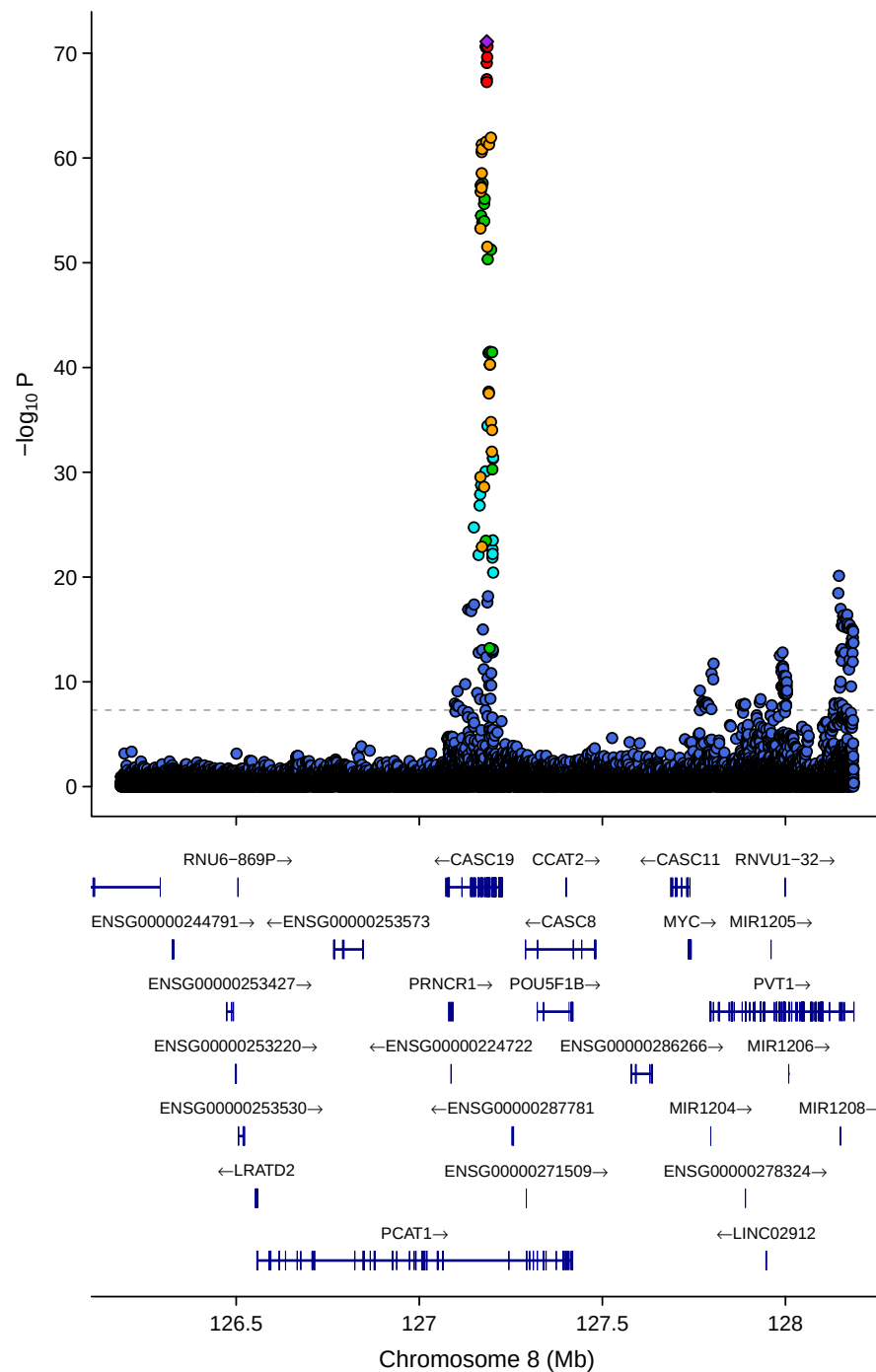


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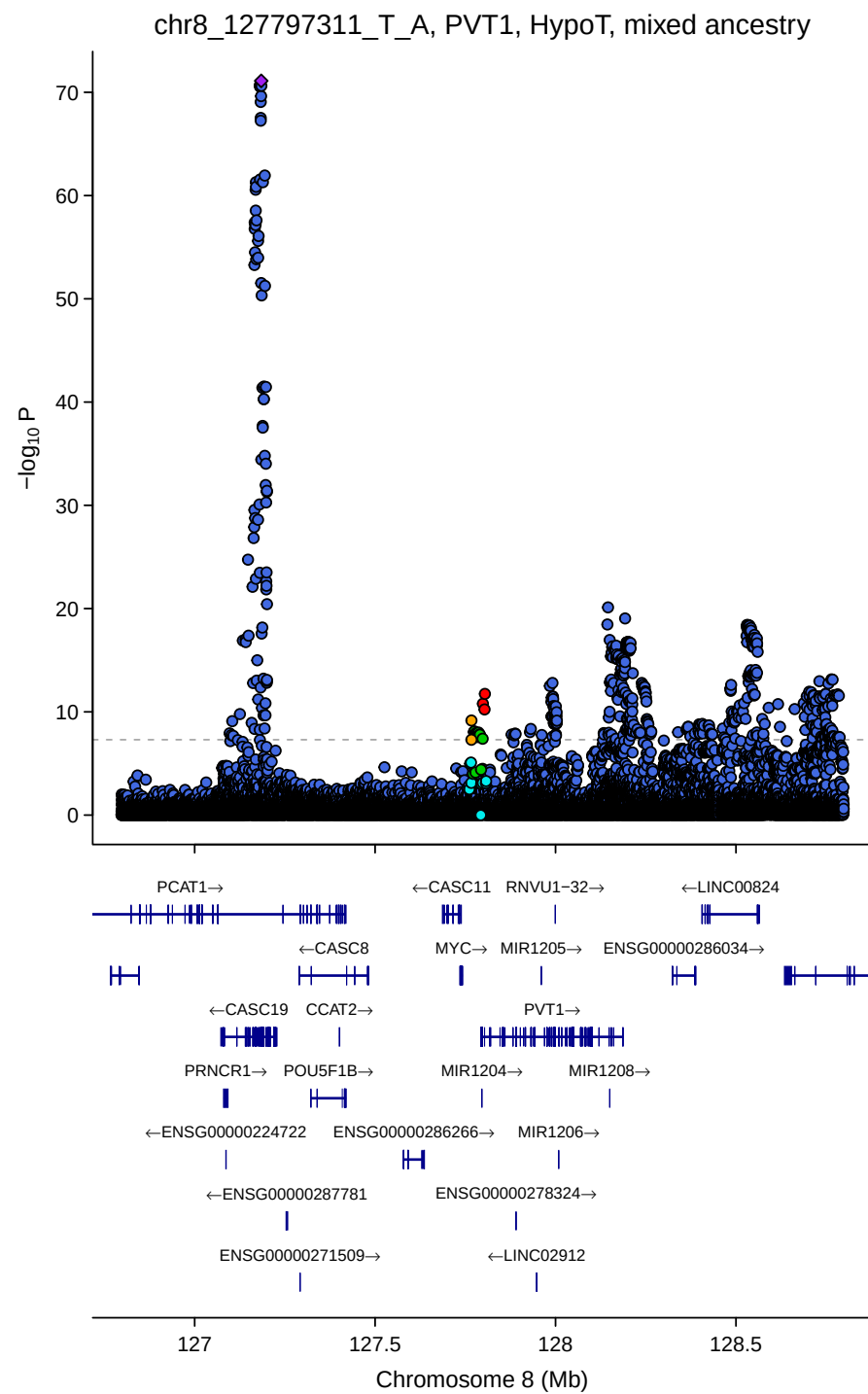
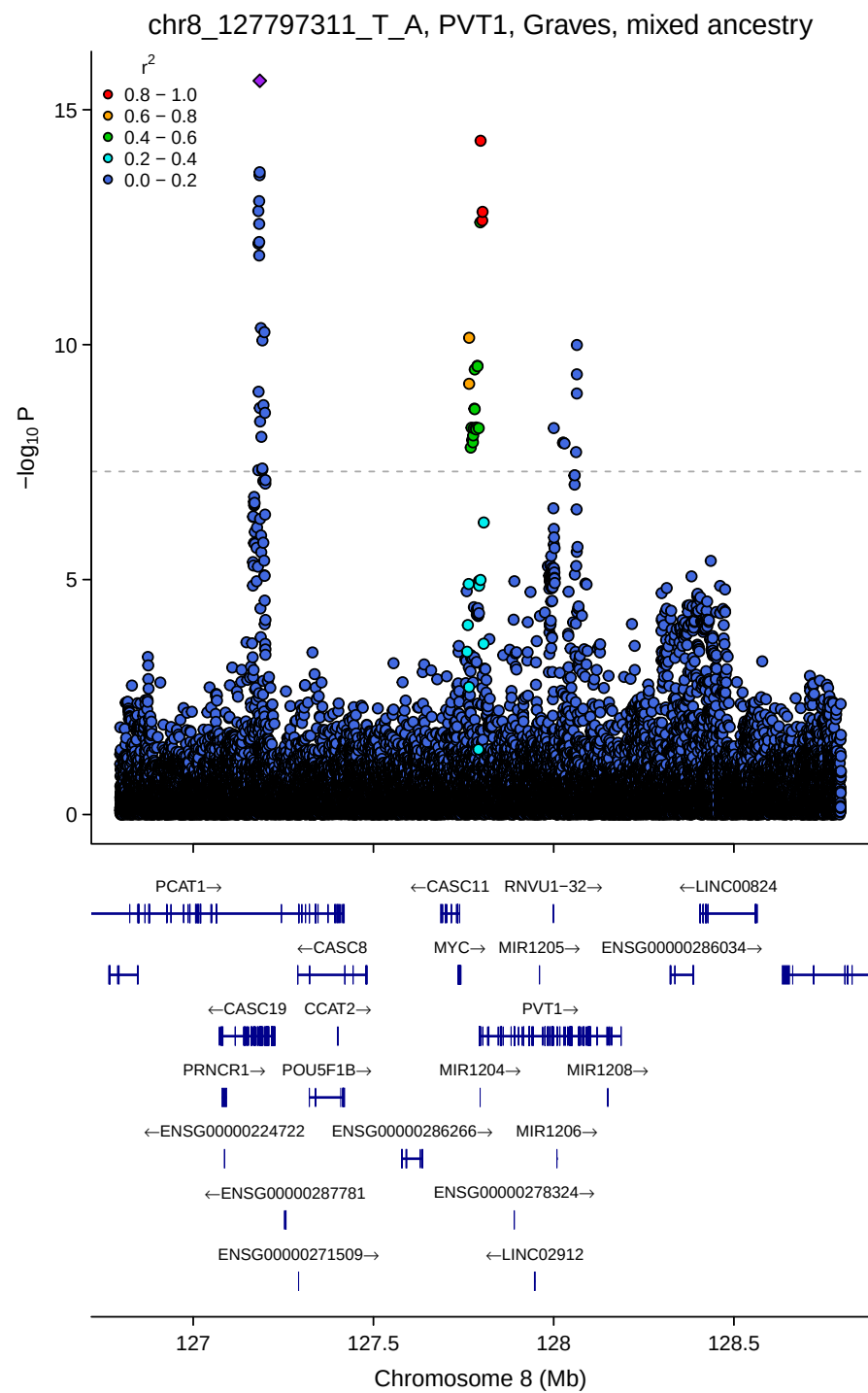
