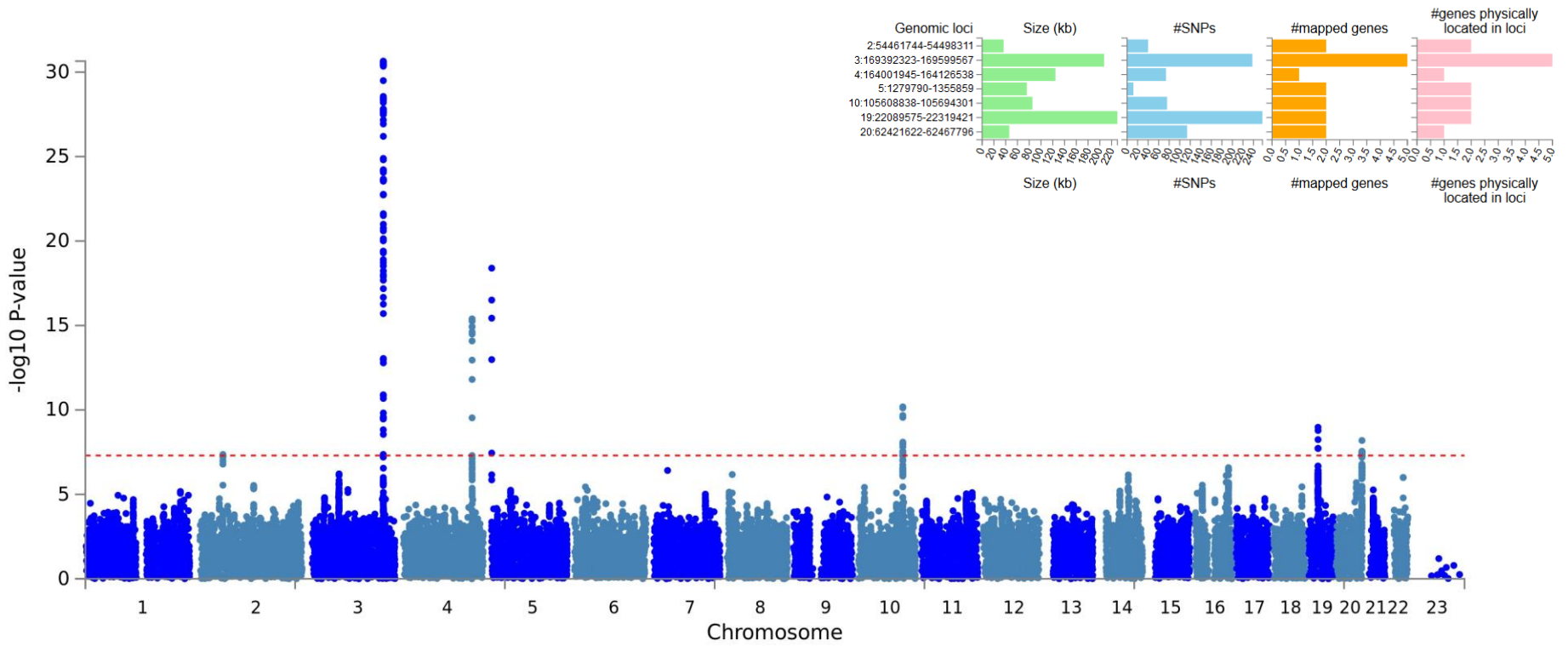


SNP-based GWAS for Leukocyte Telomere Length- EUR from ENGAGE consortia

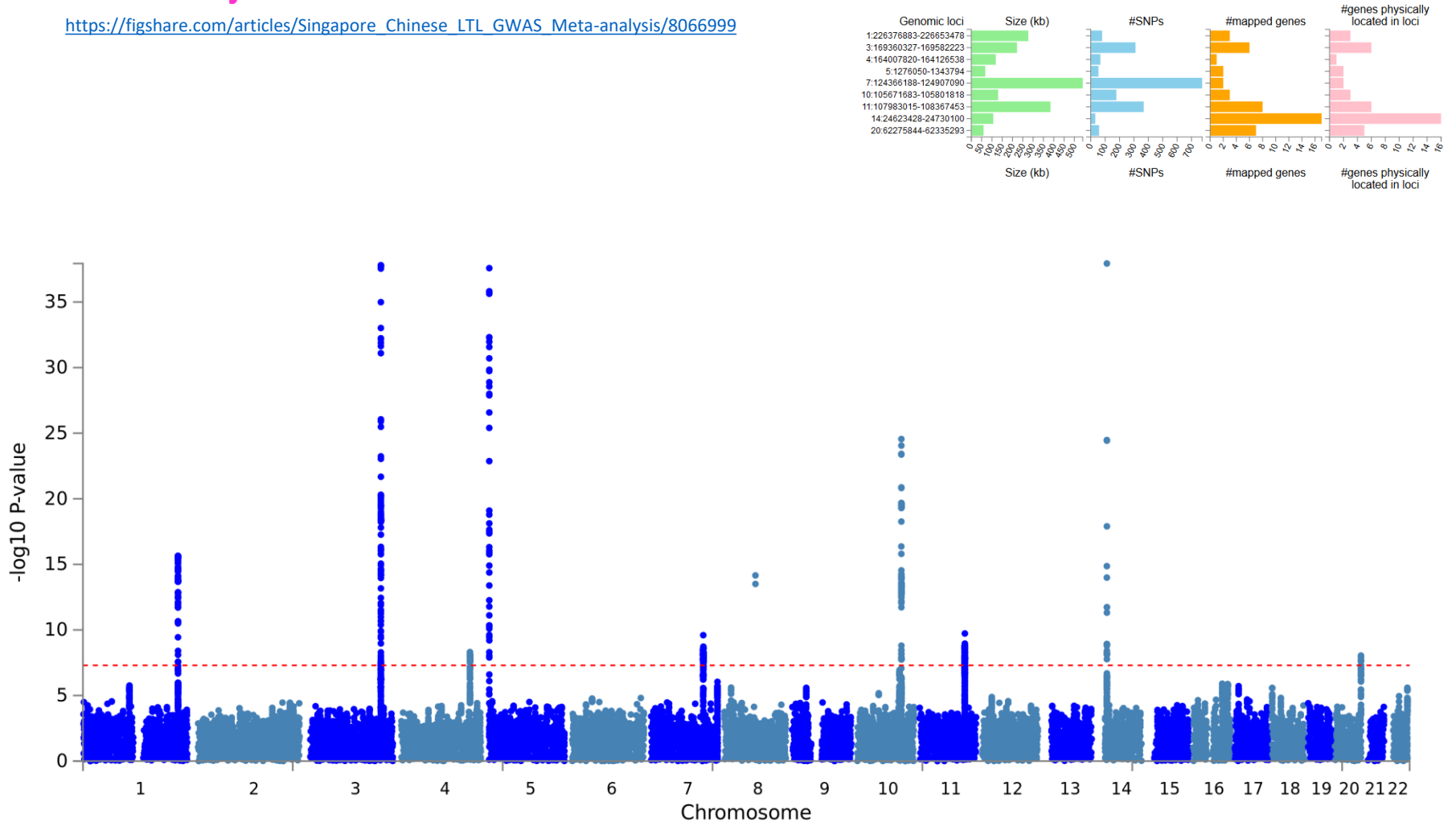
Summary per genomic risk locus ?



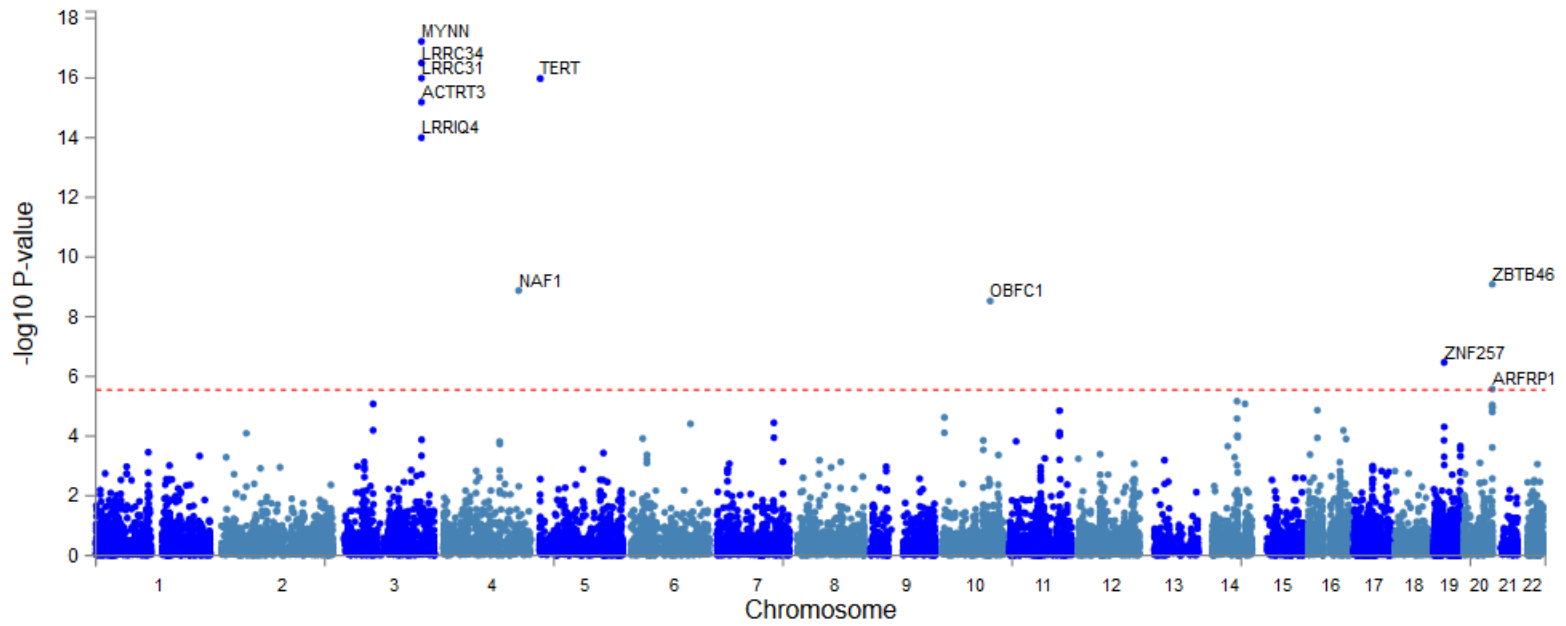
SNP-based GWAS for Leukocyte Telomere Length- EAS from Dorajoo et. al 2019

https://figshare.com/articles/Singapore_Chinese_LTL_GWAS_Meta-analysis/8066999

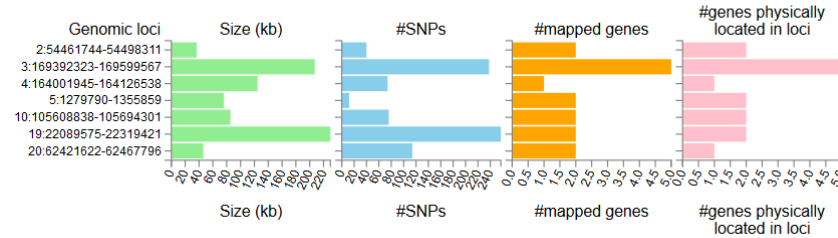
Summary per genomic risk locus ?



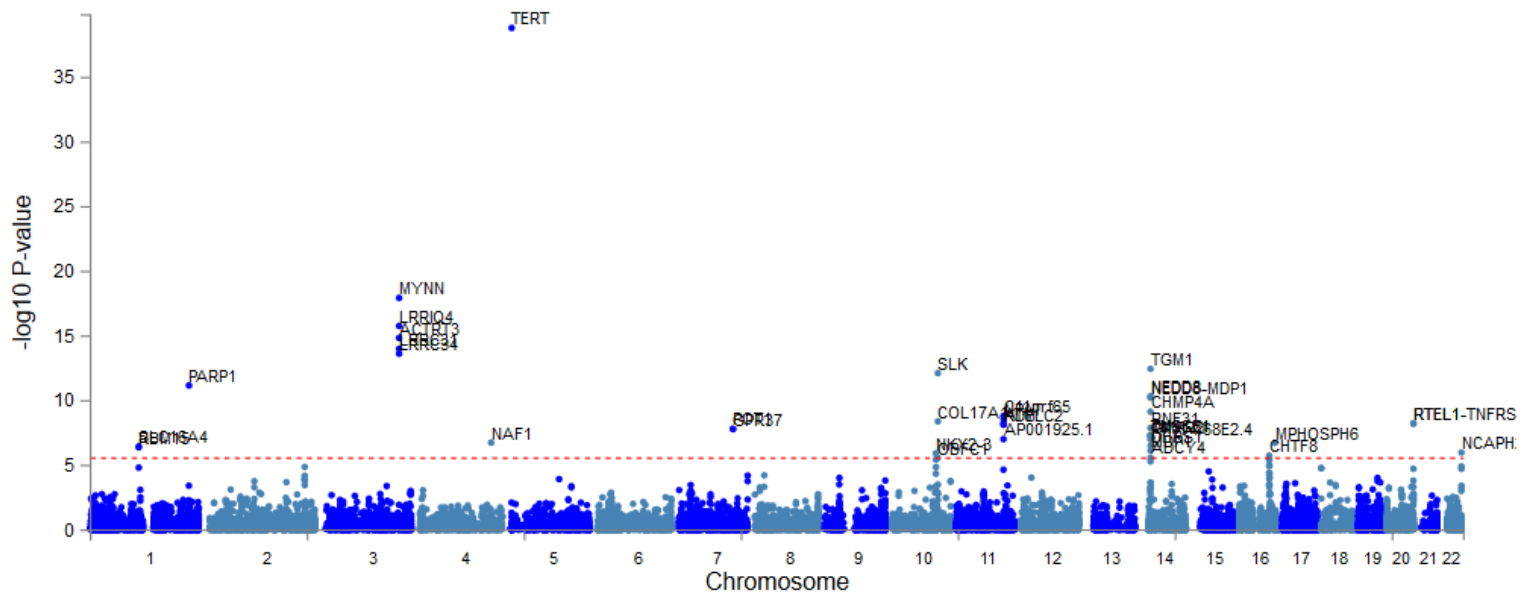
Gene (positional mapping)-based GWAS European Ancestry



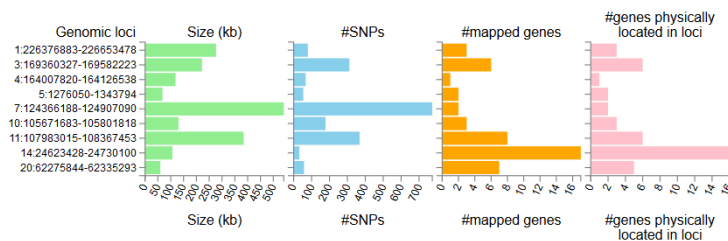
Summary per genomic risk locus ?



