SUPPLEMENTARY INFORMATION

Allele-specific chromatin architecture shapes imprinted domains and coordinates a distal enhancer and antisense transcription at the mouse *Mest-Copg2* domain

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- **Supplementary Figures**
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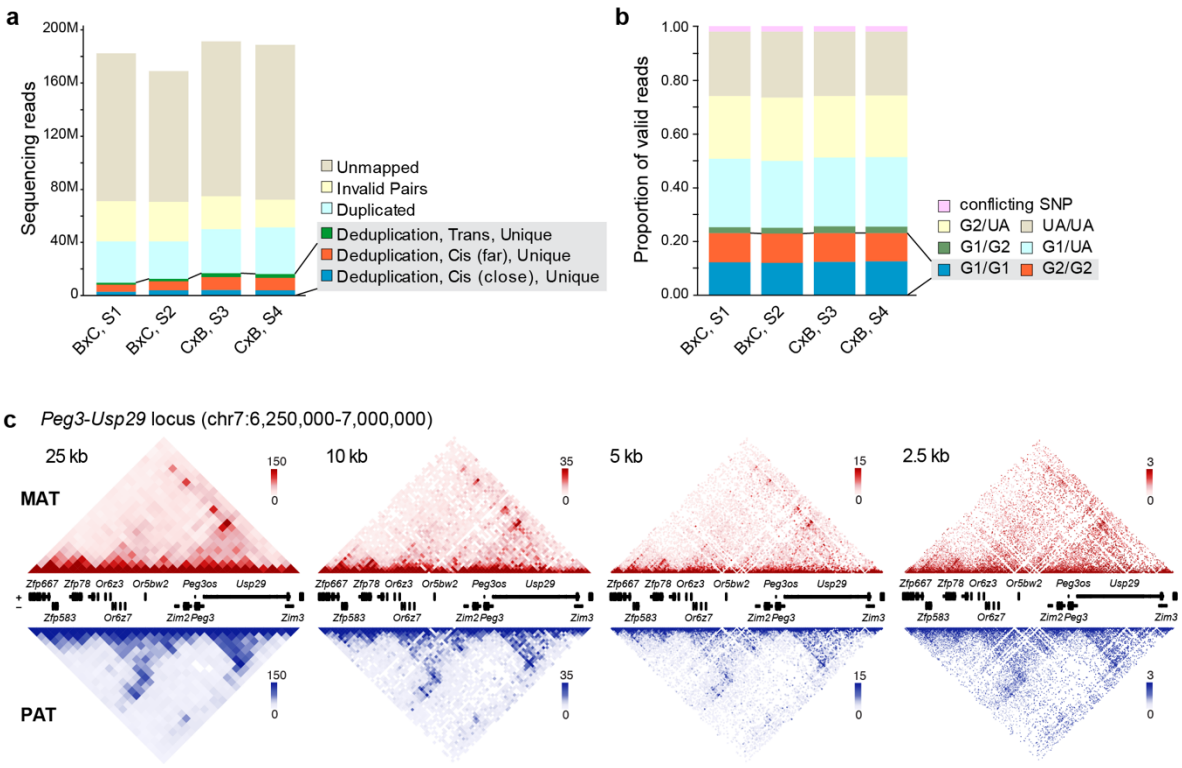
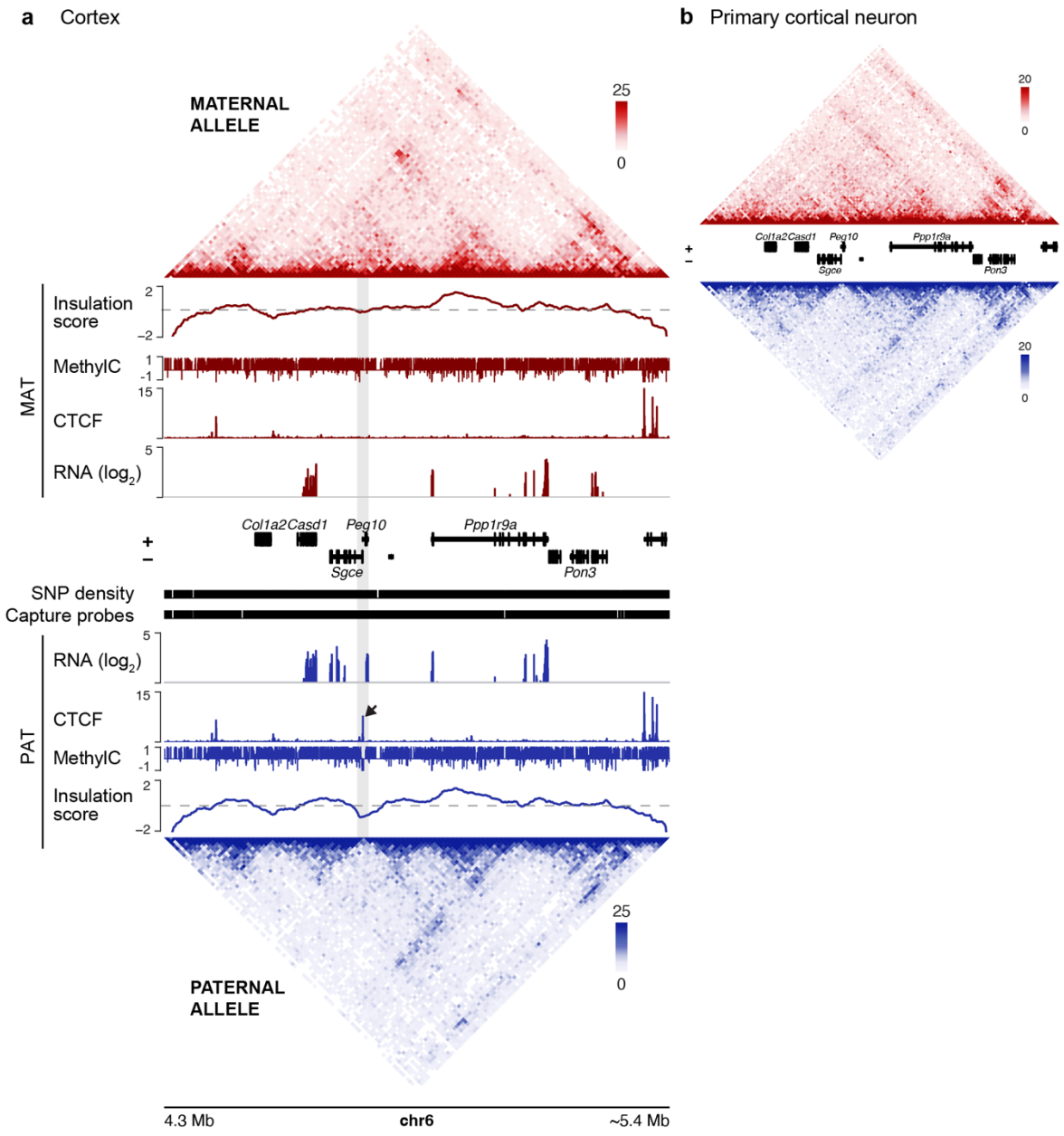
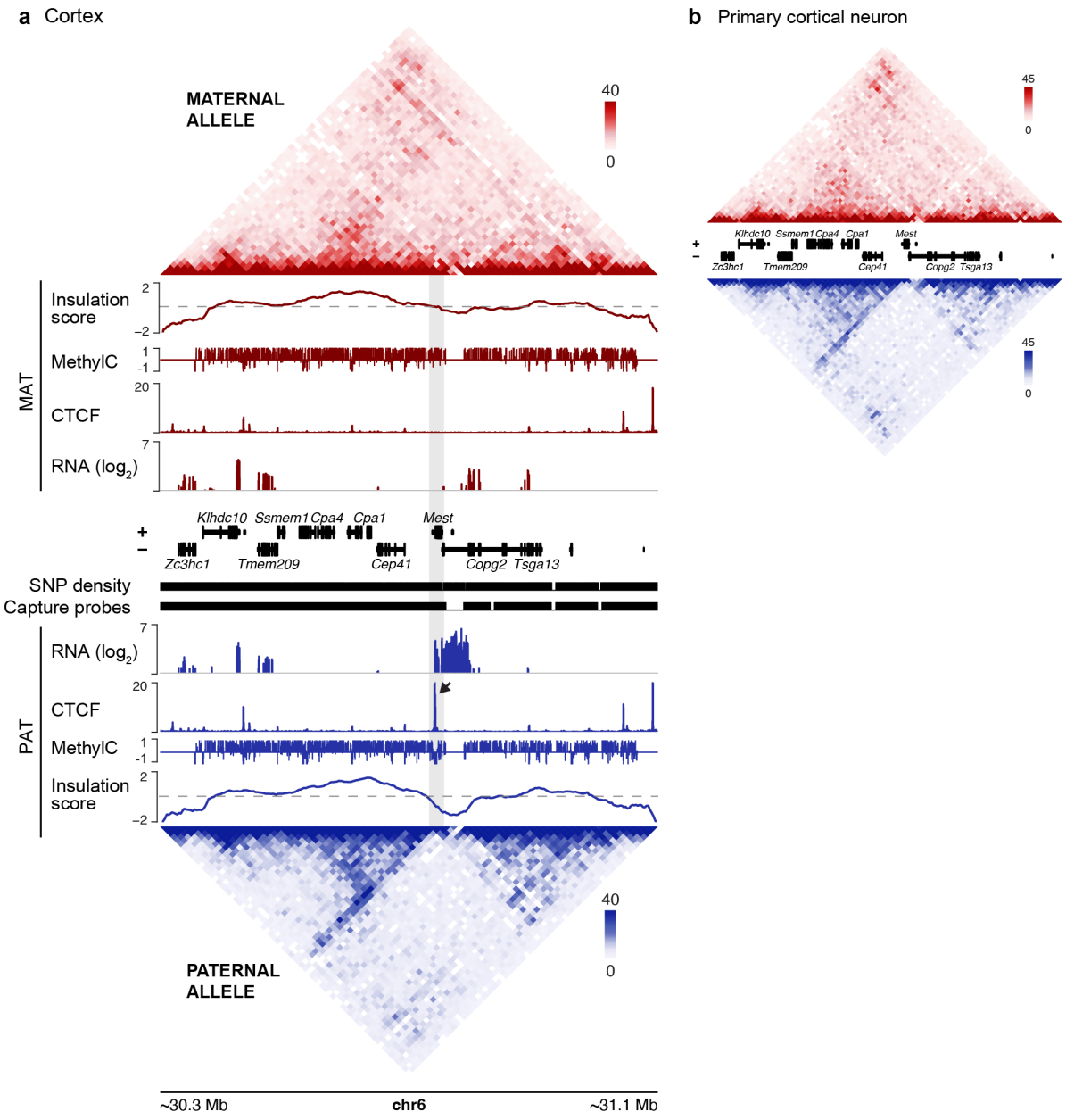