chr8\_127184843\_A\_G, PRNCR1;CASC19, Graves, mixed ancestry



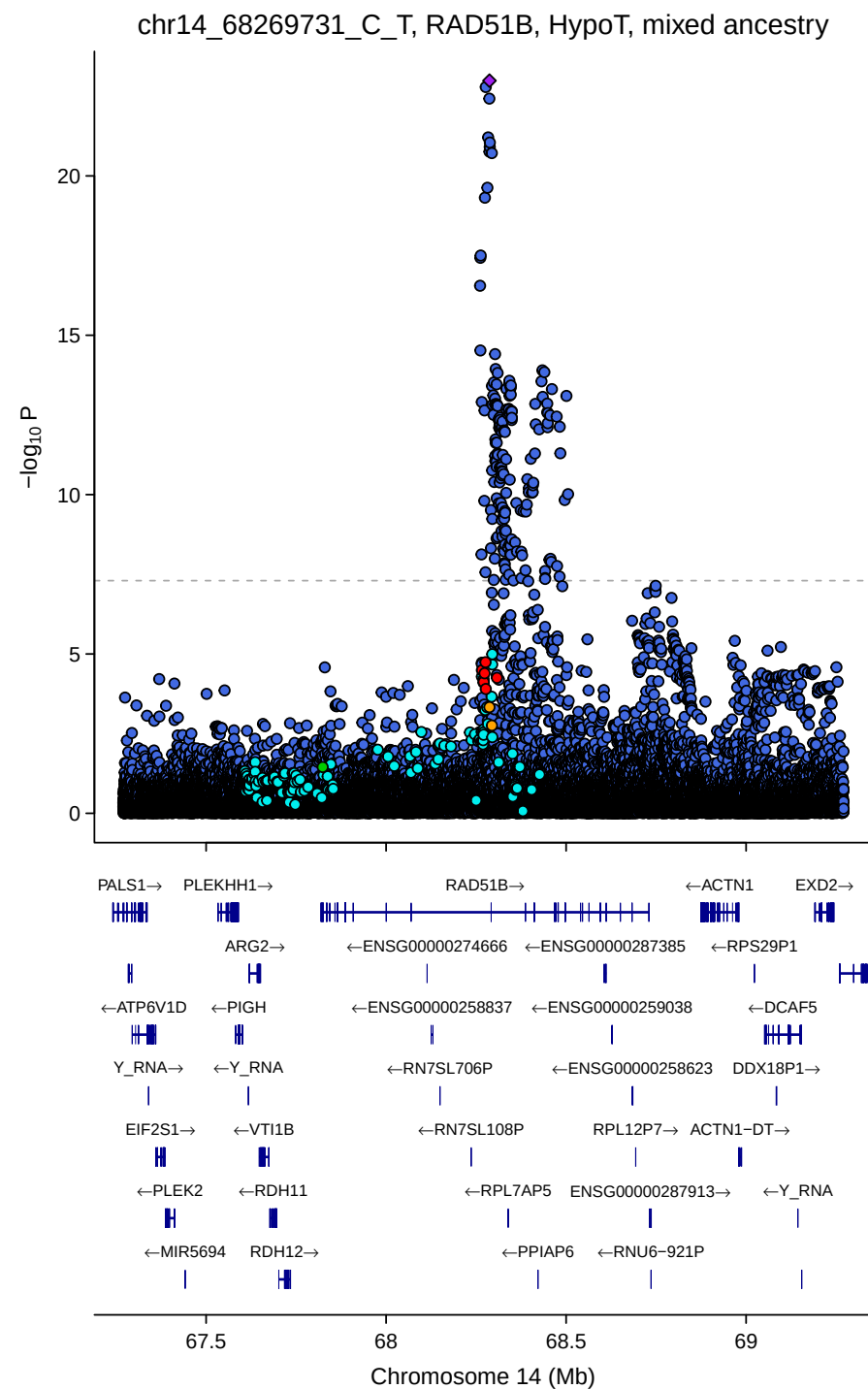
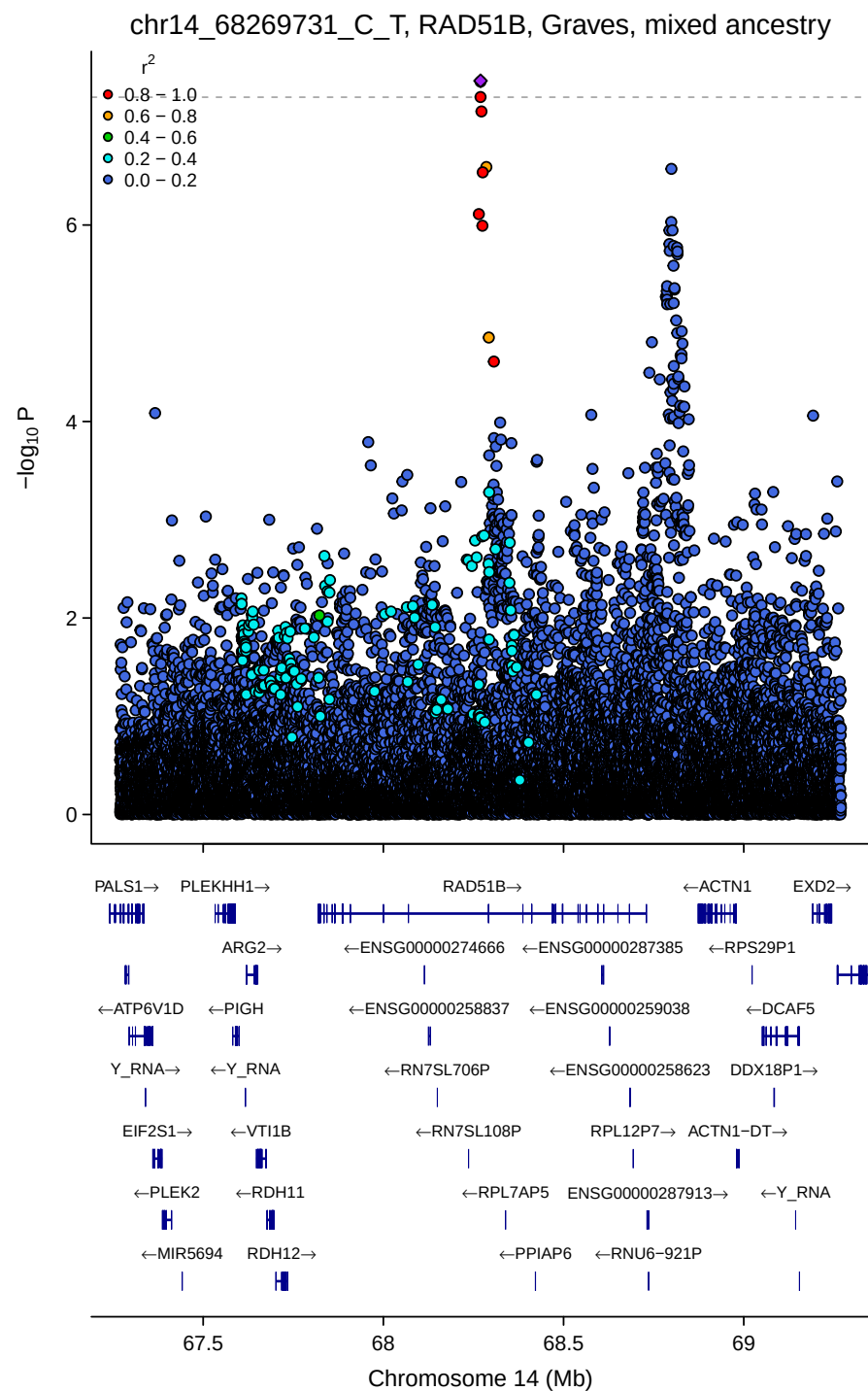
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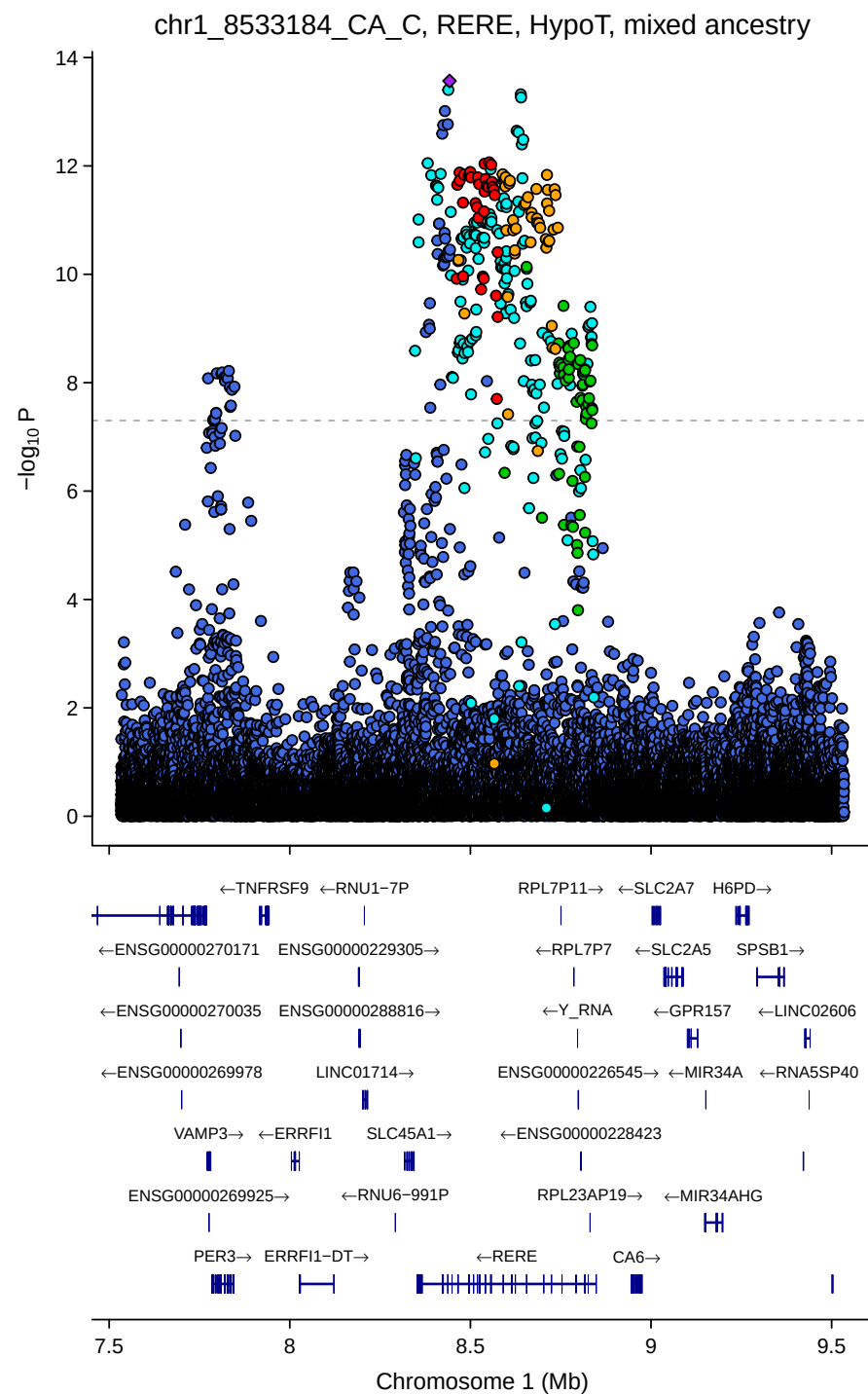
