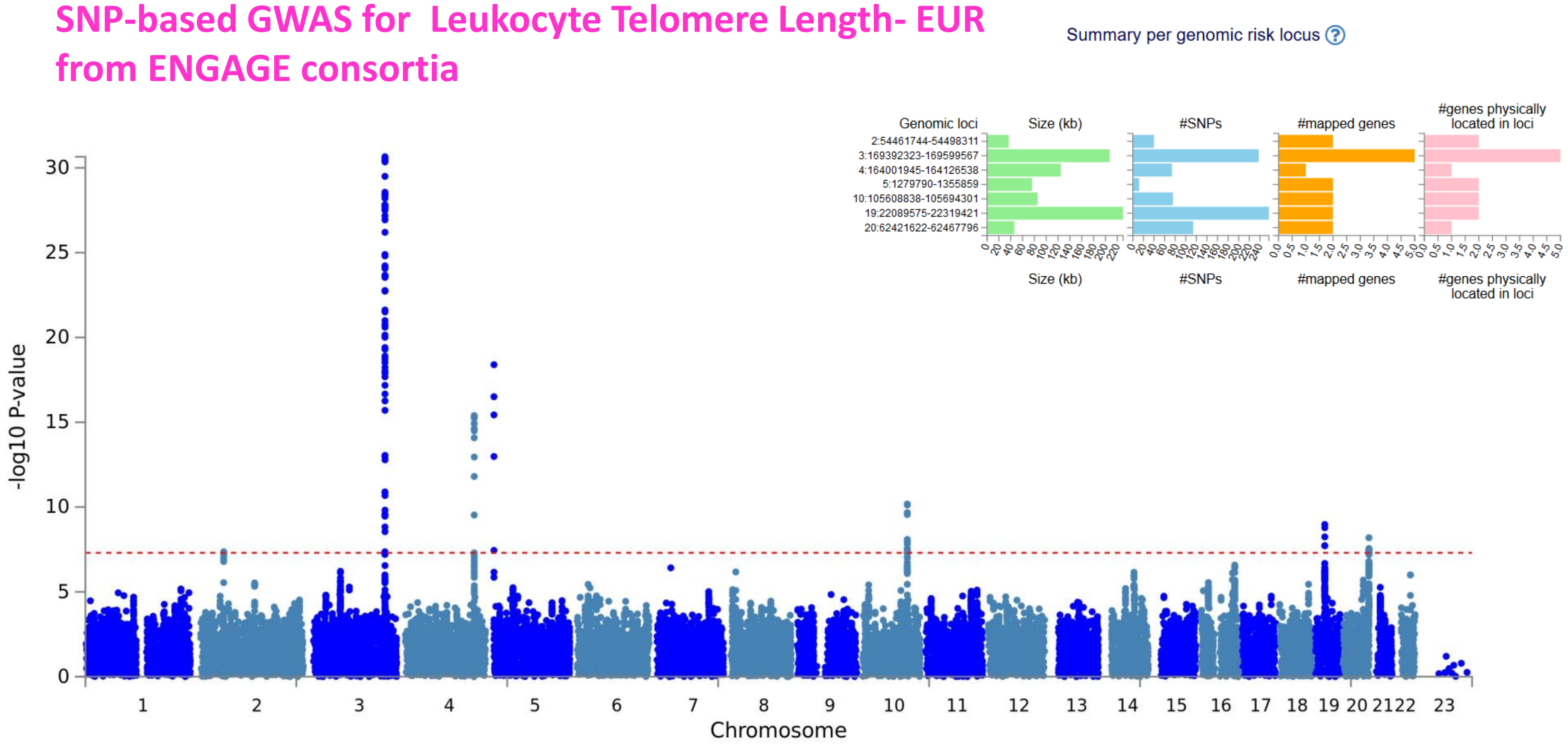
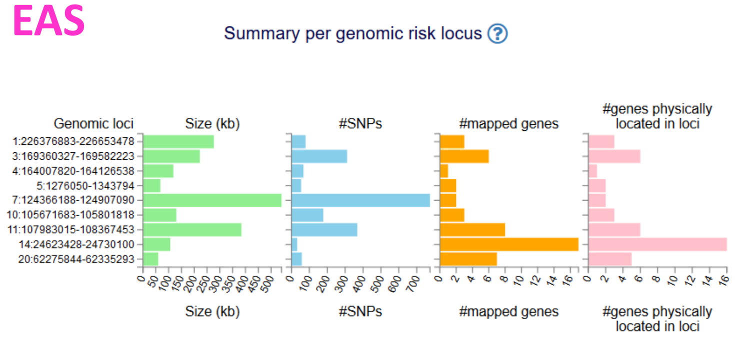
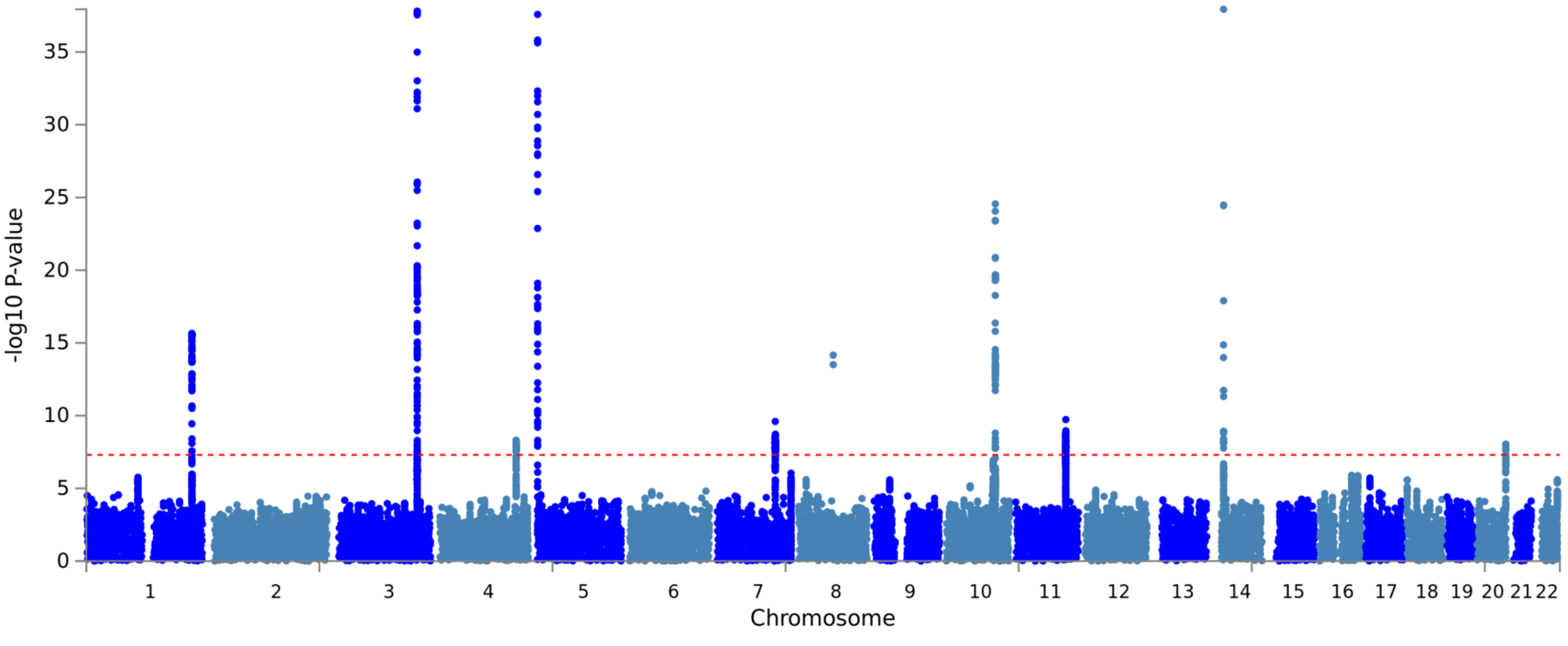
SNP-based GWAS for Leukocyte Telomere Length- EUR from ENGAGE consortia



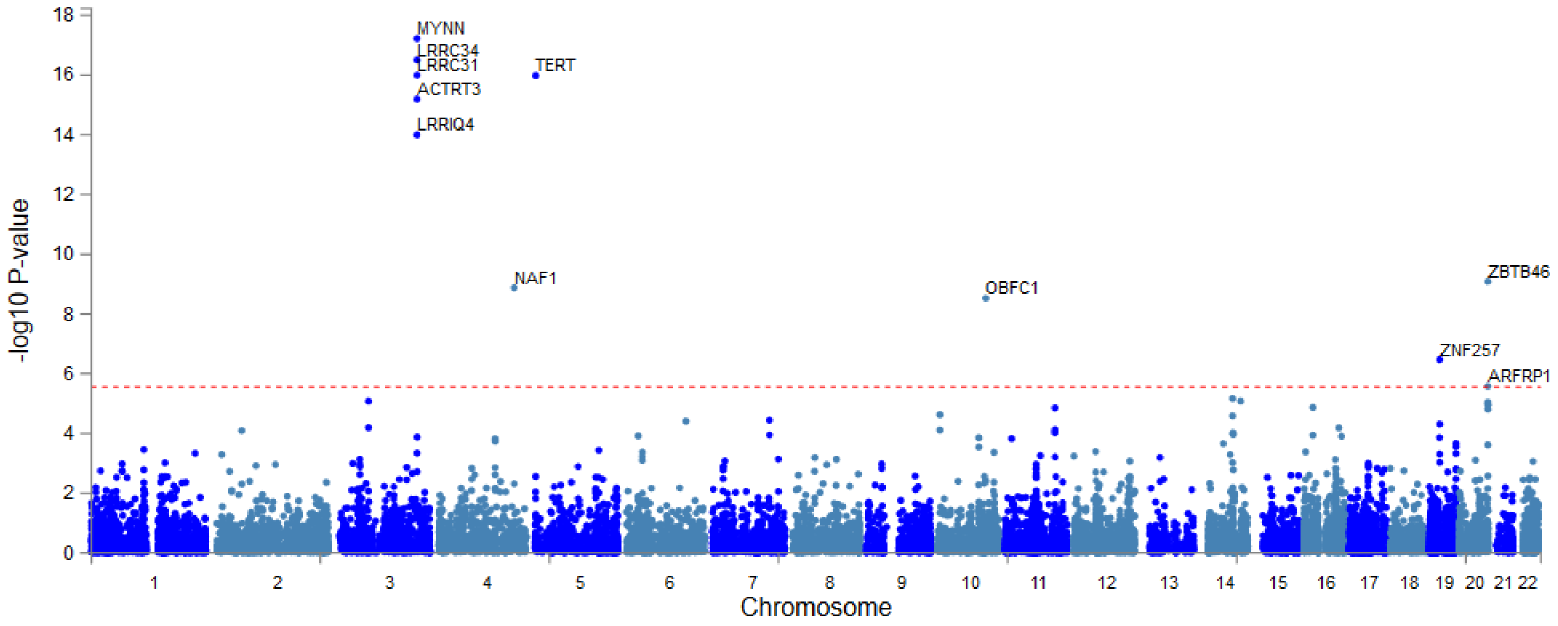
SNP-based GWAS for Leukocyte Telomere Length- EAS from Dorajoo et. al 2019