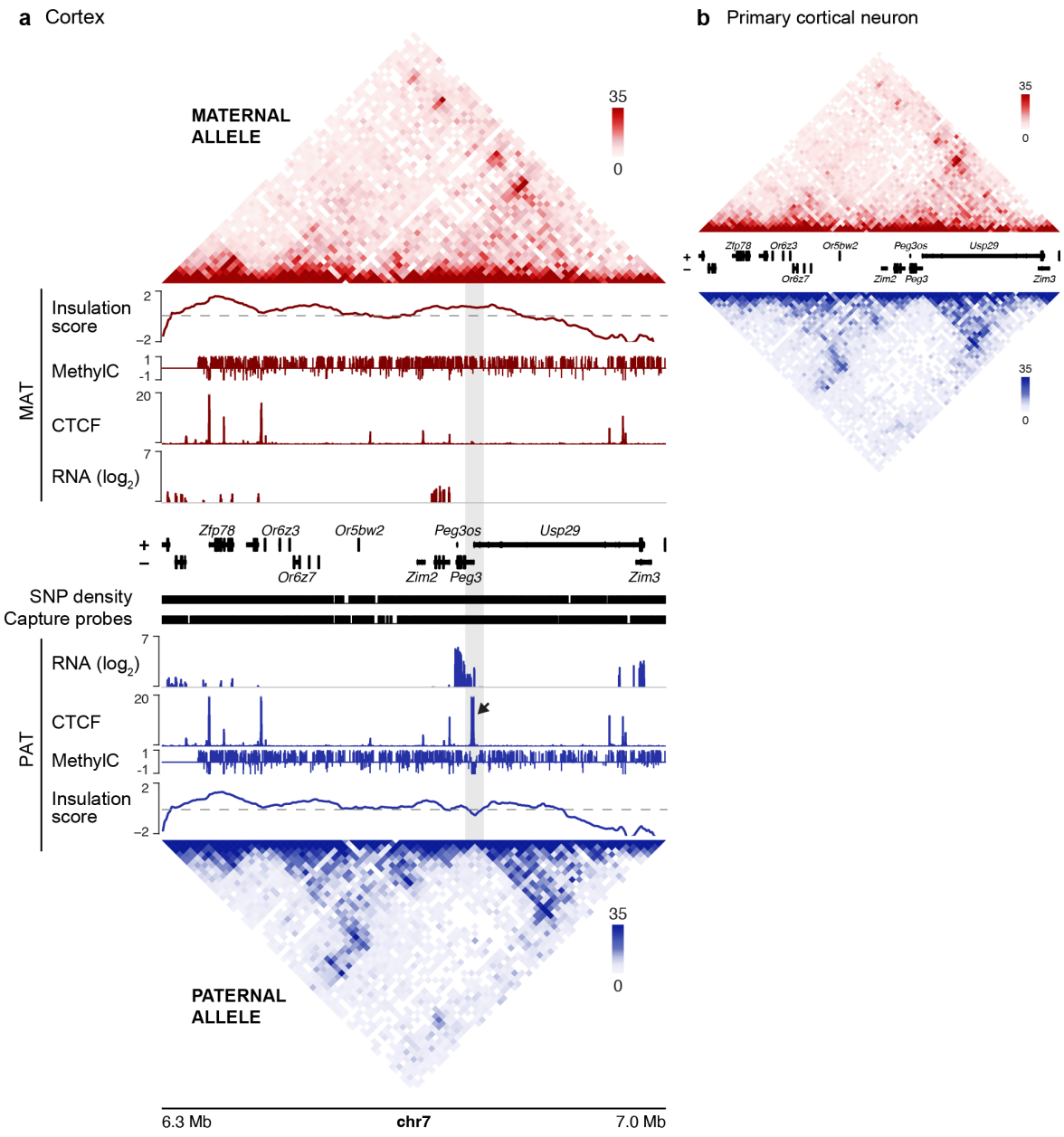
Supplementary Figure 1. Imprinted domains exhibit allele-specific chromatin architectures. (**a**) Number of paired-end reads generated by Capture Hi-C from hybrid mouse cortical samples (BL6 x CAST [BxC] and CAST x BL6 [CxB]). Deduplicated and ligated read pairs (gray box) were used for allele assignment. (**b**) Deduplicated reads were assigned to parental alleles based on SNPs. Same genome read pairs (G1-G1 and G2-G2; gray box) were used to generate Hi-C contract matrices. G1, genome 1 (BL6); G2, genome 2 (CAST); UA; unassigned. (**c**) Representative contact matrices at the *Peg3-Usp29* domain shown at 25, 10, 5, and 2.5 kb resolution. Maternal and paternal signals are shown red and blue, respectively. Matrices were normalized using square root vanilla coverage and displayed with GRCm39 annotations.



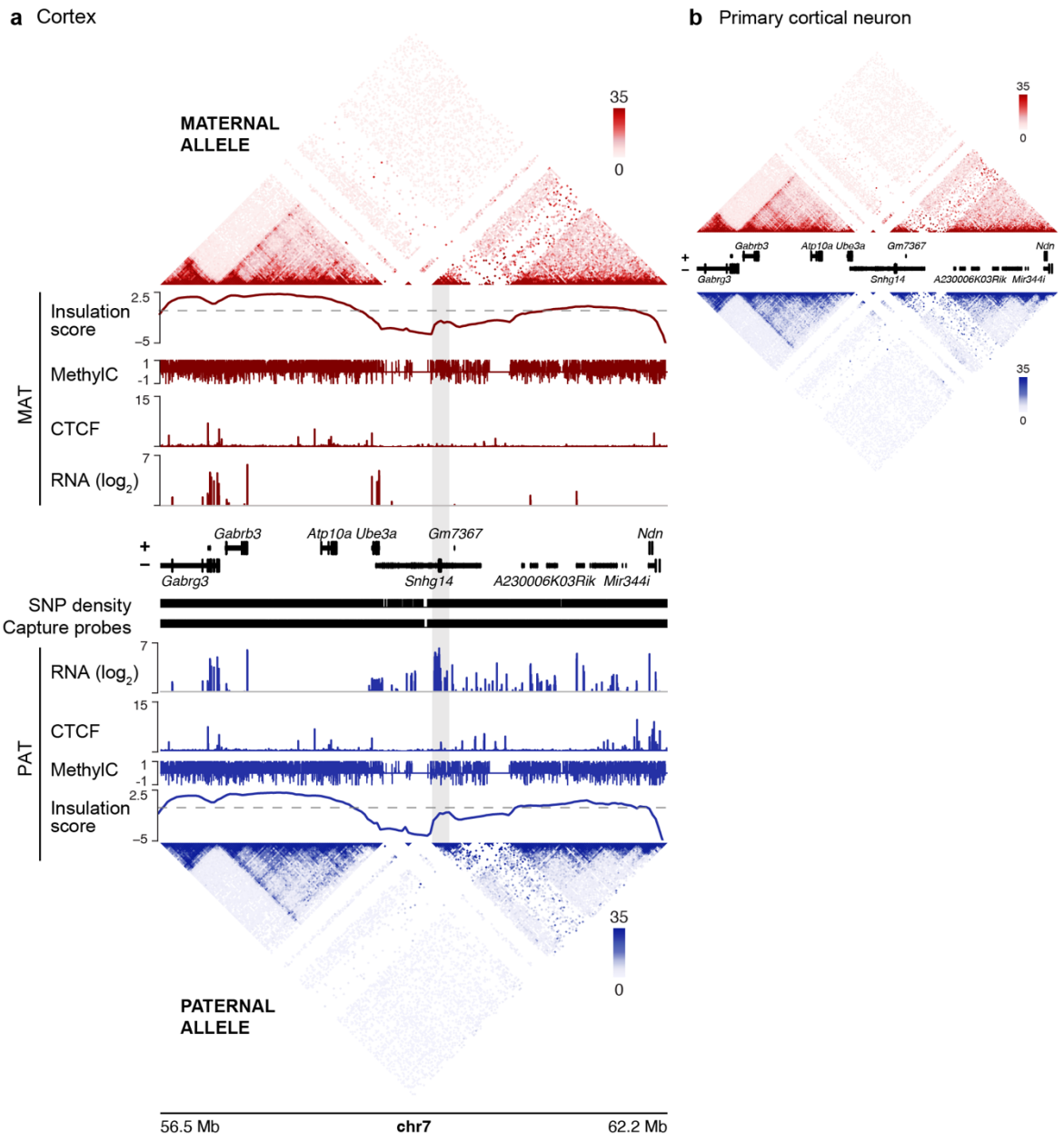
Supplementary Figure 2. Allele-specific chromatin architecture across imprinted domains. (**a**) Capture Hi-C contact matrices from hybrid mouse cortex at *Peg10-Sgce* imprinted domain, shown with insulation scores and aligned epigenetic and transcriptional profiles. Tracks include DNA methylation from hybrid cortex (MethylC)[1] and CTCF CUT&Tag and RNA-seq (log2 scale) from hybrid primary cortical neurons. Maternal and paternal signals are shown in red and blue, respectively. Gene annotations, CAST SNP density, and capture probe positions are shown in black. Gray shaded region highlights the ICR. (**b**) Capture Hi-C contact matrices at the same domains in primary cortical neurons.