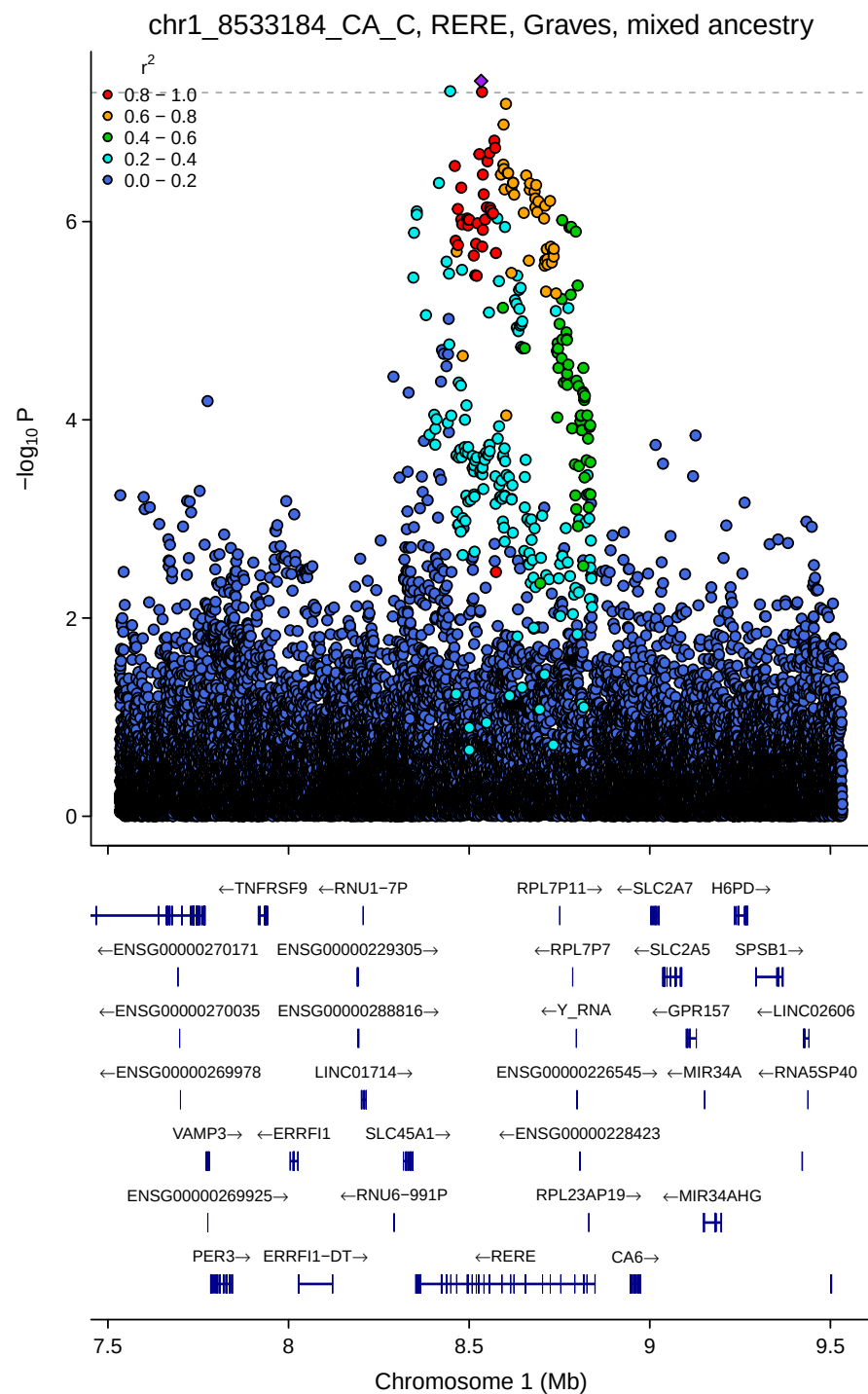
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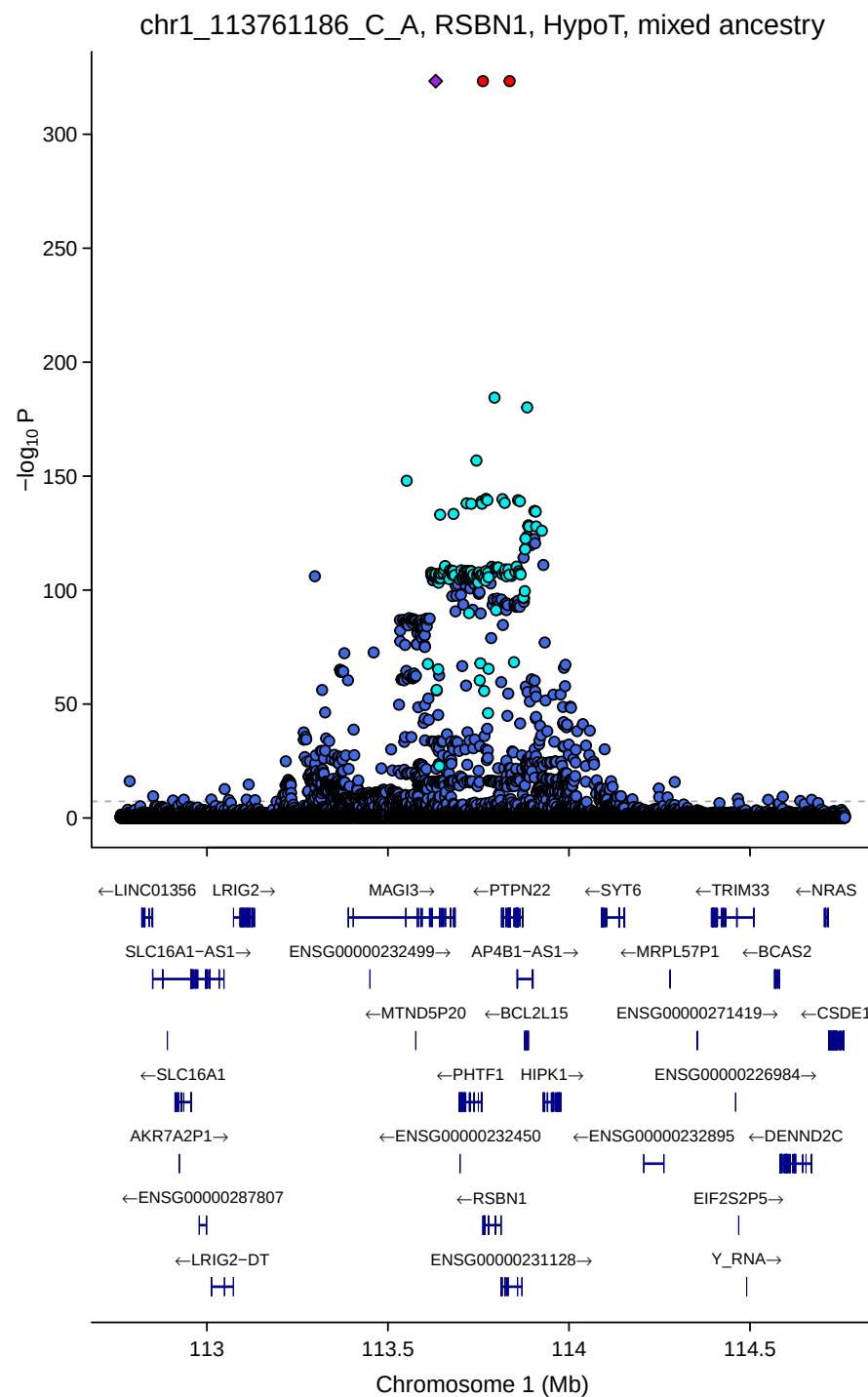
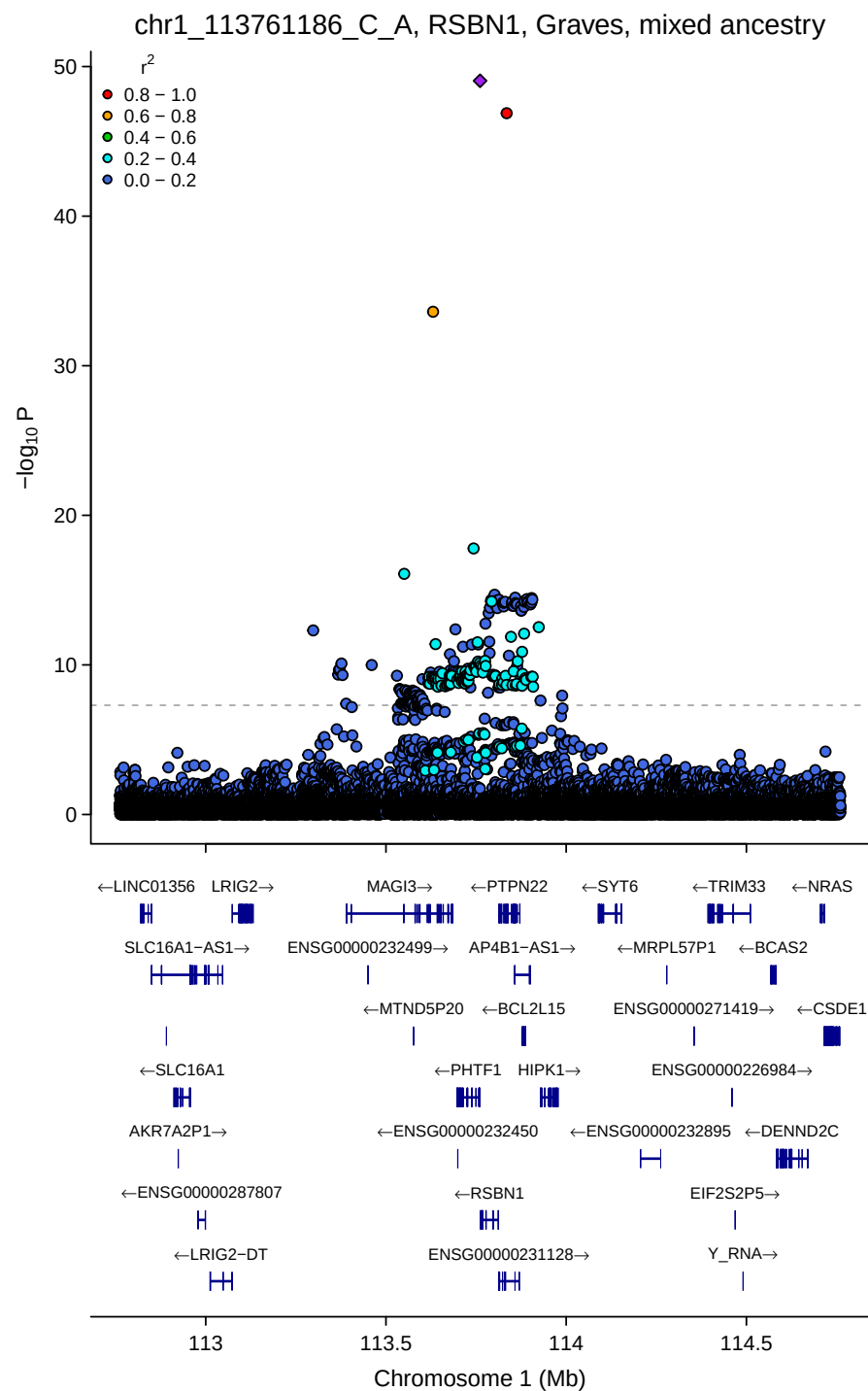
Supplementary Figure 3.2