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

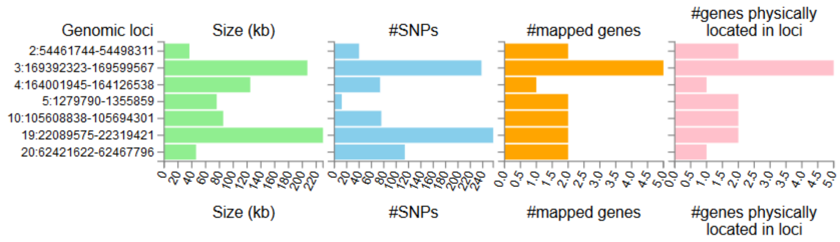




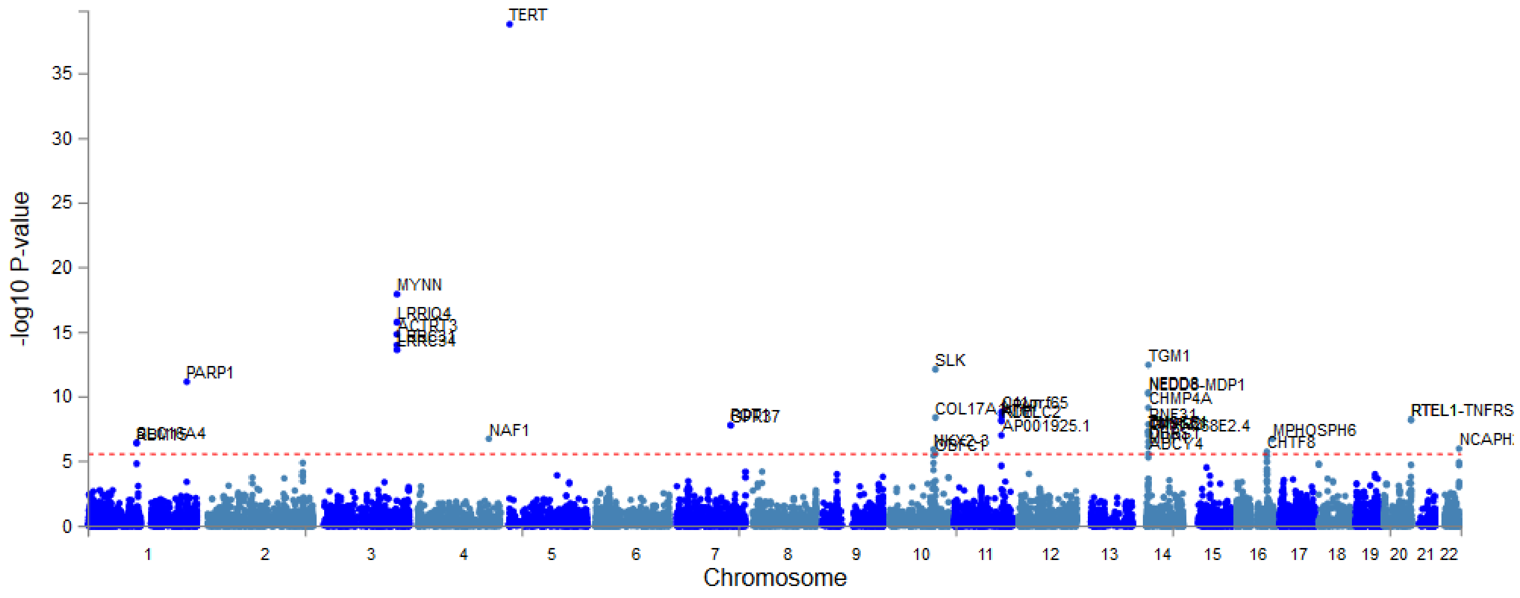
Gene (positional mapping)-based GWAS European Ancestry



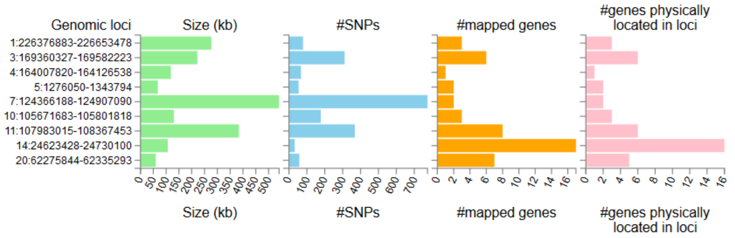
Summary per genomic risk locus



Gene (positional mapping)-based GWAS East Asian Ancestry



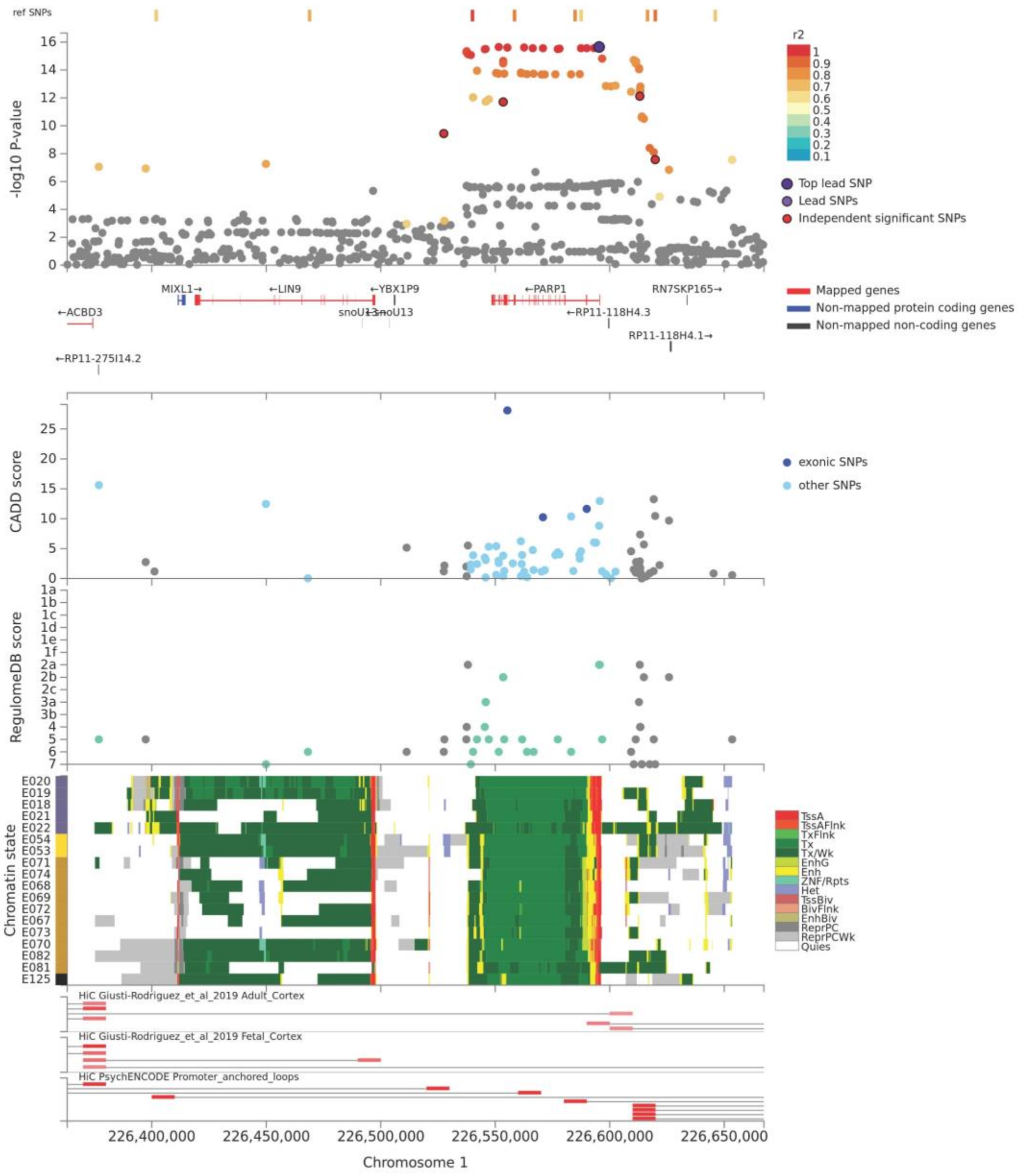
Summary per genomic risk locus

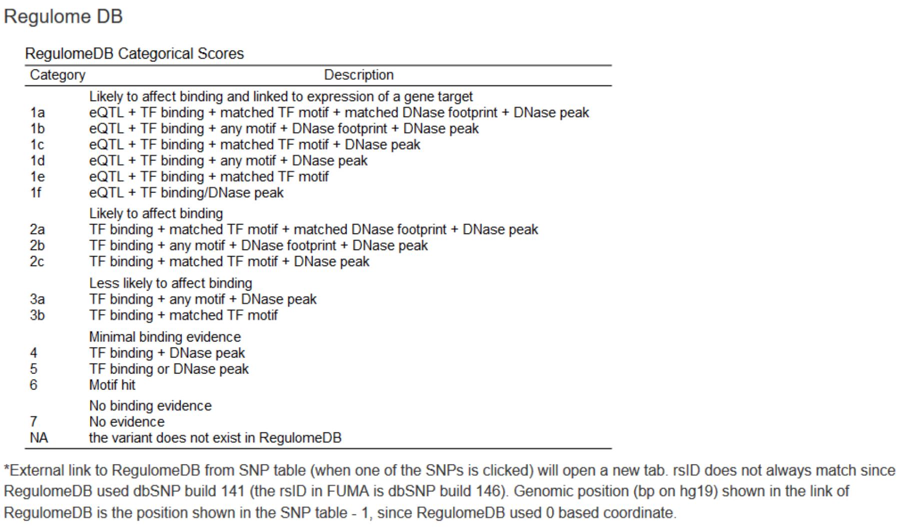


Regional Plots for each locus

Chromosome 1

EAS



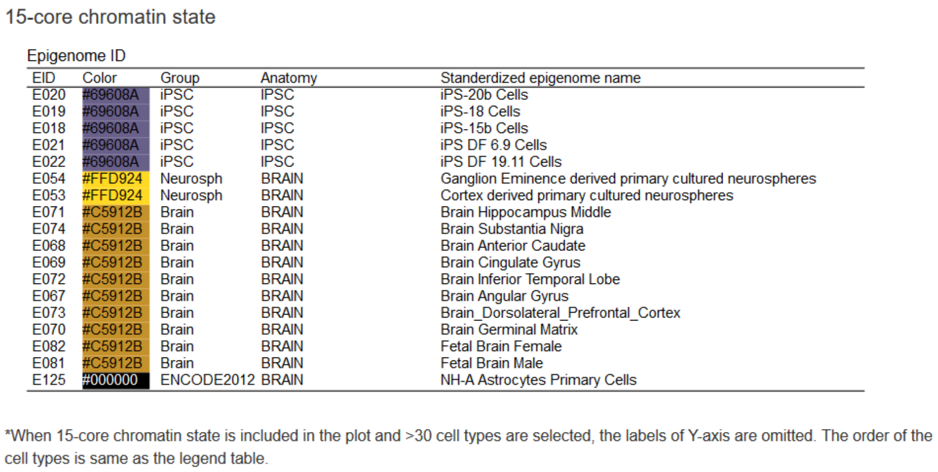


Regulome DB

RegulomeDB Categorical Scores

Category	Description
	Likely to affect binding and linked to expression of a gene target
1a	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
	Likely to affect binding
2a	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
	Less likely to affect binding
3a	TF binding + any motif + DNase peak
3b	TF binding + matched TF motif
	Minimal binding evidence
4	TF binding + DNase peak
5	TF binding or DNase peak
6	Motif hit
	No binding evidence
7	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