Gene (positional mapping)-based GWAS East Asian Ancestry



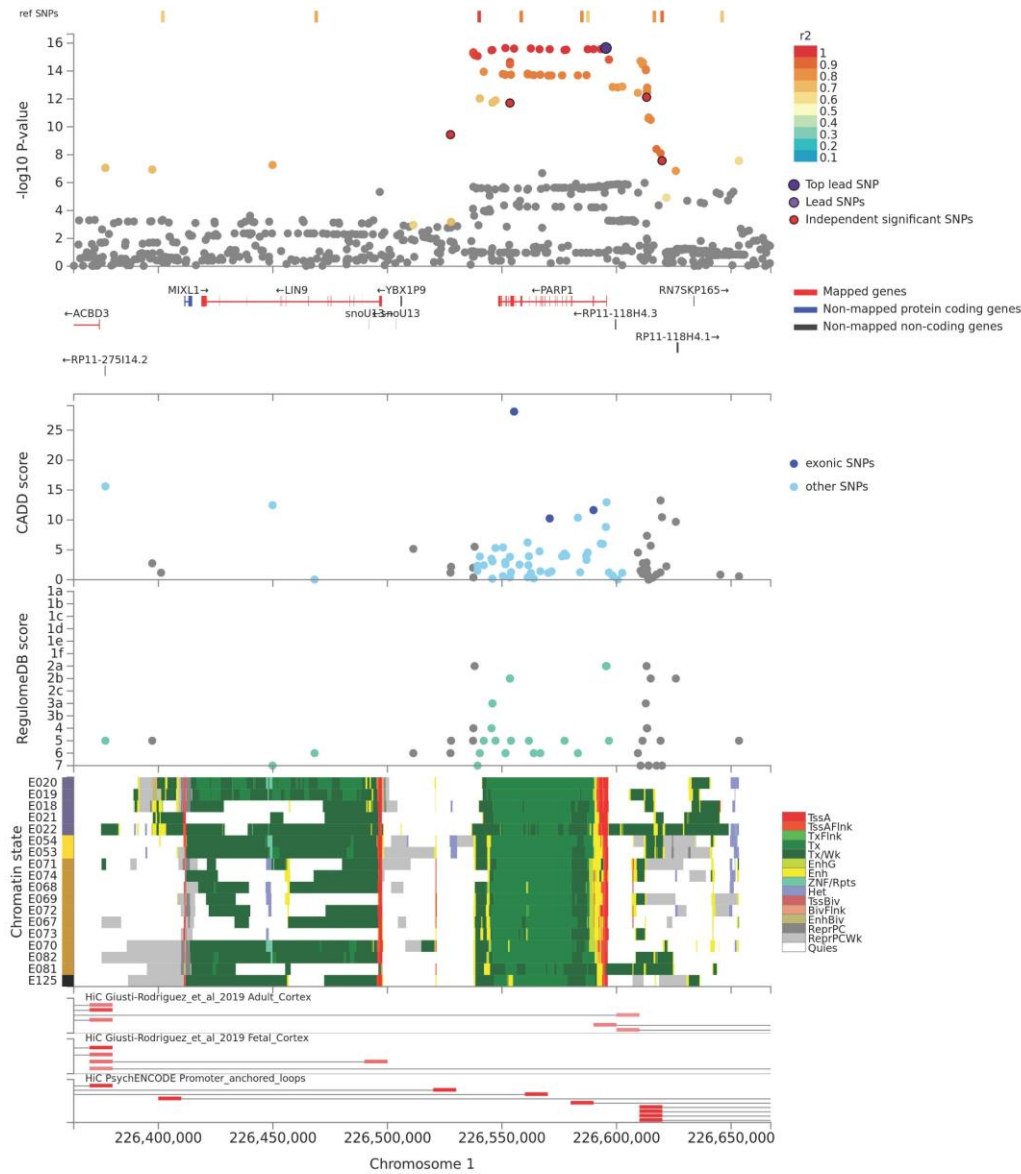
Summary per genomic risk locus ?



Regional Plots for each locus

Chromosome 1

EAS



Regulome DB

Category	Description
1a	Likely to affect binding and linked to expression of a gene target
1b	eQTL + TF binding + matched TF motif + matched DNase footprint + DNase peak
1c	eQTL + TF binding + any motif + DNase footprint + DNase peak
1d	eQTL + TF binding + matched TF motif + DNase peak
1e	eQTL + TF binding + any motif + DNase peak
1f	eQTL + TF binding + matched TF motif
2a	Likely to affect binding
2b	TF binding + matched TF motif + matched DNase footprint + DNase peak
2c	TF binding + any motif + DNase footprint + DNase peak
3a	TF binding + matched TF motif + DNase peak
3b	TF binding + any motif + DNase peak
3c	TF binding + matched TF motif
4	Less likely to affect binding
5	TF binding + DNase peak
6	TF binding or DNase peak
7	Minimal binding evidence
NA	TF binding + DNase peak
NA	TF binding or DNase peak
NA	Motif hit
NA	No binding evidence
NA	No evidence
NA	the variant does not exist in RegulomeDB

15-core chromatin state

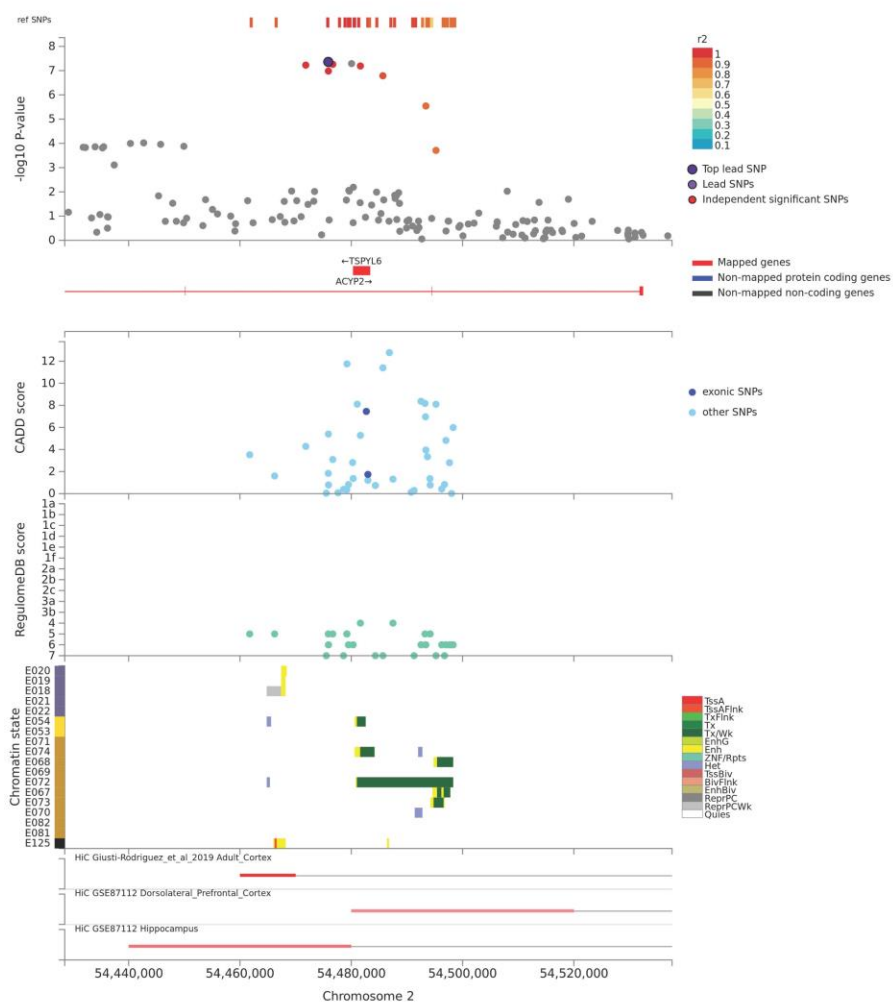
Epigenome ID		Group	Anatomy	Standardized epigenome name
EID	Color			
E020	#9608A	iPSC	iPSC	iPS-20b Cells
E019	#9608A	iPSC	iPSC	iPS-18 Cells
E018	#9608A	iPSC	iPSC	iPS-15b Cells
E021	#9608A	iPSC	iPSC	iPS DF 6.9 Cells
E022	#9608A	iPSC	iPSC	iPS DF 19.11 Cells
E054	#FFD924	Neurosp	BRAIN	Ganglion Eminence derived primary cultured neurospheres
E053	#FFD924	Neurosp	BRAIN	Cortex derived primary cultured neurospheres
E071	#C5912B	Brain	BRAIN	Brain Hippocampus Middle
E074	#C5912B	Brain	BRAIN	Brain Substantia Nigra
E068	#C5912B	Brain	BRAIN	Brain Anterior Caudate
E069	#C5912B	Brain	BRAIN	Brain Inferior Temporal Lobe
E072	#C5912B	Brain	BRAIN	Brain Cingulate Gyrus
E067	#C5912B	Brain	BRAIN	Brain Angular Gyrus
E073	#C5912B	Brain	BRAIN	Brain_Dorsolateral_Prefrontal_Cortex
E070	#C5912B	Brain	BRAIN	Brain Germinal Matrix
E082	#C5912B	Brain	BRAIN	Fetal Brain Female
E081	#C5912B	Brain	BRAIN	Fetal Brain Male
E125	#000000	ENCODE2012	BRAIN	NH-A Astrocytes Primary Cells

*External link to RegulomeDB from SNP table (when one of the SNPs is clicked) will open a new tab. rsID does not always match since RegulomeDB used dbSNP build 141 (the rsID in FUMA is dbSNP build 146). Genomic position (bp on hg19) shown in the link of RegulomeDB is the position shown in the SNP table - 1, since RegulomeDB used 0 based coordinate.

*When 15-core chromatin state is included in the plot and >30 cell types are selected, the labels of Y-axis are omitted. The order of the cell types is same as the legend table.

Chromosome 2

EUR



Regulome DB

RegulomeDB Categorical Scores

Category	Description
1a	Likely to affect binding and linked to expression of a gene target
1b	eQTL + TF binding + matched TF motif + matched DNase footprint + DNase peak
1c	eQTL + TF binding + any motif + DNase footprint + DNase peak
1d	eQTL + TF binding + matched TF motif + DNase peak
1e	eQTL + TF binding + any motif + DNase peak
1f	eQTL + TF binding + matched TF motif
2a	eQTL + TF binding/DNase peak
2b	Likely to affect binding
2c	TF binding + matched TF motif + matched DNase footprint + DNase peak
3a	TF binding + any motif + DNase footprint + DNase peak
3b	TF binding + matched TF motif + DNase peak
4	Less likely to affect binding
5	TF binding + any motif + DNase peak
6	TF binding + matched TF motif
7	Minimal binding evidence
NA	TF binding + DNase peak
	TF binding or DNase peak
	Motif hit
	No binding evidence
	No evidence
	the variant does not exist in RegulomeDB

15-core chromatin state

Epigenome ID

EID	Color	Group	Anatomy	Standardized epigenome name
E020	#89608A	iPSC	iPSC	iPS-20b Cells
E019	#89608A	iPSC	iPSC	iPS-18 Cells
E018	#89608A	iPSC	iPSC	iPS-15b Cells
E021	#89608A	iPSC	iPSC	iPS DF 6.9 Cells
E022	#89608A	iPSC	iPSC	iPS DF 19.11 Cells
E054	#FFD924	Neurosph	BRAIN	Ganglion Eminence derived primary cultured neurospheres
E053	#FFD924	Neurosph	BRAIN	Cortex derived primary cultured neurospheres
E071	#C5912B	Brain	BRAIN	Brain Hippocampus Middle
E074	#C5912B	Brain	BRAIN	Brain Substantia Nigra
E068	#C5912B	Brain	BRAIN	Brain Anterior Caudate
E069	#C5912B	Brain	BRAIN	Brain Cingulate Gyrus
E072	#C5912B	Brain	BRAIN	Brain Inferior Temporal Lobe
E067	#C5912B	Brain	BRAIN	Brain Angular Gyrus
E073	#C5912B	Brain	BRAIN	Brain_Dorsolateral_Prefrontal_Cortex
E070	#C5912B	Brain	BRAIN	Brain Germinal Matrix
E082	#C5912B	Brain	BRAIN	Fetal Brain Female
E081	#C5912B	Brain	BRAIN	Fetal Brain Male
E125	#000000	ENCODE2012	BRAIN	NH-A Astrocytes Primary Cells