Supplementary Figure 3.2

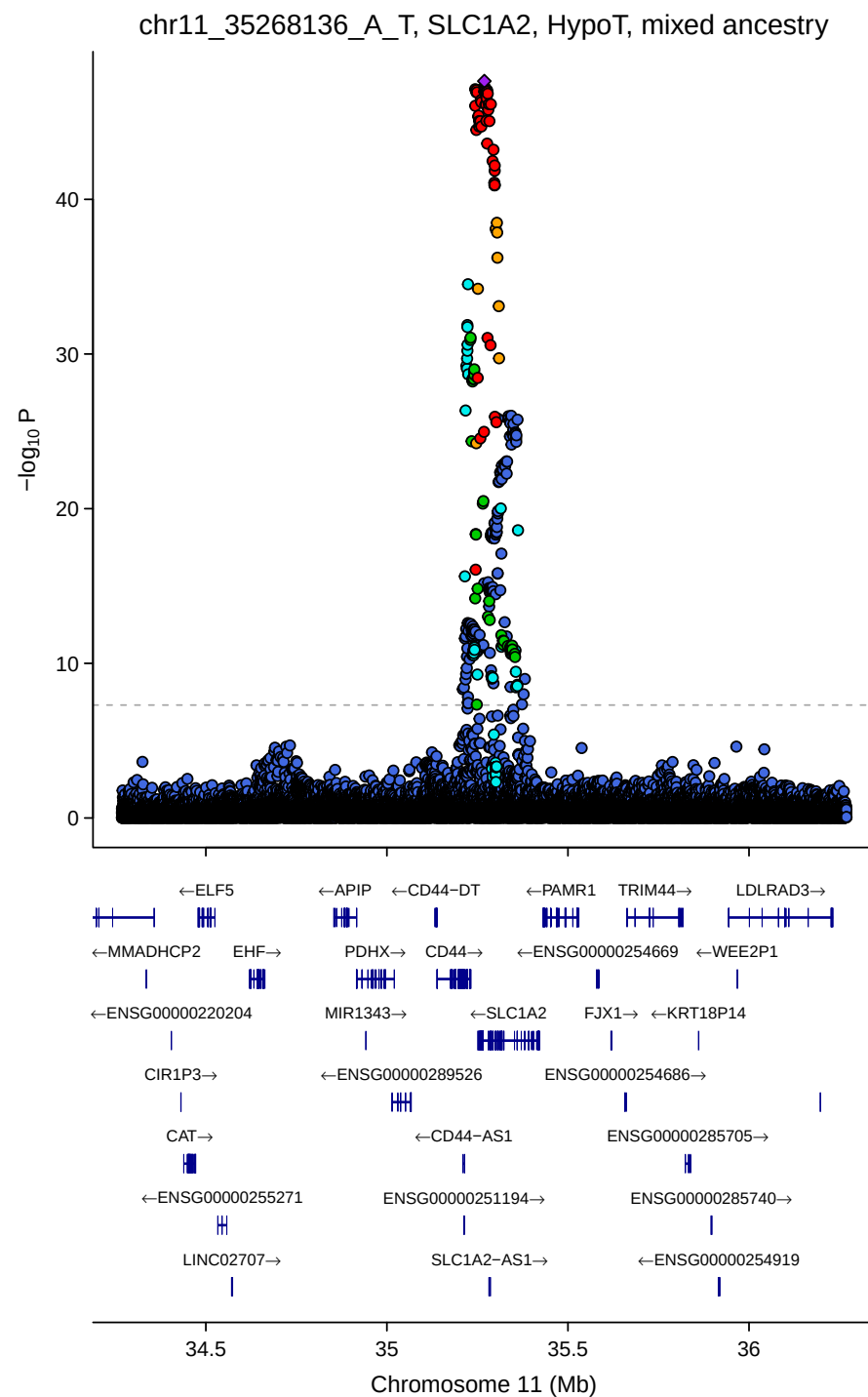
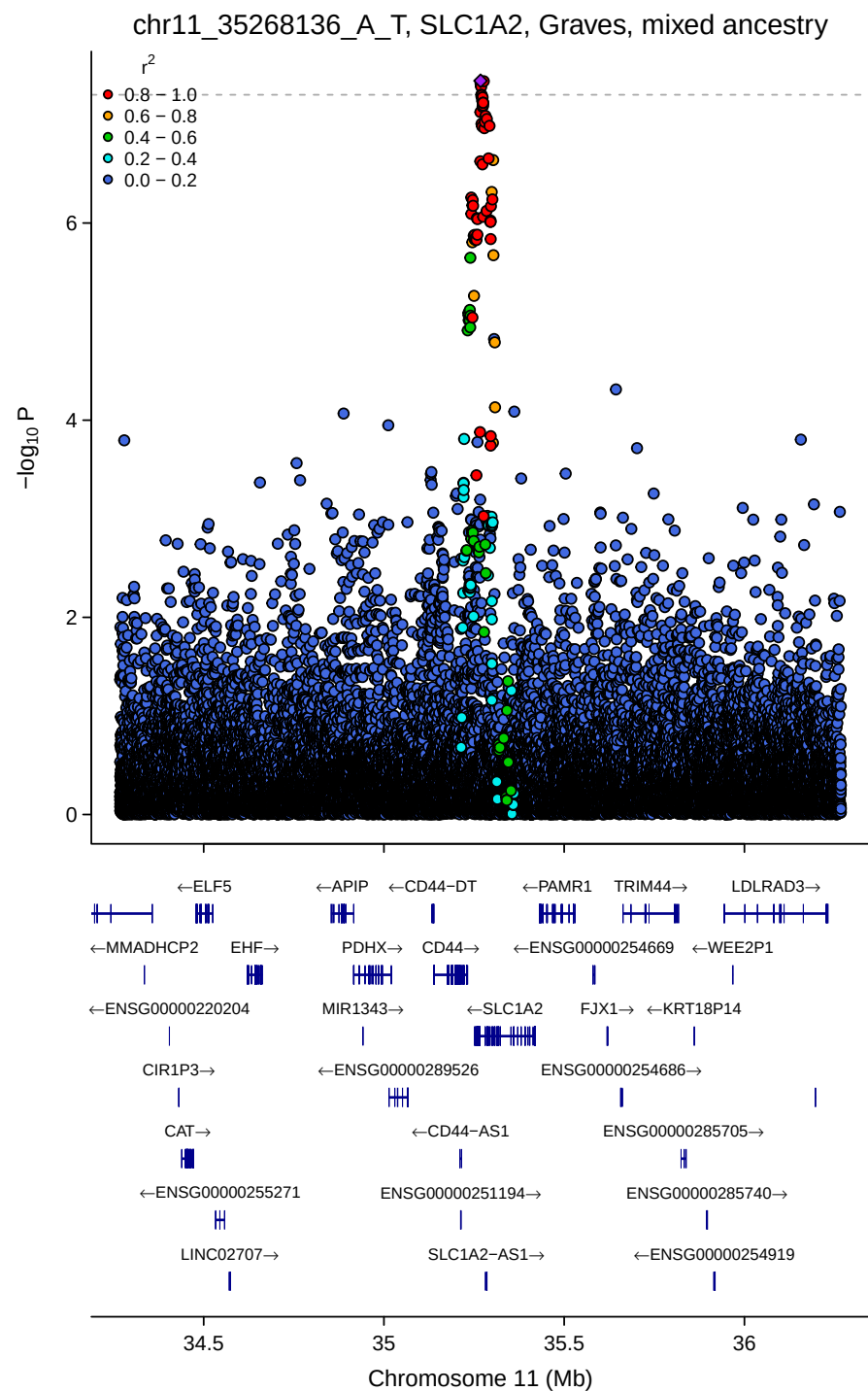


Supplementary Figure 3.2

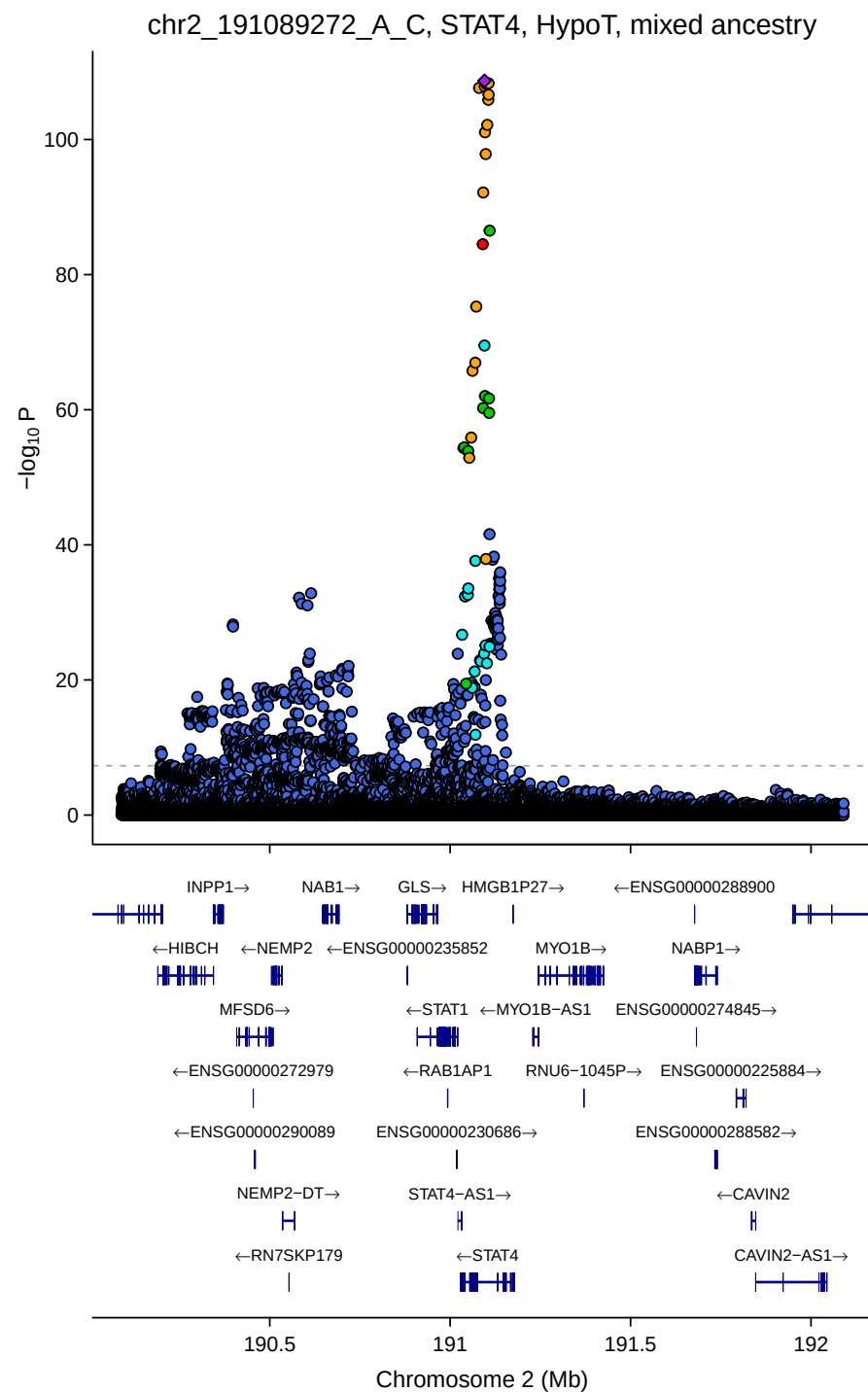
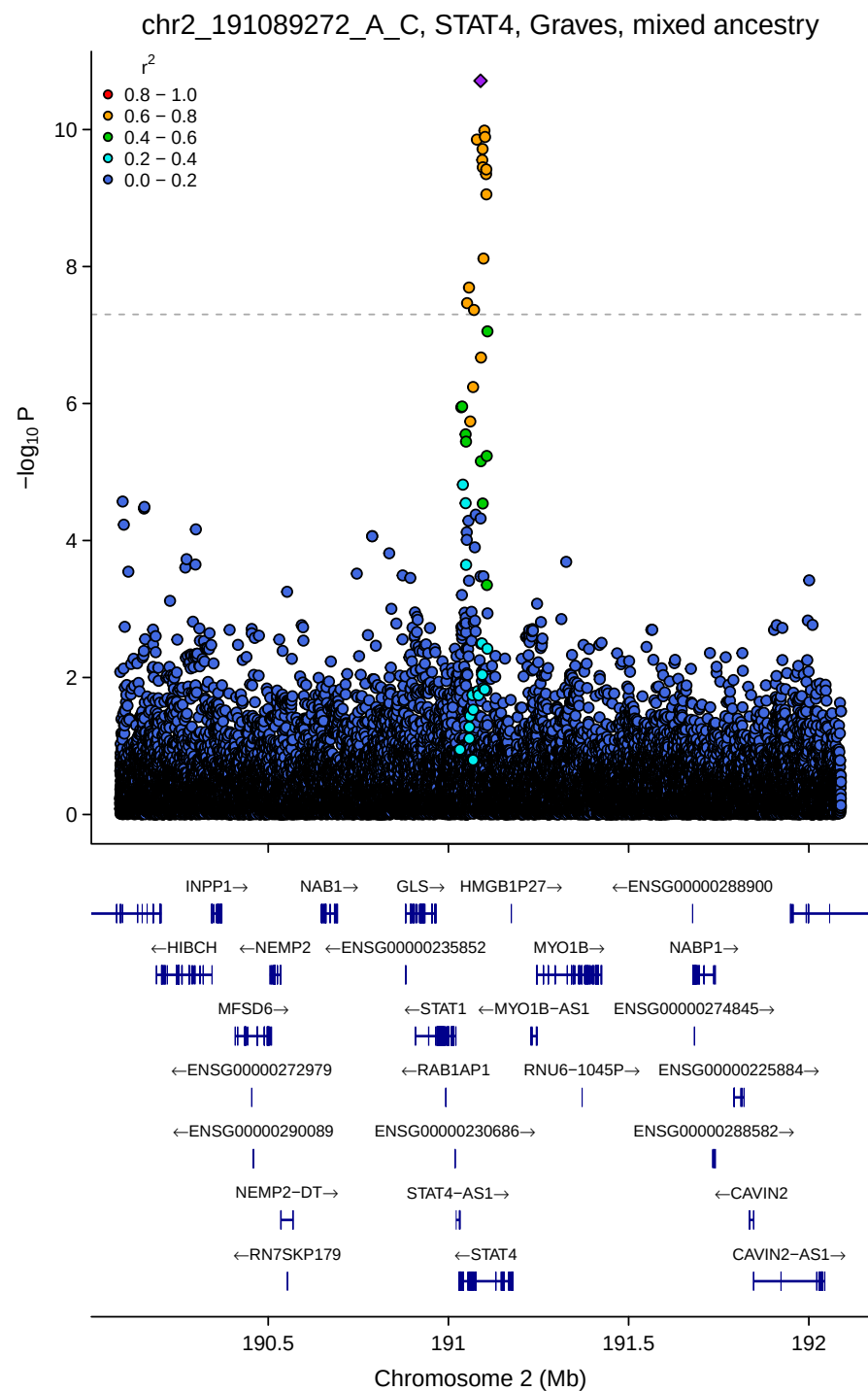