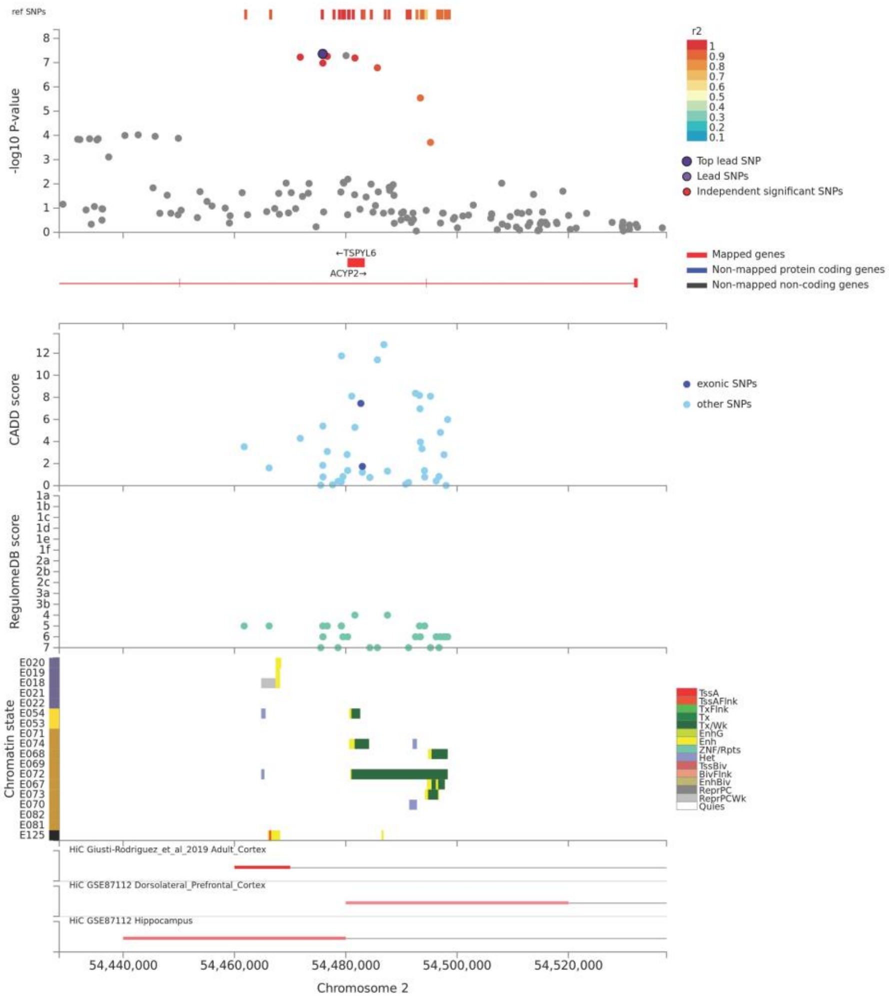
Epigenome ID

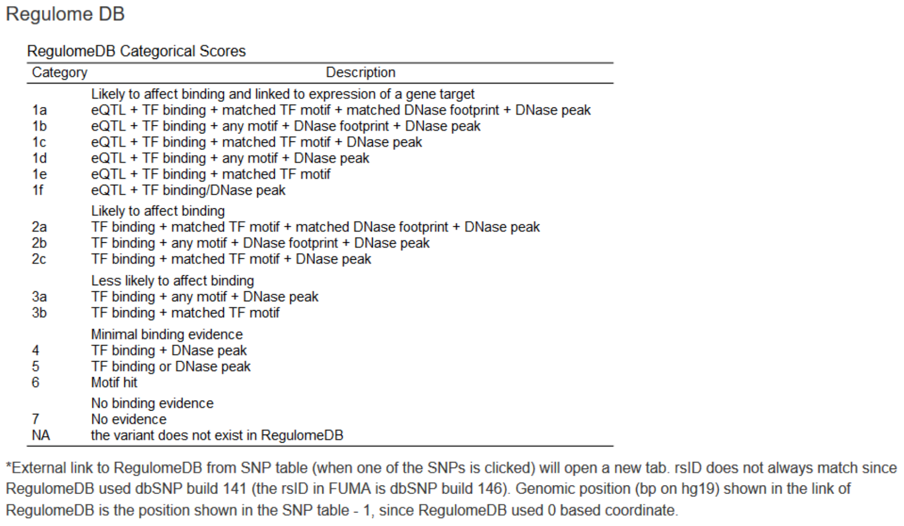
EID	Color	Group	Anatomy	Standerdized epigenome name
E020	#69608A	iPSC	IPSC	iPS-20b Cells
E019	#69608A	iPSC	IPSC	iPS-18 Cells
E018	#69608A	iPSC	IPSC	iPS-15b Cells
E021	#69608A	iPSC	IPSC	iPS DF 6.9 Cells
E022	#69608A	iPSC	IPSC	iPS DF 19.11 Cells
E054	#FFD924	Neurosph	BRAIN	Ganglion Eminence derived primary 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 2

EUR



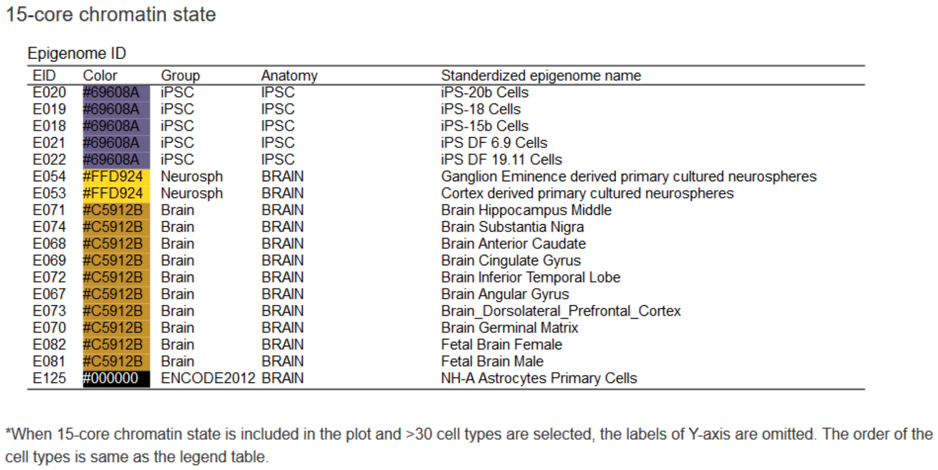


Regulome DB

RegulomeDB Categorical Scores

Category	Description
	Likely to affect binding and linked to expression of a gene target
1a	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
	Likely to affect binding
2a	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
	Less likely to affect binding
3a	TF binding + any motif + DNase peak
3b	TF binding + matched TF motif
	Minimal binding evidence
4	TF binding + DNase peak
5	TF binding or DNase peak
6	Motif hit
	No binding evidence
7	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.



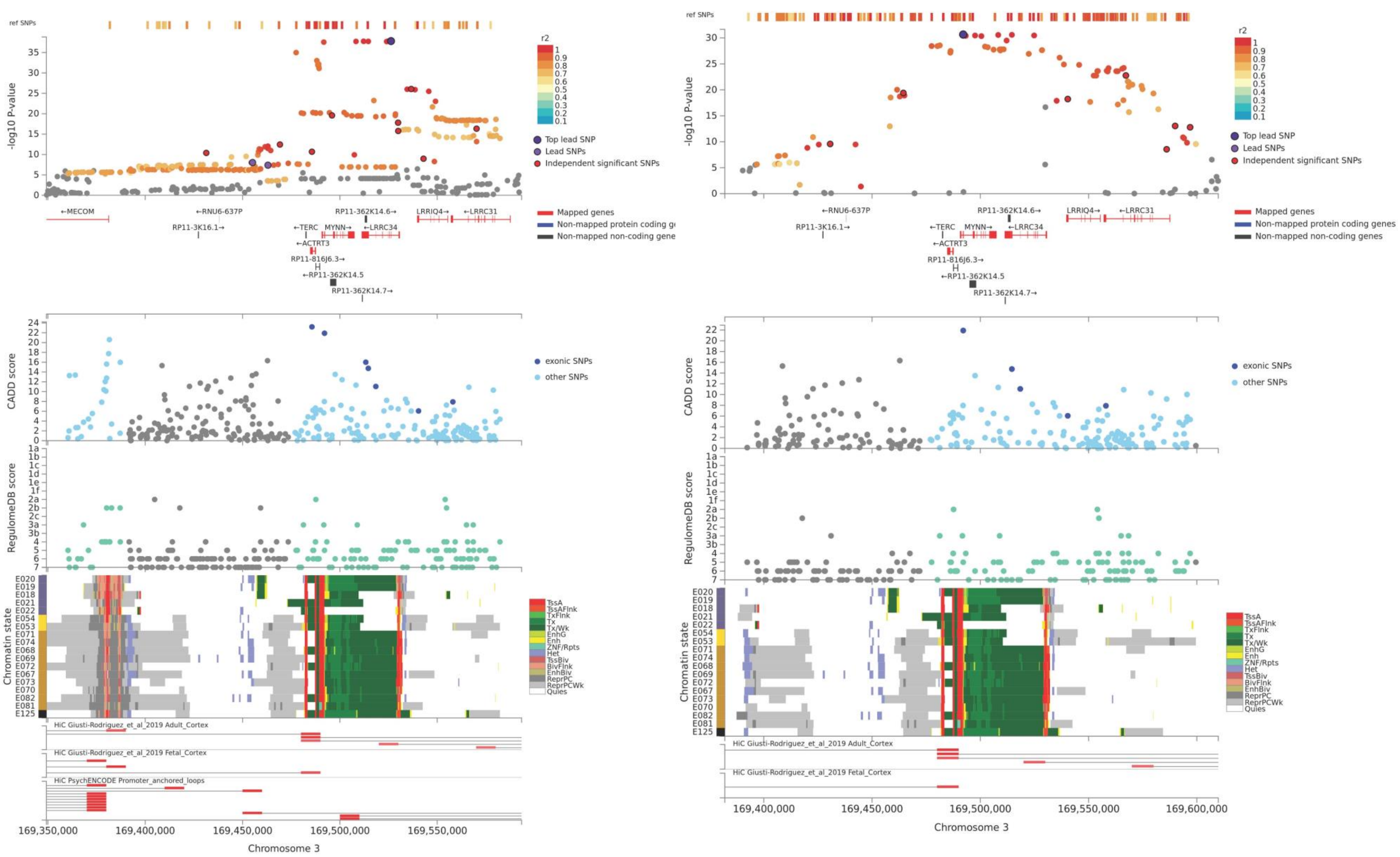
15-core chromatin state

Epigenome ID

EID	Color	Group	Anatomy	Standerdized 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.