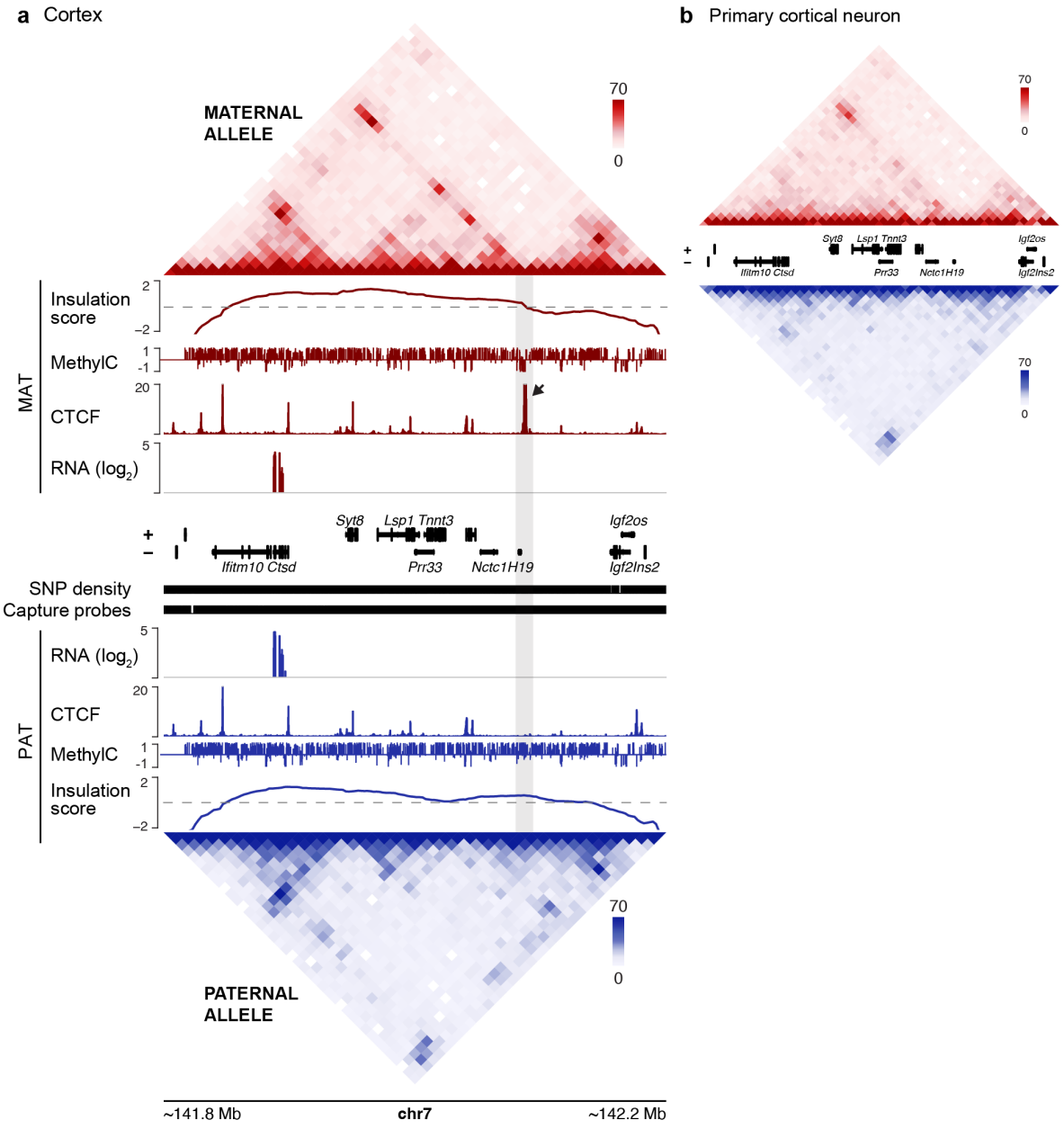
Supplementary Figure 3. Allele-specific chromatin architecture across imprinted domains. (**a**) Capture Hi-C contact matrices from hybrid mouse cortex at *Mest-Copg2* imprinted domain, shown with insulation scores and aligned epigenetic and transcriptional profiles. Tracks include DNA methylation from hybrid cortex (MethylC)[1] and CTCF CUT&Tag and RNA-seq (log2 scale) from hybrid primary cortical neurons. Maternal and paternal signals are shown in red and blue, respectively. Gene annotations, CAST SNP density, and capture probe positions are shown in black. Gray shaded region highlights the ICR. (**b**) Capture Hi-C contact matrices at the same domains in primary cortical neurons.



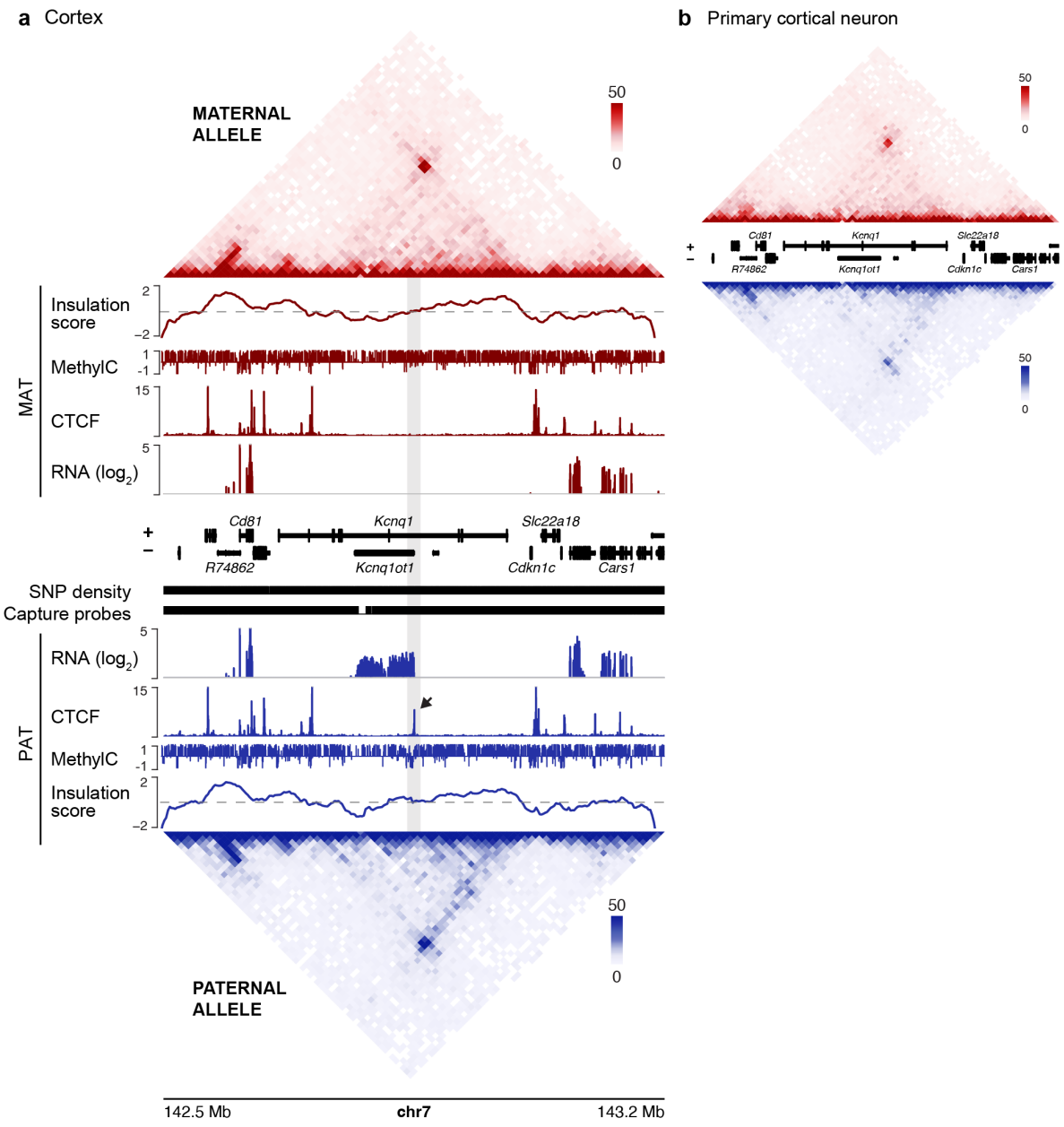
Supplementary Figure 4. Allele-specific chromatin architecture across imprinted domains. (**a**) Capture Hi-C contact matrices from hybrid mouse cortex at *Peg3-Usp29* imprinted domain, shown with insulation scores and aligned epigenetic and transcriptional profiles. Tracks include DNA methylation from hybrid cortex (MethylC)[1] and CTCF CUT&Tag and RNA-seq (log2 scale) from hybrid primary cortical neurons. Maternal and paternal signals are shown in red and blue, respectively. Gene annotations, CAST SNP density, and capture probe positions are shown in black. Gray shaded region highlights the ICR. (**b**) Capture Hi-C contact matrices at the same domains in primary cortical neurons.