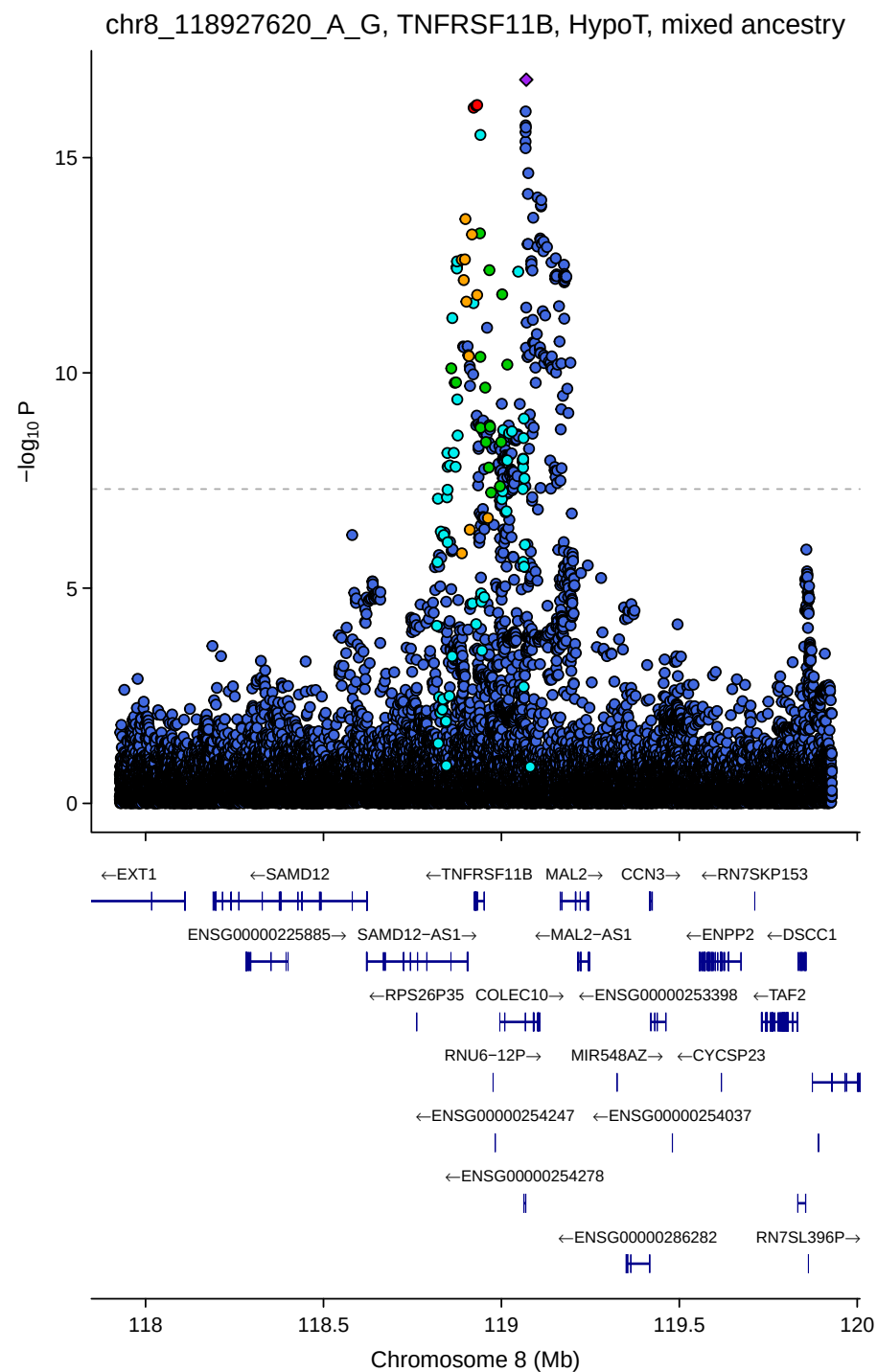
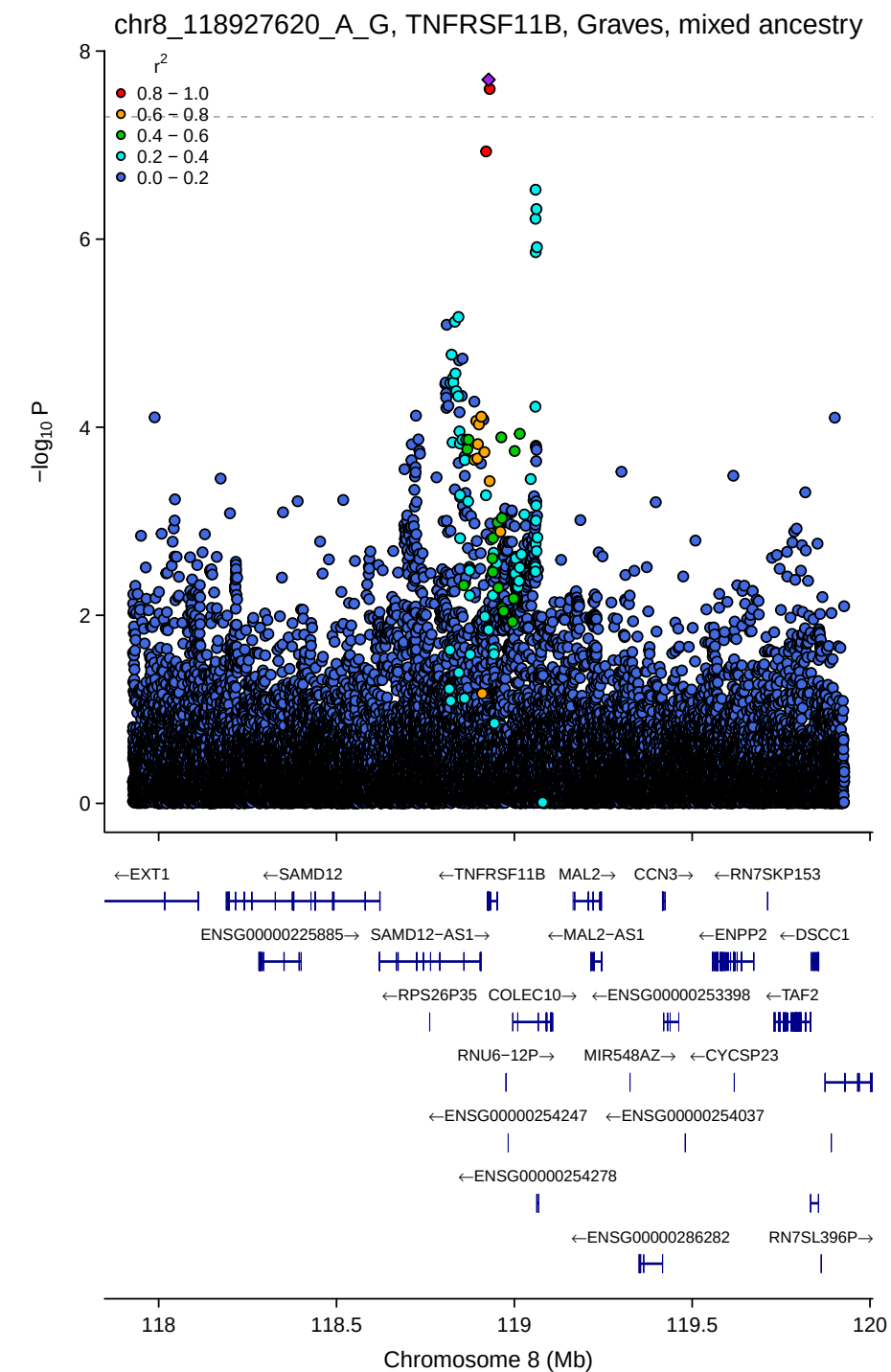
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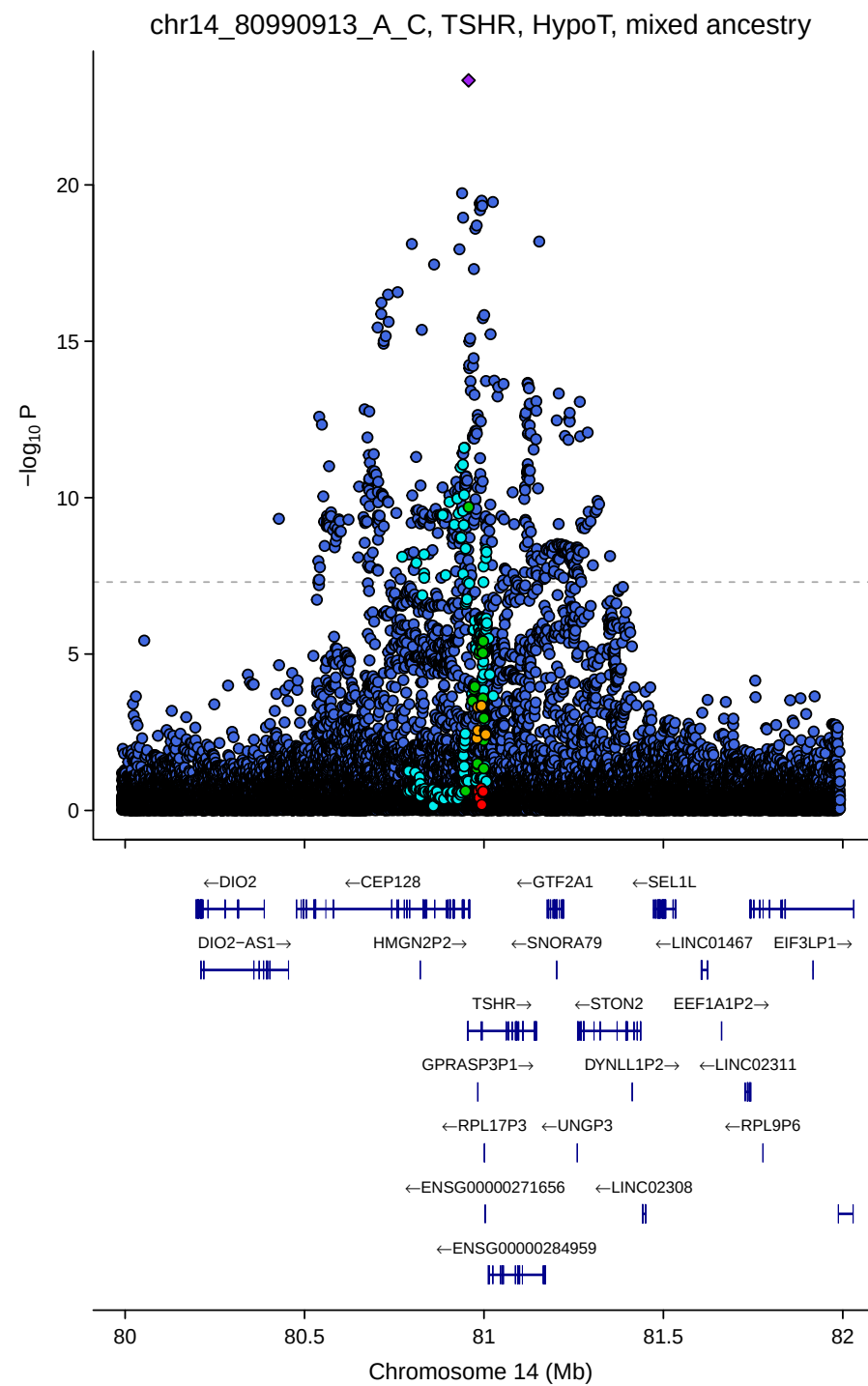