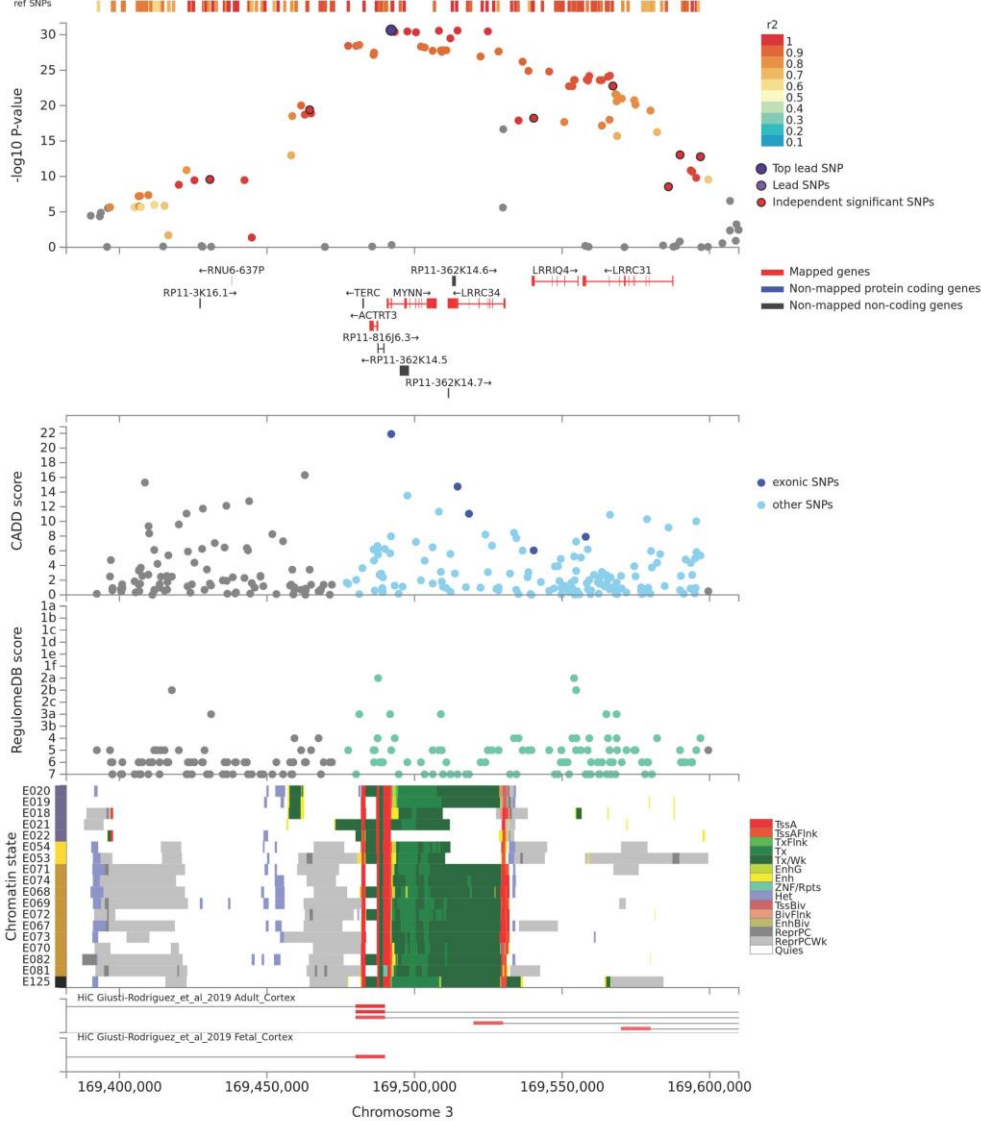
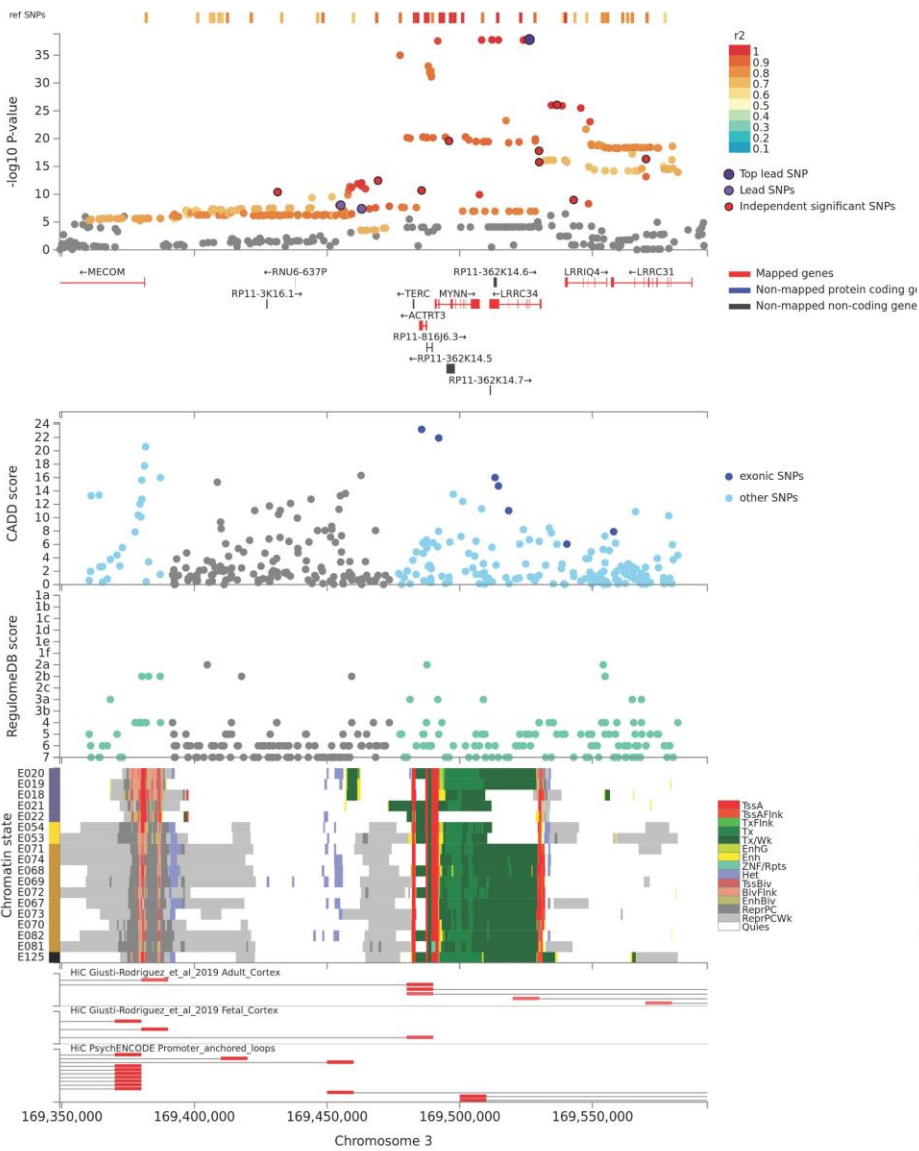
*External link to RegulomeDB from SNP table (when one of the SNPs is clicked) will open a new tab. rsID does not always match since RegulomeDB used dbSNP build 141 (the rsID in FUMA is dbSNP build 146). Genomic position (bp on hg19) shown in the link of RegulomeDB is the position shown in the SNP table - 1, since RegulomeDB used 0 based coordinate.

*When 15-core chromatin state is included in the plot and >30 cell types are selected, the labels of Y-axis are omitted. The order of the cell types is same as the legend table.

Chromosome 3

EAS

EUR



Regulome DB

RegulomeDB Categorical Scores

Category	Description
1a	Likely to affect binding and linked to expression of a gene target
1b	eQTL + TF binding + matched TF motif + matched DNase footprint + DNase peak
1c	eQTL + TF binding + any motif + DNase footprint + DNase peak
1d	eQTL + TF binding + matched TF motif + DNase peak
1e	eQTL + TF binding + any motif + DNase peak
1f	eQTL + TF binding + matched TF motif
2a	Likely to affect binding
2b	TF binding + matched TF motif + matched DNase footprint + DNase peak
2c	TF binding + any motif + DNase footprint + DNase peak
3a	TF binding + matched TF motif + DNase peak
3b	Less likely to affect binding
4	TF binding + any motif + DNase peak
5	TF binding + matched TF motif
6	Minimal binding evidence
7	TF binding + DNase peak
NA	TF binding or DNase peak
	Motif hit
	No binding evidence
	No evidence
	the variant does not exist in RegulomeDB

15-core chromatin state

Epigenome ID

EID	Color	Group	Anatomy	Standardized epigenome name
E020	#89608A	iPSC	iPSC	iPS-20b Cells
E019	#89608A	iPSC	iPSC	iPS-18 Cells
E018	#89608A	iPSC	iPSC	iPS-15b Cells
E021	#89608A	iPSC	iPSC	iPS DF 6.9 Cells
E022	#89608A	iPSC	iPSC	iPS DF 19.11 Cells
E054	#FFD924	Neurosp	BRAIN	Ganglion Eminence derived primary cultured neurospheres
E053	#FFD924	Neurosp	BRAIN	Cortex derived primary cultured neurospheres
E071	#C5912B	Brain	BRAIN	Brain Hippocampus Middle
E074	#C5912B	Brain	BRAIN	Brain Substantia Nigra
E068	#C5912B	Brain	BRAIN	Brain Anterior Caudate
E069	#C5912B	Brain	BRAIN	Brain Cingulate Gyrus
E072	#C5912B	Brain	BRAIN	Brain Inferior Temporal Lobe
E067	#C5912B	Brain	BRAIN	Brain Angular Gyrus
E073	#C5912B	Brain	BRAIN	Brain_Dorsolateral_Prefrontal_Cortex
E070	#C5912B	Brain	BRAIN	Brain Germinal Matrix
E082	#C5912B	Brain	BRAIN	Fetal Brain Female
E081	#C5912B	Brain	BRAIN	Fetal Brain Male
E125	#000000	ENCODE2012	BRAIN	NH-A Astrocytes Primary Cells

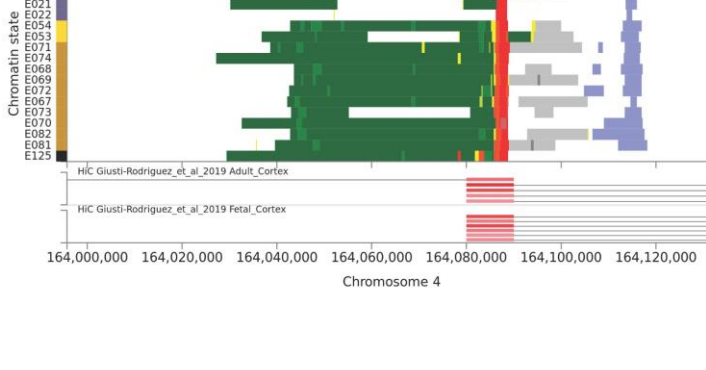
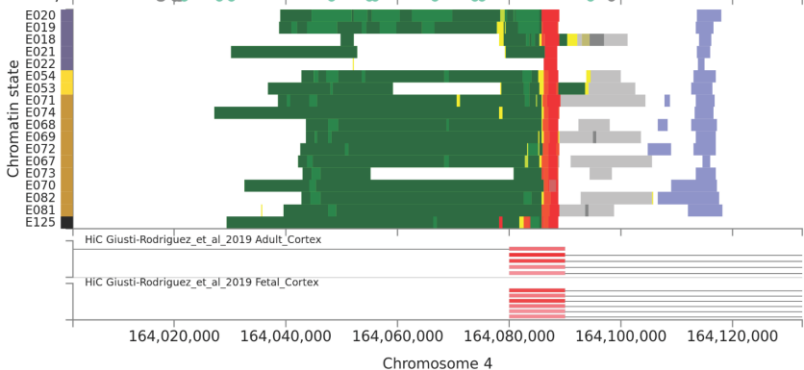
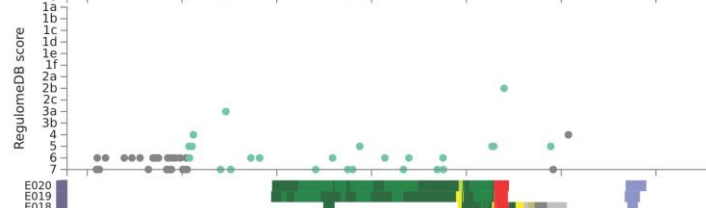
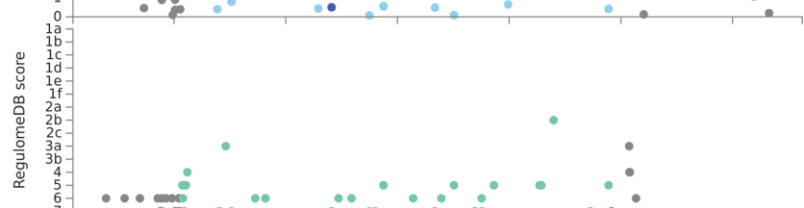
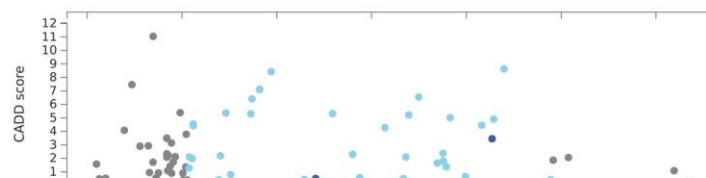
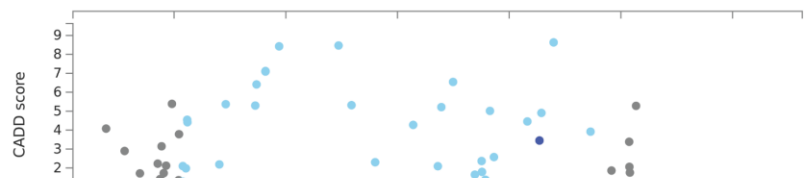
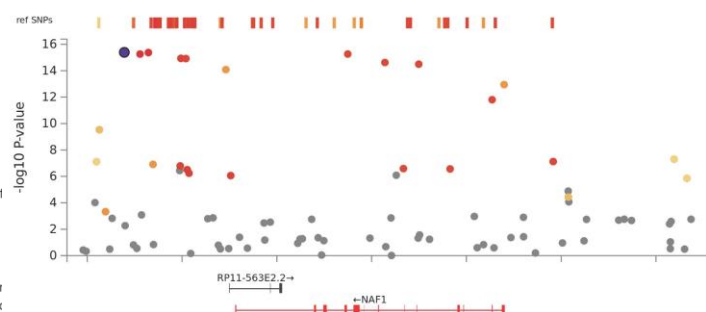
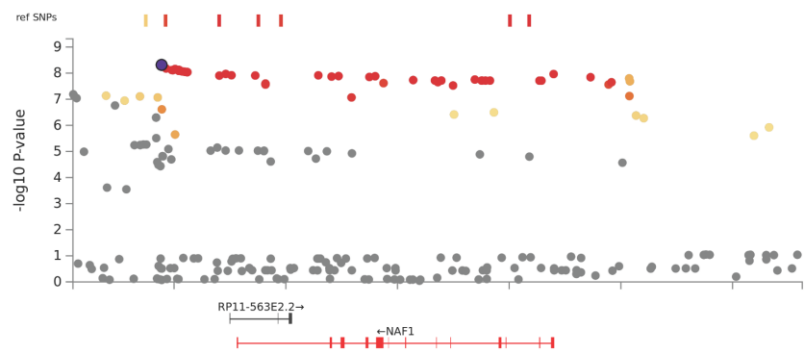
*External link to RegulomeDB from SNP table (when one of the SNPs is clicked) will open a new tab. rsID does not always match since RegulomeDB used dbSNP build 141 (the rsID in FUMA is dbSNP build 146). Genomic position (bp on hg19) shown in the link of RegulomeDB is the position shown in the SNP table - 1, since RegulomeDB used 0 based coordinate.

