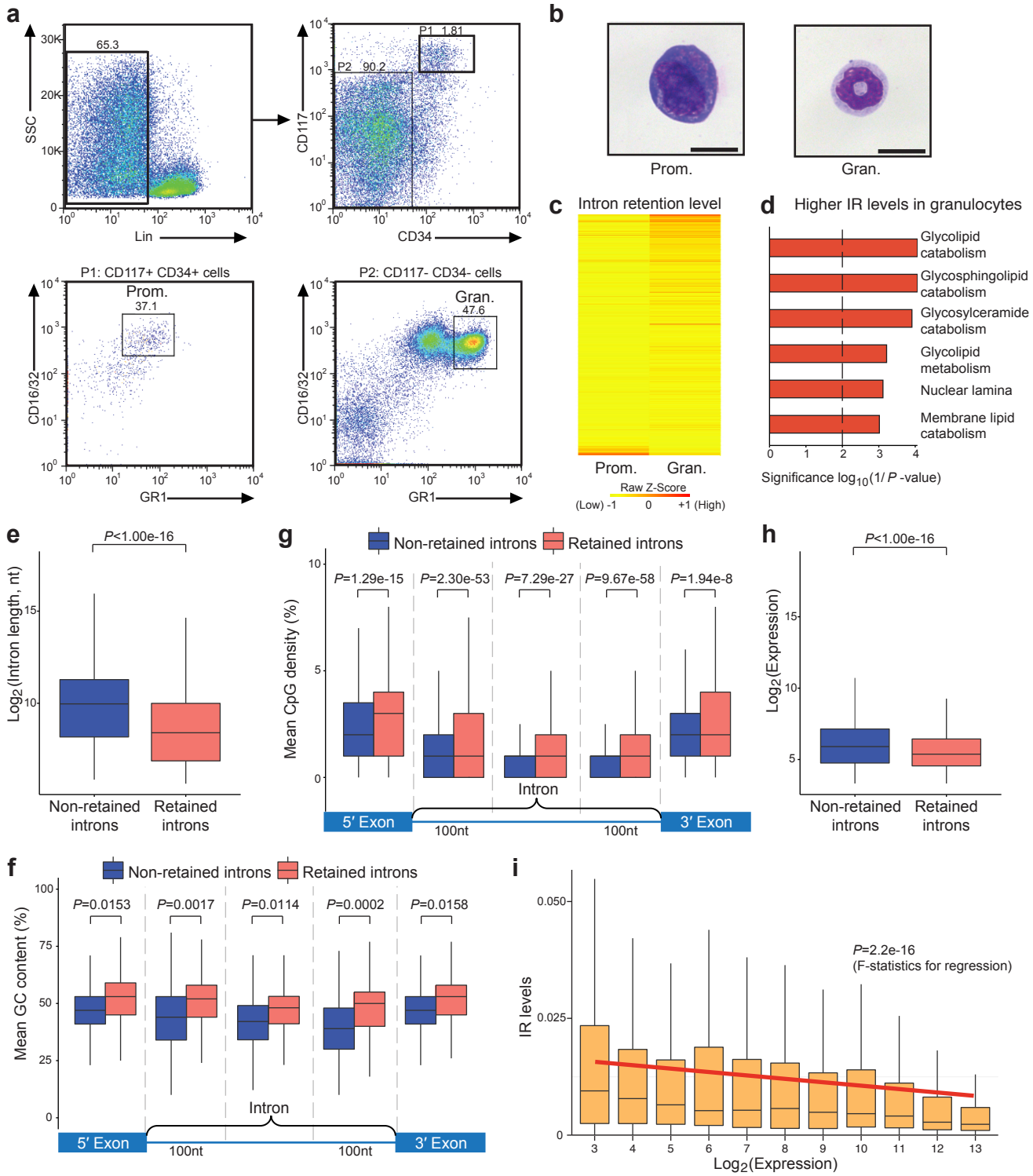
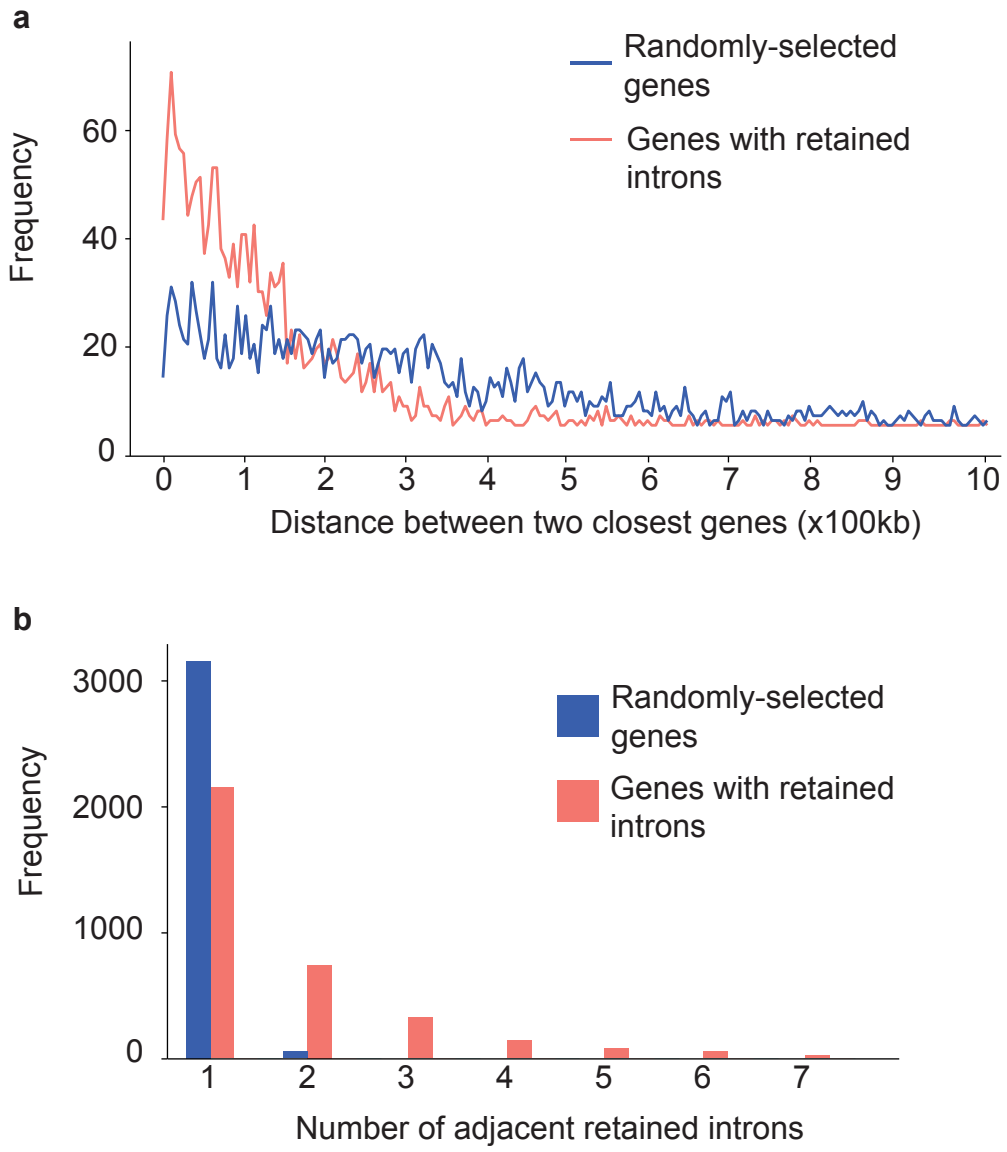