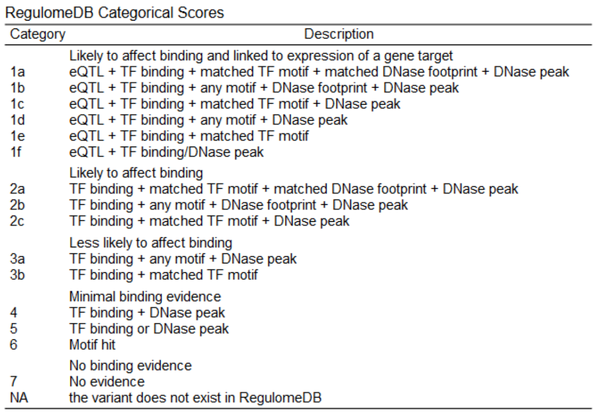
Chromosome 3



EAS

EUR

Regulome DB

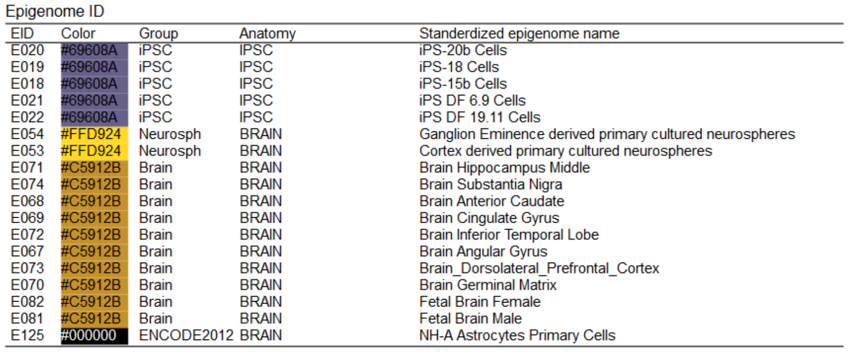


RegulomeDB Categorical Scores

Category	Description
	Likely to affect binding and linked to expression of a gene target
1a	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
	Likely to affect binding
2a	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
	Less likely to affect binding
3a	TF binding + any motif + DNase peak
3b	TF binding + matched TF motif
	Minimal binding evidence
4	TF binding + DNase peak
5	TF binding or DNase peak
6	Motif hit
	No binding evidence
7	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



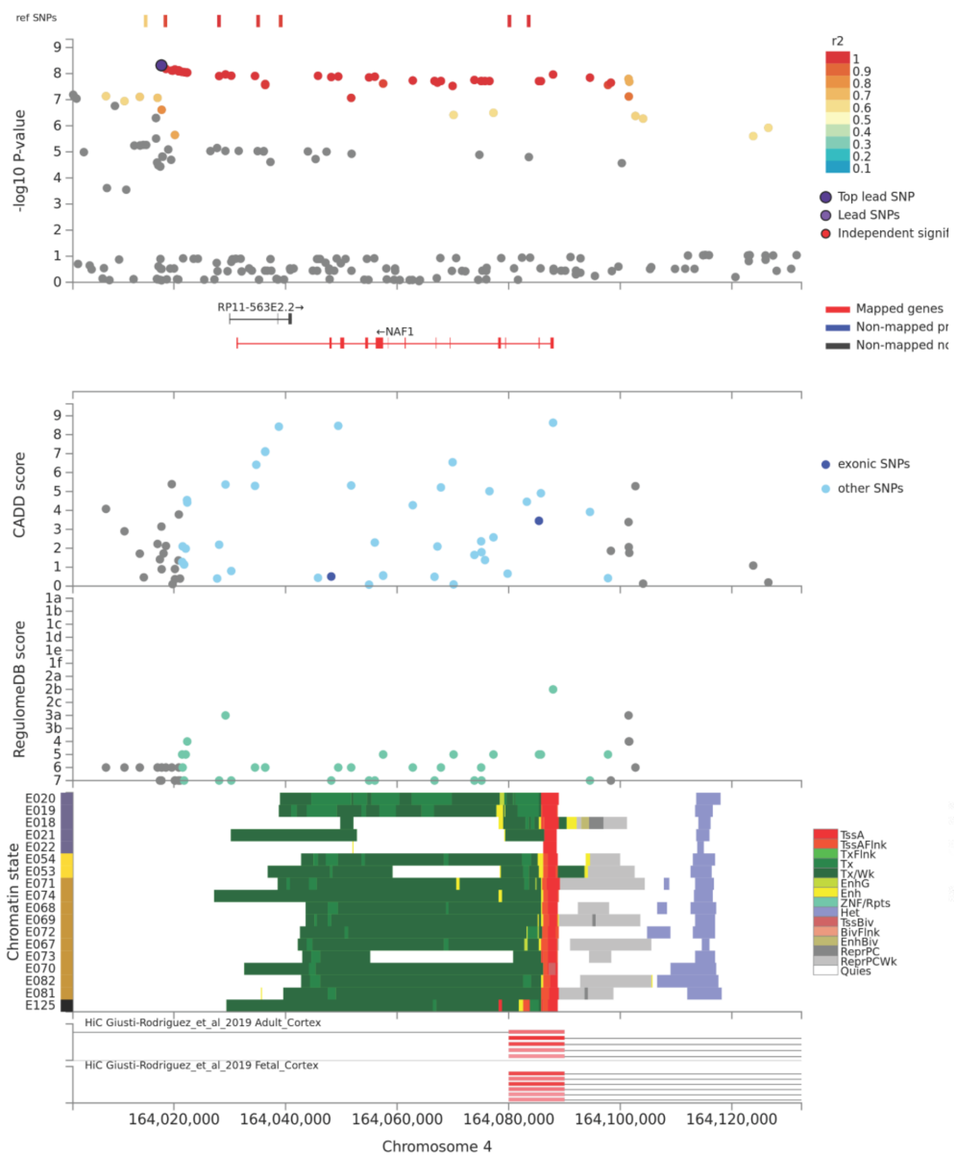
Epigenome ID

EID	Color	Group	Anatomy	Standerdized 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

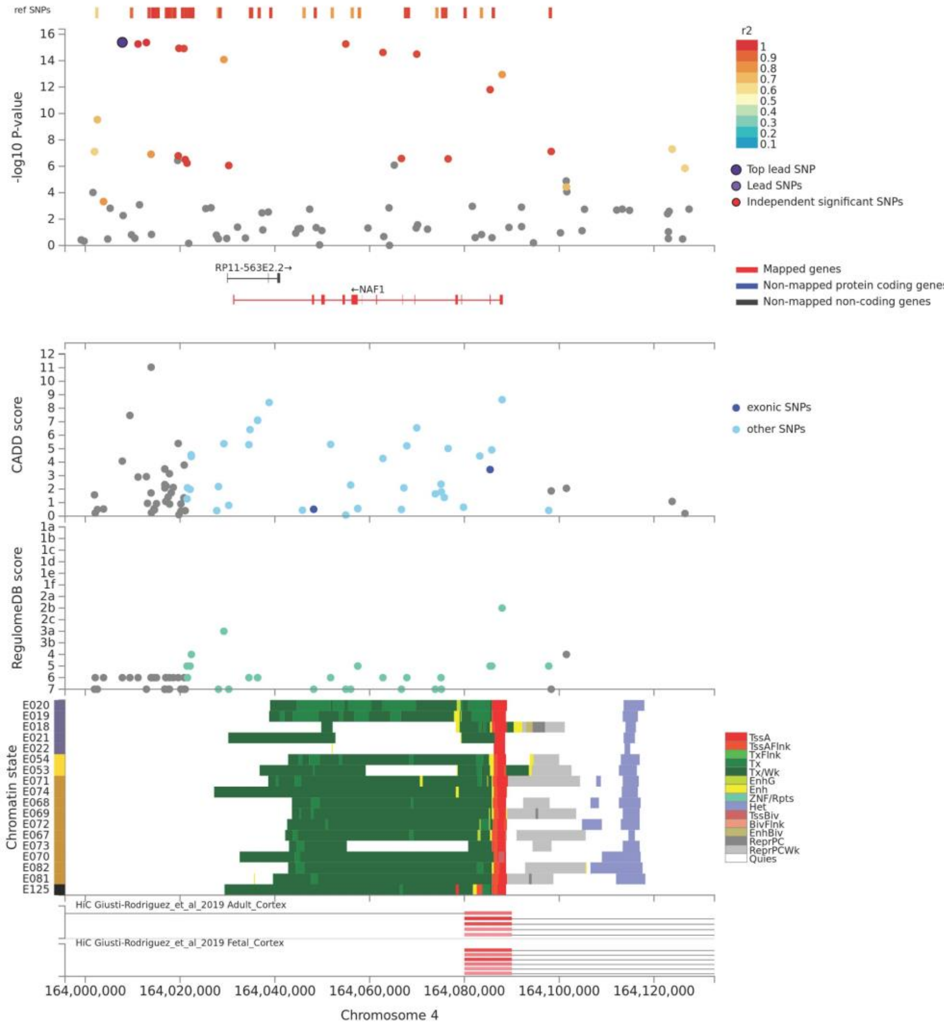
*When 15-core chromatin state is included in the plot and >30 cell types are selected, the labels of Y-axis are omitted. The order of the cell types is same as the legend table.

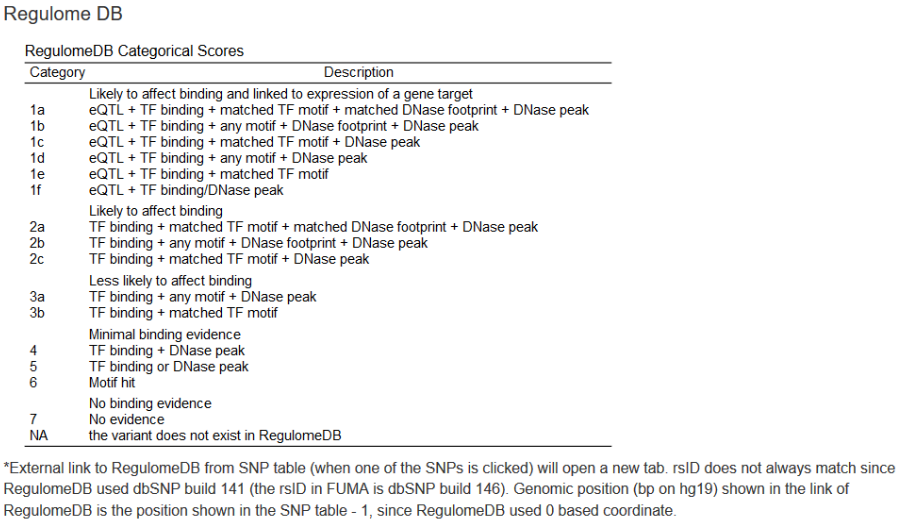
Chromosome 4

EAS



EUR



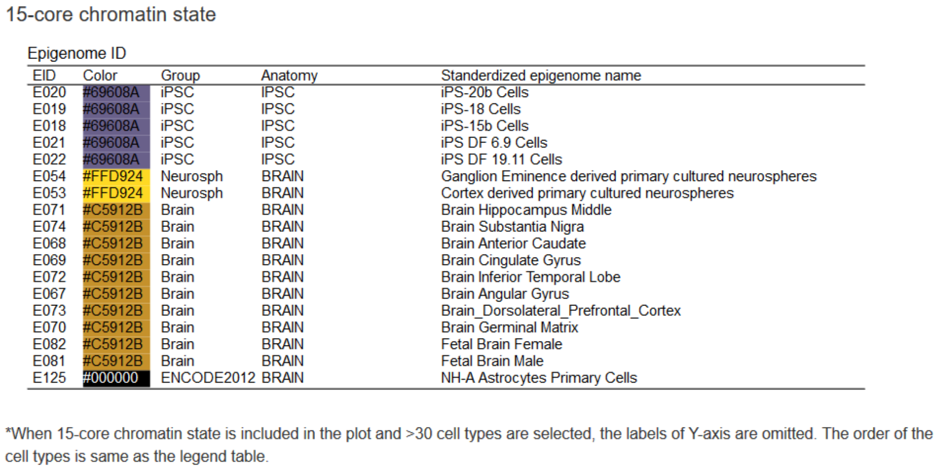


Regulome DB

RegulomeDB Categorical Scores

Category	Description
	Likely to affect binding and linked to expression of a gene target
1a	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
	Likely to affect binding
2a	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
	Less likely to affect binding
3a	TF binding + any motif + DNase peak
3b	TF binding + matched TF motif
	Minimal binding evidence
4	TF binding + DNase peak
5	TF binding or DNase peak
6	Motif hit
	No binding evidence
7	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.