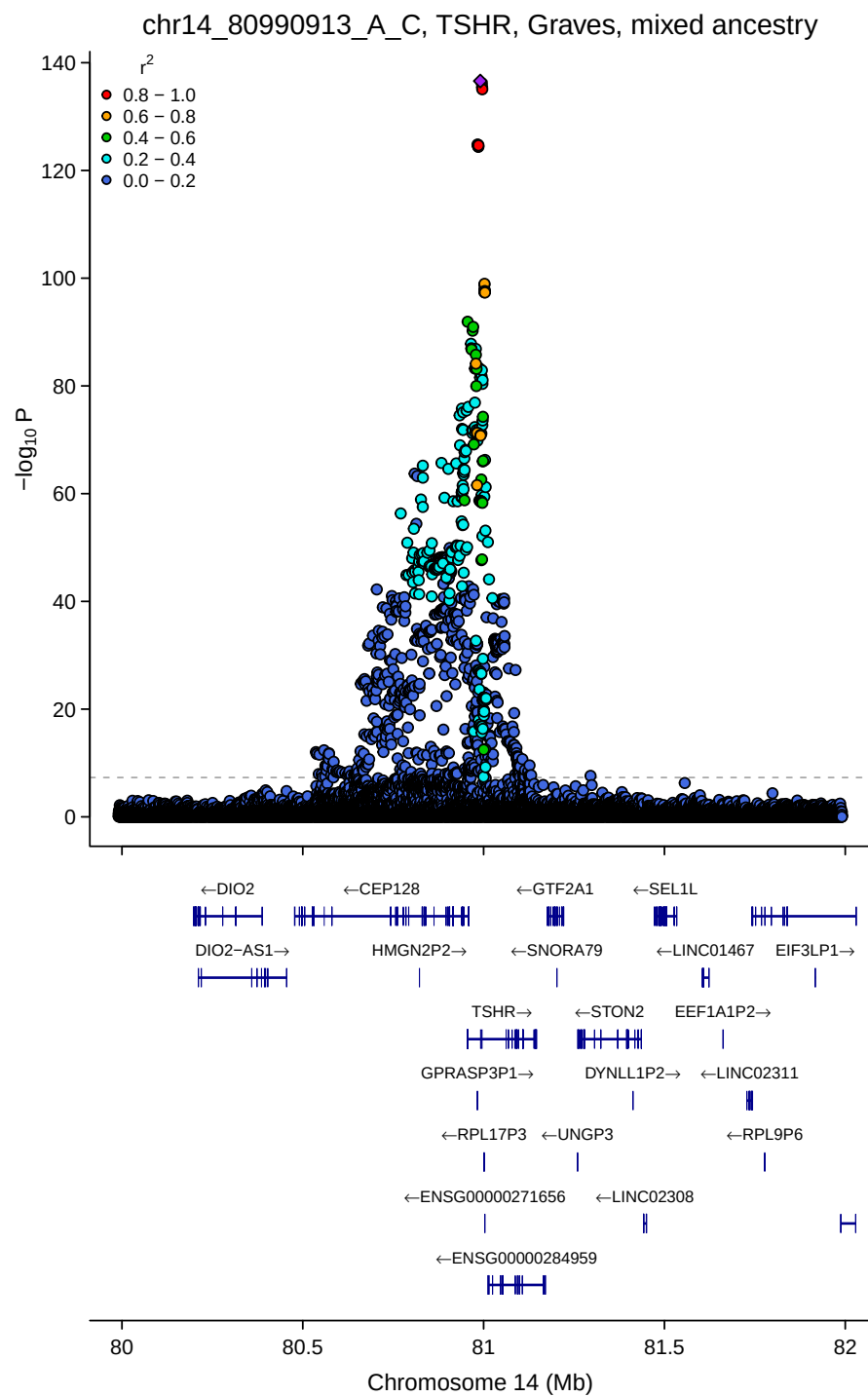
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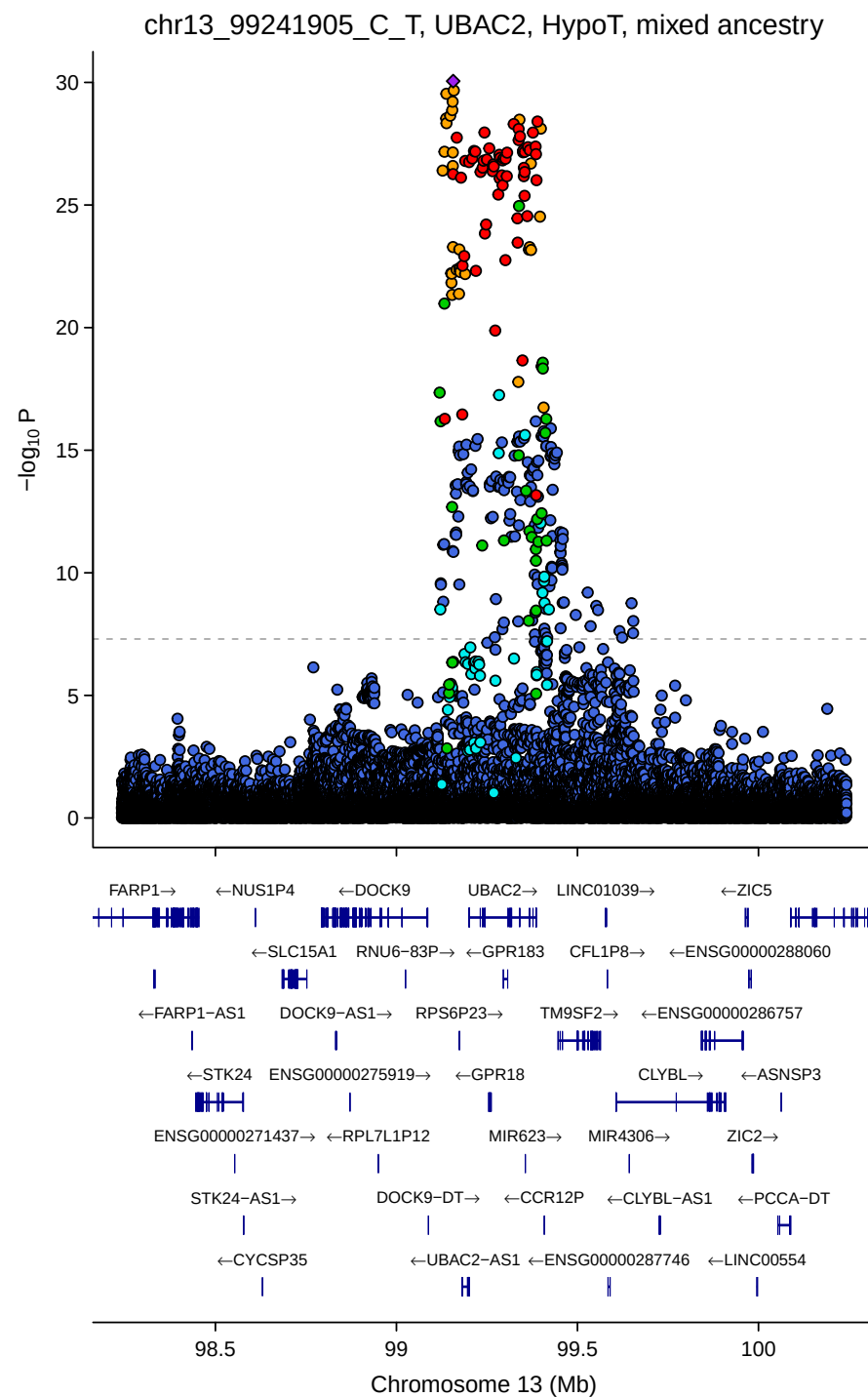
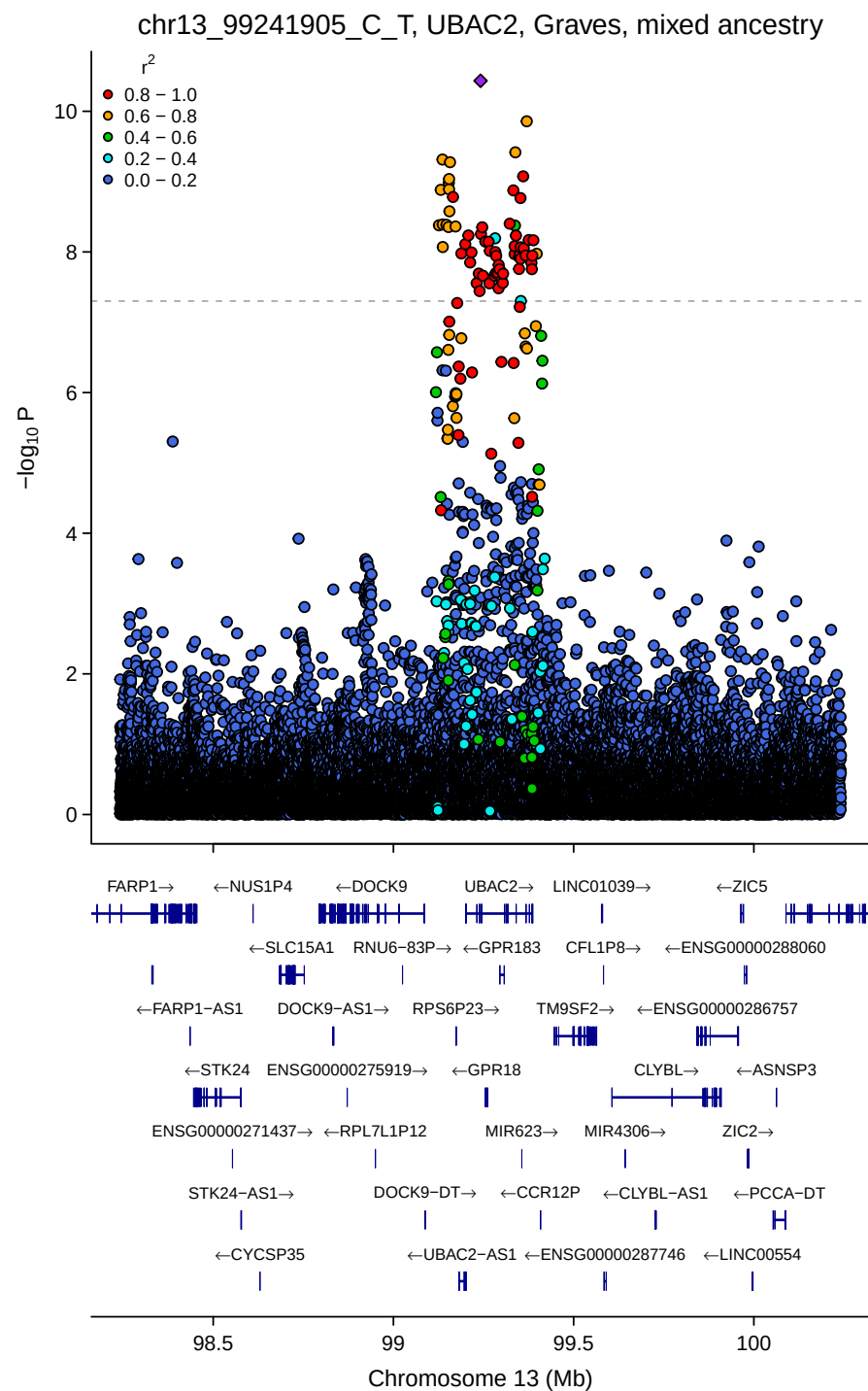
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