*When 15-core chromatin state is included in the plot and >30 cell types are selected, the labels of Y-axis are omitted. The order of the cell types is same as the legend table.

Chromosome 4

EAS

EUR



Regulome DB

RegulomeDB Categorical Scores	
Category	Description
1a	Likely to affect binding and linked to expression of a gene target
1b	eQTL + TF binding + matched TF motif + matched DNase footprint + DNase peak
1c	eQTL + TF binding + any motif + DNase footprint + DNase peak
1d	eQTL + TF binding + matched TF motif + DNase peak
1e	eQTL + TF binding + any motif + DNase peak
1f	eQTL + TF binding + matched TF motif
2a	Likely to affect binding
2b	TF binding + matched TF motif + matched DNase footprint + DNase peak
2c	TF binding + any motif + DNase footprint + DNase peak
3a	Less likely to affect binding
3b	TF binding + matched TF motif + DNase peak
4	Minimal binding evidence
5	TF binding + DNase peak
6	TF binding or DNase peak
7	Motif hit
NA	No binding evidence
	No evidence
	the variant does not exist in RegulomeDB

15-core chromatin state

Epigenome ID				
EID	Color	Group	Anatomy	Standardized epigenome name
E020	#89608A	iPSC	iPSC	iPS-20b Cells
E019	#89608A	iPSC	iPSC	iPS-18 Cells
E018	#89608A	iPSC	iPSC	iPS-15b Cells
E021	#89608A	iPSC	iPSC	iPS DF 6.9 Cells
E022	#89608A	iPSC	iPSC	iPS DF 19.11 Cells
E054	#FFD924	Neurosph	BRAIN	Ganglion Eminence derived primary cultured neurospheres
E053	#FFD924	Neurosph	BRAIN	Cortex derived primary cultured neurospheres
E071	#C5912B	Brain	BRAIN	Brain Hippocampus Middle
E074	#C5912B	Brain	BRAIN	Brain Substantia Nigra
E068	#C5912B	Brain	BRAIN	Brain Anterior Caudate
E069	#C5912B	Brain	BRAIN	Brain Cingulate Gyrus
E072	#C5912B	Brain	BRAIN	Brain Inferior Temporal Lobe
E067	#C5912B	Brain	BRAIN	Brain Angular Gyrus
E073	#C5912B	Brain	BRAIN	Brain_Dorsolateral_Prefrontal_Cortex
E070	#C5912B	Brain	BRAIN	Brain Germinal Matrix
E082	#C5912B	Brain	BRAIN	Fetal Brain Female
E081	#C5912B	Brain	BRAIN	Fetal Brain Male
E125	#000000	ENCODE2012	BRAIN	NH-A Astrocytes Primary Cells

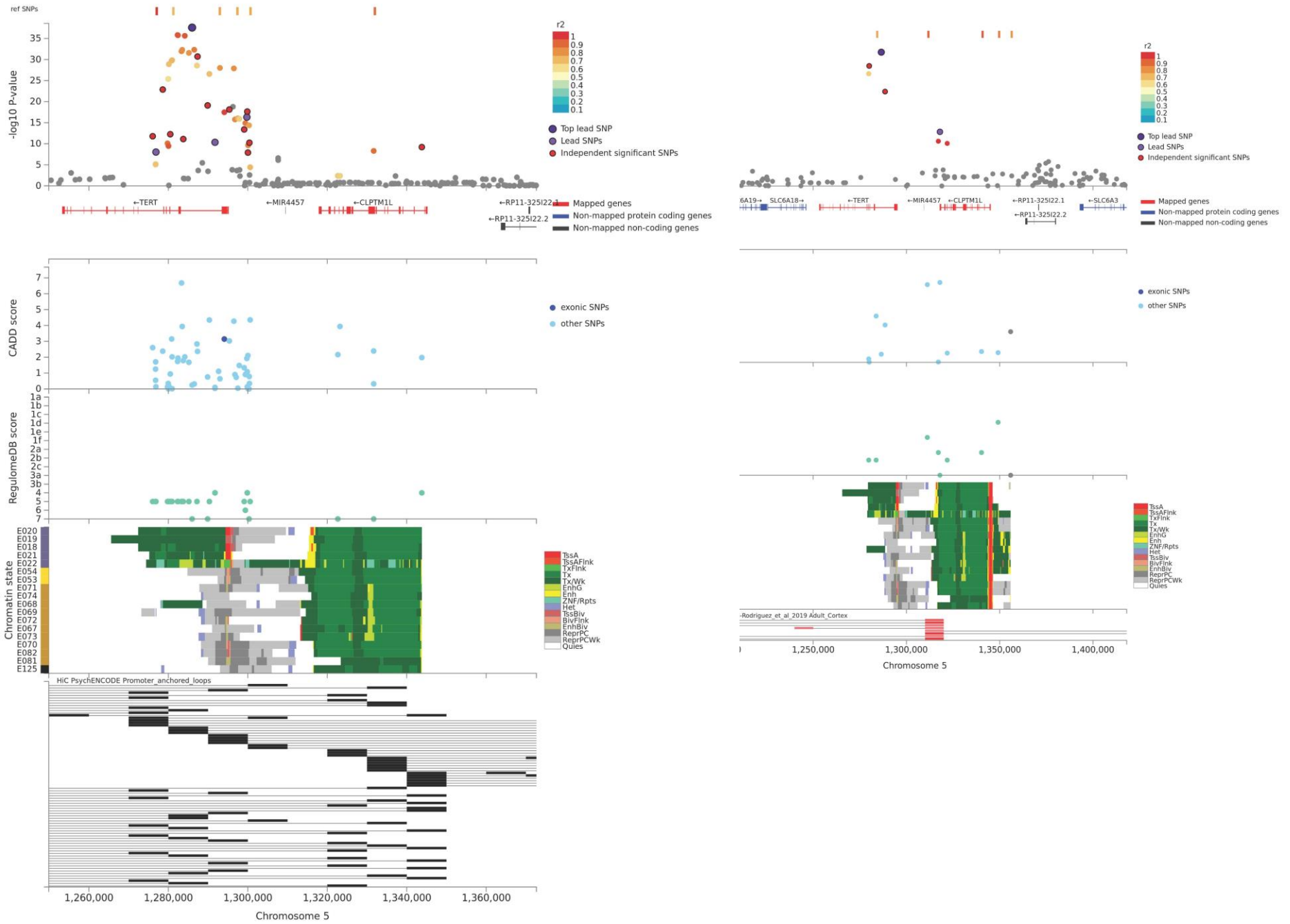
*External link to RegulomeDB from SNP table (when one of the SNPs is clicked) will open a new tab. rsID does not always match since RegulomeDB used dbSNP build 141 (the rsID in FUMA is dbSNP build 146). Genomic position (bp on hg19) shown in the link of RegulomeDB is the position shown in the SNP table - 1, since RegulomeDB used 0 based coordinate.

*When 15-core chromatin state is included in the plot and >30 cell types are selected, the labels of Y-axis are omitted. The order of the cell types is same as the legend table.

Chromosome 5

EAS

EUR



Regulome DB

Category	Description
1a	Likely to affect binding and linked to expression of a gene target
1b	eQTL + TF binding + matched TF motif + matched DNase footprint + DNase peak
1c	eQTL + TF binding + any motif + DNase footprint + DNase peak
1d	eQTL + TF binding + matched TF motif + DNase peak
1e	eQTL + TF binding + any motif + DNase peak
1f	eQTL + TF binding + matched TF motif
2a	Likely to affect binding
2b	TF binding + matched TF motif + matched DNase footprint + DNase peak
2c	TF binding + any motif + DNase footprint + DNase peak
3a	Less likely to affect binding
3b	TF binding + matched TF motif
4	Minimal binding evidence
5	TF binding + DNase peak
6	TF binding or DNase peak
7	Motif hit
NA	No binding evidence
	No evidence
	the variant does not exist in RegulomeDB

*External link to RegulomeDB from SNP table (when one of the SNPs is clicked) will open a new tab. rsID does not always match since RegulomeDB used dbSNP build 141 (the rsID in FUMA is dbSNP build 146). Genomic position (bp on hg19) shown in the link of RegulomeDB is the position shown in the SNP table - 1, since RegulomeDB used 0 based coordinate.

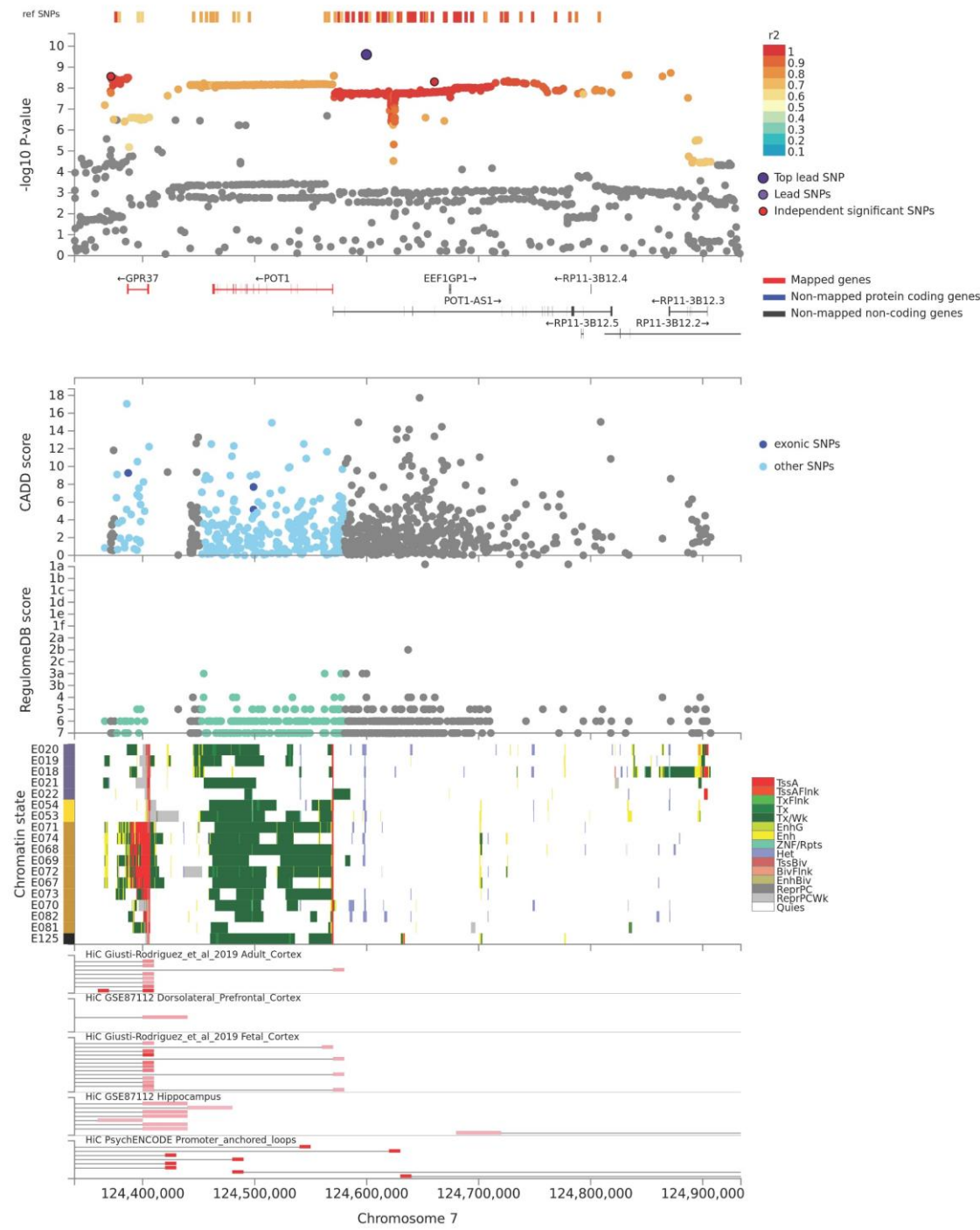
15-core chromatin state

Epigenome ID				
EID	Color	Group	Anatomy	Standardized epigenome name
E020	#69608A	iPSC	IPSC	iPS-20b Cells
E019	#69608A	iPSC	IPSC	iPS-18 Cells
E018	#69608A	iPSC	IPSC	iPS-15b Cells
E021	#69608A	iPSC	IPSC	iPS DF 6.9 Cells
E022	#69608A	iPSC	IPSC	iPS DF 19.11 Cells
E054	#FFD924	Neurosph	BRAIN	Ganglion Eminence derived primary cultured neurospheres
E053	#FFD924	Neurosph	BRAIN	Cortex derived primary cultured neurospheres
E071	#C5912B	Brain	BRAIN	Brain Hippocampus Middle
E074	#C5912B	Brain	BRAIN	Brain Substantia Nigra
E068	#C5912B	Brain	BRAIN	Brain Anterior Caudate
E069	#C5912B	Brain	BRAIN	Brain Cingulate Gyrus
E072	#C5912B	Brain	BRAIN	Brain Inferior Temporal Lobe
E067	#C5912B	Brain	BRAIN	Brain Angular Gyrus
E073	#C5912B	Brain	BRAIN	Brain_Dorsolateral_Prefrontal_Cortex
E070	#C5912B	Brain	BRAIN	Brain Germinal Matrix
E082	#C5912B	Brain	BRAIN	Fetal Brain Female
E081	#C5912B	Brain	BRAIN	Fetal Brain Male
E125	#000000	ENCODE2012	BRAIN	NH-A Astrocytes Primary Cells

*When 15-core chromatin state is included in the plot and >30 cell types are selected, the labels of Y-axis are omitted. The order of the cell types is same as the legend table.