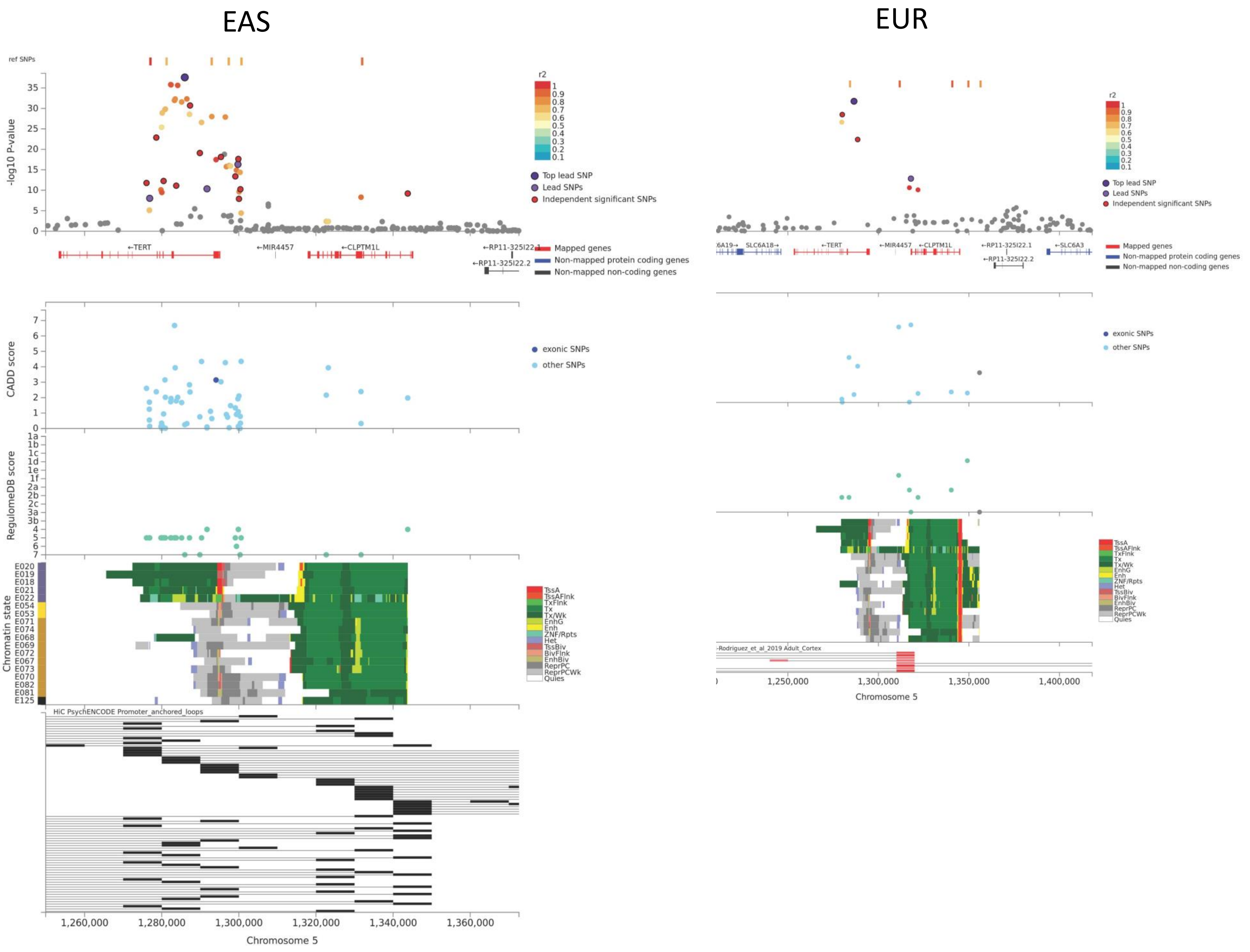
15-core chromatin state

Epigenome ID

EID	Color	Group	Anatomy	Standerdized 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 5



Regulome DB

RegulomeDB Categorical Scores

Category	Description
	Likely to affect binding and linked to expression of a gene target
1a	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
	Likely to affect binding
2a	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
	Less likely to affect binding
3a	TF binding + any motif + DNase peak
3b	TF binding + matched TF motif
	Minimal binding evidence
4	TF binding + DNase peak
5	TF binding or DNase peak
6	Motif hit
	No binding evidence
7	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

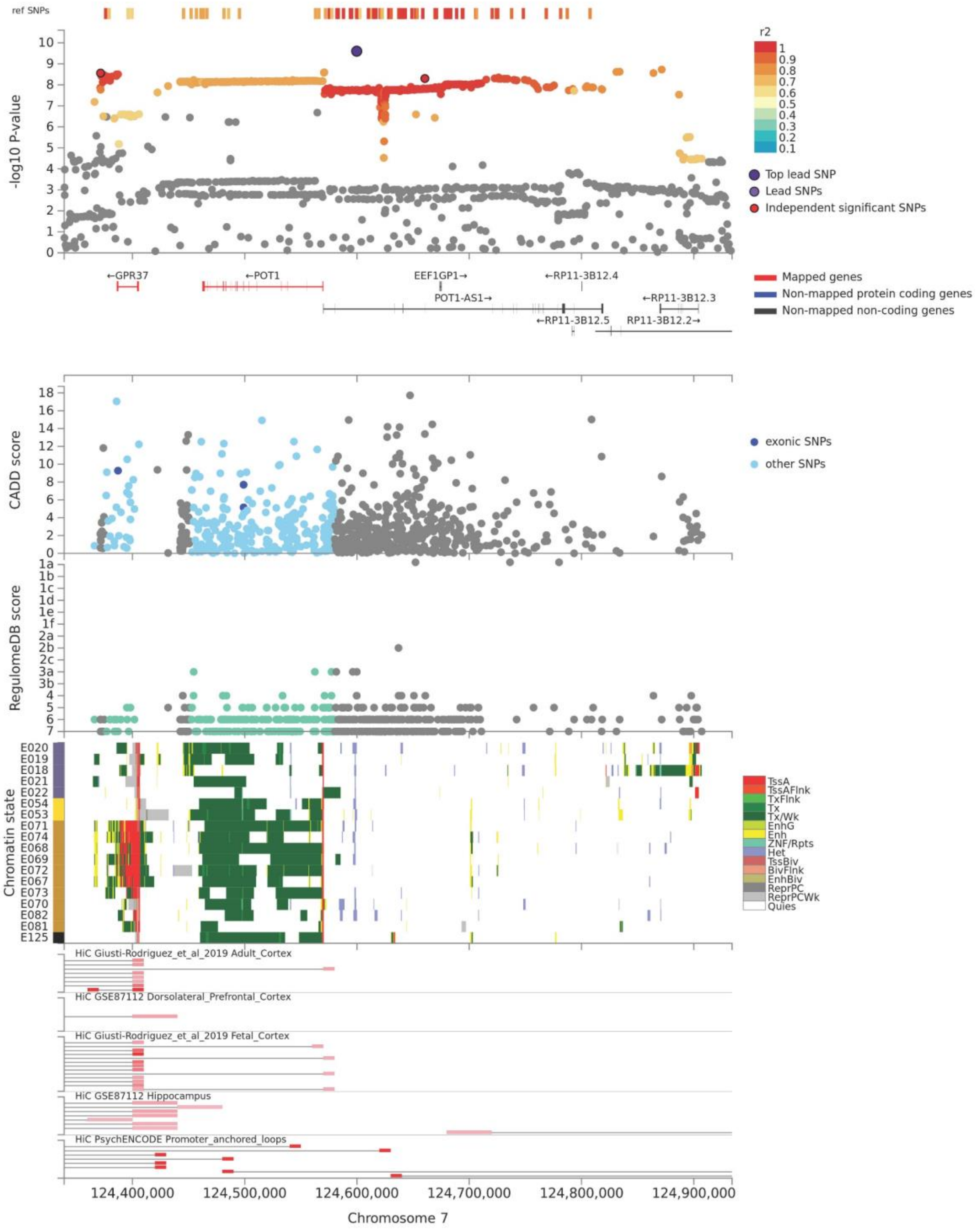
Epigenome ID

EID	Color	Group	Anatomy	Standerdized 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

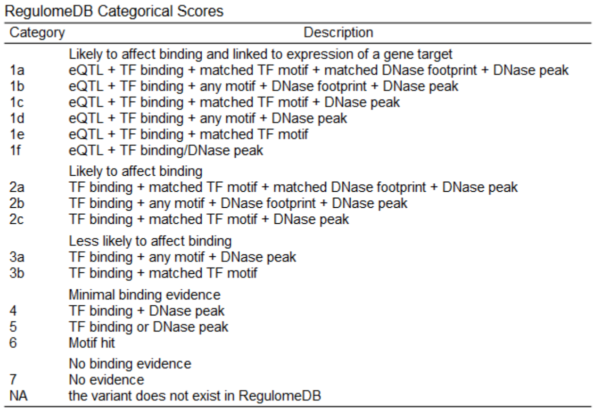
*When 15-core chromatin state is included in the plot and >30 cell types are selected, the labels of Y-axis are omitted. The order of the cell types is same as the legend table.

Chromosome 7

EAS



Regulome DB

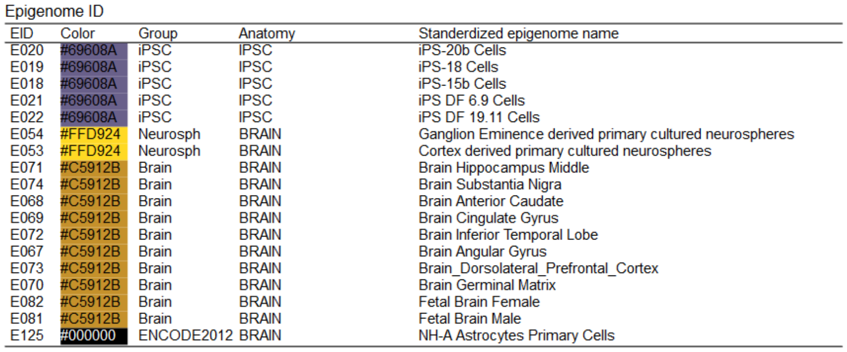


RegulomeDB Categorical Scores

Category	Description
	Likely to affect binding and linked to expression of a gene target
1a	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
	Likely to affect binding
2a	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
	Less likely to affect binding
3a	TF binding + any motif + DNase peak
3b	TF binding + matched TF motif
	Minimal binding evidence
4	TF binding + DNase peak
5	TF binding or DNase peak
6	Motif hit
	No binding evidence
7	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