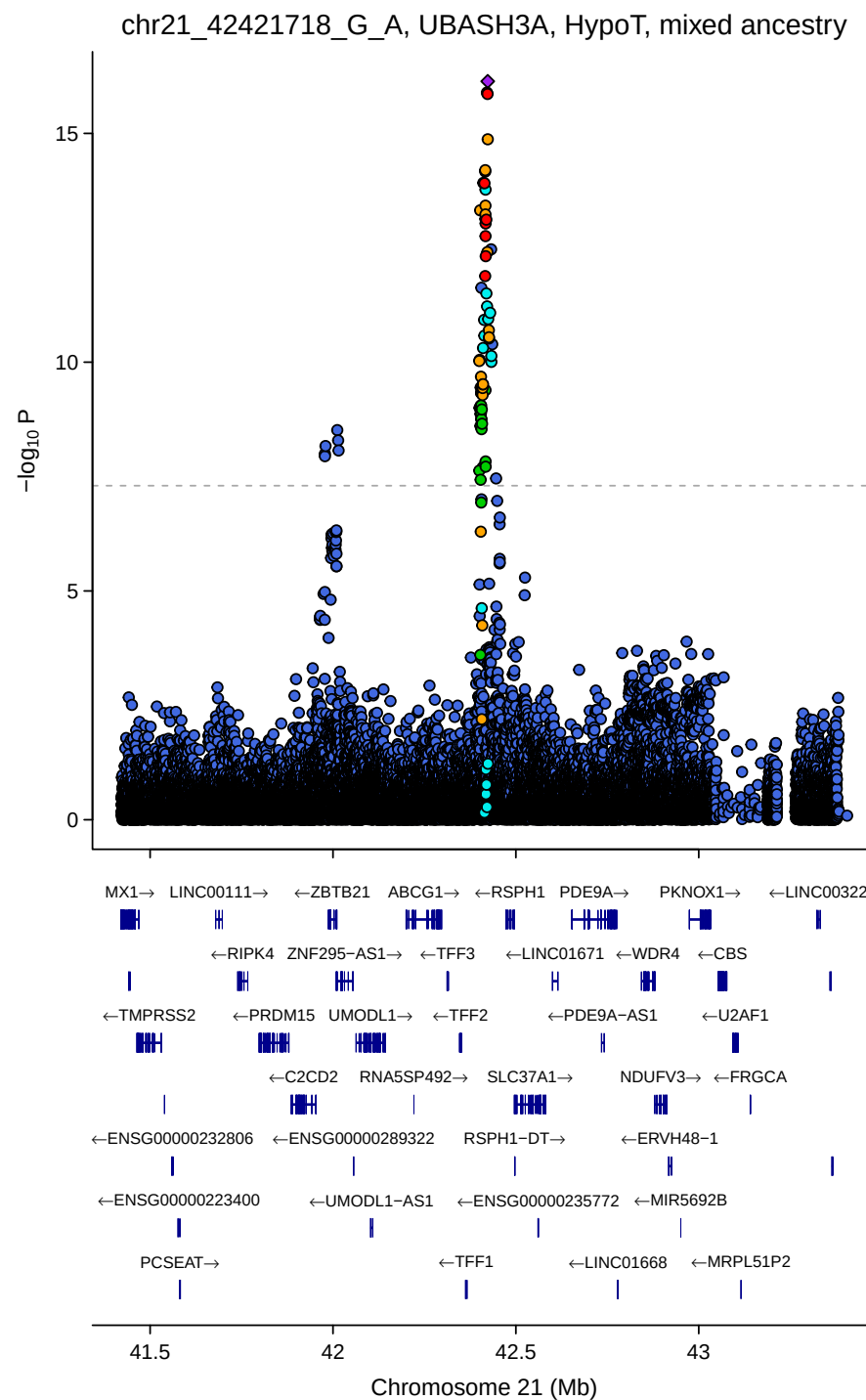
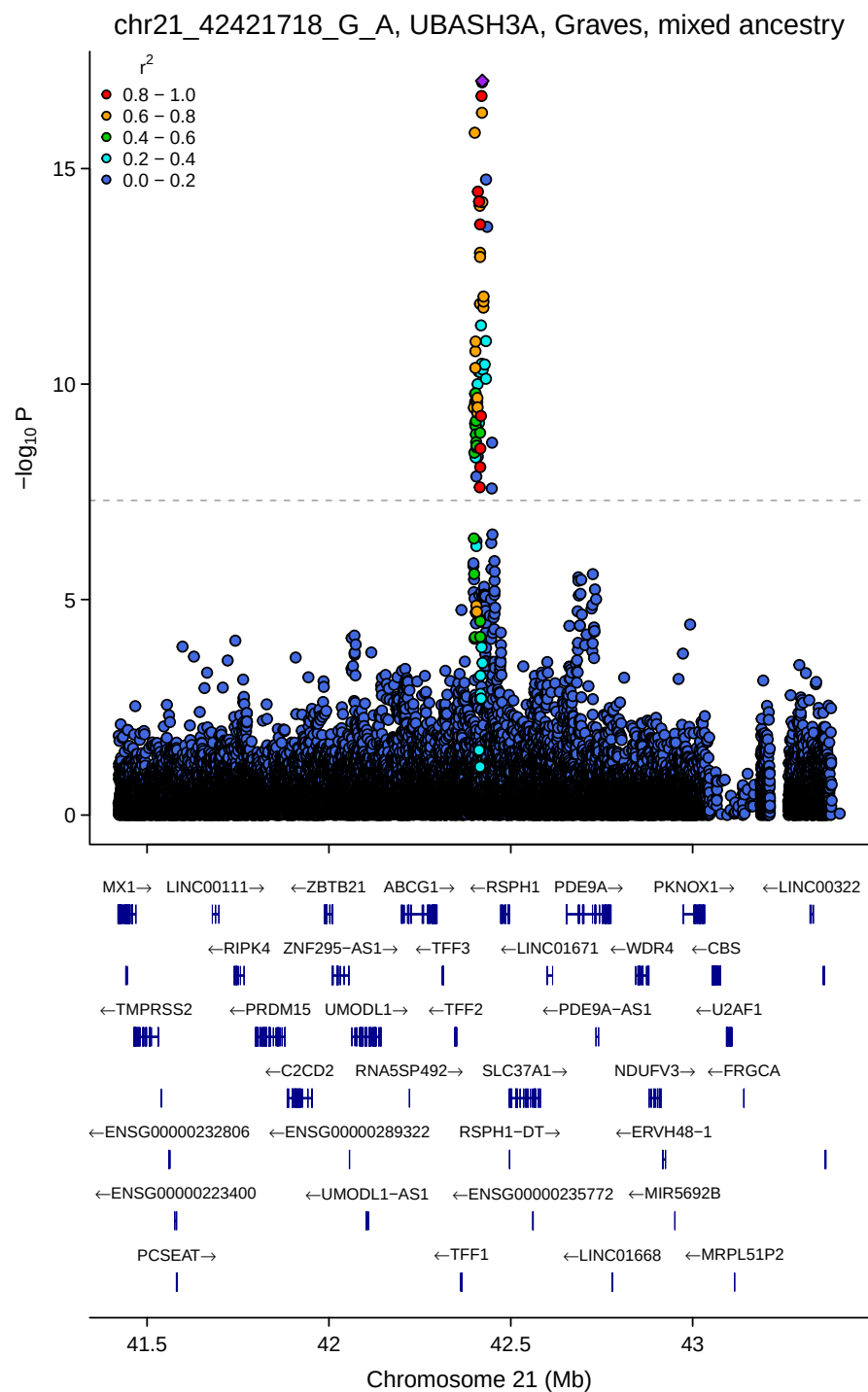
Supplementary Figure 3.2



Supplementary Figure 3.2

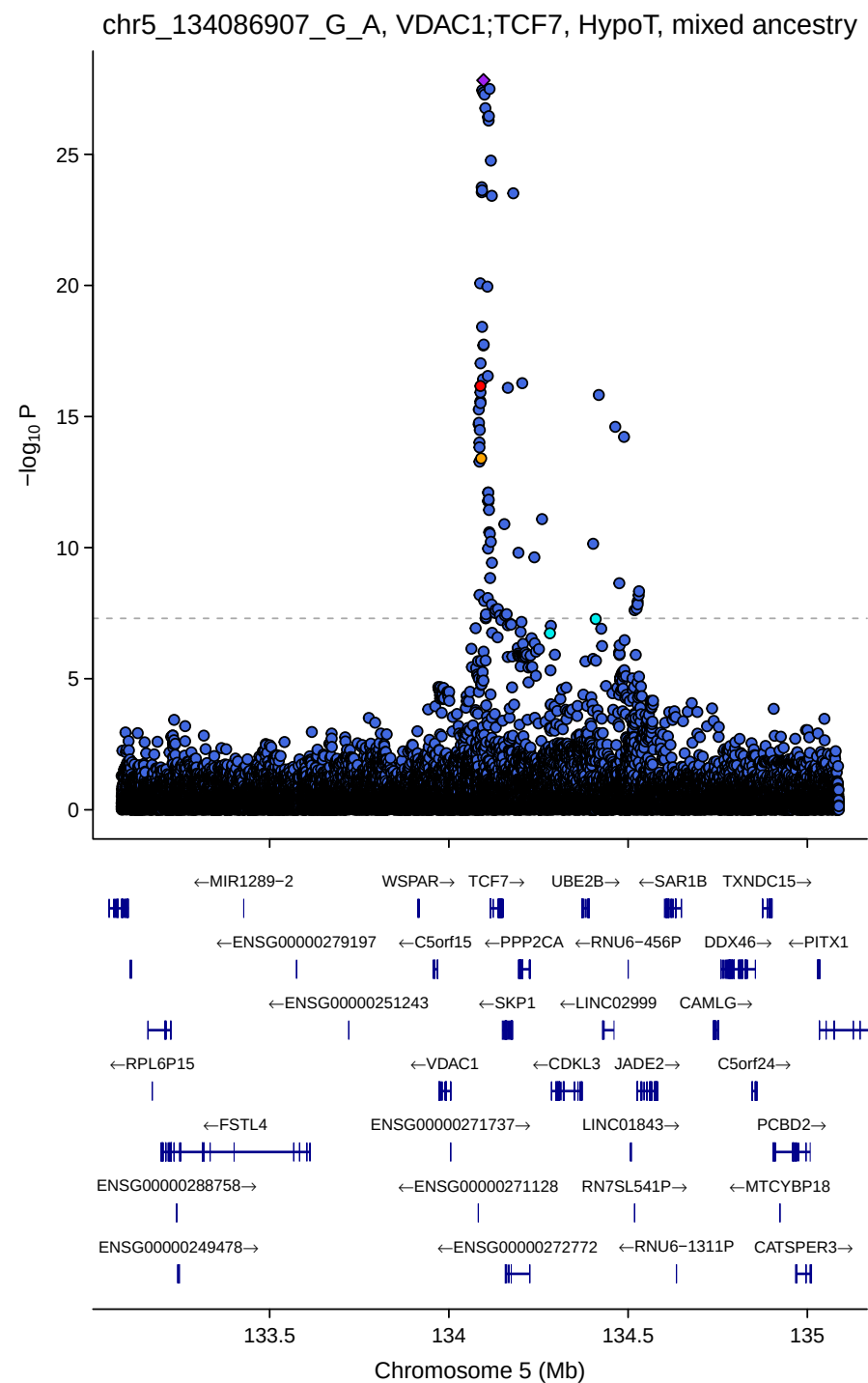
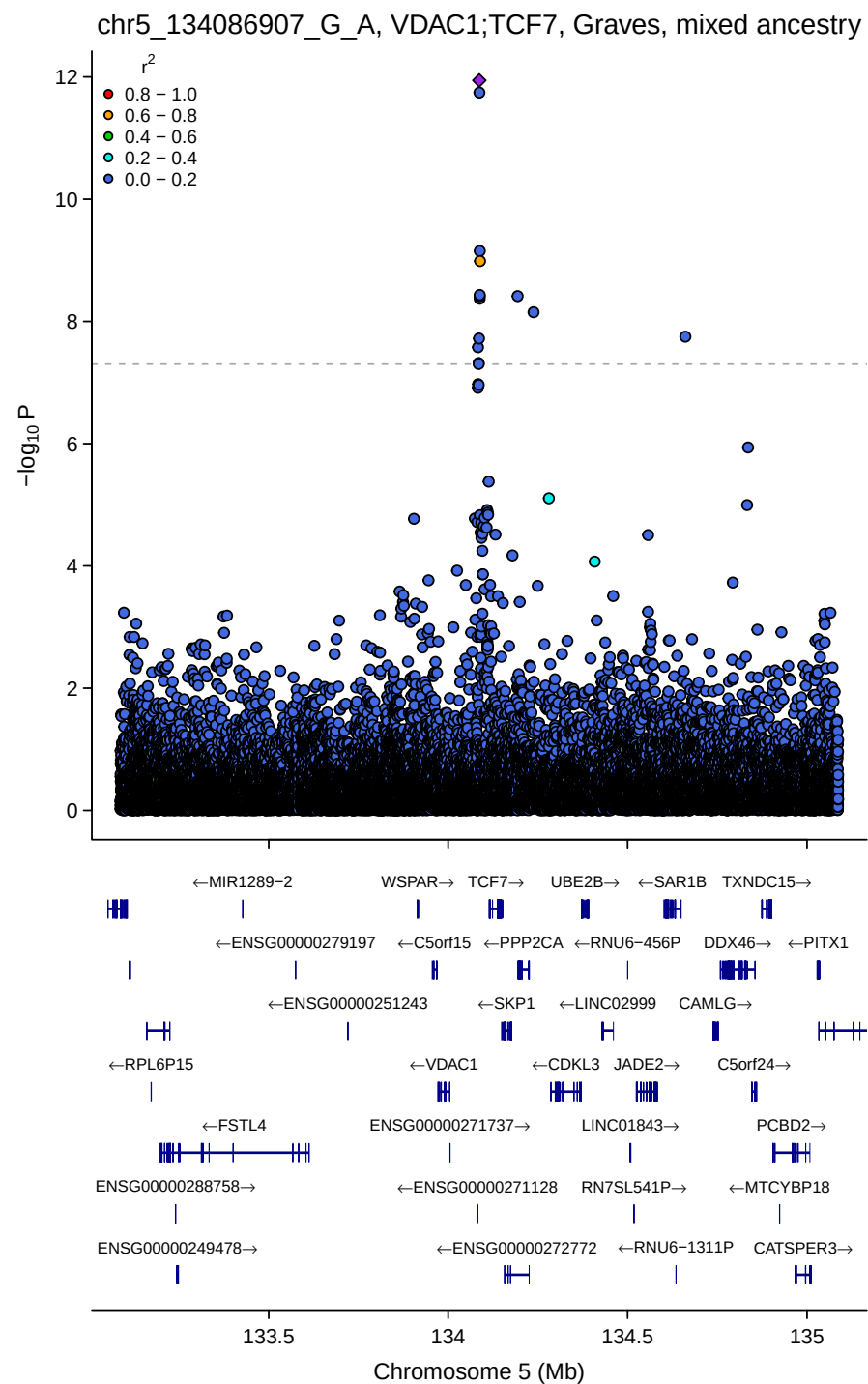