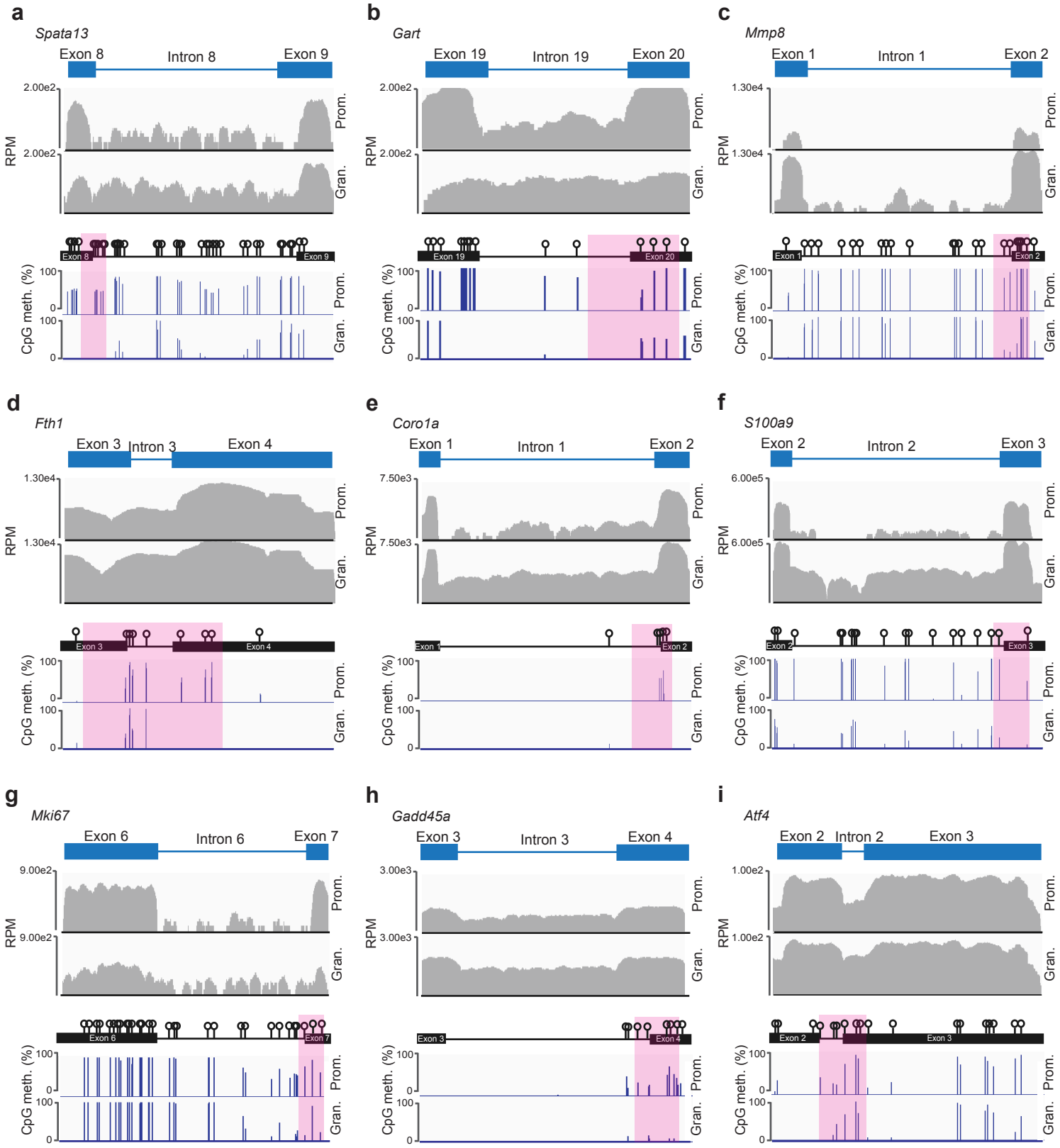