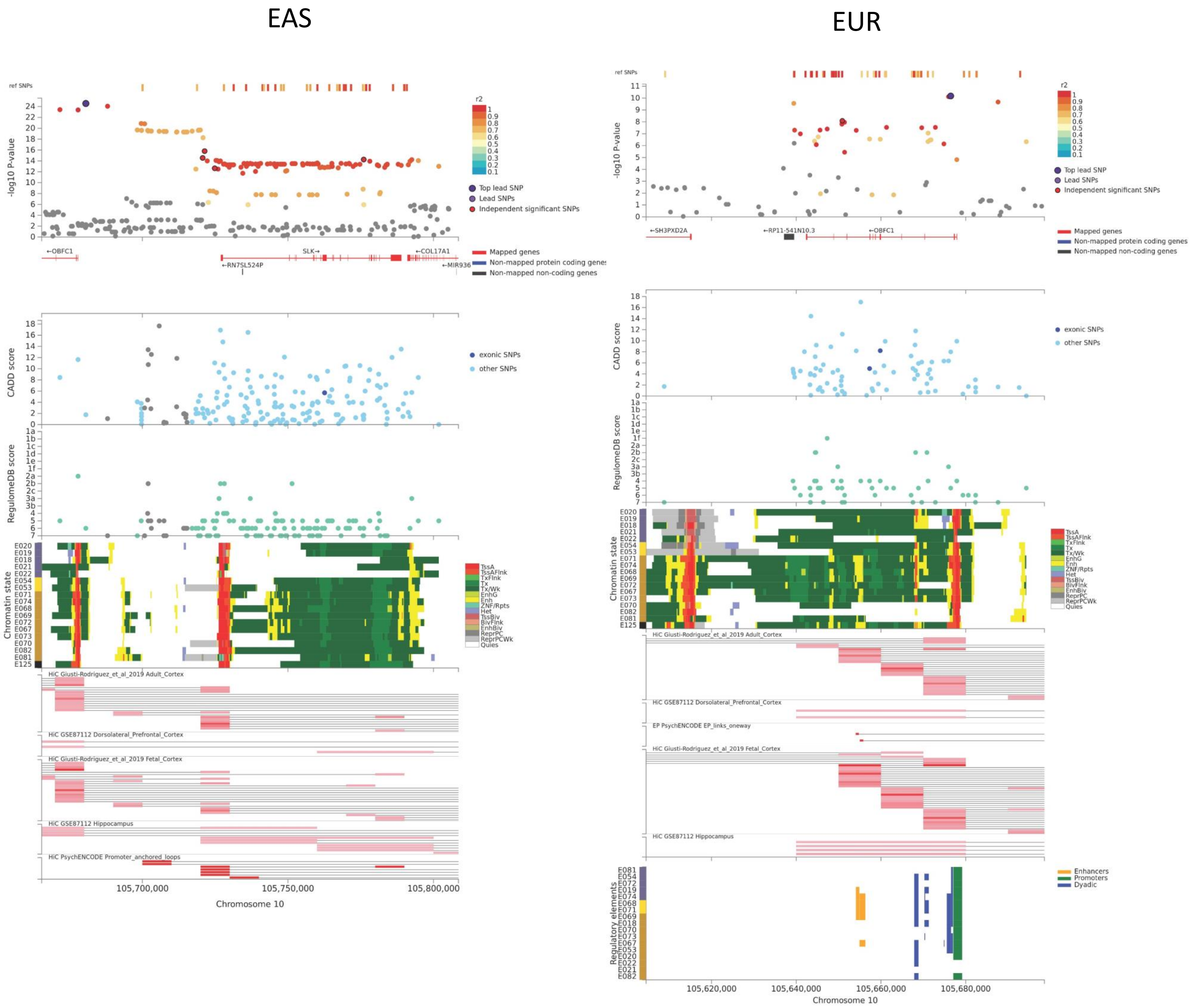


Epigenome ID

EID	Color	Group	Anatomy	Standerdized 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 10



Regulome DB

RegulomeDB Categorical Scores

Category	Description
	Likely to affect binding and linked to expression of a gene target
1a	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
	Likely to affect binding
2a	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
	Less likely to affect binding
3a	TF binding + any motif + DNase peak
3b	TF binding + matched TF motif
	Minimal binding evidence
4	TF binding + DNase peak
5	TF binding or DNase peak
6	Motif hit
	No binding evidence
7	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

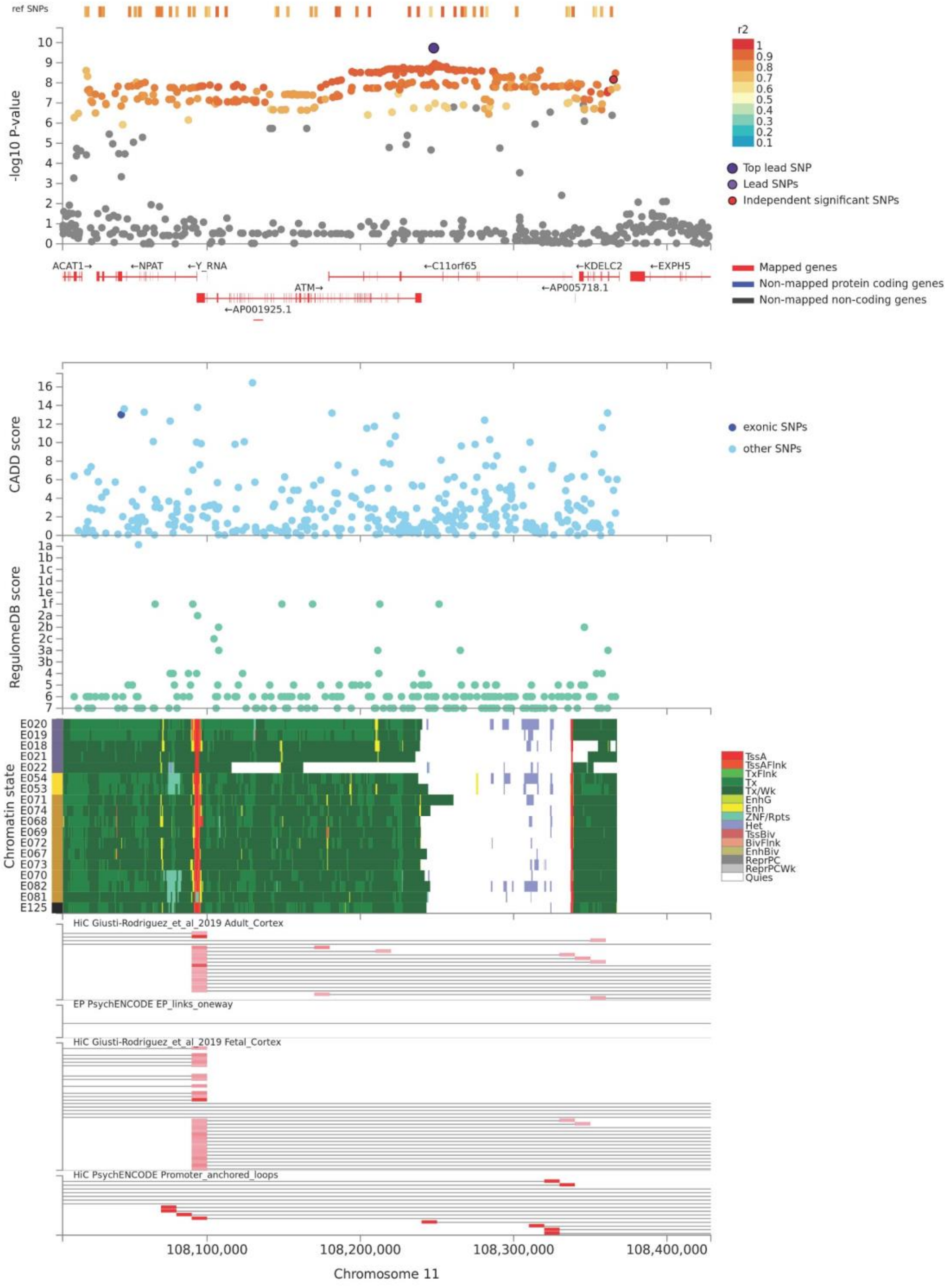
Epigenome ID

EID	Color	Group	Anatomy	Standerdized 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 11

EAS



Regulome DB

RegulomeDB Categorical Scores

Category	Description
	Likely to affect binding and linked to expression of a gene target
1a	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
	Likely to affect binding
2a	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
	Less likely to affect binding
3a	TF binding + any motif + DNase peak
3b	TF binding + matched TF motif
	Minimal binding evidence
4	TF binding + DNase peak
5	TF binding or DNase peak
6	Motif hit
	No binding evidence
7	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

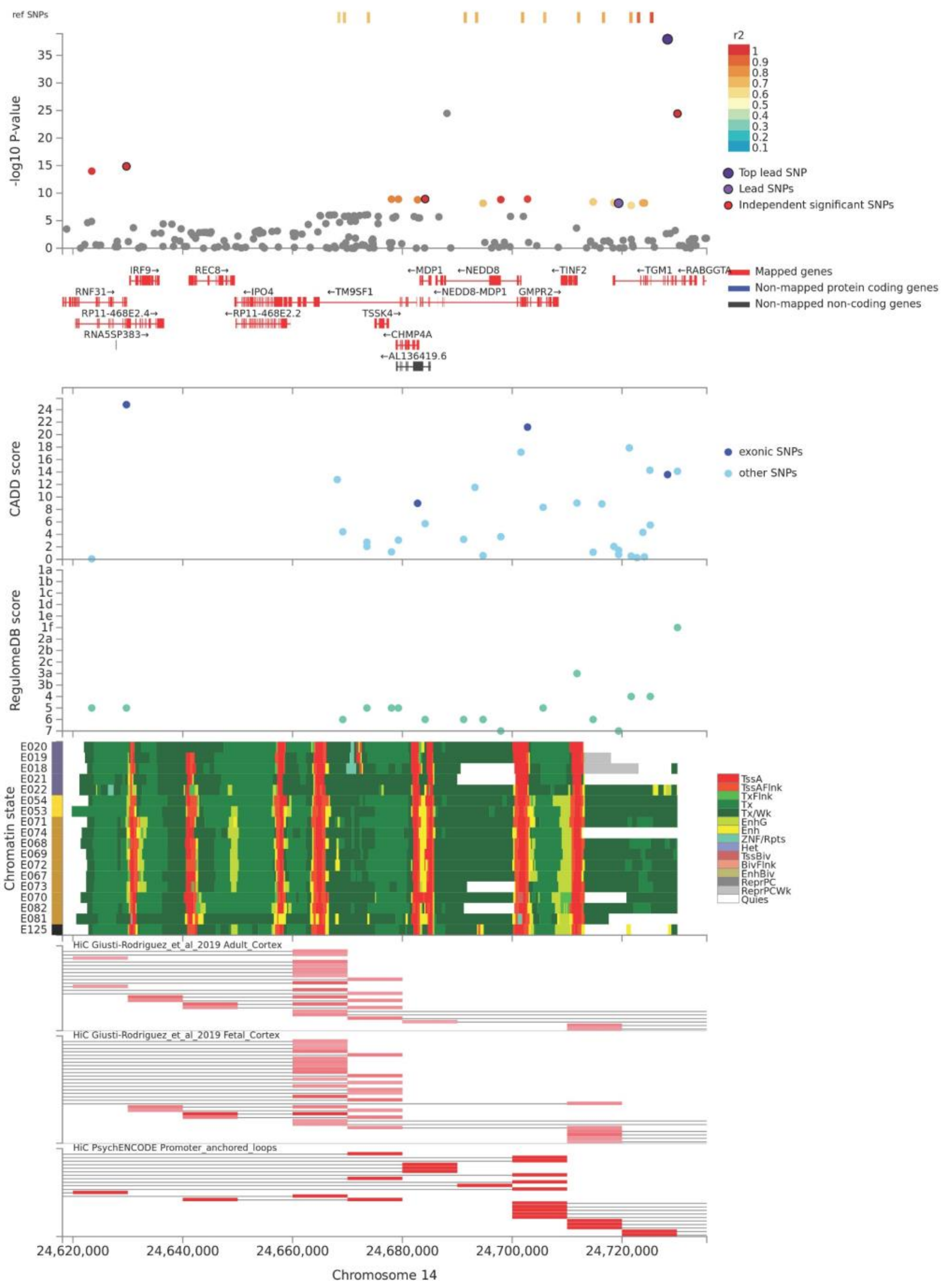
Epigenome ID

EID	Color	Group	Anatomy	Standerdized 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