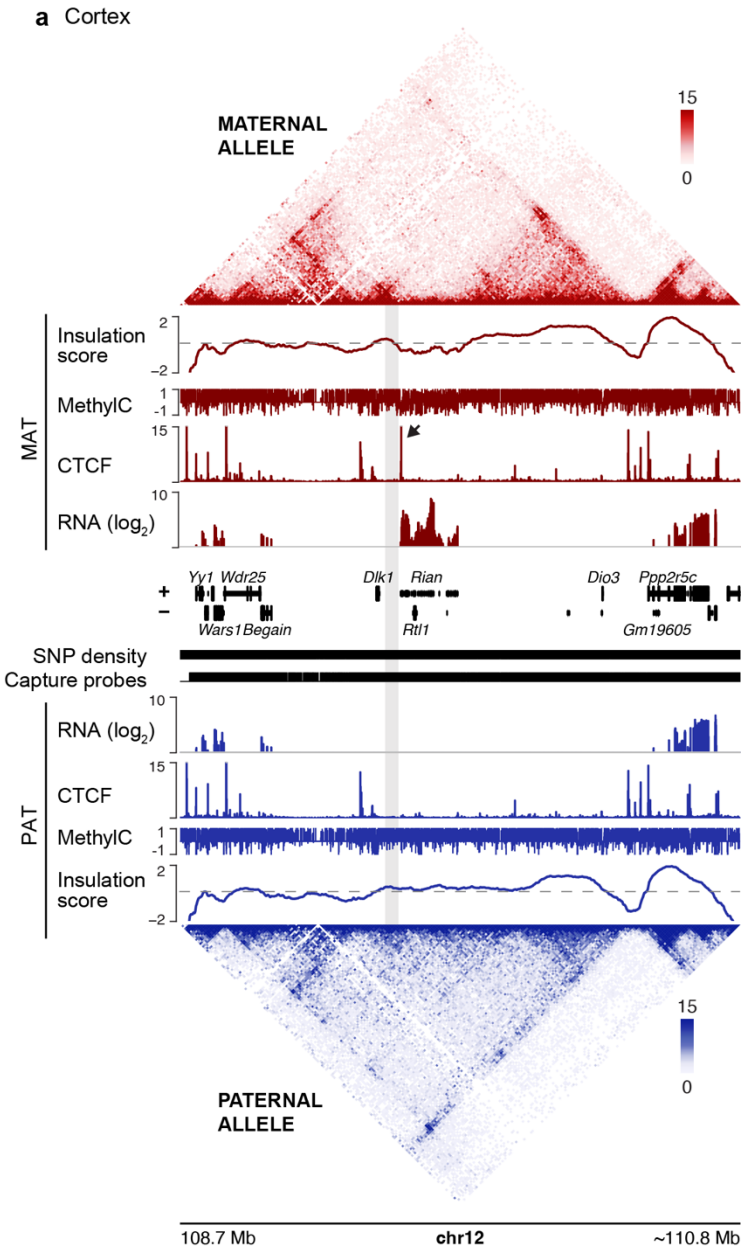
Supplementary Figure 5. Allele-specific chromatin architecture across imprinted domains. (**a**) Capture Hi-C contact matrices from hybrid mouse cortex at *Snrpn-Peg12* imprinted domain, shown with insulation scores and aligned epigenetic and transcriptional profiles. Tracks include DNA methylation from hybrid cortex (MethylC)[1] and CTCF CUT&Tag and RNA-seq (log2 scale) from hybrid primary cortical neurons. Maternal and paternal signals are shown in red and blue, respectively. Gene annotations, CAST SNP density, and capture probe positions are shown in black. Gray shaded region highlights the ICR. (**b**) Capture Hi-C contact matrices at the same domains in primary cortical neurons.



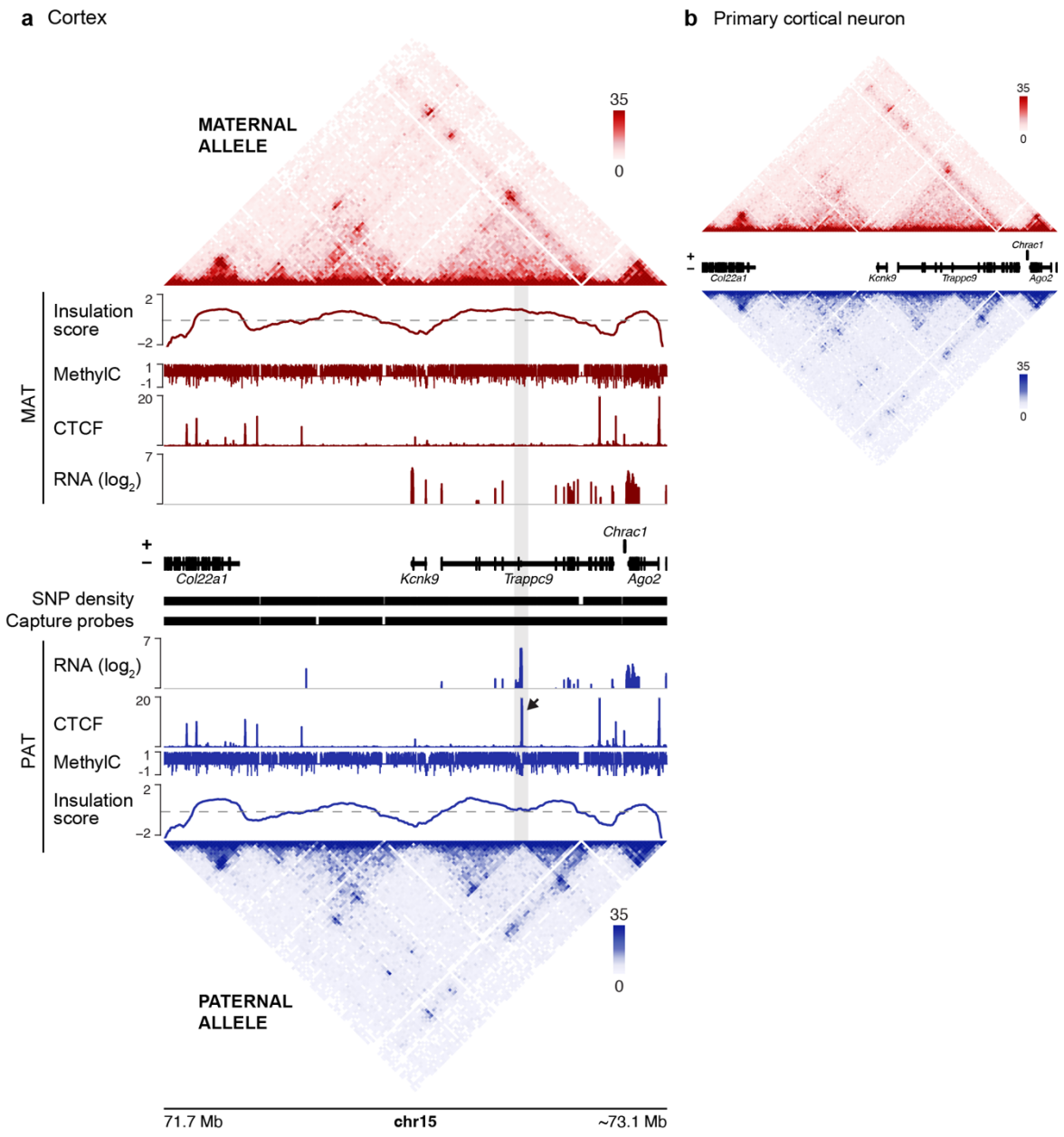
Supplementary Figure 6. Allele-specific chromatin architecture across imprinted domains. (**a**) Capture Hi-C contact matrices from hybrid mouse cortex at *H19-Igf2* imprinted domain, shown with insulation scores and aligned epigenetic and transcriptional profiles. Tracks include DNA methylation from hybrid cortex (MethylC)[1] and CTCF CUT&Tag and RNA-seq (log2 scale) from hybrid primary cortical neurons. Maternal and paternal signals are shown in red and blue, respectively. Gene annotations, CAST SNP density, and capture probe positions are shown in black. Gray shaded region highlights the ICR. (**b**) Capture Hi-C contact matrices at the same domains in primary cortical neurons.