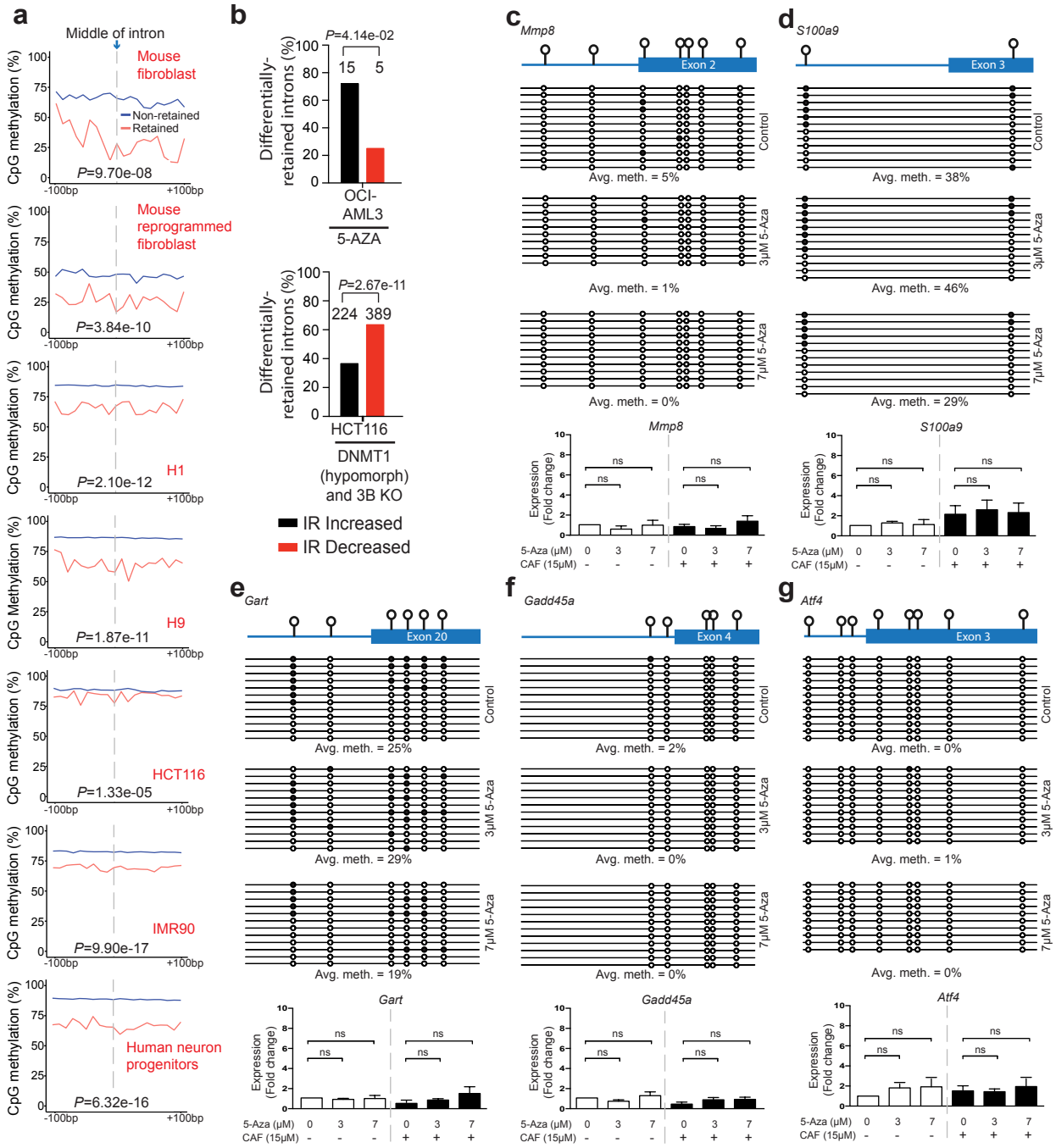

**Supplementary Figure 1. Features associated with IR in promyelocytes and granulocytes. (a)** Fluorescence-activated cell sorting strategy to isolate Lin-Kit+CD34+CD16/32+Gr-1low promyelocytes (Prom.) and Lin-Kit-CD34-CD16/32+Gr-1high granulocytes (Gran.) from mouse bone marrow. **(b)** Representative morphology of a promyelocyte and a granulocyte examined using a light microscope at 100× magnification following staining with May Grünwald Giemsa. Scale bars indicate 10 μm. **(c)** Heatmaps generated from RNA-seq data showing the expression levels of differentially-retained introns in promyelocytes and granulocytes. **(d)** Gene ontology enrichment of the genes with significantly increased IR levels in granulocytes ($P$<0.01 with Benjamini-Hochberg correction). **(e)** Box and whisker plots displaying length distribution of non-retained versus retained introns in promyelocytes and granulocytes. **(f)** GC content and **(g)** CpG density for introns and flanking exons of non-retained versus retained introns spanning ±100bp from the 5′ and 3′ splice junctions, and from the middle of introns. **(h)** Expression levels of the exons flanking non-retained and retained introns. **(i)** A series of box and whisker plots displaying the association of IR levels with gene expression in promyelocytes and granulocytes. Genes with a similar expression level were binned into categories shown on the x-axis. F-test was applied to determine the fitness of the regression model (red line) at $P$<0.05.