Supplementary Figure 3.2

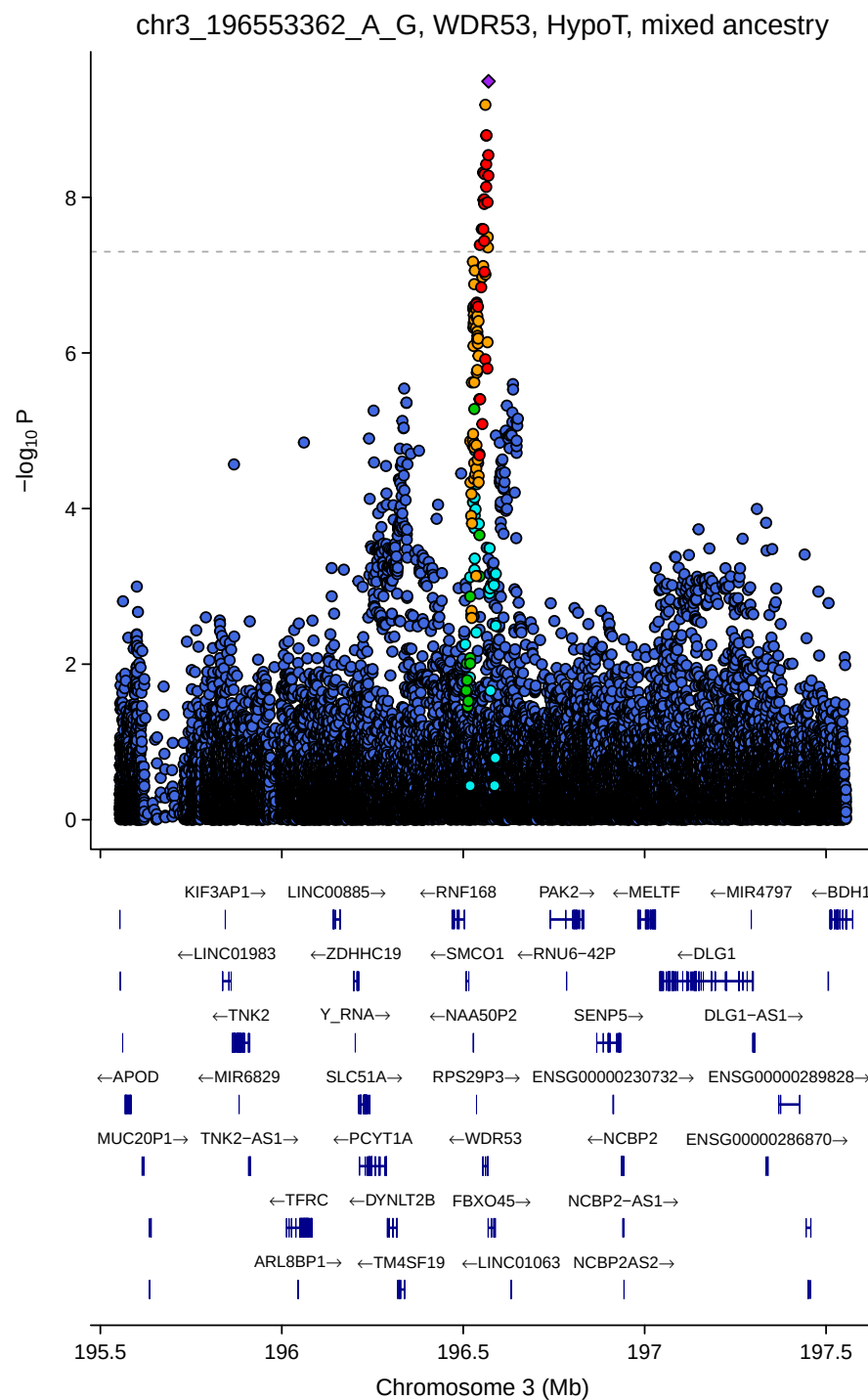
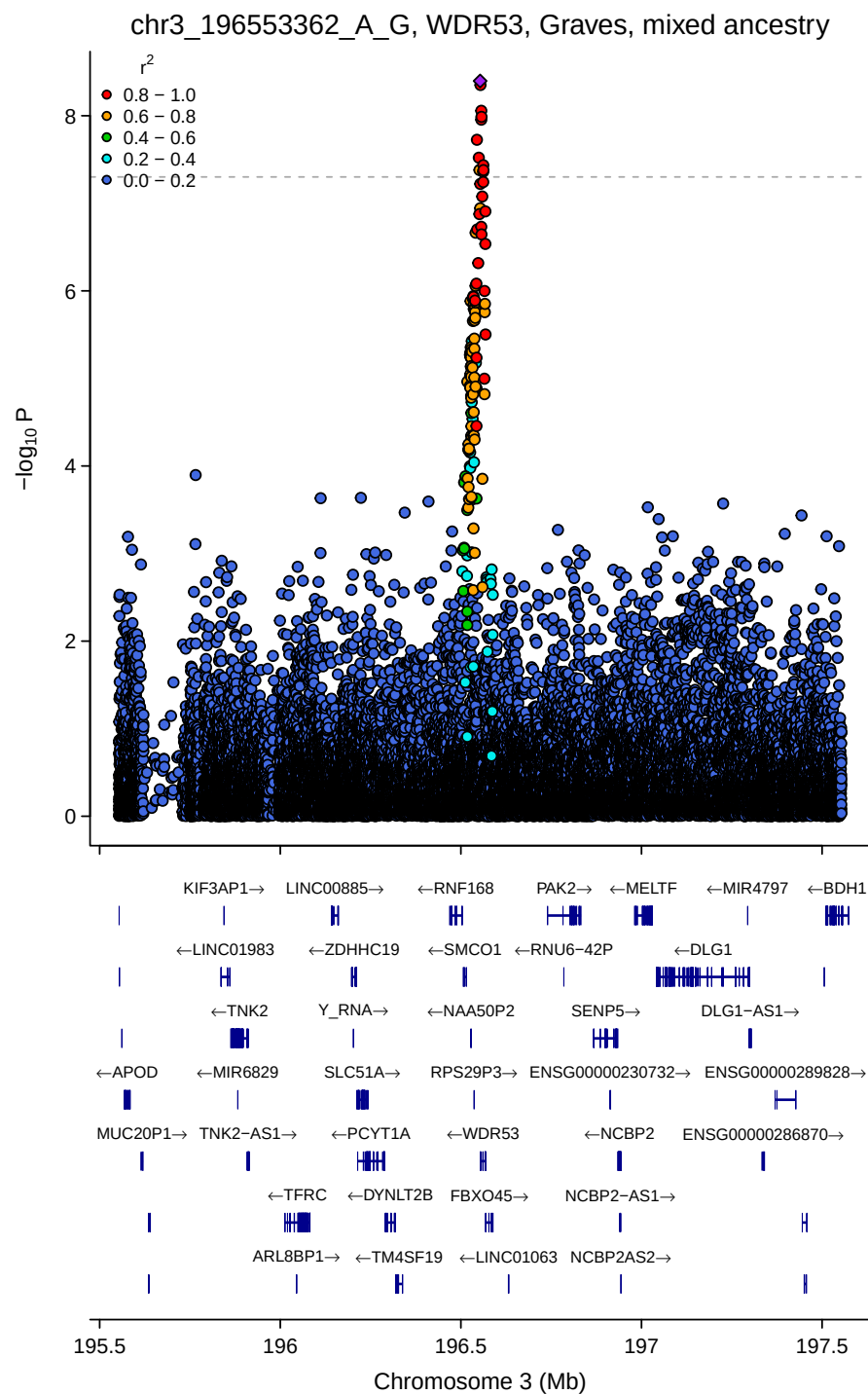




Supplementary Figure 3.2



Supplementary Figure 3.2



Supplementary Figure 3.2