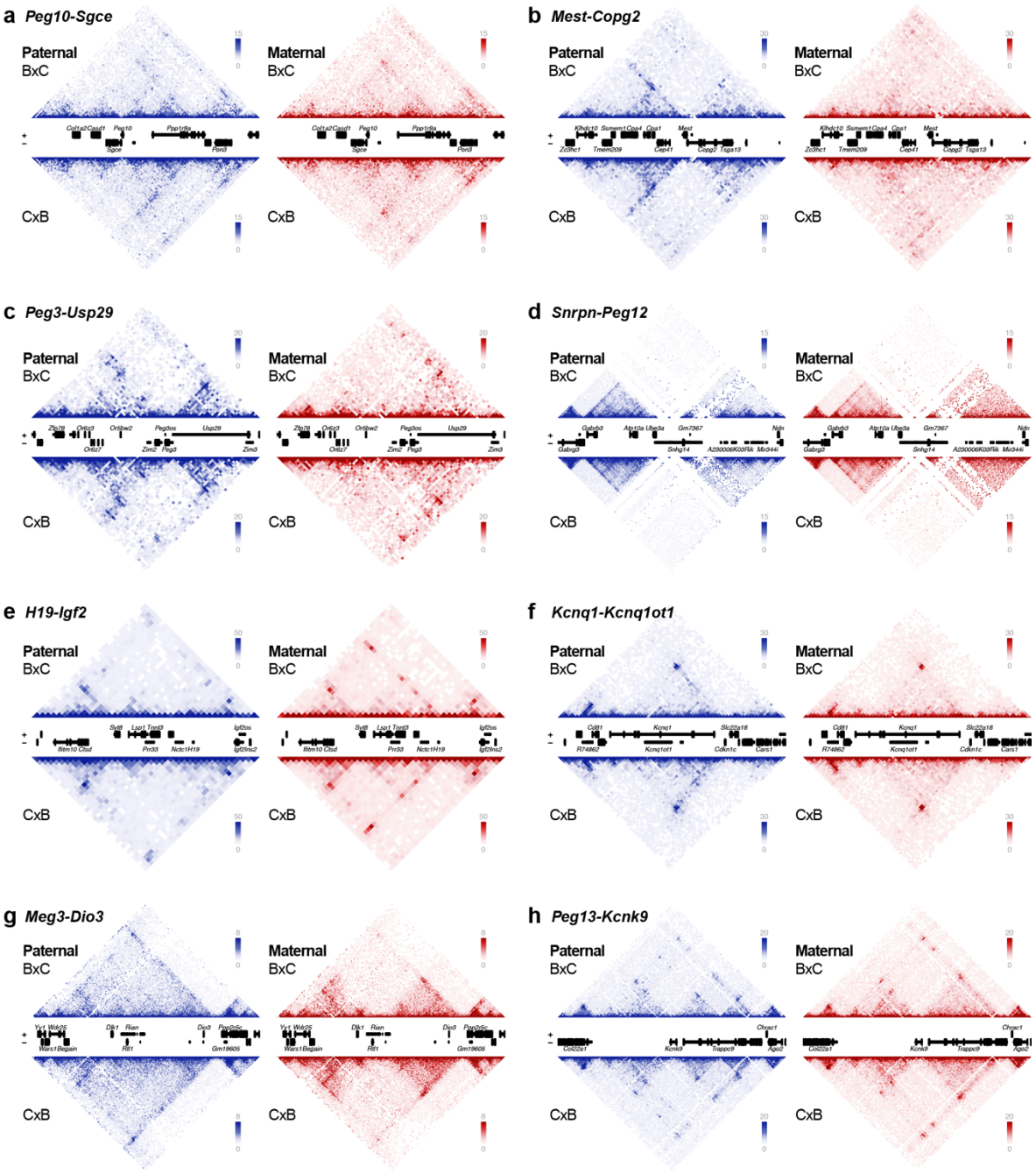
Supplementary Figure 7. Allele-specific chromatin architecture across imprinted domains. (**a**) Capture Hi-C contact matrices from hybrid mouse cortex at *Kcnq1-Kcnq1ot1* imprinted domain, shown with insulation scores and aligned epigenetic and transcriptional profiles. Tracks include DNA methylation from hybrid cortex (MethylC)[1] and CTCF CUT&Tag and RNA-seq (log2 scale) from hybrid primary cortical neurons. Maternal and paternal signals are shown in red and blue, respectively. Gene annotations, CAST SNP density, and capture probe positions are shown in black. Gray shaded region highlights the ICR. (**b**) Capture Hi-C contact matrices at the same domains in primary cortical neurons.



Supplementary Figure 8. Allele-specific chromatin architecture across imprinted domains. (**a**) Capture Hi-C contact matrices from hybrid mouse cortex at *Meg3-Dio3* imprinted domain, shown with insulation scores and aligned epigenetic and transcriptional profiles. Tracks include DNA methylation from hybrid cortex (MethylC)[1] and CTCF CUT&Tag and RNA-seq (log2 scale) from hybrid primary cortical neurons. Maternal and paternal signals are shown in red and blue, respectively. Gene annotations, CAST SNP density, and capture probe positions are shown in black. Gray shaded region highlights the ICR.

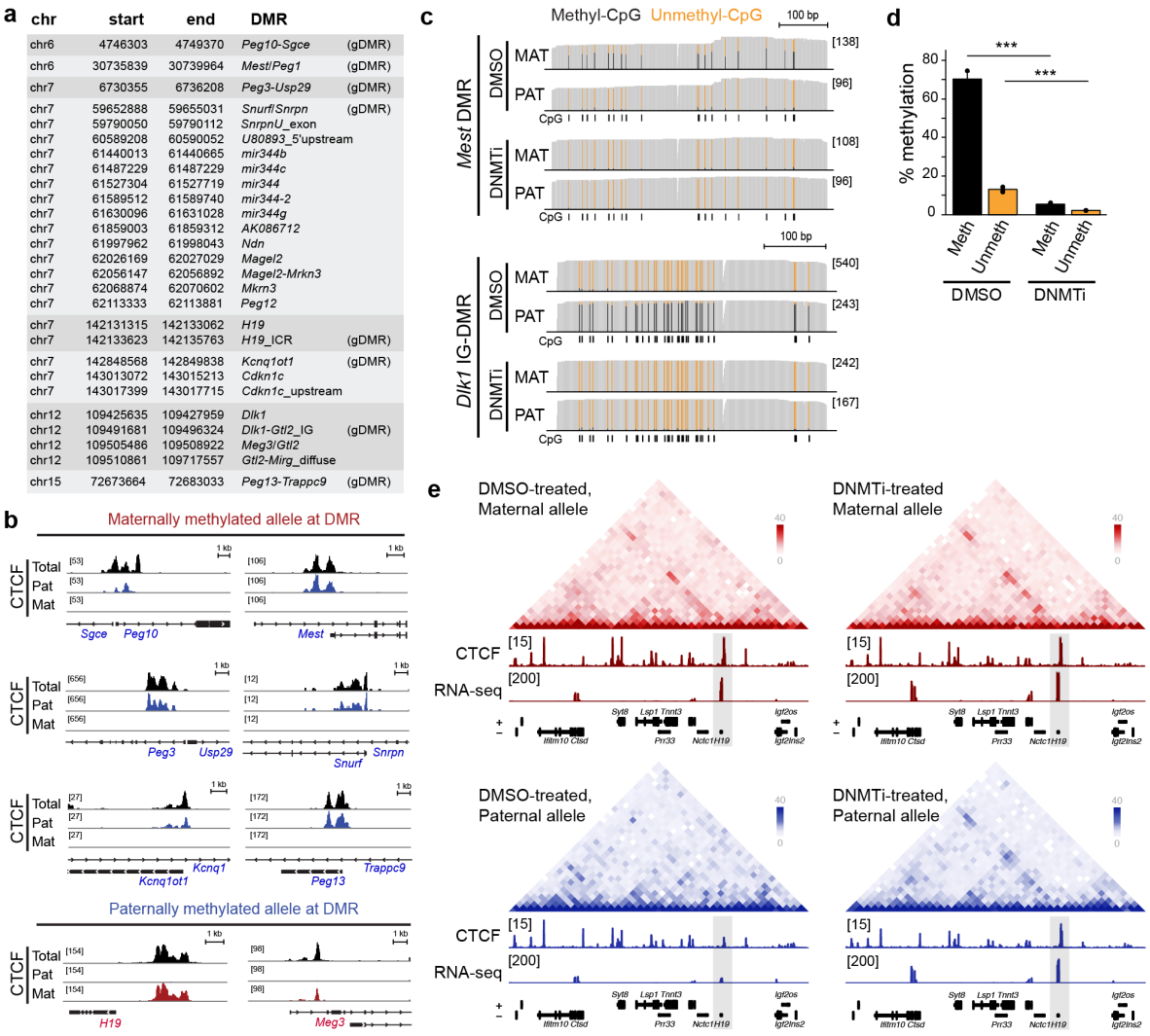


Supplementary Figure 9. Allele-specific chromatin architecture across imprinted domains. (**a**) Capture Hi-C contact matrices from hybrid mouse cortex at *Peg13-Kcnk9* imprinted domain, shown with insulation scores and aligned epigenetic and transcriptional profiles. Tracks include DNA methylation from hybrid cortex (MethylC)[1] and CTCF CUT&Tag and RNA-seq (log2 scale) from hybrid primary cortical neurons. Maternal and paternal signals are shown in red and blue, respectively. Gene annotations, CAST SNP density, and capture probe positions are shown in black. Gray shaded region highlights the ICR. (**b**) Capture Hi-C contact matrices at the same domains in primary cortical neurons.