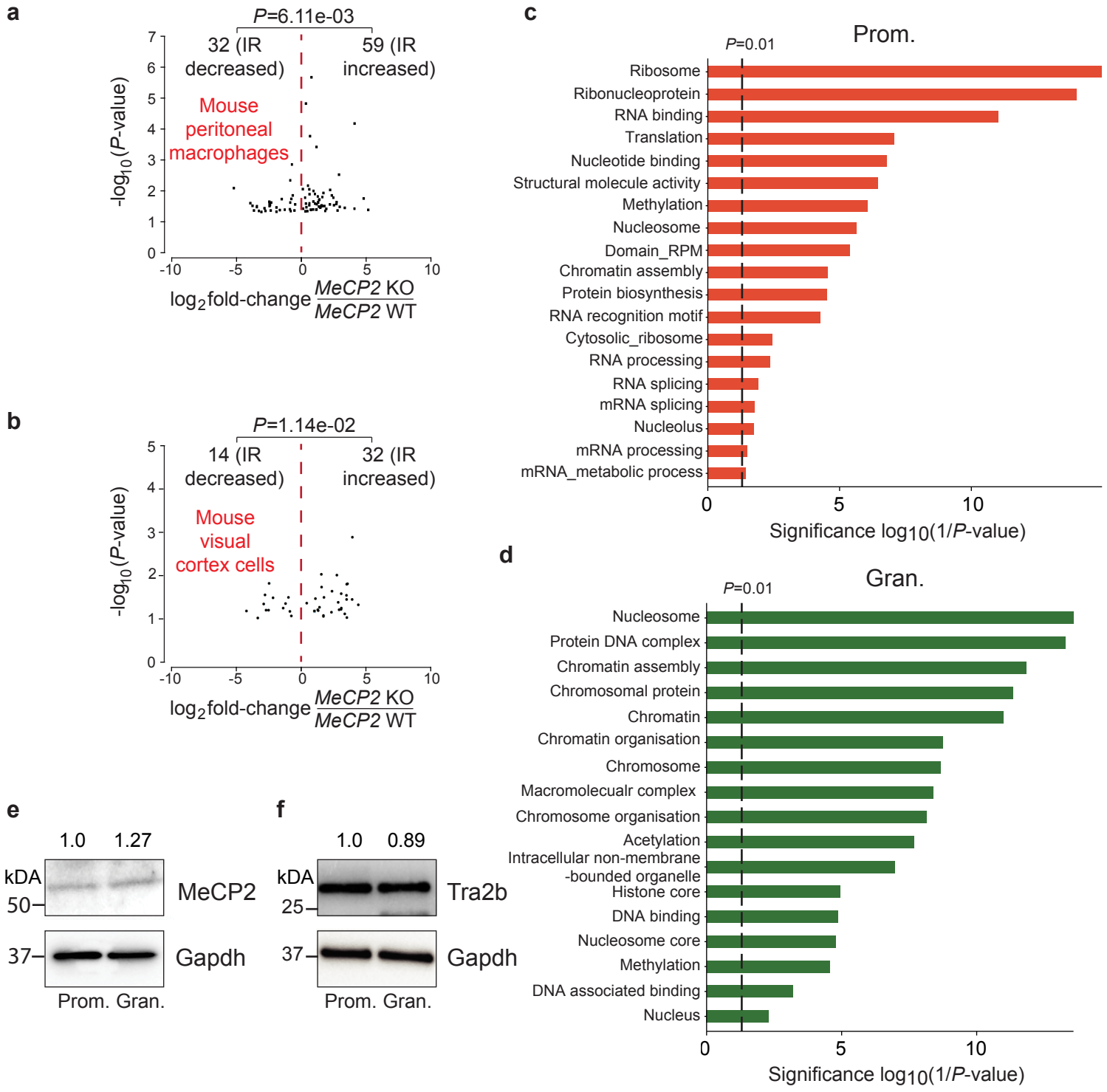

**Supplementary Figure 2. Retained introns within genes and genomic positions of genes with retained introns are clustered. (a)** Genomic distance between 2 closest genes with retained introns in granulocytes (n=1739) and in a control set where the same number of genes were randomly selected amongst genes expressed in granulocytes (>10 Fragments Per Kilobase of transcript per Million mapped reads, FPKM). **(b)** Frequency of adjacent retained introns, separated only by one or more annotated exon(s) within the same gene in granulocytes compared to a control set where the same number of introns were randomly selected within the same gene.




**Supplementary Figure 3. Higher levels of IR in granulocytes are associated with lower levels of DNA methylation near 5' and/or 3' splice junctions.** RNA-seq reads (RPM values) within introns and flanking exons in promyelocytes (Prom.) and granulocytes (Gran.) shown on the same scale using IGV v2.3 software for murine genes **(a)** *Spata13*, **(b)** *Gart*, **(c)** *Mmp8*, **(d)** *Fth1*, **(e)** *Coro1a*, **(f)** *S100a9*, **(g)** *Mki67*, **(h)** *Gadd45a* and **(i)** *Atf4*. Shown beneath the mRNA-seq data are average methylation levels (0-100%) at individual CpGs (indicated by lollipops on the maps) detected by WGBS within specific introns and flanking exons of these genes. A ±100bp region around splice junctions, with reduced DNA methylation in granulocytes, is shaded in pink.

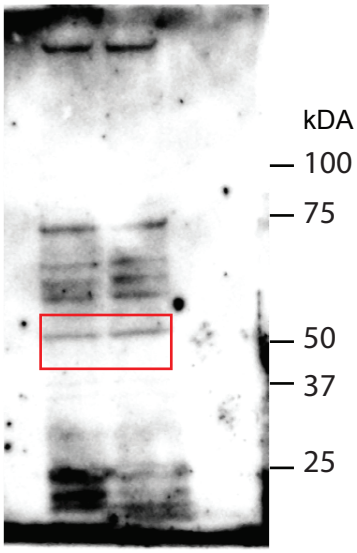



**Supplementary Figure 4. Increased IR occurs consequent to reduced DNA methylation levels. (a)** Average DNA methylation levels spanning ±100bp from the middle of the intron in the DNA encoding non-retained (blue) and retained (red) introns in primary mouse fibroblasts, mouse reprogrammed fibroblasts, human cell lines (H1, H9, HCT116, IMR90) and human primary neuron progenitors. **(b)** Percentage (%) of introns in OCI-AML cells treated with 5-Aza-2′deoxycitidine (5-Aza) or engineered DNMT3B and hypomorphic DNMT1 double-KO HCT116 cells that increased (black) or decreased in IR (red) compared to control. Number of events with increased or decreased IR is shown above the bars. Binomial test was used to determine significance at $P<0.05$. **(c-g)** Clonal bisulfite sequencing displaying DNA methylation changes near 3′ splice junctions of *Mmp8* intron 1, *S100a9* intron 2, *Gart* intron 19, *Gadd45a* intron 3 and *Atf4* intron 2 in MPRO cells following treatment with 3 and 7 μM 5-Aza. Each row represents a single cloned PCR amplicon aligned to the exon-intron map shown. Each lollipop on the map represents a CpG site. Black and white circles denote methylated and unmethylated CpGs respectively. Lower panel: IR levels determined by qRT-PCR for the same indicated introns in MPRO cells, with and without exposure to 5-Aza at 3 or 7 μM, and in the absence (-) or presence (+) of NMD inhibition via caffeine (CAF) treatment. Two-tailed t-test was used to determine significance at $P<0.05$. Bars display mean ± standard error of the mean. Independent qRT-PCR experiments were performed three times in triplicate (n=3). ns, not significant; Avg. meth., average methylation levels.

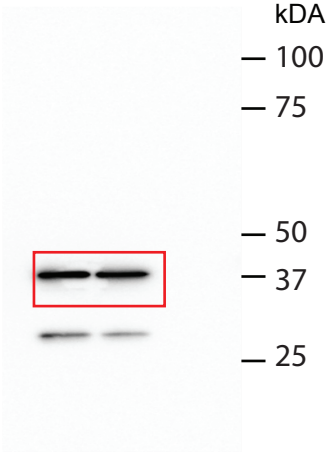



**Supplementary Figure 5. MeCP2 levels and occupancy are associated with IR and splicing factor recruitment.** Association between IR ratio fold changes and their significance in the MeCP2-knockout primary mouse peritoneal macrophages **(a)** and visual cortex cells **(b)**. Binomial test was used to determine the significant bias between increased and decreased IR at $P<0.05$. Gene ontology analysis of the proteins that interact with MeCP2 in promyelocytes (Prom.) **(c)** and granulocytes (Gran.) **(d)** using RIME ($P<0.01$ with Benjamini-Hochberg correction). **(e and f)** Western blots showing total levels of MeCP2 and Tra2b proteins in promyelocytes and granulocytes. Gapdh was the loading control, with relative levels shown above normalized to Gapdh. Molecular weight markers in kilodalton (kDA) are indicated.