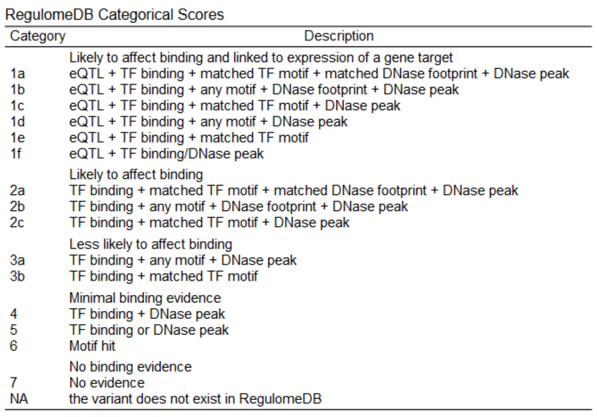
*When 15-core chromatin state is included in the plot and >30 cell types are selected, the labels of Y-axis are omitted. The order of the cell types is same as the legend table.

Chromosome 14

EAS



Regulome DB

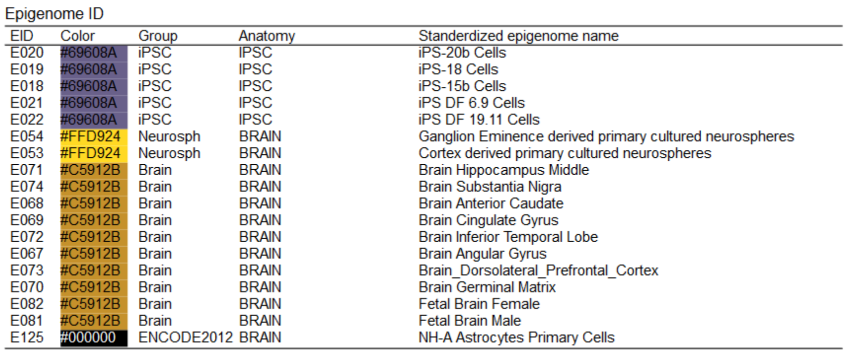


RegulomeDB Categorical Scores

Category	Description
	Likely to affect binding and linked to expression of a gene target
1a	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
	Likely to affect binding
2a	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
	Less likely to affect binding
3a	TF binding + any motif + DNase peak
3b	TF binding + matched TF motif
	Minimal binding evidence
4	TF binding + DNase peak
5	TF binding or DNase peak
6	Motif hit
	No binding evidence
7	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



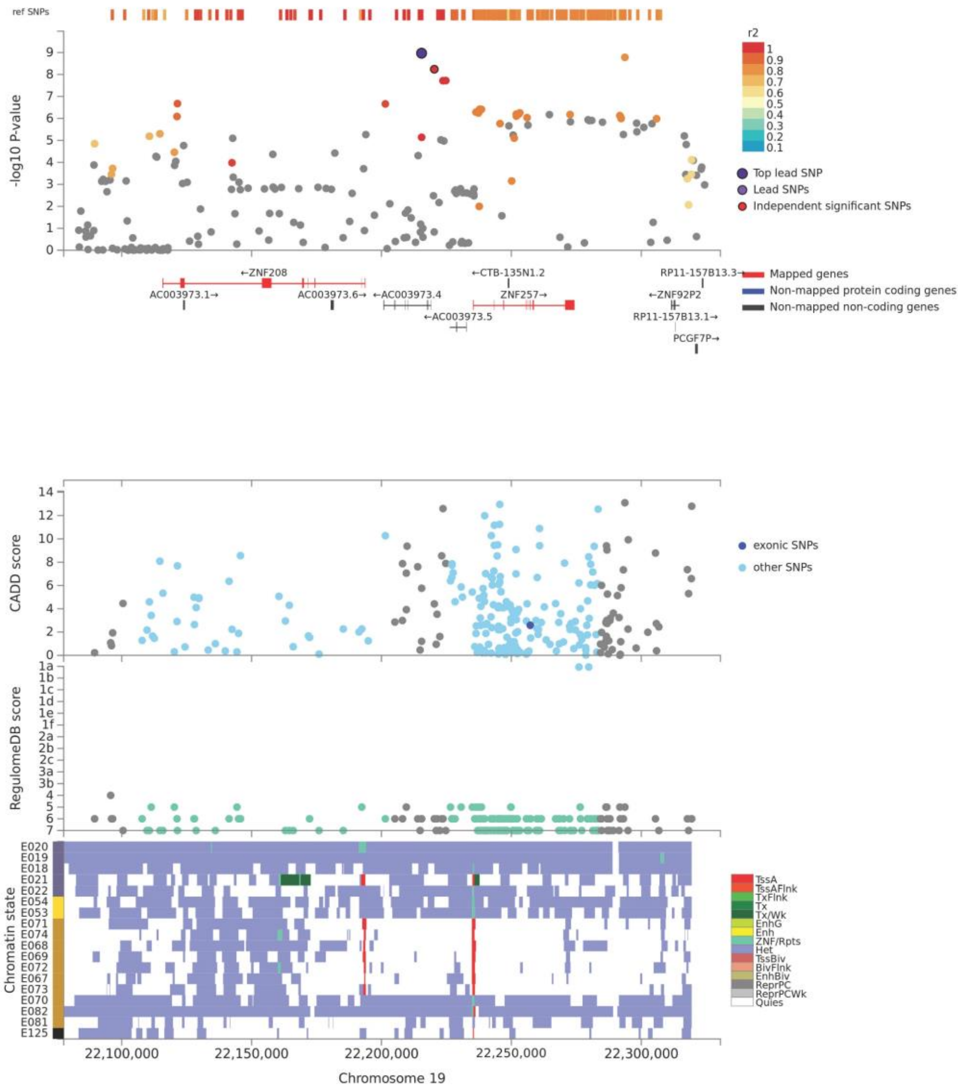
Epigenome ID

EID	Color	Group	Anatomy	Standerdized 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
	Likely to affect binding and linked to expression of a gene target
1a	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
	Likely to affect binding
2a	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
	Less likely to affect binding
3a	TF binding + any motif + DNase peak
3b	TF binding + matched TF motif
	Minimal binding evidence
4	TF binding + DNase peak
5	TF binding or DNase peak
6	Motif hit
	No binding evidence
7	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

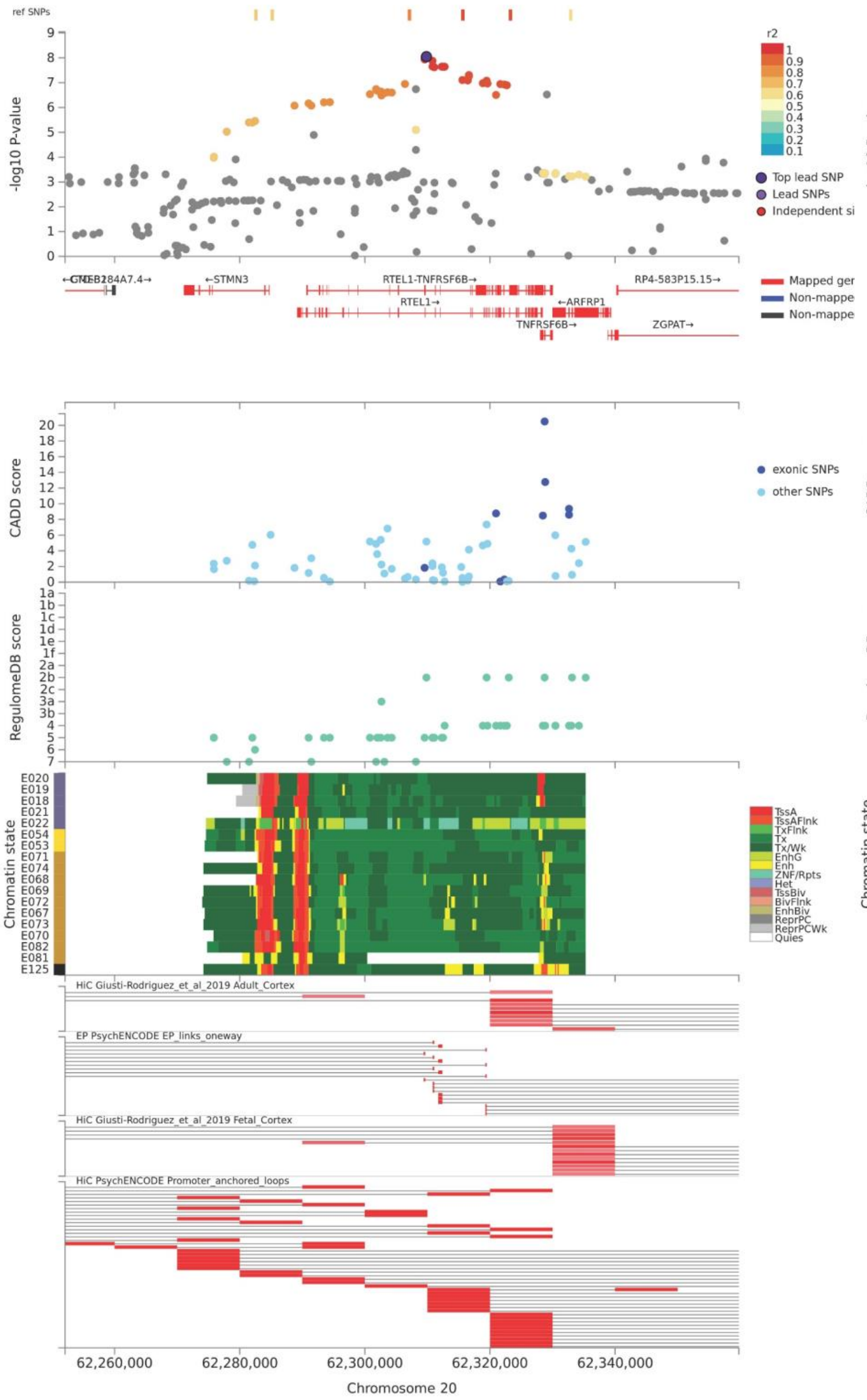
Epigenome ID

EID	Color	Group	Anatomy	Standerdized 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