Chromosome 7

EAS



Regulome DB

RegulomeDB Categorical Scores

Category	Description
1a	Likely to affect binding and linked to expression of a gene target eQTL + TF binding + matched TF motif + matched DNase footprint + DNase peak
1b	eQTL + TF binding + any motif + DNase footprint + DNase peak
1c	eQTL + TF binding + matched TF motif + DNase peak
1d	eQTL + TF binding + any motif + DNase peak
1e	eQTL + TF binding + matched TF motif
1f	eQTL + TF binding/DNase peak
2a	Likely to affect binding TF binding + matched TF motif + matched DNase footprint + DNase peak
2b	TF binding + any motif + DNase footprint + DNase peak
2c	TF binding + matched TF motif + DNase peak
3a	Less likely to affect binding TF binding + any motif + DNase peak
3b	TF binding + matched TF motif
4	Minimal binding evidence TF binding + DNase peak
5	TF binding or DNase peak
6	Motif hit
7	No binding evidence
NA	No evidence the variant does not exist in RegulomeDB

15-core chromatin state

Epigenome ID				
EID	Color	Group	Anatomy	Standardized epigenome name
E020	#69608A	iPSC	IPSC	iPS-20b Cells
E019	#69608A	iPSC	IPSC	iPS-18 Cells
E018	#69608A	iPSC	IPSC	iPS-15b Cells
E021	#69608A	iPSC	IPSC	iPS DF 6.9 Cells
E022	#69608A	iPSC	IPSC	iPS DF 19.11 Cells
E054	#FFD924	Neurosph	BRAIN	Ganglion Eminence derived primary cultured neurospheres
E053	#FFD924	Neurosph	BRAIN	Cortex derived primary cultured neurospheres
E071	#C5912B	Brain	BRAIN	Brain Hippocampus Middle
E074	#C5912B	Brain	BRAIN	Brain Substantia Nigra
E068	#C5912B	Brain	BRAIN	Brain Anterior Caudate
E069	#C5912B	Brain	BRAIN	Brain Cingulate Gyrus
E072	#C5912B	Brain	BRAIN	Brain Inferior Temporal Lobe
E067	#C5912B	Brain	BRAIN	Brain Angular Gyrus
E073	#C5912B	Brain	BRAIN	Brain_Dorsolateral_Prefrontal_Cortex
E070	#C5912B	Brain	BRAIN	Brain Germinal Matrix
E082	#C5912B	Brain	BRAIN	Fetal Brain Female
E081	#C5912B	Brain	BRAIN	Fetal Brain Male
E125	#000000	ENCODE2012	BRAIN	NH-A Astrocytes Primary Cells

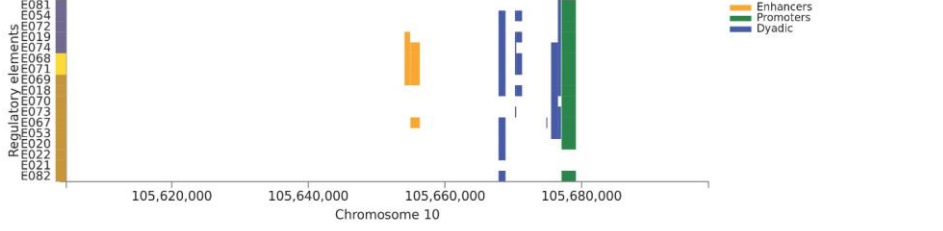
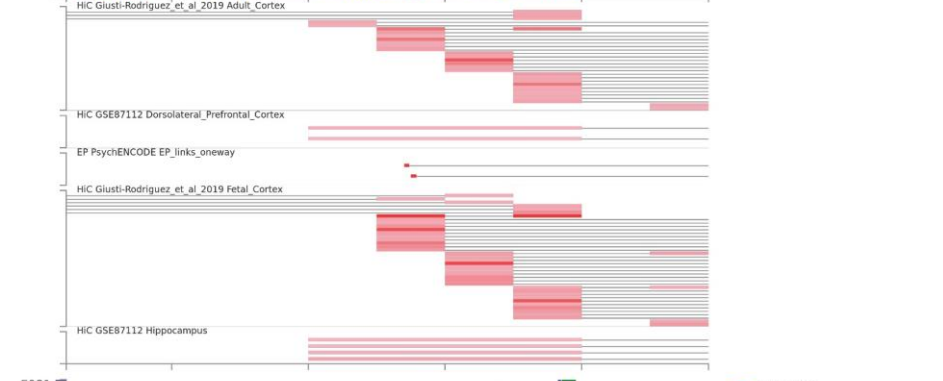
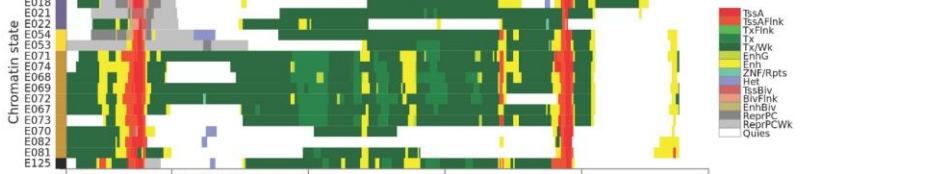
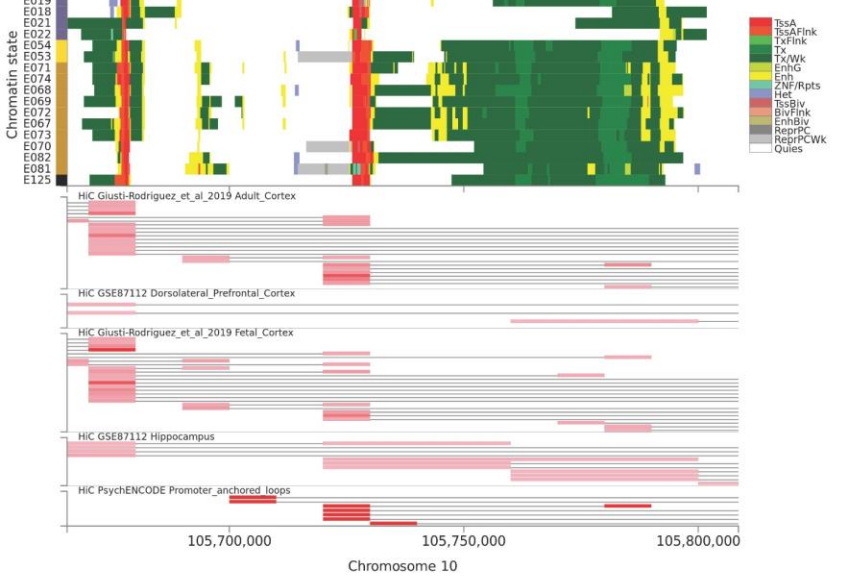
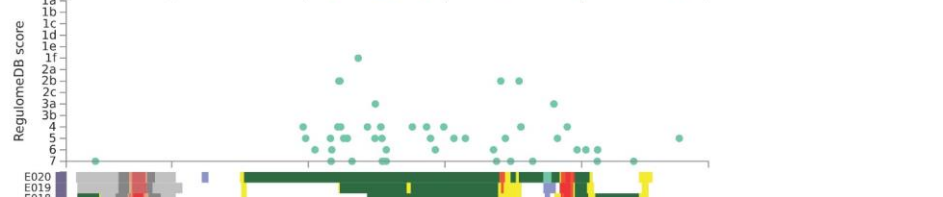
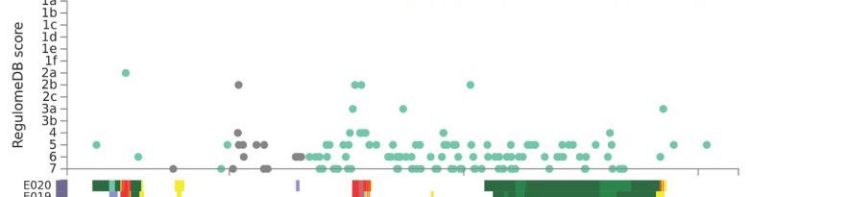
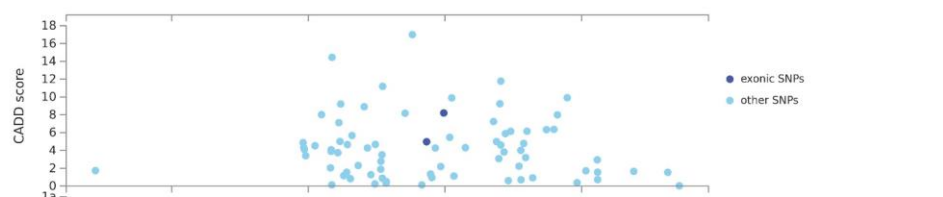
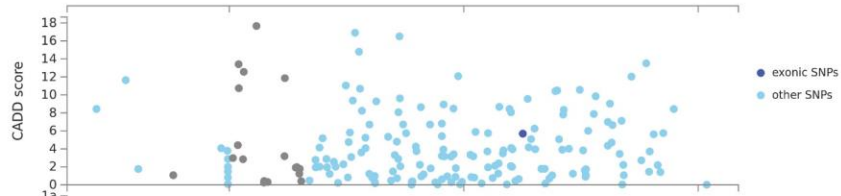
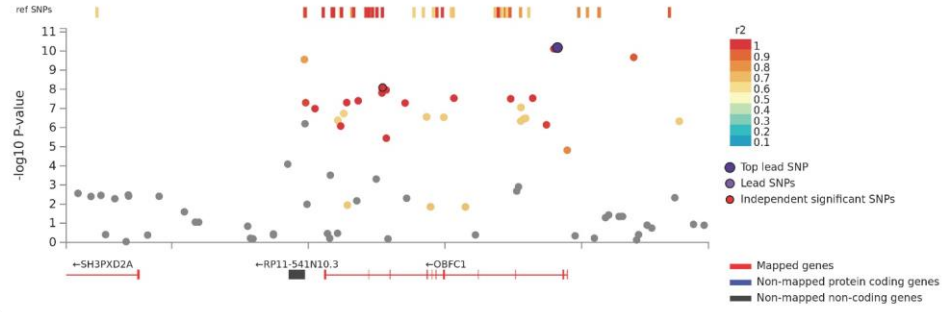
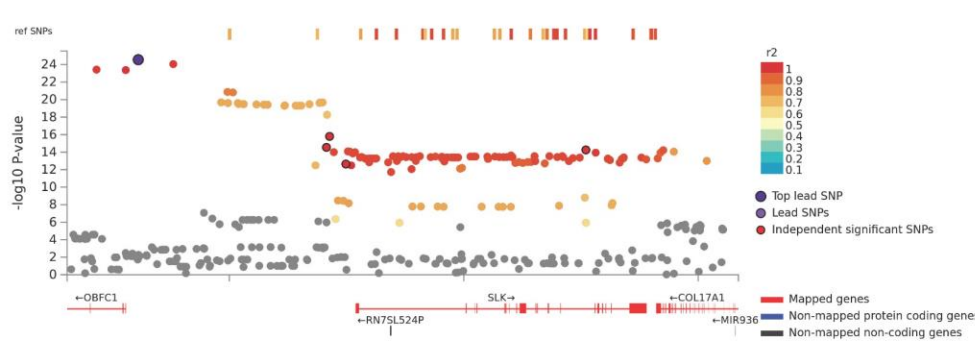
*External link to RegulomeDB from SNP table (when one of the SNPs is clicked) will open a new tab. rsID does not always match since RegulomeDB used dbSNP build 141 (the rsID in FUMA is dbSNP build 146). Genomic position (bp on hg19) shown in the link of RegulomeDB is the position shown in the SNP table - 1, since RegulomeDB used 0 based coordinate.

*When 15-core chromatin state is included in the plot and >30 cell types are selected, the labels of Y-axis are omitted. The order of the cell types is same as the legend table.

Chromosome 10

EAS

EUR



Regulome DB

Category	Description
1a	Likely to affect binding and linked to expression of a gene target
1b	eQTL + TF binding + matched TF motif + matched DNase footprint + DNase peak
1c	eQTL + TF binding + any motif + DNase footprint + DNase peak
1d	eQTL + TF binding + matched TF motif + DNase peak
1e	eQTL + TF binding + any motif + DNase peak
1f	eQTL + TF binding + matched TF motif
2a	Likely to affect binding
2b	TF binding + matched TF motif + matched DNase footprint + DNase peak
2c	TF binding + any motif + DNase footprint + DNase peak
3a	Less likely to affect binding
3b	TF binding + any motif + DNase peak
3c	TF binding + matched TF motif
4	Minimal binding evidence
5	TF binding + DNase peak
6	TF binding or DNase peak
7	Motif hit
NA	No binding evidence
NA	No evidence
NA	the variant does not exist in RegulomeDB

*External link to RegulomeDB from SNP table (when one of the SNPs is clicked) will open a new tab. rsID does not always match since RegulomeDB used dbSNP build 141 (the rsID in FUMA is dbSNP build 146). Genomic position (bp on hg19) shown in the link of RegulomeDB is the position shown in the SNP table - 1, since RegulomeDB used 0 based coordinate.