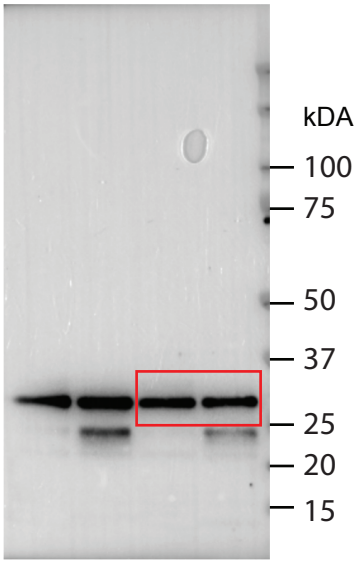
Supplementary Fig. 5e MeCP2



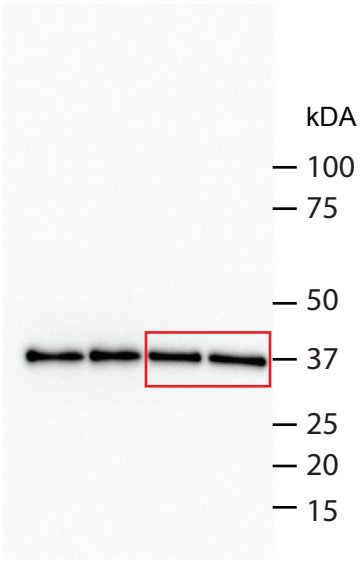

Supplementary Fig. 5e Gapdh



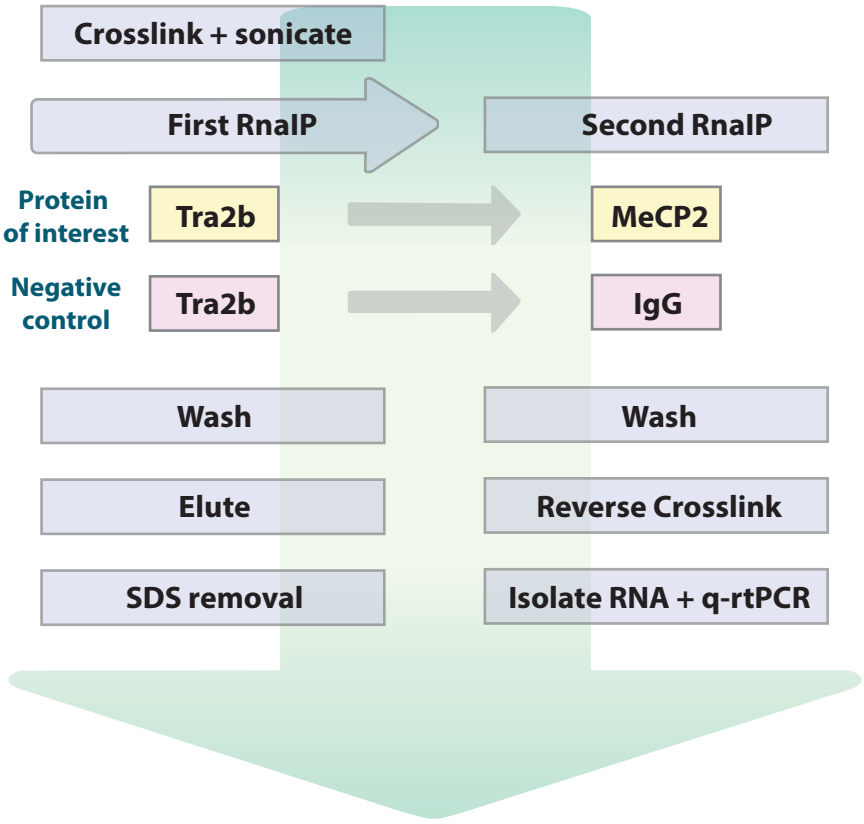

Supplementary Fig. 5f Tra2b




Supplementary Fig. 5f Gapdh




**Supplementary Figure 6.** Uncropped western blots for cropped images (in red boxes) presented in Supplementary Figures 5e and 5f. Molecular weight markers in kilodalton (kDA) are indicated.




**Supplementary Figure 7. Workflow of the RNA-IP-reIP experiment to determine reduced co-occupancies of MeCP2 and Tra2b at splice junctions near retained introns.**

**Supplementary Table 1. WGBS, ChIP and RNA-seq data analyzed.**

| **Paired WGBS and RNA-seq** | | | |
|---|---|---|---|
| **Cell line/Primary cells** | **BS-seq ID** | **RNA-seq ID** | **Organism** |
| Wildtype fibroblast | GSM1134890 | GSM1134903 | mouse |
| Fibroblast reprogrammed for 3 weeks | GSM1134892 | GSM1134902 | mouse |
| H1 | GSM429321 | GSM438361 | human |
| H9 | GSM1521762 | GSM1521768 | human |
| Neuron progenitor | GSM1521763 | GSM1521770 | human |
| IMR90 | GSM432687 | GSM1151056 | human |
| HCT116 | GSM1465024 | GSM1151050 | human |
| | | | |
| **RNA-seq of DNMT knockout or 5-Aza treated cells and controls** | | | |
| **Cell line/Primary cells** | **Control ID** | **KO/Treated ID** | **Organism** |
| B cell | GSM1229021 | GSM1229013 | mouse |
| Hematopoietic stem cell | GSM1206271 | GSM1229019 | mouse |
| OCI-AML3 | GSM1329859-61 | GSM1329862-64 | human |
| HCT116 | GSM1151050 | GSM1151051 | human |
| | | | |
| **RNA-seq of MeCP2 knockdown or knockout cells and controls** | | | |
| **Cell line/Primary cells** | **Control ID** | **KO/Treated ID** | **Organism** |
| IMR90 | GSM1151048 | GSM1151053 | human |
| Peritoneal macrophage | GSM1617050 | GSM1617051 | mouse |
| Cerebellum | GSM1063328 | GSM1063324 | mouse |
| Visual cortex | GSM1643940-42 | GSM1643943-45 | mouse |

**Supplementary Table 2. Proteins that coimmunoprecipitated with MeCP2 in promyelocytes and/or granulocytes as detected by the RIME assay.**