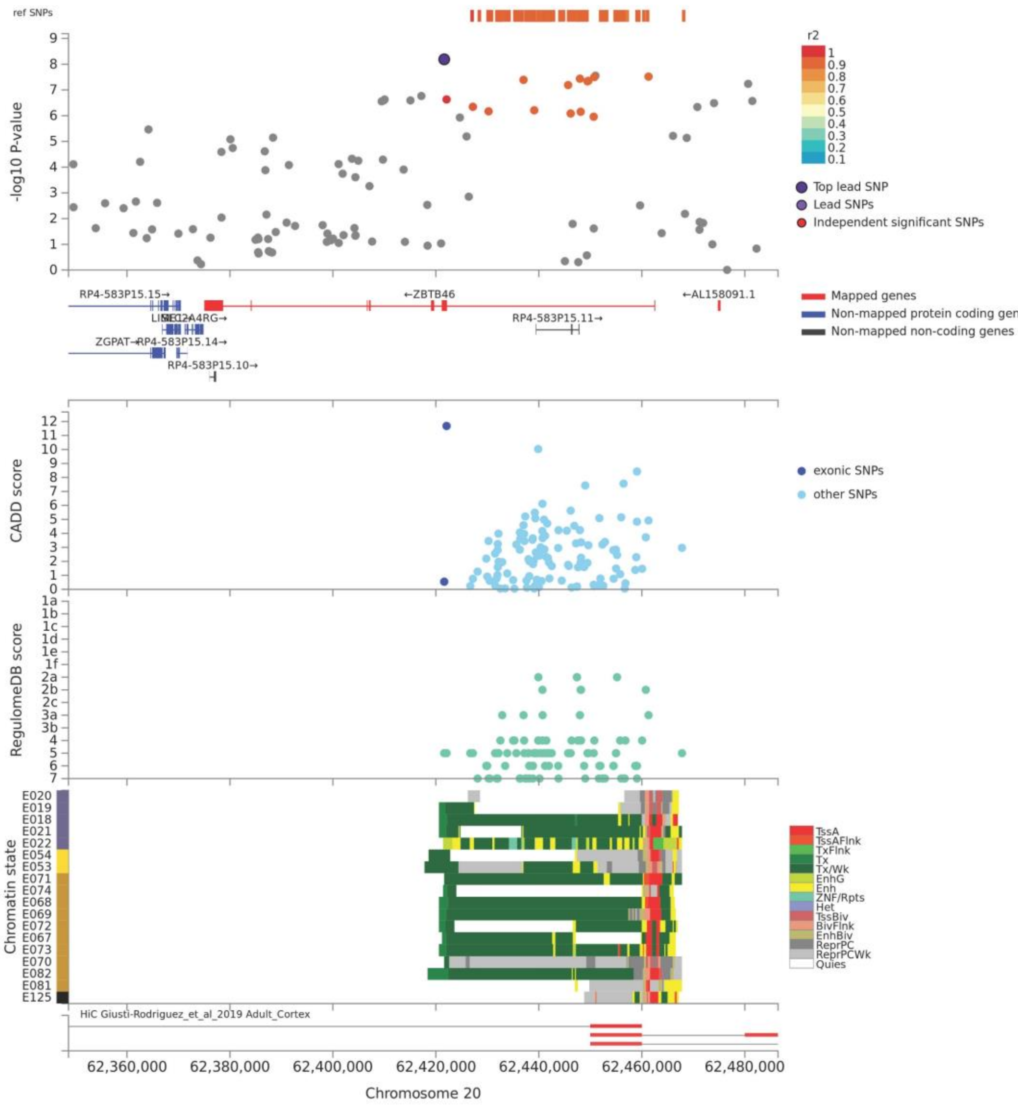
*When 15-core chromatin state is included in the plot and >30 cell types are selected, the labels of Y-axis are omitted. The order of the cell types is same as the legend table.

Chromosome 20

EAS



EUR



Regulome DB

RegulomeDB Categorical Scores

Category	Description
	Likely to affect binding and linked to expression of a gene target
1a	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
	Likely to affect binding
2a	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
	Less likely to affect binding
3a	TF binding + any motif + DNase peak
3b	TF binding + matched TF motif
	Minimal binding evidence
4	TF binding + DNase peak
5	TF binding or DNase peak
6	Motif hit
	No binding evidence
7	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

Epigenome ID

EID	Color	Group	Anatomy	Standerdized 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.

Chromatin mapping – Circos Plots

Locus shared between both populations

EUR

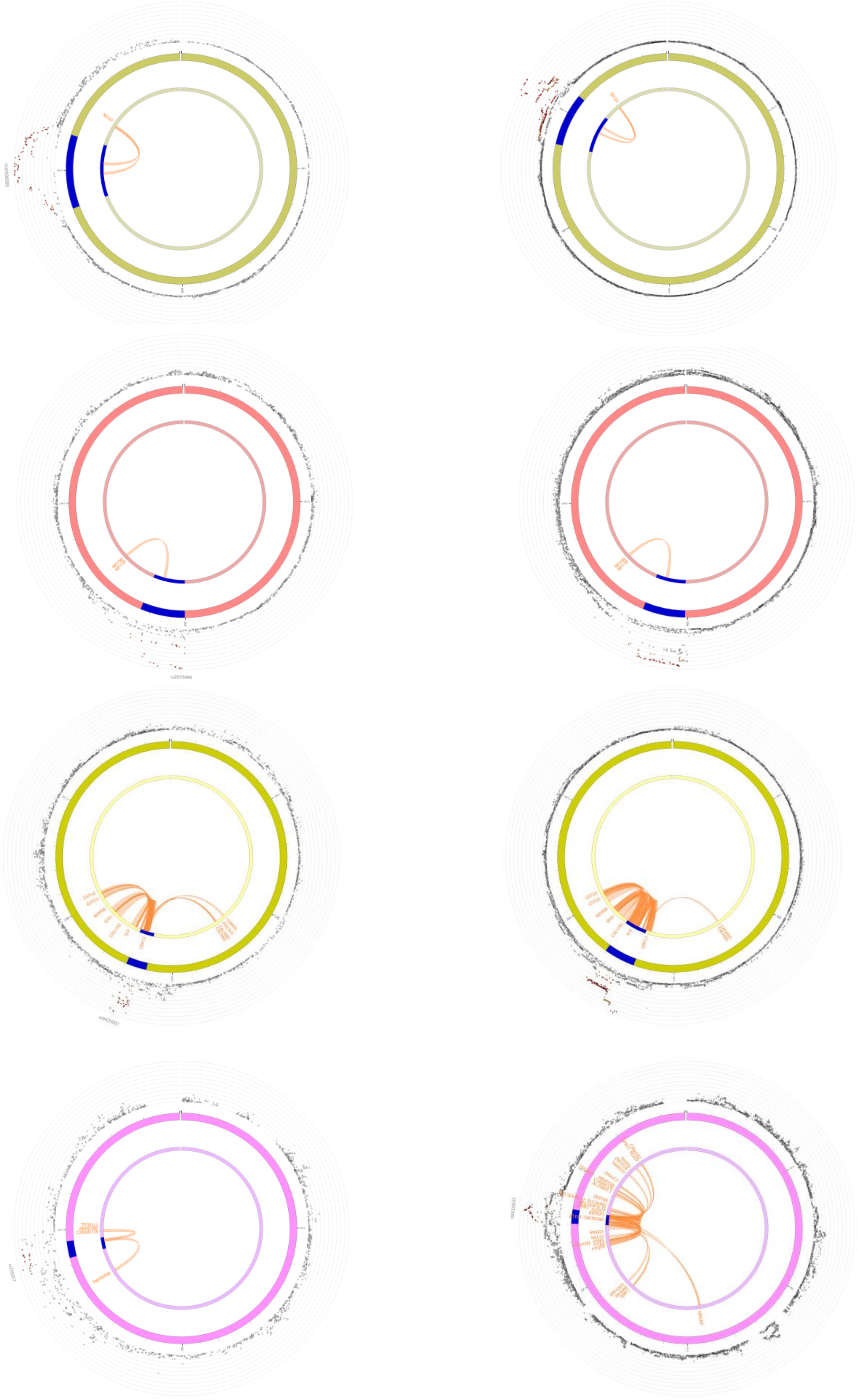
EAS

Chromosome 3

Chromosome 4

Chromosome 10

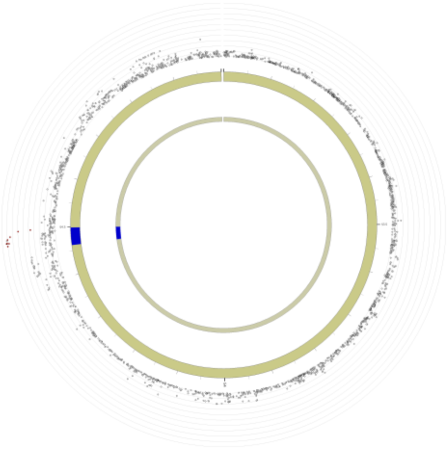
Chromosome 20



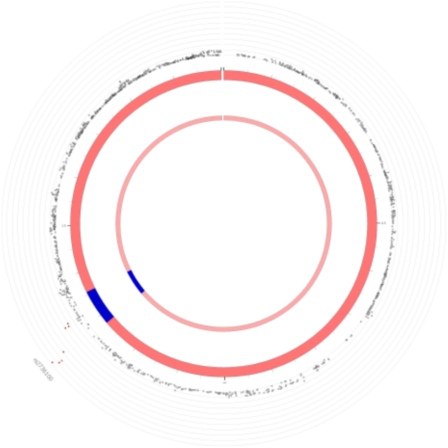
Locus NOT shared between both populations

EUR

Chromosome 2



Chromosome 5

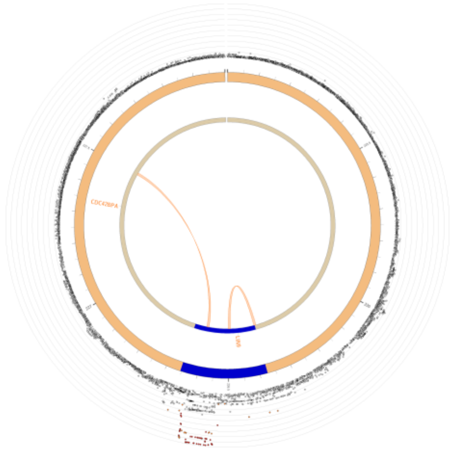


Chromosome 19

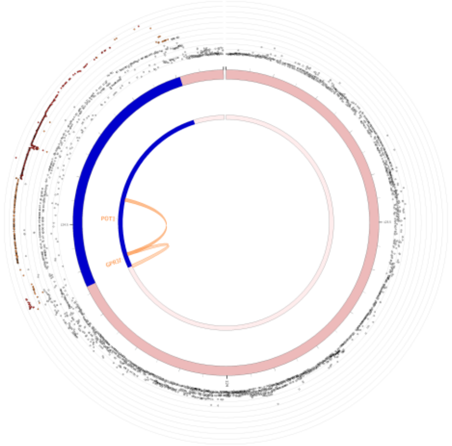
Locus NOT shared between both populations

EAS

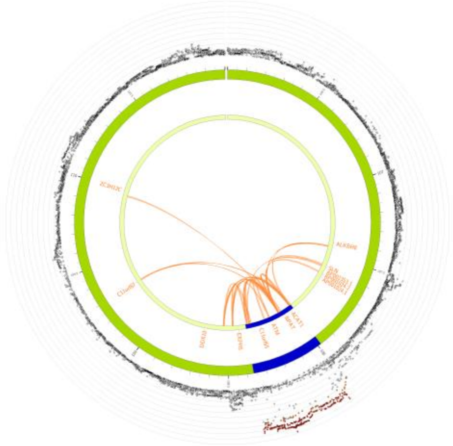
Chromosome 1



Chromosome 7



Chromosome 11



Chromosome 15