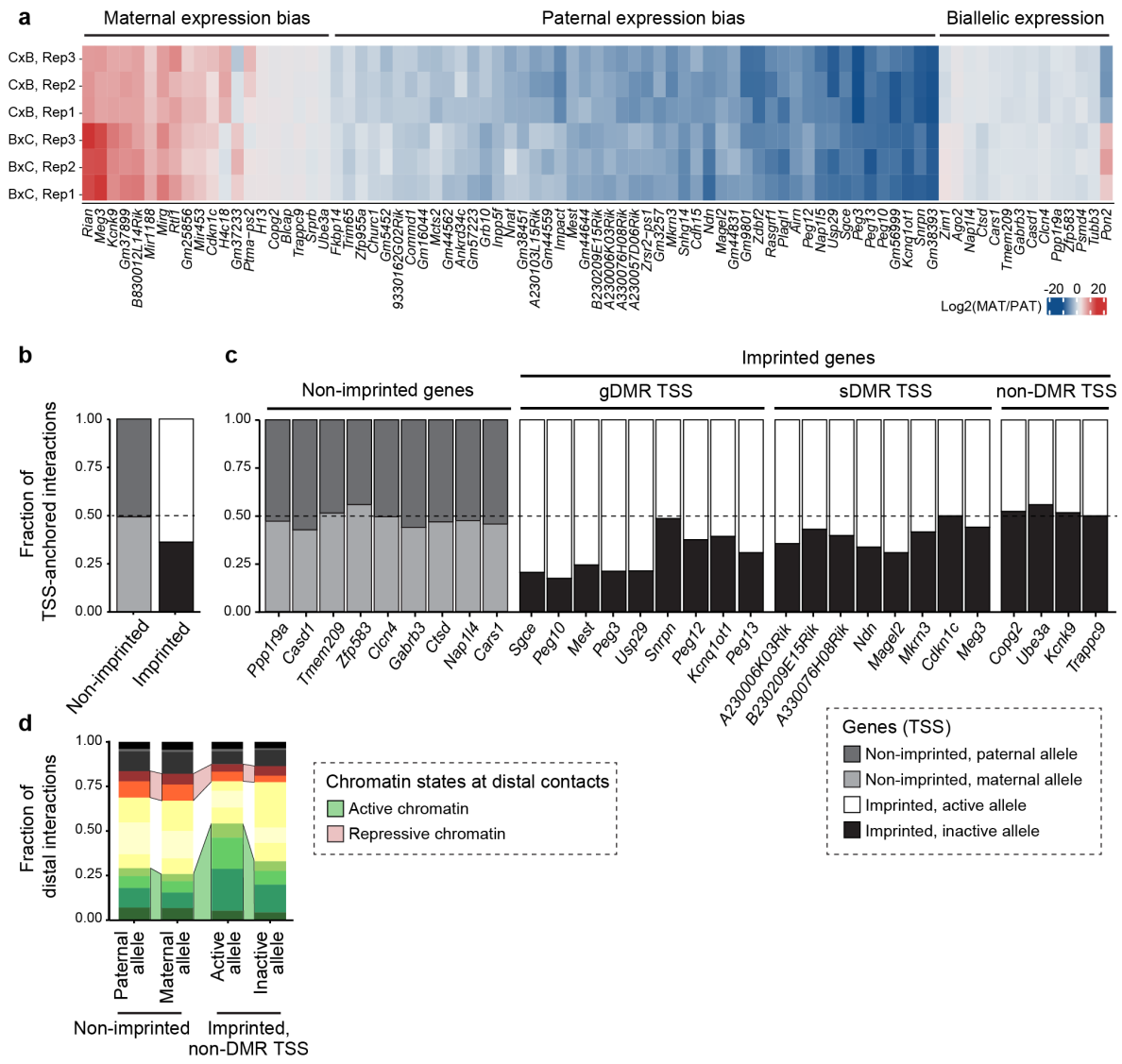
Supplementary Figure 10. Allele-specific chromatin architectures are consistent between reciprocal crosses.

(**a-h**) Capture Hi-C contact matrices from hybrid mouse cortex at eight imprinted domains, shown separately for maternal (red) and paternal (blue) alleles. Data are shown for reciprocal crosses (BL6 x CAST [BxC] and CAST x BL6 [CxB]) using GRCm39 annotations.



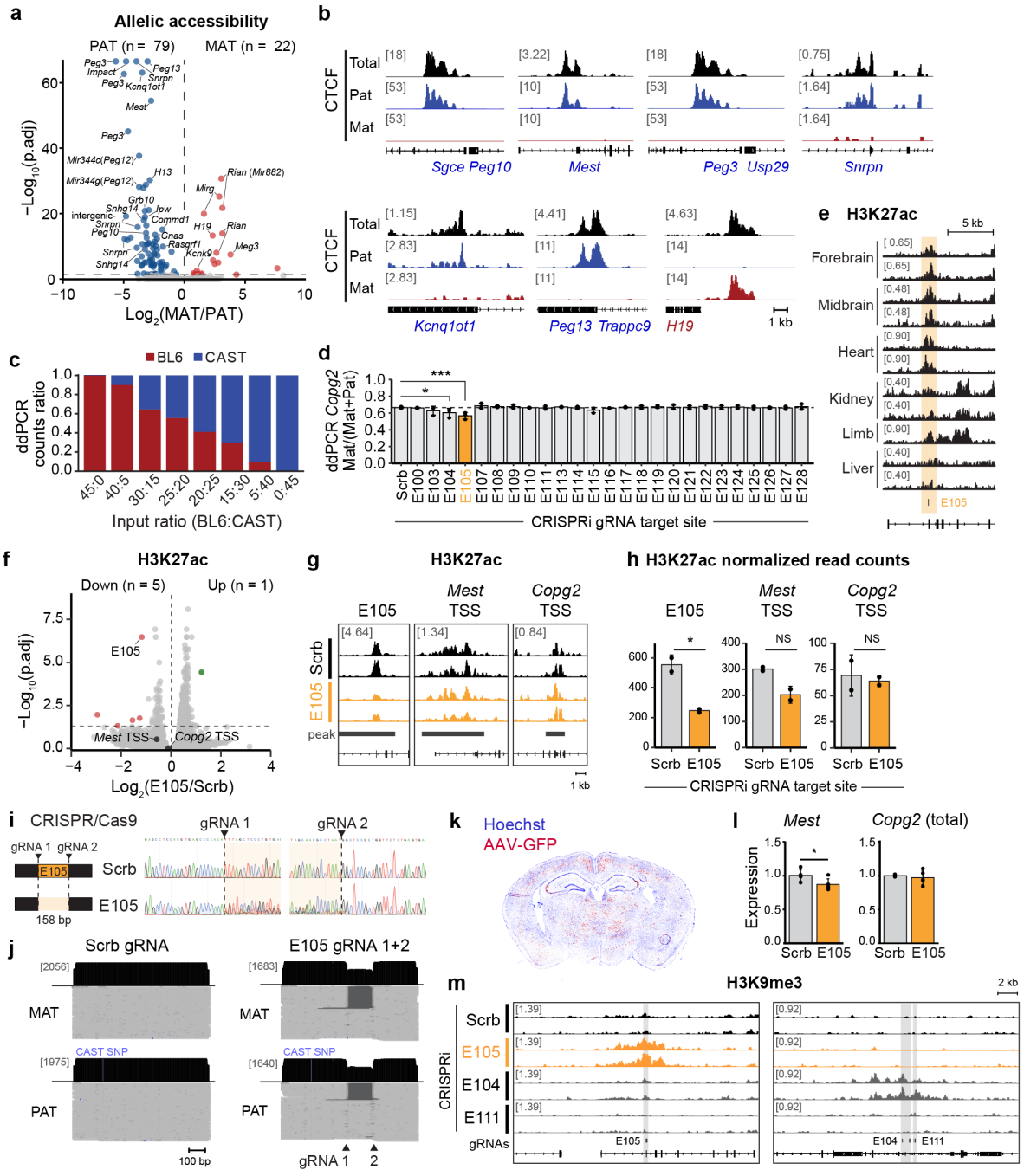
Supplementary Figure 11. Methylation-sensitive CTCF binding at ICRs organizes allele-specific chromatin architecture.

(**a**) Annotated DMRs within capture regions in mouse cortex[1]. (**b**) Counts per million (CPM)-normalized total and allele-specific CTCF signal at indicated DMRs in primary cortical neurons. (**c**) Representative nanopore sequencing tracks from bisulfite-treated genomic DNA in DMSO- and DNMTi-treated mESCs. (**d**) Average CpG methylation across analyzed gDMRs, including *Peg10-Sgce*, *Mest*/*Peg1*, *Peg3-Usp29*, *Snurf*/*Snrpn*, *H19* ICR, *Dlk1-Gtl2* intergenic, and *Peg13-Trappc9*. Meth = normally methylated allele, Unmeth = normally unmethylated allele. Data are presented as mean values +/- SD. n = 3 biological replicates per group. ***p < 0.0001 (Two-sided t-test). (**e**) Capture Hi-C matrices, CTCF CUT&Tag, and RNA-seq tracks at the *H19-Igf2* domain in DMSO- and DNMTi-treated mESCs, shown separately for maternal and paternal alleles.



Supplementary Figure 12. Imprinted gene promoters exhibit allelic differences in distal chromatin contacts in primary cortical neurons.