| Detected in Promyelocytes | | | Detected in Granulocytes | | |
|---|---|---|---|---|---|
| **Name** | **Total number of peptide** | **References to known MeCP2 interactors** | **Name** | **Total number of peptide** | **References to known MeCP2 interactors** |
| Histone H1.3 | 40 | | Histone H1.5 | 47 | |
| Nucleolar RNA helicase 2 | 30 | Huttlin, E. L., et al. (2015). Cell | Histone H1.1 | 26 | |
| Histone H3.1 | 29 | Lambert, J. P., et al. (2015). J Proteomics | Histone H3.1 | 24 | Lambert, J. P., et al. (2015). J Proteomics |
| 40S ribosomal protein S8 | 21 | Huttlin, E. L., et al. (2015). Cell | Histone H1.4 | 17 | |
| Histone H4 | 18 | | Histone H4 | 12 | |
| Histone H1.4 | 15 | | Protein S100-A9 | 8 | |
| 60S ribosomal protein L4 | 15 | | Histone H1.3 | 7 | |
| Serine/arginine-rich splicing factor 2 | 13 | | Histone H2A type 1-H | 7 | |
| U1 small nuclear ribonucleoprotein 70 kDa | 13 | | 60S ribosomal protein L6 | 6 | |
| Core histone macro-H2A.1 | 12 | Chahrour, M., et al. (2008). Science | 60S ribosomal protein L23a | 3 | |
| Scaffold attachment factor B1 | 11 | | Histone H2B type 1-C/E/G | 3 | |
| 60S ribosomal protein L13 | 11 | Huttlin, E. L., et al. (2015). Cell | Histone H2B type 2-B | 3 | |
| 40S ribosomal protein S6 | 10 | | | | |
| 60S ribosomal protein L7a | 10 | Huttlin, E. L., et al. (2015). Cell | | | |
| 60S ribosomal protein L8 | 10 | Huttlin, E. L., et al. (2015). Cell | | | |
| Nucleolin | 10 | Maxwell, S. S., et al. (2013). RNA Biol | | | |
| 60S ribosomal protein L7 | 9 | | | | |
| Serine/arginine-rich splicing factor 6 | 9 | Tsujimura, K., et al. (2015). Cell Rep | | | |
| 60S ribosomal protein L29 | 9 | Huttlin, E. L., et al. (2015). Cell | | | |
| SAFB-like transcription modulator | 9 | | | | |
| 60S ribosomal protein L18 | 9 | Huttlin, E. L., et al. (2015). Cell | | | |
| rRNA 2'-O-methyltransferase fibrillarin | 9 | | | | |
| Serine/arginine-rich splicing factor 10 | 9 | | | | |
| Transformer-2 protein homolog beta | 8 | | | | |
| 60S ribosomal protein L23a | 8 | | | | |
| Peptidyl-prolyl cis-trans isomerase A | 8 | | | | |
| Serine/arginine-rich splicing factor 1 | 7 | | | | |
| Serine/arginine-rich splicing factor 3 | 7 | | | | |
| RNA-binding protein 39 | 6 | | | | |
| Echinoderm microtubule-associated protein-like 4 | 6 | | | | |
| Nucleophosmin | 6 | Li, R. et al. (2016) Plos Genet | | | |
| Serine/arginine-rich splicing factor 4 | 6 | Tsujimura, K., et al. (2015). Cell Rep | | | |
| 40S ribosomal protein S24 | 5 | | | | |
| 40S ribosomal protein S11 | 4 | | | | |
| Putative RNA-binding protein Luc7-like 2 | 4 | | | | |
| Serine/arginine-rich splicing factor 7 | 4 | Tsujimura, K., et al. (2015). Cell Rep | | | |
| Transformer-2 protein homolog alpha | 4 | | | | |
| RNA-binding protein with serine-rich domain 1 | 3 | | | | |
| Histone H2B type 2-B | 3 | | | | |
| Protein RCC2 | 3 | | | | |
| Bcl-2-associated transcription factor 1 | 3 | | | | |

**Note:** Proteins detected in both promyelocytes and granulocytes are highlighted in green
Splicing factors are highlighted in red


Maxwell, S. S., et al. (2013). "Chromatin context and ncRNA highlight targets of MeCP2 in brain." RNA Biol 10(11): 1741-1757.
Tsujimura, K., et al. (2015). "miR-199a Links MeCP2 with mTOR signaling and Its dysregulation leads to Rett Syndrome phenotypes." Cell Rep 12(11): 1887-1901.
Chahrour, M., et al. (2008). "MeCP2, a key contributor to neurological disease, activates and represses transcription." Science 320(5880): 1224-1229.
Huttlin, E. L., et al. (2015). "The BioPlex network: A systematic exploration of the human interactome." Cell 162(2): 425-440.
Lambert, J. P., et al. (2015). "Proximity biotinylation and affinity purification are complementary approaches for the interactome mapping of chromatin-associated protein complexes." J Proteomics 118: 81-94.
Li, R., et al. (2016). "Misregulation of alternative splicing in a mouse model of Rett Syndrome." Plos Genet 12(6): e1006129.

**Supplementary Table 3. Primer pairs used.**

| **RT-qPCR Primers to quantify intronic and exonic expression** | | | |
|---|---|---|---|
| **cDNA target** | **Primer** | **Sequence (5'-3')** | **Related Figures** |
| *Lmnb1* intron 5 | Forward | CAAGCTTGAGAATGCCAGAC | 2c |
| | Reverse | TGTCTCATCTGGGACAAAAGA | 2c |
| Lmnb1 exons 5-6 | Forward | GCCAGACTCTCCTCAGAGATG | 2c |
| | Reverse | AACACGCTCTAGACTCTTTCTGC | 2c |
| *Ngp* intron 3 | Forward | CAGTCCTCCGTGACTCATCA | 2d |
| | Reverse | CCACCATCACAGCAGAGAGA | 2d |
| *Ngp* exons 3-4 | Forward | GACAGGGATTGCAGTCGAGA | 2d |
| | Reverse | CACCTCCCTCCTCTTTCCAG | 2d |
| *Spata13* intron 8 | Forward | TGAGAGAAGGGACGTGGAGA | 2e |
| | Reverse | GCAGCTGGTACAGCAGAAGG | 2e |
| *Spata13* exons 8-9 | Forward | TTGCGCAGCTAGCCACTATT | 2e |
| | Reverse | CCTGGGTGGTTGTTGCAGTA | 2e |
| *S100a8* intron 2 | Forward | GCCCTCCAAGTTGCTTTCTG | 2f |
| | Reverse | ATCGCAAGGAACTCCTCGAA | 2f |
| *S100a8* exons 2-3 | Forward | AGGAAATCACCATGCCCTCT | 2f |
| | Reverse | CTCCTTGTGGCTGTCTTTGTG | 2f |
| *Atf4* intron 2 | Forward | CCTGGTGTGCCCTTTTCATA | Supplementary 4g |
| | Reverse | CTGGGAAAAGAAATTCAGGTG | Supplementary 4g |
| *Atf4* exons 2-3 | Forward | GCAAGGAGGATGCCTTTTC | Supplementary 4g |
| | Reverse | AGAGCTCATCTGGCATGGTT | Supplementary 4g |
| *Mmp8* intron 1 | Forward | GCAGGTGCCACTCCTCTAAG | Supplementary 4c |
| | Reverse | TGGAGGTGACAGAGAGCAGA | Supplementary 4c |
| *Mmp8* exons 1-2 | Forward | GCCTTCCCAGTACCTGAACA | Supplementary 4c |
| | Reverse | AGCGCTGCATCTCTTTAAGC | Supplementary 4c |
| *S100a9* intron 2 | Forward | GCAATGTGTGGTGCCCTATT | Supplementary 4d |
| | Reverse | TGTCTCACCATCCTCCCAAC | Supplementary 4d |
| *S100a9* exons 2-3 | Forward | AGGAAGGAAGGACACCCTGA | Supplementary 4d |
| | Reverse | GTTTGTGTCCAGGTCCTCCA | Supplementary 4d |
| *Gart* intron 19 | Forward | AGCCGAGGATGTACCACTGT | Supplementary 4e |
| | Reverse | CACTTAGAGGGTGGCTGAGG | Supplementary 4e |
| *Gart* exons 19-20 | Forward | TGGTATTCCCACCAGGGTAA | Supplementary 4e |
| | Reverse | CATGAACCCTGCAAGACAGA | Supplementary 4e |
| *Gadd45a* intron 3 | Forward | TGCCTGGTTACTTGTTGCTG | Supplementary 4f |
| | Reverse | AAGACCTCCCTTCCAAGCAT | Supplementary 4f |
| *Gadd45a* exons 3-4 | Forward | TGGTGACGAACCCACATTCAT | Supplementary 4f |
| | Reverse | ATTCGGATGCCATCACCGTT | Supplementary 4f |