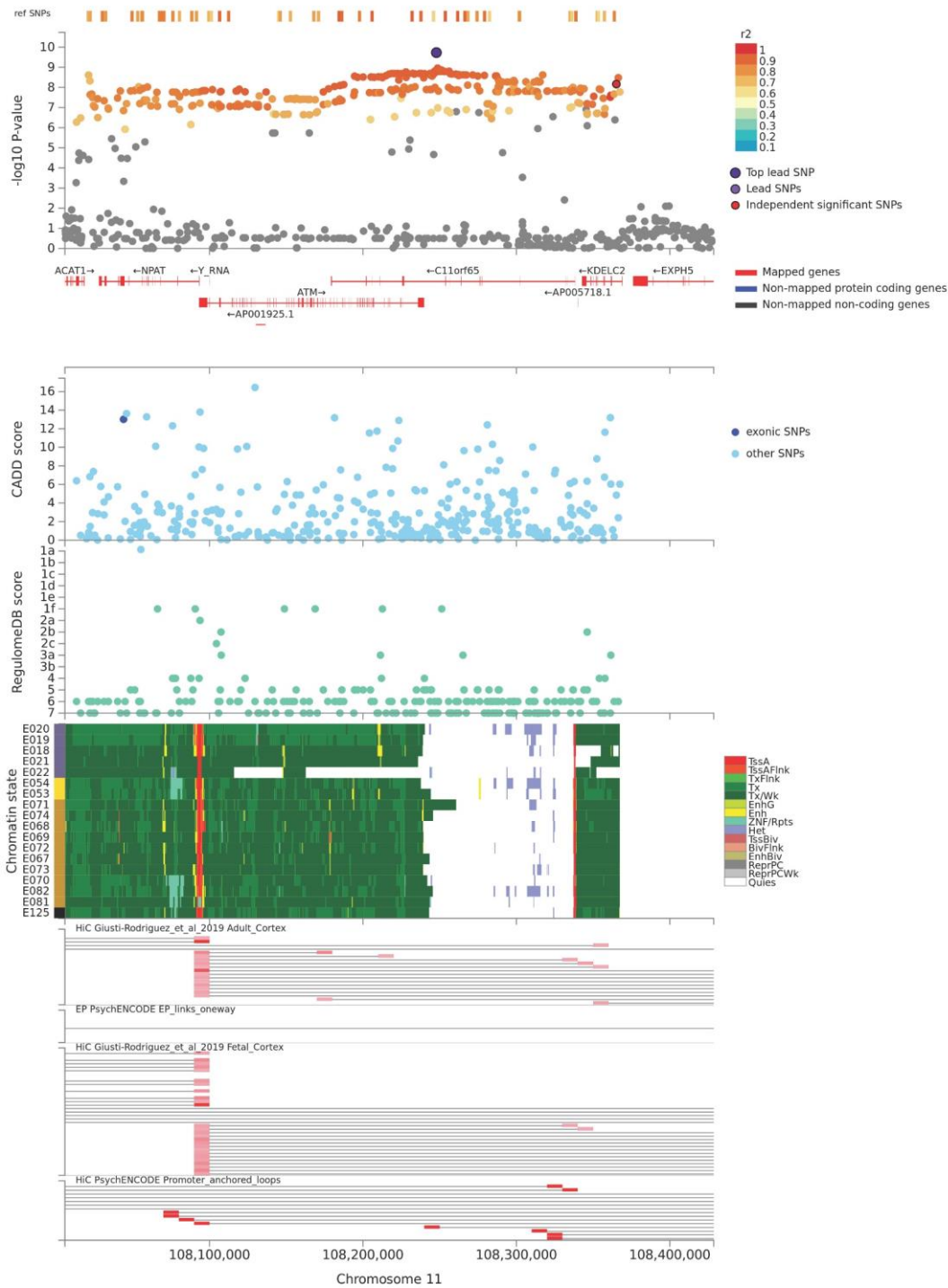
15-core chromatin state

EID	Color	Group	Anatomy	Standardized epigenome name
E020	#89608A	iPSC	IPSC	iPS-20b Cells
E019	#89608A	iPSC	IPSC	iPS-18 Cells
E018	#89608A	iPSC	IPSC	iPS-15b Cells
E021	#89608A	iPSC	IPSC	iPS DF 6.9 Cells
E022	#89608A	iPSC	IPSC	iPS DF 19.11 Cells
E054	#FFD924	Neurosph	BRAIN	Ganglion Eminence derived primary cultured neurospheres
E053	#FFD924	Neurosph	BRAIN	Cortex derived primary cultured neurospheres
E071	#C5912B	Brain	BRAIN	Brain Hippocampus Middle
E074	#C5912B	Brain	BRAIN	Brain Substantia Nigra
E068	#C5912B	Brain	BRAIN	Brain Anterior Caudate
E069	#C5912B	Brain	BRAIN	Brain Cingulate Gyrus
E072	#C5912B	Brain	BRAIN	Brain Inferior Temporal Lobe
E067	#C5912B	Brain	BRAIN	Brain Angular Gyrus
E073	#C5912B	Brain	BRAIN	Brain_Dorsolateral_Prefrontal_Cortex
E070	#C5912B	Brain	BRAIN	Brain Germinal Matrix
E082	#C5912B	Brain	BRAIN	Fetal Brain Female
E081	#C5912B	Brain	BRAIN	Fetal Brain Male
E125	#000000	ENCODE2012	BRAIN	NH-A Astrocytes Primary Cells

*When 15-core chromatin state is included in the plot and >30 cell types are selected, the labels of Y-axis are omitted. The order of the cell types is same as the legend table.

Chromosome 11

EAS



Regulome DB

Category	Description
1a	Likely to affect binding and linked to expression of a gene target eQTL + TF binding + matched TF motif + matched DNase footprint + DNase peak
1b	eQTL + TF binding + any motif + DNase footprint + DNase peak
1c	eQTL + TF binding + matched TF motif + DNase peak
1d	eQTL + TF binding + any motif + DNase peak
1e	eQTL + TF binding + matched TF motif
1f	eQTL + TF binding/DNase peak
2a	Likely to affect binding TF binding + matched TF motif + matched DNase footprint + DNase peak
2b	TF binding + any motif + DNase footprint + DNase peak
2c	TF binding + matched TF motif + DNase peak
3a	Less likely to affect binding TF binding + any motif + DNase peak
3b	TF binding + matched TF motif
4	Minimal binding evidence TF binding + DNase peak
5	TF binding or DNase peak
6	Motif hit
7	No binding evidence
NA	No evidence the variant does not exist in RegulomeDB

15-core chromatin state

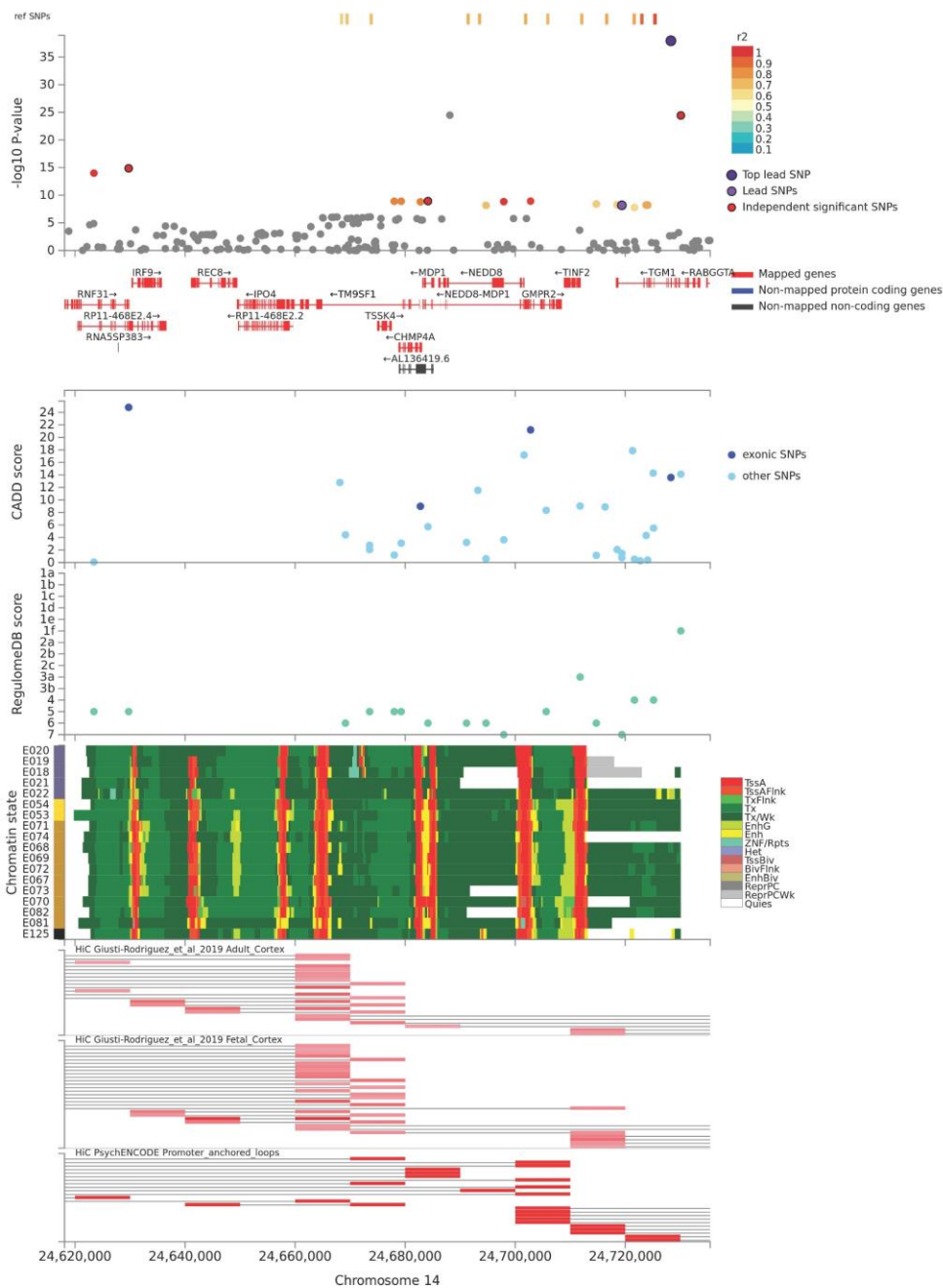
Epigenome ID				
EID	Color	Group	Anatomy	Standardized epigenome name
E020	#69608A	iPSC	IPSC	iPS-20b Cells
E019	#69608A	iPSC	IPSC	iPS-18 Cells
E018	#69608A	iPSC	IPSC	iPS-15b Cells
E021	#69608A	iPSC	IPSC	iPS DF 6.9 Cells
E022	#69608A	iPSC	IPSC	iPS DF 19.11 Cells
E054	#FFD924	Neurosph	BRAIN	Ganglion Eminence derived primary cultured neurospheres
E053	#FFD924	Neurosph	BRAIN	Cortex derived primary cultured neurospheres
E071	#C5912B	Brain	BRAIN	Brain Hippocampus Middle
E074	#C5912B	Brain	BRAIN	Brain Substantia Nigra
E068	#C5912B	Brain	BRAIN	Brain Anterior Caudate
E069	#C5912B	Brain	BRAIN	Brain Cingulate Gyrus
E072	#C5912B	Brain	BRAIN	Brain Inferior Temporal Lobe
E067	#C5912B	Brain	BRAIN	Brain Angular Gyrus
E073	#C5912B	Brain	BRAIN	Brain_Dorsolateral_Prefrontal_Cortex
E070	#C5912B	Brain	BRAIN	Brain Germinal Matrix
E082	#C5912B	Brain	BRAIN	Fetal Brain Female
E081	#C5912B	Brain	BRAIN	Fetal Brain Male
E125	#000000	ENCODE2012	BRAIN	NH-A Astrocytes Primary Cells

*External link to RegulomeDB from SNP table (when one of the SNPs is clicked) will open a new tab. rsID does not always match since RegulomeDB used dbSNP build 141 (the rsID in FUMA is dbSNP build 146). Genomic position (bp on hg19) shown in the link of RegulomeDB is the position shown in the SNP table - 1, since RegulomeDB used 0 based coordinate.

*When 15-core chromatin state is included in the plot and >30 cell types are selected, the labels of Y-axis are omitted. The order of the cell types is same as the legend table.

Chromosome 14

EAS



Regulome DB

Category	Description
1a	Likely to affect binding and linked to expression of a gene target
1b	eQTL + TF binding + matched TF motif + matched DNase footprint + DNase peak
1c	eQTL + TF binding + any motif + DNase footprint + DNase peak
1d	eQTL + TF binding + matched TF motif + DNase peak
1e	eQTL + TF binding + any motif + DNase peak
1f	eQTL + TF binding + matched TF motif
2a	Likely to affect binding
2b	TF binding + matched TF motif + matched DNase footprint + DNase peak
2c	TF binding + any motif + DNase footprint + DNase peak
3a	TF binding + matched TF motif + DNase peak
3b	TF binding + any motif + DNase peak
3c	TF binding + matched TF motif
4	Less likely to affect binding
5	TF binding + DNase peak
6	TF binding or DNase peak
7	Motif hit
NA	No binding evidence
	No evidence
	the variant does not exist in RegulomeDB

*External link to RegulomeDB from SNP table (when one of the SNPs is clicked) will open a new tab. rsID does not always match since RegulomeDB used dbSNP build 141 (the rsID in FUMA is dbSNP build 146). Genomic position (bp on hg19) shown in the link of RegulomeDB is the position shown in the SNP table - 1, since RegulomeDB used 0 based coordinate.