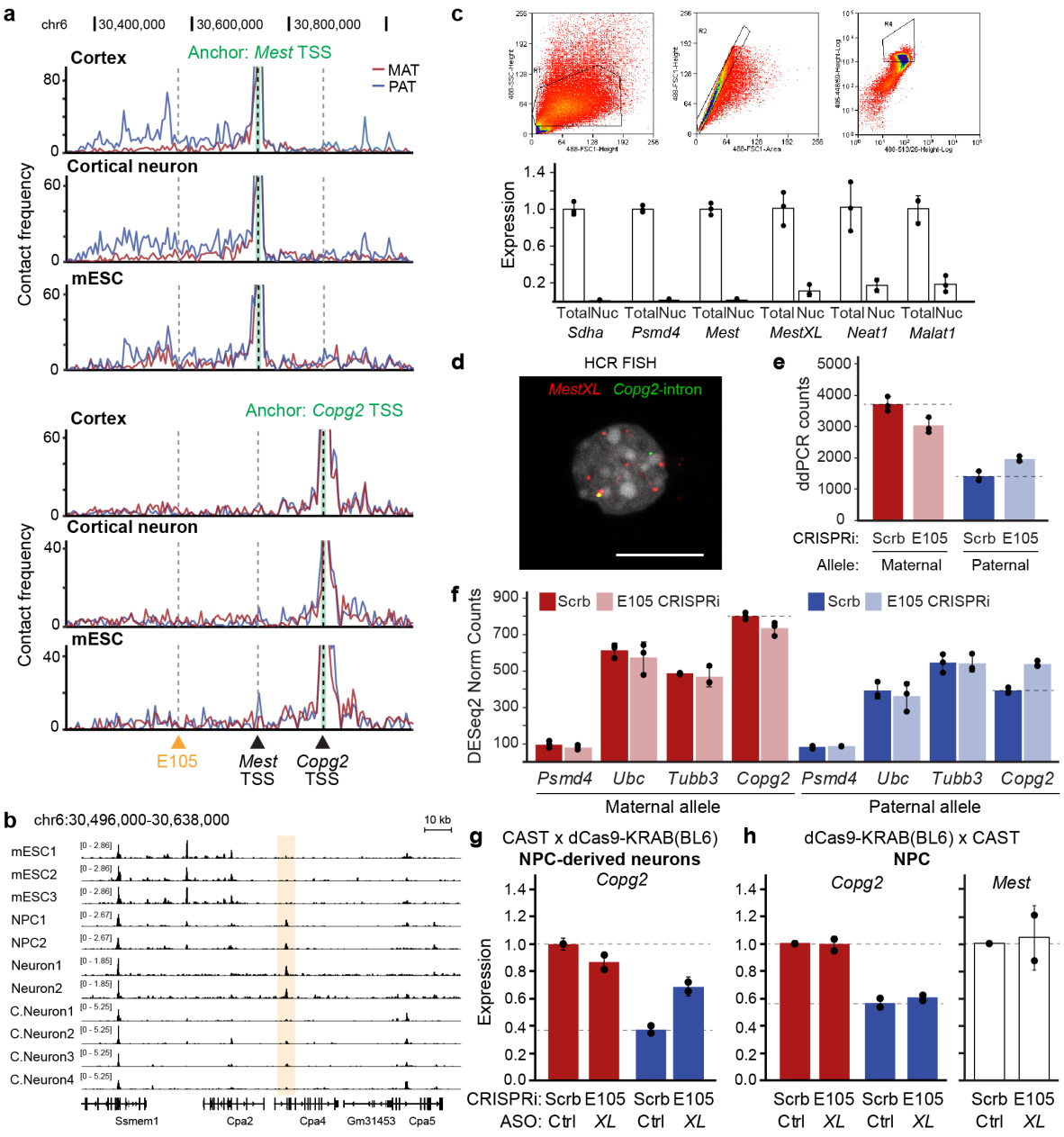
(**a**) Heatmap of allele-specific RNA expression from primary cortical neurons. Rows correspond to biological replicates from reciprocal crosses. (**b,c**) Fraction of TSS-anchored contacts per allele for non-imprinted and imprinted genes. (**d**) Fraction of TSS-anchored contacts stratified by chromatin state of distal interacting regions. n = 4 biological replicates.



Supplementary Figure 13. CRISPRi screening identifies candidate regulatory elements.

(**a**) Volcano plot of allele-specific ATAC-seq peaks in mouse cortex. n = 3 biological replicates per reciprocal cross (BL6 x CAST and CAST x B6). (**b**) Counts per million (CPM)-normalized total and allele-specific CTCF signal at indicated DMRs in NPC-derived neurons. (**c**) Validation of *Copg2* ddPCR probes using synthetic oligonucleotides containing BL6- or CAST-specific SNPs mixed at known ratios. (**d**) Allelic *Copg2* expression in NPC-derived neurons following CRISPRi

same as in Figure 5d, represented as maternal fraction. Source data are provided as a Source Data file. (**e**) H3K27ac profiles at the E105 region across E15.5 mouse tissues (ENCODE). (**f-h**) H3K27ac profiles in NPC-derived neurons following CRISPRi targeting. (**f**) Volcano plot of differential H3K27ac signal. (**g**) H3K27ac tracks at regions of interest. (**h**) Quantification of H3K27ac signal at regions of interest. (**i**) Schematic of E105 dual gRNA targeting approach using Cas9, and Sanger sequencing traces confirming indels at E105. (**j**) Nanopore sequencing traces of PCR-amplified E105 region confirming heterogeneous population of indels and deletions. (**k**) Representative brain sections showing AAV-derived GFP signal (red). (**l**) Relative *Mest* and *Copg2* expression following in vivo CRISPRi targeting. Data are presented as mean values +/- SD. n = 5 mice; *p = 0.0353 (Two-sided t-test). (**m**) CPM-normalized H3K9me3 tracks at regions of interest following CRISPRi targeting. The gray shaded regions highlight putative enhancer/target sites.



Supplementary Figure 14. Allele-specific chromatin interactions and *MestXL* function.

(**a**) Virtual 4C profiles from mouse cortex, primary cortical neurons, and mESCs anchored at *Mest* or *Copg2* TSSs showing allele-specific contact frequencies. Maternal and paternal contacts are shown in red and blue, respectively. The green shaded regions indicate anchor points. (**b**) CTCF tracks from mESC, NPCs, NPC-derived neurons, and primary cortical neurons at E105 region. (**c**) RT-qPCR analysis of *MestXL* enrichment in nuclear versus total RNA fractions in NPC-derived neurons. Nuclear fractions were obtained by flow cytometry. A scatter plot to remove debris (FSC-H vs SSC-H), a doublet discrimination plot (FSC-A vs FSC-H), and a nuclei gate (R4) based on

Hoechst (405-448/59H vs open 488-513/26H) are shown. Expression was normalized to *Meg3.* Data are presented as mean values +/- SD. n = 3 biological replicates. Source data are provided as a Source Data file. (**d**) Fluorescence in situ hybridization for *MestXL* (red) and *Copg2* intron (green). Nuclei counterstain in gray. Scale bar = 10 μm. Images were acquired in a single experiment. A representative image is shown from 6 images taken. (**e**) Absolute RT-ddPCR counts showing maternal and paternal *Copg2* transcript levels following CRISPRi targeting in NPC-derived neurons. Data are presented as mean values +/- SD. n = 3 biological replicates. Source data are provided as a Source Data file. (**f**) DEseq2-normalized RNA-seq counts showing allele-specific *Copg2* expression following CRISPRi targeting in NPC-derived neurons. (**g**) Allele-specific *Copg2* expression measured by RT-ddPCR following CRISPRi targeting of E105 and *MestXL* knockdown in CAST x dCas9-KRAB(BL6) NPC-derived neurons. Data are presented as mean values +/- SD. n = 2 biological replicates. Source data are provided as a Source Data file. (**h**) Allele-specific *Copg2* expression measured by RT-ddPCR following CRISPRi targeting of E105 and *MestXL* knockdown in dCas9-KRAB x CAST NPCs. Data are presented as mean values +/- SD. n = 2 biological replicates. Source data are provided as a Source Data file.

Supplementary Table 1. Guide RNA sequences

Target Name	gRNA sequence	Coordinates (GRCm39/mm39)	Method
Scrb	GCCTCGCCTTATCGTCACCT	NA	CRISPRi, CRISPR/Cas9
E100_g1	TGTCAGTGAGAGTGTACAAT	chr6:30526999-30527018 (-)	CRISPRi
E100_g2	GCTCTGAAAACAGACAGGCA	chr6:30527148-30527167 (+)	CRISPRi
E100_g3	CTGCTCGAATCACTCCACAG	chr6:30527064-30527083 (-)	CRISPRi
E100_g4	GAAAGGGAGGCAATCAGCAG	chr6:30526950-30526969 (-)	CRISPRi
E103_g1	TATACGTACAGAGACTGTTT	chr6:30653734-30653753 (-)	CRISPRi
E103_g2	AAGAGCTATGGAGAAACACA	chr6:30653650-30653669 (+)	CRISPRi
E103_g3	ATGAGGCCCATGAAGTCAGA	chr6:30654575-30654594 (-)	CRISPRi
E103_g4	ACCCAGCAGCAGTAACCTAA	chr6:30654430-30654449 (+)	CRISPRi
E104_g1	GTCCACTGCCCAATACTGAA	chr6:30674244-30674263 (+)	CRISPRi
E104_g2	TGGAAAAGCCGGCAAGCCGC	chr6:30674296-30674315 (-)	CRISPRi
E104_g2	TAAATTATAGGAACCCAATG	chr6:30674940-30674959 (-)	CRISPRi
E104_g4	GTTGCTAAGAGACAGCTCCA	chr6:30675051-30675070 (+)	CRISPRi
E105*_g1	TGTCACAGGGAGCTAAATGT	chr6:30572832-30572851 (-)	CRISPRi, CRISPR/Cas9
E105*_g2	AGAGAACCAGCGGAGCCATT	chr6:30572990-30573009 (-)	CRISPRi, CRISPR/Cas9
E105_g3	CCTTTGACGCGAGTGAATAC	chr6:30572911-30572930 (-)	CRISPRi
E105_g4	GAAGTCCATCCAGATTAAAC	chr6:30572778-30572797 (+)	CRISPRi
E107_g1	AACATAAAAAGTGCTCGACT	chr6:30432978-30432997 (+)	CRISPRi
E107_g2	CTATAAGAATGTGTGCAGTC	chr6:30432917-30432936 (+)	CRISPRi
E107_g3	ACCATGAATTTATGCAAATC	chr6:30432877-30432896 (+)	CRISPRi
E107_g4	GAAGTGAGCATTCTCATTTC	chr6:30432849-30432868 (+)	CRISPRi
E108_g1	CTGCTCGAATCACTCCACAG	chr6:30527064-30527083 (-)	CRISPRi
E108_g2	GAAAGGGAGGCAATCAGCAG	chr6:30526950-30526969 (-)	CRISPRi
E108_g3	TGATTGGCTCAGAGCAATCA	chr6:30527027-30527046 (-)	CRISPRi
E108_g4	GGGCAGAAGGAGGATCTGCT	chr6:30526979-30526998 (-)	CRISPRi
E109_g1	AACAGTTCGGGTATCTACAC	chr6:30528948-30528967 (-)	CRISPRi
E109_g2	TTGAGACAGGATGAGAATAT	chr6:30529009-30529028 (+)	CRISPRi
E109_g3	TCAAGCATTCCAGCACACCT	chr6:30528881-30528900 (-)	CRISPRi
E109_g4	TGTGAGATCAGCAACAGTTC	chr6:30528960-30528979 (-)	CRISPRi
E110_g1	GGGTCCTGCAGCGAATACTC	chr6:30569698-30569717 (-)	CRISPRi
E110_g2	TCCGCAGGCAGCTCAGCGGT	chr6:30569516-30569535 (+)	CRISPRi
E110_g3	AGCCACATGAAGAGCTGCAG	chr6:30569597-30569616 (-)	CRISPRi
E110_g4	TGAACTGGGCAACCAGGACA	chr6:30569850-30569869 (-)	CRISPRi
E111_g1	CAGAACACAGAGCTGGGACA	chr6:30675561-30675580 (+)	CRISPRi
E111_g2	GACTAGTGGAGAAGGGCTGC	chr6:30675429-30675448 (+)	CRISPRi