| **Primers for chromatin immunoprecipitation** | | | |
|---|---|---|---|
| **Target** | **Primer** | **Sequence (5'-3')** | **Related Figures** |
| *Gadd45a-in3*ex4 | Forward | GCAGGATCCTTCCATTGTGA | 3b |
| | Reverse | ACAGAATGTTCGGGGTTTGG | 3b |
| *Coro1a*-in1ex2 | Forward | GTTGCTCTGGGGATGACAAA | 3b |
| | Reverse | ATTTGCTGGAGCGAACCAC | 3b |
| *Mmp8*-in1ex2 | Forward | CGGAGCAATTTCACAGCAAG | 3b |
| | Reverse | GCTTCTCTGCAACCATCGTG | 3b |
| *S100a9*-in2ex3 | Forward | GACACTCCCTGTGCTTCAGA | 3b |
| | Reverse | GTCCTGGTTTGTGTCCAGGT | 3b |
| *Gart*-in19ex20 | Forward | TGCTGATCCTCTGAAAATAGGC | 3b |
| | Reverse | CTTCCAGGACGTGGTCAACT | 3b |
| *Spata13-ex*8in8 | Forward | GGATCCTGCTTTCTTGAGCA | 3b |
| | Reverse | GTCTTTGGCGGAGACATCTT | 3b |
| *Fth1*-in3ex4 | Forward | TTGGGAGAGCTGACCAGTAA | 3b |
| | Reverse | CGTGGTCACCCAGTTCTTTA | 3b |
| *Mki67*-in6ex7 | Forward | GCGCCATGTTTCAGTGTCTT | 3b |
| | Reverse | CATAGGCATTCCCTCACTCTTG | 3b |

| | | | |
|---|---|---|---|
| *Atf4*-in2ex3 | Forward | TCTGCCTCCCGAATATGACA | 3b,c |
| | Reverse | CCATTCGAAACAGAGCATCG | 3b,c |
| *Smarcd1*-ex9in9 | Forward | TCTCAGCGGATGAAGTTCTCA | 3b |
| | Reverse | GCACACACTCACCTGATGACA | 3b |
| *Nomo1*-ex24in24 | Forward | GAAGGAGTTCCGCTTTGAGC | 3b |
| | Reverse | ACACGCACCTGTAGGCAGTT | 3b |
| *Pam*-ex2in2 | Forward | GCCTTCAGAAGCCCACTTTC | 3b |
| | Reverse | CAACGTCCTTCCTCCAGTCT | 3b |
| *Xist*-CpG | Forward | CAGCGCAATTGGTTGCTTT | 3b |
| | Reverse | CCATTATGGCTTCTGCGTGA | 3b |
| *IAP* | Forward | GCTTTCGTTTTTGGGGCTTGG | 3b |
| | Reverse | CTTACTCCGCGTTCTCACGAC | 3b |
| *Gapdh*-CpG | Forward | GTCTCTGGAACAGGGAGGAG | 3b |
| | Reverse | CCCTTGAGCTAGGACTGGAT | 3b |
| *Actb*-CpG | Forward | GGAATGTGGCTGCAAAGAGT | 3b |
| | Reverse | ATCACTCAGAACGGACACCA | 3b |
| *Lmnb1*-in4 (P1) | Forward | TACCAGAAGGGCTTGGGTTT | 4a,b |
| | Reverse | GGAAGCCACTGTCAGCCTTA | 4a,b |
| *Lmnb1*-ex5in5 (P2) | Forward | AGCCGGATGAGGATCGAGAG | 3b,c and 4a,b |
| | Reverse | AGCCTTCCAGCTACACCTCA | 3b,c and 4a,b |
| *Lmnb1*-in5-1 (P3) | Forward | TGGTGAGGTGCCTTCTTTCT | 4a,b |
| | Reverse | GTCACTTGTCGCTGGGGTAT | 4a,b |
| *Lmnb1*-in5-2 (P4) | Forward | TCAGGAGCTTGGAATGGCTA | 4a,b |
| | Reverse | TGCACTGTATTTGCCCTCCT | 4a,b |
| *Lmnb1*-in5-3 (P5) | Forward | CTGAGGGTTGTTGGGTCACT | 4a,b |
| | Reverse | GCATAGGTCACACTGGCAGA | 4a,b |
| *Lmnb1*-in5-5 (P6) | Forward | CTCGGCTTCTGGACCTTCTC | 4a,b |
| | Reverse | GCACGTTCATGTGTGCAATC | 4a,b |
| *Lmnb1*-in5-6 (P7) | Forward | CCGATTGAGACTGGTGCATT | 4a,b |
| | Reverse | CGCCAGCATATTCCTTCTCA | 4a,b |
| *Lmnb1*-in5ex6 (P8) | Forward | GTGCTCCTTTGACCCTGAAG | 4a,b |
| | Reverse | CTGCATCTGGTCCCTGATCT | 4a,b |
| *Ngp*-ex3in3 (P1) | Forward | AACCTCCCTGACCTTGACCT | 4a,b |
| | Reverse | AGAGGCCTGGAGTGGACAT | 4a,b |
| *Ngp*-in3-1 (P2) | Forward | TGGGAGACACTGAGTTGCTG | 4a,b |
| | Reverse | TGACAAAGGACATGCCACAC | 4a,b |
| *Ngp*-in3-2 (P3) | Forward | TTCCCACTGTTAGGGGAGTG | 4a,b |
| | Reverse | AGGCTTCCATAGGCTGTCAT | 4a,b |
| *Ngp*-in3-3 (P4) | Forward | CCCCAATTCAGATCTGCTCA | 4a,b |
| | Reverse | CAGCTACAAGGGCATGATGA | 4a,b |
| *Ngp*-in3ex4 (P5) | Forward | CTGCTGTGATGGTGGTGACT | 3b,c and 4a,b |
| | Reverse | ATGTGAGGGGGCACATCTT | 3b,c and 4a,b |
| *S100a8*-ex2in2 (P1) | Forward | AGGAAATCACCATGCCCTCT | 4a,b |
| | Reverse | CCATCCCAGCACCATTAGAA | 4a,b |
| *S100a8*-in2 (P2) | Forward | TTCTAATGGTGCTGGGATGG | 4a,b |
| | Reverse | AAGCGAGGACTATCTGTGGA | 4a,b |
| *S100a8*-in2ex3 (P3) | Forward | TCCACAGATAGTCCTCGCTTA | 3b and 4a,b |
| | Reverse | ATCGCAAGGAACTCCTCGAA | 3b and 4a,b |
| *Lmnb1*-ex3in3 (P1) | Forward | GGATTTGGAGAATCGCTGTC | 4c,d |
| | Reverse | GGCCAGGACTATGCAGAGAA | 4c,d |
| *Lmnb1*-in3-1 (P2) | Forward | CTCTGTAACAAAGCCGCACA | 4c,d |
| | Reverse | CTGCAAGGCATCTCCTATCC | 4c,d |
| *Lmnb1*-in3-2 (P3) | Forward | AGACCCTGCCTGCATACATC | 4c,d |
| | Reverse | CAATCCCTACGGACACCTCT | 4c,d |
| *Lmnb1*-in3ex4 (P4) | Forward | TTGAGTCAGGACAGGCACAG | 4c,d |
| | Reverse | GGTCTCATGCTTCCTCCTTG | 4c,d |
| *Smarcd1*-ex9in9 (P1) | Forward | TCTCAGCGGATGAAGTTCTCA | 4c,d |
| | Reverse | GCACACACTCACCTGATGACA | 4c,d |
| *Smarcd1*-in9-1 (P2) | Forward | ACCAACTTGTGCTTGCCTGT | 4c,d |
| | Reverse | TAGCATGGGCCAGAGAAGAG | 4c,d |