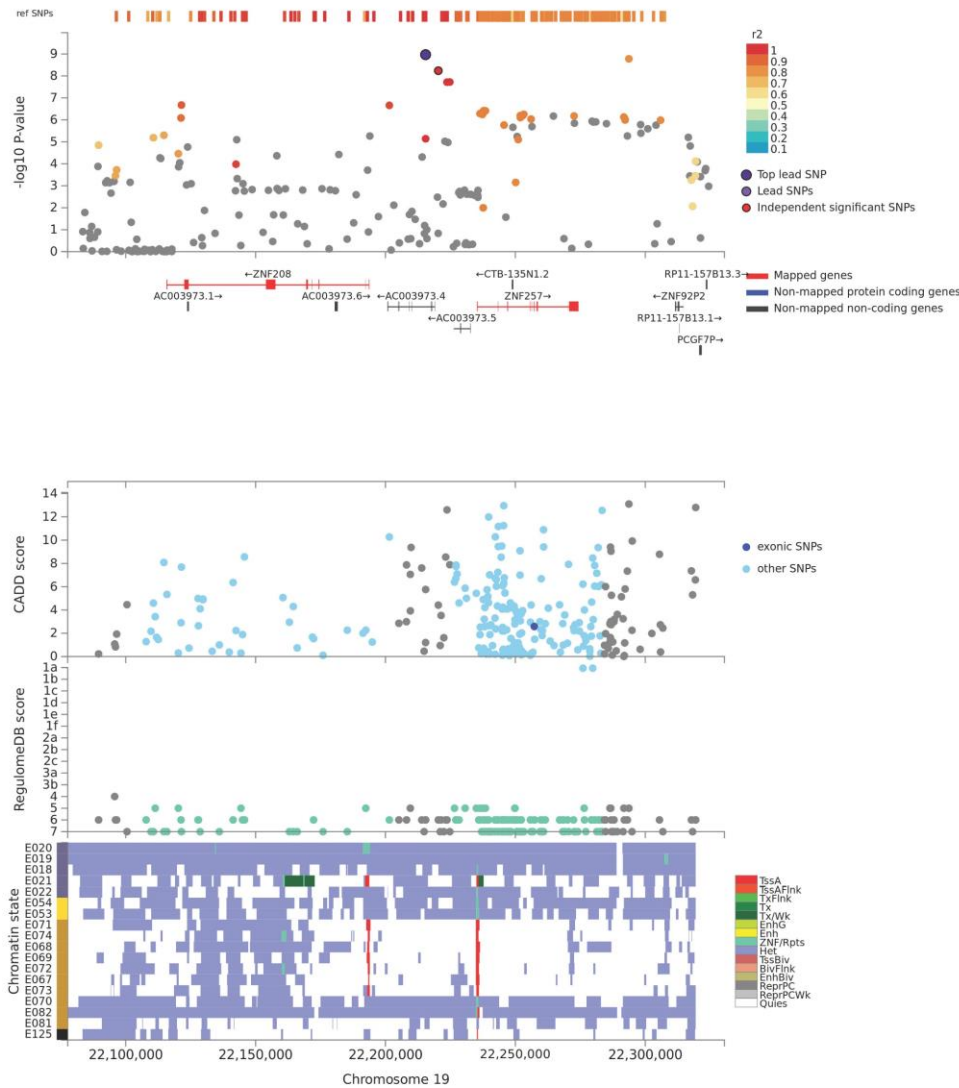
15-core chromatin state

Epigenome ID				
EID	Color	Group	Anatomy	Standardized epigenome name
E020	#69608A	iPSC	IPSC	iPS-20b Cells
E019	#69608A	iPSC	IPSC	iPS-18 Cells
E018	#69608A	iPSC	IPSC	iPS-15b Cells
E021	#69608A	iPSC	IPSC	iPS DF 6.9 Cells
E022	#69608A	iPSC	IPSC	iPS DF 19.11 Cells
E054	#FFD924	Neurosph	BRAIN	Ganglion Eminence derived primary cultured neurospheres
E053	#FFD924	Neurosph	BRAIN	Cortex derived primary cultured neurospheres
E071	#C5912B	Brain	BRAIN	Brain Hippocampus Middle
E074	#C5912B	Brain	BRAIN	Brain Substantia Nigra
E068	#C5912B	Brain	BRAIN	Brain Anterior Caudate
E069	#C5912B	Brain	BRAIN	Brain Cingulate Gyrus
E072	#C5912B	Brain	BRAIN	Brain Inferior Temporal Lobe
E067	#C5912B	Brain	BRAIN	Brain Angular Gyrus
E073	#C5912B	Brain	BRAIN	Brain_Dorsolateral_Prefrontal_Cortex
E070	#C5912B	Brain	BRAIN	Brain Germinal Matrix
E082	#C5912B	Brain	BRAIN	Fetal Brain Female
E081	#C5912B	Brain	BRAIN	Fetal Brain Male
E125	#000000	ENCODE2012	BRAIN	NH-A Astrocytes Primary Cells

*When 15-core chromatin state is included in the plot and >30 cell types are selected, the labels of Y-axis are omitted. The order of the cell types is same as the legend table.

Chromosome 19

EUR



Regulome DB

RegulomeDB Categorical Scores

Category	Description
1a	Likely to affect binding and linked to expression of a gene target eQTL + TF binding + matched TF motif + matched DNase footprint + DNase peak
1b	eQTL + TF binding + any motif + DNase footprint + DNase peak
1c	eQTL + TF binding + matched TF motif + DNase peak
1d	eQTL + TF binding + any motif + DNase peak
1e	eQTL + TF binding + matched TF motif
1f	eQTL + TF binding/DNase peak
2a	Likely to affect binding TF binding + matched TF motif + matched DNase footprint + DNase peak
2b	TF binding + any motif + DNase footprint + DNase peak
2c	TF binding + matched TF motif + DNase peak
3a	Less likely to affect binding TF binding + any motif + DNase peak
3b	TF binding + matched TF motif
4	Minimal binding evidence TF binding + DNase peak
5	TF binding or DNase peak
6	Motif hit
7	No binding evidence
NA	No evidence the variant does not exist in RegulomeDB

*External link to RegulomeDB from SNP table (when one of the SNPs is clicked) will open a new tab. rsID does not always match since RegulomeDB used dbSNP build 141 (the rsID in FUMA is dbSNP build 146). Genomic position (bp on hg19) shown in the link of RegulomeDB is the position shown in the SNP table - 1, since RegulomeDB used 0 based coordinate.

15-core chromatin state

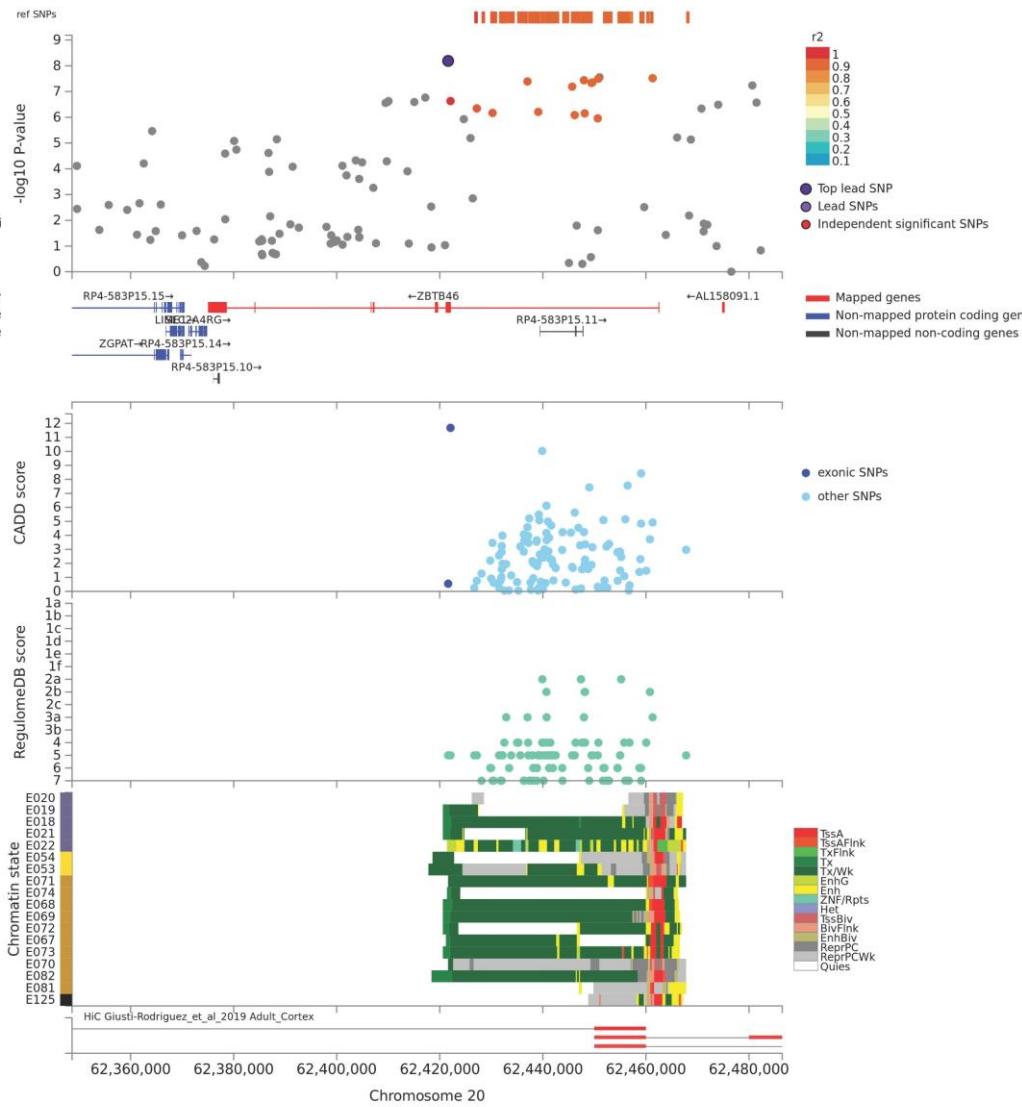
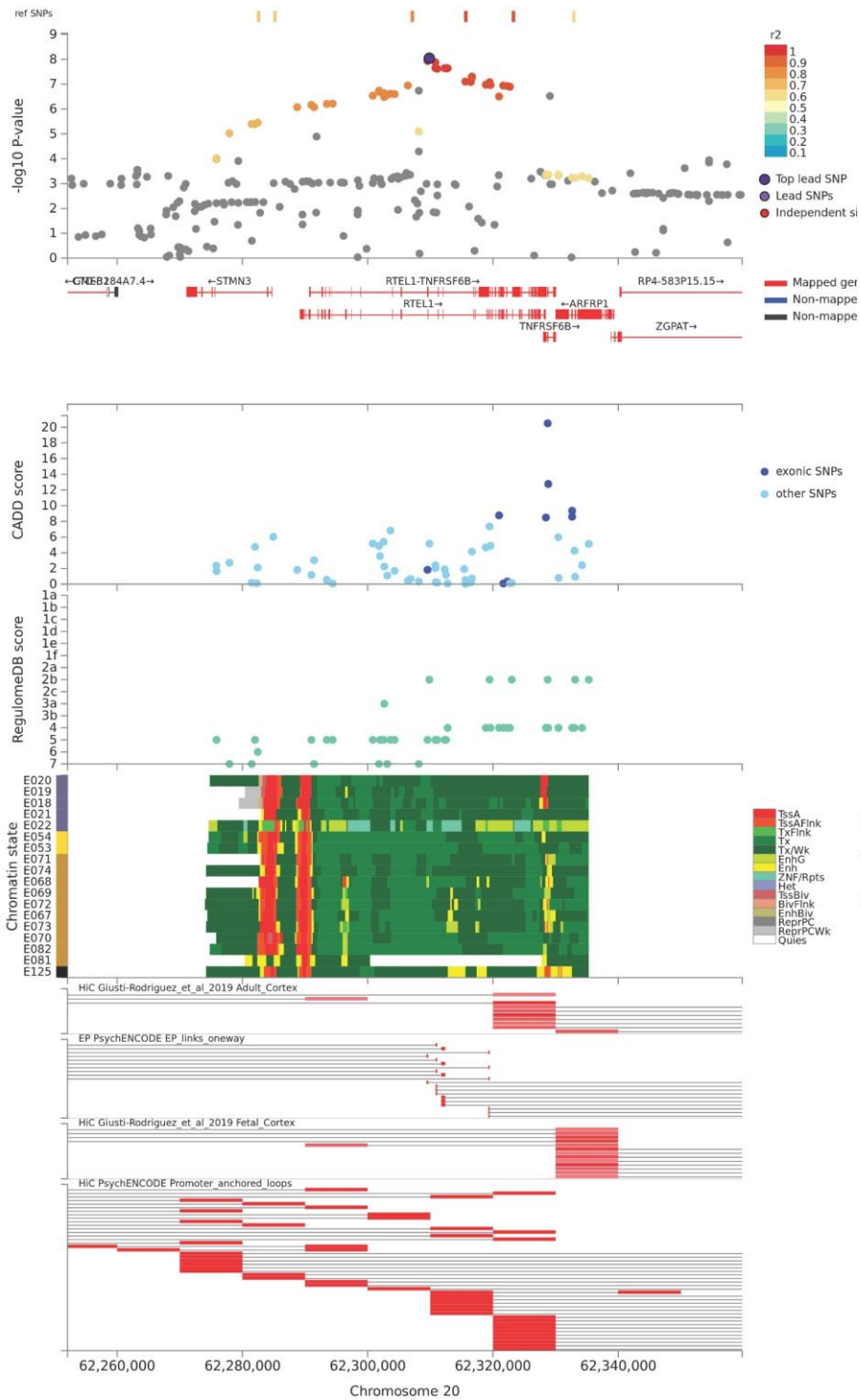
Epigenome ID		Color	Group	Anatomy	Standardized epigenome name
E020	#69608A		iPSC	IPSC	iPS-20b Cells
E019	#69608A		iPSC	IPSC	iPS-18 Cells
E018	#69608A		iPSC	IPSC	iPS-15b Cells
E021	#69608A		iPSC	IPSC	iPS DF 6.9 Cells
E022	#69608A		iPSC	IPSC	iPS DF 19.11 Cells
E054	#FFD924		Neurosph	BRAIN	Ganglion Eminence derived primary cultured neurospheres
E053	#FFD924		Neurosph	BRAIN	Cortex derived primary cultured neurospheres
E071	#C5912B		Brain	BRAIN	Brain Hippocampus Middle
E074	#C5912B		Brain	BRAIN	Brain Substantia Nigra
E068	#C5912B		Brain	BRAIN	Brain Anterior Caudate
E069	#C5912B		Brain	BRAIN	Brain Cingulate Gyrus
E072	#C5912B		Brain	BRAIN	Brain Inferior Temporal Lobe
E067	#C5912B		Brain	BRAIN	Brain Angular Gyrus
E073	#C5912B		Brain	BRAIN	Brain_Dorsolateral_Prefrontal_Cortex
E070	#C5912B		Brain	BRAIN	Brain Germinal Matrix
E082	#C5912B		Brain	BRAIN	Fetal Brain Female
E081	#C5912B		Brain	BRAIN	Fetal Brain Male
E125	#000000		ENCODE2012	BRAIN	NH-A Astrocytes Primary Cells

*When 15-core chromatin state is included in the plot and >30 cell types are selected, the labels of Y-axis are omitted. The order of the cell types is same as the legend table.