E111_g3	TGGCCTCTGAGGCTCCCTGA	chr6:30675594-30675613 (-)	CRISPRi
E113_g1	AAGCGAGTAAGGTGTCAGAT	chr6:30469665-30469684 (-)	CRISPRi
E113_g2	TACCCAGAGACAGAGGTCGT	chr6:30469381-30469400 (+)	CRISPRi
E113_g3	CTGCAGGGCCTCTCGAGGAT	chr6:30469459-30469478 (-)	CRISPRi
E114_g1	GCTGAGTCCAGATATGTAGA	chr6:30477433-30477452 (-)	CRISPRi
E114_g2	GTGGGGACAGGAATGCAGAG	chr6:30477392-30477411 (+)	CRISPRi
E114_g3	GATGGCTTGCTCTTCACAGC	chr6:30477312-30477331 (+)	CRISPRi
E114_g4	AGCACATGACCACAGTACCC	chr6:30477203-30477222 (+)	CRISPRi
E115_g1	TCAGAGAGCGCATCGATTCC	chr6:30401708-30401727 (-)	CRISPRi
E115_g2	GTGCTTATGGGACAGAATTC	chr6:30401565-30401584 (+)	CRISPRi
E115_g3	CTATAGCTAAAAGAGATGGG	chr6:30401752-30401771 (-)	CRISPRi
E115_g4	TAGTCGAAGACCGAGCGGGG	chr6:30401644-30401663 (-)	CRISPRi
E116_g1	TTAGTAATGCAGAAAACCTA	chr6:30403470-30403489 (-)	CRISPRi
E116_g2	TTACACCATGAACTTCATGT	chr6:30403576-30403595 (+)	CRISPRi
E116_g3	TCCTCTCTGCTACCACATGA	chr6:30403632-30403651 (+)	CRISPRi
E116_g4	AAGAACAGCCATTTGTCCAG	chr6:30403728-30403747 (+)	CRISPRi
E117_g1	AGCTCCACGTTACTAAGGGT	chr6:30442518-30442537 (-)	CRISPRi
E117_g2	CTAGCTCCCGACCTTCAAGT	chr6:30442468-30442487 (-)	CRISPRi
E117_g3	TACACCAACCCTTAGTAACG	chr6:30442511-30442530 (+)	CRISPRi
E117_g4	ACCCAACAAGCCATCTTCCC	chr6:30442423-30442442 (+)	CRISPRi
E118_g1	GCATCTAGTGGGTACGCAAC	chr6:30460139-30460158 (+)	CRISPRi
E118_g2	GGAATTAGGACGGGGTACCA	chr6:30460696-30460715 (+)	CRISPRi
E118_g3	GAATAGAGTACTTTAGCTCA	chr6:30460258-30460277 (+)	CRISPRi
E118_g4	GGACCAGCGCTGCTCGCCAG	chr6:30460071-30460090 (-)	CRISPRi
E119_g1	TAATTATAAAGCTCGTACTG	chr6:30509507-30509526 (-)	CRISPRi
E119_g2	CATGCGCAGAGGCAAGACTA	chr6:30509731-30509750 (+)	CRISPRi
E119_g3	AGCTGAGCCTAGCGAGACAA	chr6:30509370-30509389 (-)	CRISPRi
E120_g1	TGGGATGGACAAGCAGACTT	chr6:30545779-30545798 (-)	CRISPRi
E120_g2	GCAATGAATCCAGTCTGGTG	chr6:30545438-30545457 (-)	CRISPRi
E120_g3	ACAGAAGGAGAATAATATCT	chr6:30545697-30545716 (-)	CRISPRi
E120_g4	AGAGGTTAACTCCTAAAGGC	chr6:30545212-30545231 (+)	CRISPRi
E121_g1	GCATCTGTAATTGAGTGACT	chr6:30547060-30547079 (-)	CRISPRi
E121_g2	GTGACTCATCATCCCCGTGA	chr6:30546960-30546979 (+)	CRISPRi
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E122_g1	GCTGGCTGCACACCCGTGAA	chr6:30552214-30552233 (-)	CRISPRi
E122_g2	GGGAAGCTGCGTAAGAAGTG	chr6:30552388-30552407 (+)	CRISPRi
E122_g3	TGCTGCCTGGGGCTGTGACA	chr6:30552236-30552255 (-)	CRISPRi
E122_g4	TGAACCGGGCTACAGCCTGC	chr6:30552290-30552309 (-)	CRISPRi
E123_g1	ATGAGATCATCCCCCTCTGT	chr6:30553783-30553802 (-)	CRISPRi

E123_g2	AATAGCTCGCTGCATTGGGT	chr6:30553748-30553767 (-)	CRISPRi
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E123_g4	AAGCAGAAATGAACTCATCT	chr6:30553860-30553879 (-)	CRISPRi
E124_g1	GAGCCCCAACGCTACAGCAA	chr6:30580431-30580450 (+)	CRISPRi
E124_g2	AGCCAGGGTCTCTATCAGAT	chr6:30580385-30580404 (-)	CRISPRi
E124_g3	GGCTCCATGGGTCAGAGCGT	chr6:30580416-30580435 (-)	CRISPRi
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E125_g4	AGCACAGAGAGGCATTGGTC	chr6:30585324-30585343 (-)	CRISPRi
E126_g1	AAACCTGAGAACGCGTCAGA	chr6:30649982-30650001 (+)	CRISPRi
E126_g2	TCATCTAAAAACCCCAGAGA	chr6:30650067-30650086 (+)	CRISPRi
E126_g3	GTCCTGGCCAAGAAGAGCTC	chr6:30649939-30649958 (+)	CRISPRi
E126_g4	AGTTCCTCCAGGCAACATCT	chr6:30649890-30649909 (-)	CRISPRi
E127_g1	TAGATTAGTAGCCAGACGTG	chr6:30693705-30693724 (-)	CRISPRi
E127_g2	GCAGTAAACGGAGCTTCTAT	chr6:30693806-30693825 (-)	CRISPRi
E127_g3	ACCGGCGGGTGCCACTGACG	chr6:30693447-30693466 (+)	CRISPRi
E127_g4	GCCACTTCCCGCCTTCCGGG	chr6:30693522-30693541 (+)	CRISPRi
E128_g1	AAAGATAACGCTGAGGATAT	chr6:30716798-30716817 (+)	CRISPRi
E128_g2	GCTGGCAGCTCTTACATTAC	chr6:30716840-30716859 (+)	CRISPRi
E128_g3	TAAATACGCAATATACGAGA	chr6:30716743-30716762 (-)	CRISPRi
E128_g4	ATCAGAGAGAAGTAGATACG	chr6:30716573-30716592 (+)	CRISPRi

Supplementary Table 2. Primers

Experiment	Oligo	Sequence
Bisulfite PCR	Peg10_ICR_F	GGTATAGGTATAAGATTTGTAGTTTTTT
	Peg10_ICR_R	AATTTCCACAAACTATTACTAAACACC
	Mest_ICR_F	TAGAGAATTTGTTTATTTTTTAGTTATT
	Mest_ICR_R	ATAAAAAAAACCTTCCCATATATTAATA
	Peg3_ICR_F	GTGGTGATTTAGGATTATAAAGTTTTT
	Peg3_ICR_R	CCCTAAACTATATCTAACTCCATTTATA
	Snrpn_ICR_F	AAATTTAGAATGTTTTGGTTAAATAGGA
	Snrpn_ICR_R	CCTCTCCCACATAATAAAAATCTATATA
	Dlk1_ICR_F	GGGTAAGTTTTATGGTTTATTGTATATAA
	Dlk1_ICR_R	TAAACTACAATCTATATAATCACAACAC
	H19_ICR_F	ATTTTAGTTTTTGTTTTTATGGTTATGG
	H19_ICR_R	TAATACAACACACATTTCTTAAATAACT
	Peg13_ICR_F	TGGTAGGGAAGGTTATTTATATAAATATT
	Peg13_ICR_R	ACTACTACAACCTAATTCTAAATAAAAC
qRT-PCR	Mest_F	TGGTCGGAAGCCCTGAGATA
	Mest_R	GCGATCACTCGATGGAACCT
	Mest-XL_F	GGGAACAGGAGATGCAGTGAA
	Mest-XL_F	TCCAGTTGAACCCCTACTTTGC
	Copg2_F	AGCTCTCCTAAACCAGCCTTG
	Copg2_R	AGTCCAGATTGCAGGCAGTAA
	Psmd4_F	CAGCCGATTCTTGGCTAAAC
	Psmd4_R	TCCAGACCTAAGCAGCATGA
	Meg3_F	GCTGCCCATCTCCACAGAAG
	Meg3_R	CTTCCTGGGGTCCTCGC

Supplementary References

1. Xie, W. *et al.* Base-Resolution Analyses of Sequence and Parent-of-Origin Dependent DNA Methylation in the Mouse Genome. *Cell* **148**, 816–831 (2012).