| | | | |
|---|---|---|---|
| *Smarcd1*-in9-2 (P3) | Forward | AGCAAGATGGTTCAGCAGGT | 4c,d |
| | Reverse | GGTGAGAGGACCATTTGTGG | 4c,d |
| *Smarcd1*-in9ex10 (P4) | Forward | TCATCCCTGGACCATCTTTC | 4c,d |
| | Reverse | CAGAGTGTCATCCACCTCCA | 4c,d |
| *TBP*-ex5in5 (P1) | Forward | AAGAGAGCCACGGACAACTG | 4c,d |
| | Reverse | CCCACTAGAAACAAAGCATTCC | 4c,d |
| *TBP*-in5-1 (P2) | Forward | TGGTTTGCTCTGATTACTCTGC | 4c,d |
| | Reverse | AATGGCAGTGCTACAACCAG | 4c,d |
| *TBP*-in5-2 (P3) | Forward | AGGTCATAATGAGGTGATGACG | 4c,d |
| | Reverse | TGTGGCACATTACTGTCAAGC | 4c,d |
| *TBP*-in5ex6 (P4) | Forward | TGGTTTCTGTTGAGGACACG | 4c,d |
| | Reverse | TTCTTGCTGCTAGTCTGGATTG | 4c,d |
| Chr6-intergenic | Forward | TACCAATGTCCACCCTCTGA | 4b,d |
| | Reverse | GACAACATCCACACGTCCAG | 4b,d |

| **Primers for bisulfite sequencing** | | | |
|---|---|---|---|
| **Target** | **Primer** | **Sequence (5'-3')** | **Related Figures** |
| *Lmnb1*-in4ex5in5 | Forward | TTAGTTGGTTATTAGAAGGGTTTGG | 1d and 2c |
| | Reverse | AAAAAAATAACACCAAAAAAACAAC | 1d and 2c |
| *Ngp*-in3ex4 | Forward | ATTTTGGGGTTTGGGAATATTATAT | 1d and 2d |
| | Reverse | TATACAAAAAACACCTCCCTCCTC | 1d and 2d |
| *S100a8*-in2ex3 | Forward | TTTGTGTAGGTGAGGAGGTGTT | 1d and 2f |
| | Reverse | AACCCAACCCTAAACCAAAAA | 1d and 2f |
| *Spata13*-ex8in8 | Forward | AAATTGTTTAATTGTTTTTAAGTAAATAAA | 2e |
| | Reverse | ACAACACCCTCTAAAATATCTTTAAC | 2e |
| *Atf4*-in2ex3 | Forward | TATGGATGATGGTTTGGTTAGTGT | Supplementary 4g |
| | Reverse | CAAAATCAAACTTCCTATCTCCTTC | Supplementary 4g |
| *MMp8*-in1ex2 | Forward | AATTTTTGTTATTGTTTTTTGTTTGT | Supplementary 4c |
| | Reverse | CCAAAATCAAACACTCCACATC | Supplementary 4c |
| *S100a9*-in2ex3 | Forward | AGTATTGTGTTTTAAATTAAATTTAGATTT | Supplementary 4d |
| | Reverse | TTACCATAACTATAACCATACCCAC | Supplementary 4d |
| *Gart*-in19ex20 | Forward | TTGGGTTTGTTTTTTTGTTGTATTT | Supplementary 4e |
| | Reverse | TCAATCAATCTAAACACTTCCTACC | Supplementary 4e |
| *Gadd45a*-in3ex4 | Forward | ATTTATTAGGGTATATGTTTGGAAGG | Supplementary 4f |
| | Reverse | ACAATTTAATTCAATTATTTCCATTC | Supplementary 4f |

| **Primers for RNA-IP and RNA-IP-reIP** | | | |
|---|---|---|---|
| **Target** | **Primer** | **Sequence (5'-3')** | **Related Figures** |
| *Malat1* | Forward | GTTACCAGCCCAAACCTCAA | 5c |
| | Reverse | CACTTGTGGGGAGACCTTGT | 5c |
| *Tra2a* | Forward | GAATTGGGGAAGAATACACGAA | 5d |
| | Reverse | AGGACCCATTCATTCTTCCAG | 5d |
| *Lmnb1* | Forward | GAGAATGCCAGACTCTCCTCA | 5e,f,i |
| | Reverse | GAGGCTCTCGATCCTCATCC | 5e,f.i |
| *Ngp* | Forward | GACAGGGATTGCAGTCGAGA | 5e,f,i |
| | Reverse | CACCTCCCTCCTCTTTCCAG | 5e,f,i |
| *S100a8* | Forward | TCGTGACAATGCCGTCTGAA | 5e,f,i |
| | Reverse | AGGGCATGGTGATTTCCTTGT | 5e,f,i |
| *Smarcd1* | Forward | TCTCAGAGATCCCTCAGCGG | 5g,h,i |
| | Reverse | CCACCTCCACGTCAATGTCA | 5g,h,i |
| *Tbp* | Forward | AAGAGAGCCACGGACAACTG | 5g,h,i |
| | Reverse | GCTCCTGTGCACACCATTTT | 5g,h,i |