Chromosome 20

EAS

EUR



Regulome DB

Category	Description
1a	Likely to affect binding and linked to expression of a gene target
1b	eQTL + TF binding + matched TF motif + matched DNase footprint + DNase peak
1c	eQTL + TF binding + any motif + DNase footprint + DNase peak
1d	eQTL + TF binding + matched TF motif + DNase peak
1e	eQTL + TF binding + any motif + DNase peak
1f	eQTL + TF binding + matched TF motif
2a	Likely to affect binding
2b	TF binding + matched TF motif + matched DNase footprint + DNase peak
2c	TF binding + any motif + DNase footprint + DNase peak
3a	TF binding + matched TF motif + DNase peak
3b	TF binding + any motif + DNase peak
3c	TF binding + matched TF motif
4	Less likely to affect binding
5	TF binding + DNase peak
6	TF binding or DNase peak
7	Motif hit
NA	No binding evidence
7	No evidence
NA	the variant does not exist in RegulomeDB

15-core chromatin state

Epigenome ID		Group	Anatomy	Standardized epigenome name
EID	Color			
E020	#69608A	iPSC	IPSC	iPS-20b Cells
E019	#69608A	iPSC	IPSC	iPS-18 Cells
E018	#69608A	iPSC	IPSC	iPS-15b Cells
E021	#69608A	iPSC	IPSC	iPS DF 6.9 Cells
E022	#69608A	iPSC	IPSC	iPS DF 19.11 Cells
E054	#FFD924	Neurosph	BRAIN	Ganglion Eminence derived primary cultured neurospheres
E053	#FFD924	Neurosph	BRAIN	Cortex derived primary cultured neurospheres
E071	#C5912B	Brain	BRAIN	Brain Hippocampus Middle
E074	#C5912B	Brain	BRAIN	Brain Substantia Nigra
E068	#C5912B	Brain	BRAIN	Brain Anterior Caudate
E069	#C5912B	Brain	BRAIN	Brain Cingulate Gyrus
E072	#C5912B	Brain	BRAIN	Brain Inferior Temporal Lobe
E067	#C5912B	Brain	BRAIN	Brain Angular Gyrus
E073	#C5912B	Brain	BRAIN	Brain_Dorsolateral_Prefrontal_Cortex
E070	#C5912B	Brain	BRAIN	Brain Germinal Matrix
E082	#C5912B	Brain	BRAIN	Fetal Brain Female
E081	#C5912B	Brain	BRAIN	Fetal Brain Male
E125	#000000	ENCODE2012	BRAIN	NH-A Astrocytes Primary Cells

*External link to RegulomeDB from SNP table (when one of the SNPs is clicked) will open a new tab. rsID does not always match since RegulomeDB used dbSNP build 141 (the rsID in FUMA is dbSNP build 146). Genomic position (bp on hg19) shown in the link of RegulomeDB is the position shown in the SNP table - 1, since RegulomeDB used 0 based coordinate.

*When 15-core chromatin state is included in the plot and >30 cell types are selected, the labels of Y-axis are omitted. The order of the cell types is same as the legend table.

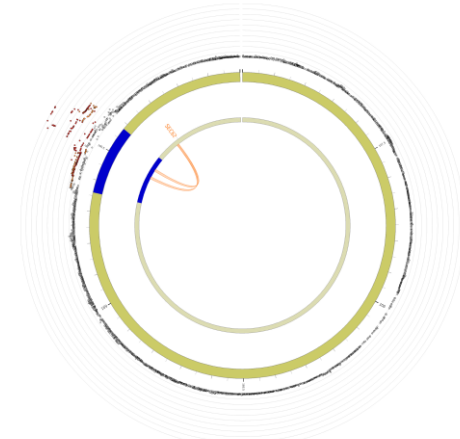
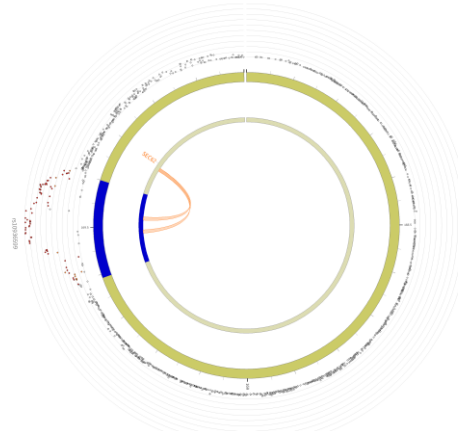
Chromatin mapping – Circos Plots

Locus shared between both populations

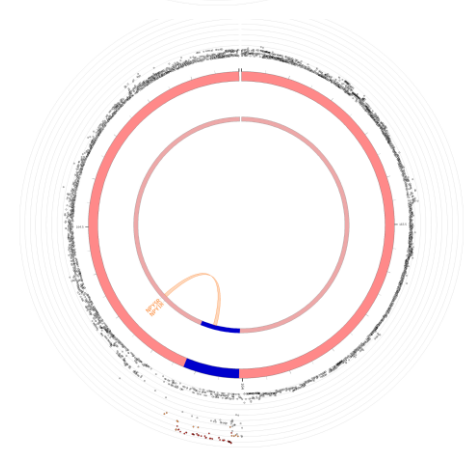
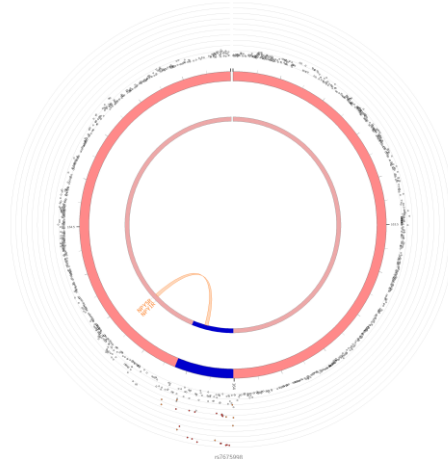
EUR

EAS

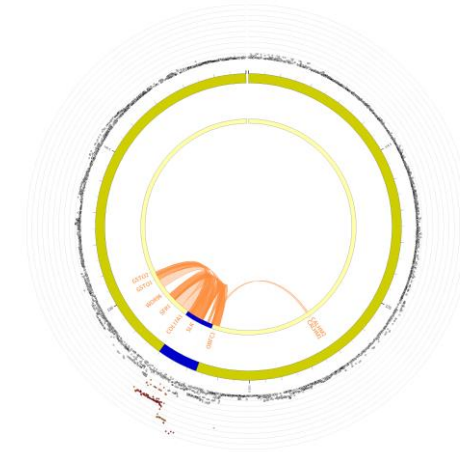
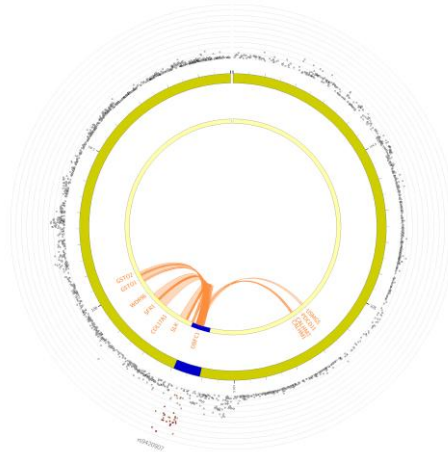
Chromosome 3



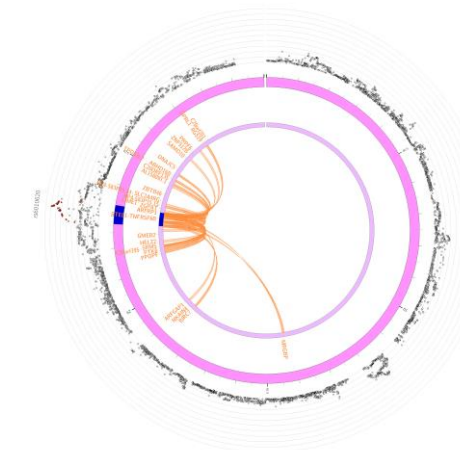
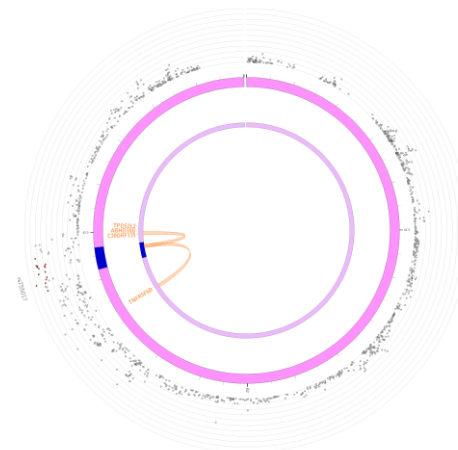
Chromosome 4



Chromosome 10



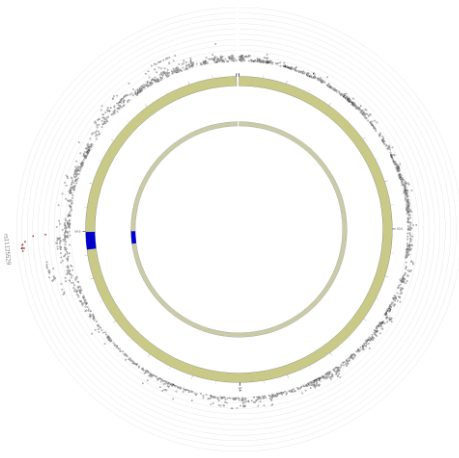
Chromosome 20



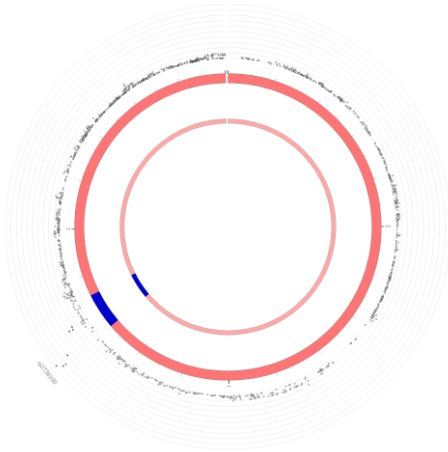
Locus NOT shared between both populations

EUR

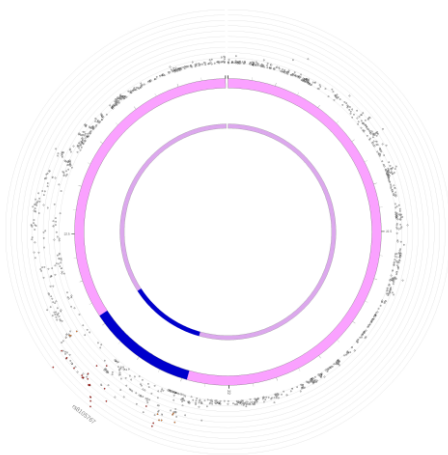
Chromosome 2



Chromosome 5



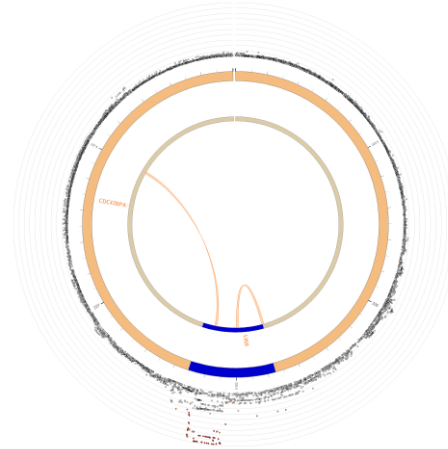
Chromosome 19



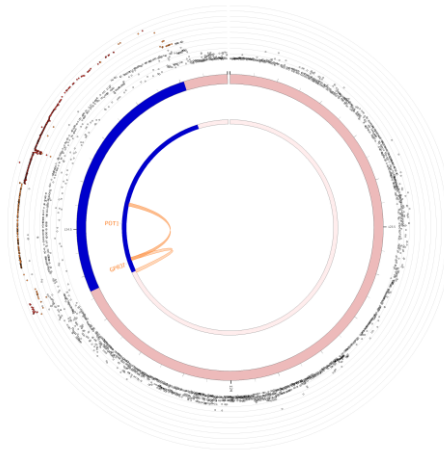
Locus NOT shared between both populations

EAS

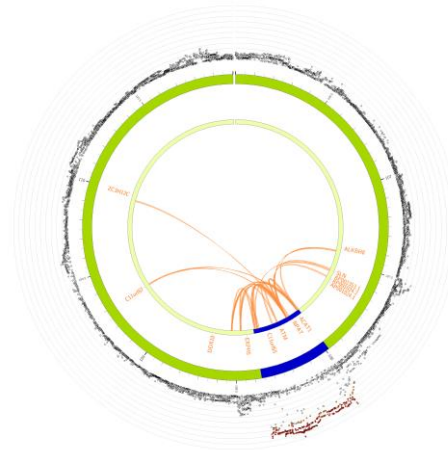
Chromosome 1



Chromosome 7



Chromosome 11



Chromosome 15

