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# **DNA methyltransferases 3A and 3B target specific sequences during mouse gastrulation**

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## **ABSTRACT**

In mammalian embryos, DNA methylation is initialized to maximal levels in the epiblast by the de-novo DNA methyltransferase DNMT3A and DNMT3B (DNMT3A/B), before gastrulation diversifies it across regulatory regions. Here we show that DNMT3A/B are differentially regulated during endoderm and mesoderm bifurcation and study the implications in-vivo and in meso-endoderm embryoid bodies. Loss of both Dnmt3a/b impairs exit from the epiblast state. More subtly, independent loss of Dnmt3a/b leads to small meso-endo bifurcation biases and transcriptional de-regulation. Epigenetically, DNMT3A/B drive distinct methylation kinetics in the epiblast, as can be predicted from their strand-specific sequence preferences. The enzymes compensate each other in the epiblast, but can later facilitate lineage specific methylation kinetics as their expression diverges. Single cell analysis shows DNMT3A/B differential activity combines with replication-linked methylation turnover to increase epigenetic plasticity in gastrulation. Together, outlines a dynamic model for the use of DNMT3A and DNMT3B sequence specificity during gastrulation.

## INTRODUCTION

During a short period following implantation, the mammalian pluripotent inner cell mass (ICM) is proliferating rapidly to form the epiblast, out of which the endoderm and mesoderm, and immediately afterward the ectoderm germ layers are specified. Gastrulation then proceeds through parallel differentiation and morphogenesis in lineages that create the basic body plan and its main cell types, as was recently charted at high single cell resolution <sup>1–3</sup>. This remarkable process is known for many years to rely on a functional epigenetic machinery, including the de-novo DNA methyltransferases DNMT3A and DNMT3B <sup>4</sup>. During epiblast formation, DNA methylation is accumulating throughout the genome, raising from minimal levels in the ICM (day 4.5 post fertilization in mice) to maximal levels just prior to the initiation of primitive streak (PS) formation and endoderm/mesoderm differentiation (day 6.5) <sup>5–7</sup>. Loss of Dnmt3a/b is linked with gastrulation defects <sup>8–11</sup>. But as DNA methylation is a global regulatory mechanism with interactions over the entire genome, DNMT3A/B can affect epiblast and germ layer programs pervasively and beyond one or few loci, in ways that are not well understood. The question of DNMT3A/B function during gastrulation is a key example for the “paradox” of epigenetic function, which in one hand show the potential for prevalent genome wide regulatory impact and on the other hand exhibit only weak and quantitative effect at any particular gene and locus. Thus, in order to understand the function of DNA methylation systematically and beyond the global developmental arrest caused by its complete loss, we have to consider quantitative effects, redundancy and competition <sup>12</sup> with multiple transcriptional and epigenetic mechanisms <sup>13–15</sup>. We also must interpret the enzymes’ function and its specialization in each gastrulating germ layer and cell type.

The potential redundancy or specificity of DNMT3A/B adds to the complexity of the DNA methylation machinery. Both enzymes are potent CpG DNA methyltransferases in-vitro and in-vivo <sup>4</sup>, but multiple studies demonstrated their variable affinity to different flanking sequences <sup>16–18</sup> or different epigenomic contexts, including enhancers, promoters or exons <sup>19</sup>. The impact of such variable specificity is unclear, in particular since each DNMT can target hundreds of thousands of regulatory elements that contain a number of CpGs each, and the mild specificity of the factors so far did not seem to be amplified by clusters of adjacent high or low affinity targets. Both DNMTs are strongly expressed during the initial buildup of DNA methylation in the epiblast, and the division of labor among them at this stage is unclear.

Separately, Dnmt3a<sup>-/-</sup> and Dnmt3b<sup>-/-</sup> embryos move through gastrulation successfully, suggesting some or all of their initial functions can be compensated. Later in development however, Dnmt3b is weakly expressed, but Dnmt3b<sup>-/-</sup> embryos are arrested shortly after gastrulation. Dnmt3a is expressed in multiple lineages during organogenesis, but Dnmt3a<sup>-/-</sup> embryos are developing almost normally before dying postnatally<sup>11</sup>. Additional experiments perturbing Dnmts expression<sup>20-24</sup> further support the idea of variable and cell type dependent impact for each of the methyltransferases. Analysis of directed endoderm differentiation in human Dnmt3a<sup>-/-</sup> ESCs suggested a role for the enzyme in de-novo methylation of endoderm-specific differentially methylated regions<sup>10,25</sup>. These data highlight the need in new sensitive and quantitative models for understanding DNMT3A/B function and specificity.

Single cell RNA-seq (scRNA-seq) recently emerged as a powerful tool for mapping gastrulation transcriptional programs and temporal dynamics<sup>1-3,26</sup>. An important outcome of this technology is a highly quantitative model for the series of transcriptional states leading epiblast cells through germ-layer formation and gastrulation. Spontaneously differentiating embryoid bodies (EB) and gastruloids<sup>27-29</sup> can now be dissected over time using scRNA-seq such that in-vitro specific single cell states and artifacts are filtered and cell types that are faithfully modelling in-vivo counterparts are retained and analyzed in-depth. Such models can then be used for understanding early effects of key gastrulation factors on the differentiation dynamics. Comparative scRNA-seq of wild type and genetically perturbed models has many advantages, in particular as they allow for separating response to knockouts over different cell types and lineages and phasing of the response over time. Importantly, single cell analysis of in-vitro models should not be regarded as universally applicable in every lineage and embryonic stage, and analysis using such models must be ascertained through unbiased in-vivo/in-vitro comparison of transcriptional and epigenomic maps.

In this study we focus on a model for the critical time window of initial endoderm and mesoderm specification (E6.5-E7.5). At this stage, methylation is already at peak levels globally, while DNMT3A/B expression is declining from high levels sharply, simultaneously with rapid proliferation and transcriptional differentiation. We stabilized a meso-endoderm embryoid bodies (MEEB) system that reconstitute faithfully and at single cell resolution the

in-vivo epiblast, primitive streak (PS), early endoderm and early mesoderm programs. We then characterize the transcriptional and epigenetic impact of DNMT3A/B knockouts (independently or simultaneously) on these stages. This result in a detailed characterization of the mechanisms by which the two surprisingly specific methyltransferases first compensate for each other to harmoniously methylate the epiblast, but then diverge in the endoderm and mesoderm, to help creating a differentiated epigenetic and transcriptional landscape. Beyond the immediate implication to our understanding of gastrulation epigenomic regulation, this model provides a blueprint for understanding DNMT3A/B mediated methylation dynamics in any other systems.

## RESULTS

### **Asymmetric expression of DNMT3A and DNMT3B in gastrulation**

Using a recent temporal model for mouse gastrulation <sup>1</sup> we traced back the expression kinetics of DNMT3A and DNMT3B from the key cell states/type in E8.0 endoderm, mesoderm and ectoderm (Fig. 1a). Peak expression for both enzymes is observed in the epiblast at E6.5, with rapid downregulation toward E7.25 established in all lineages. Interestingly however, the main endoderm lineage (labeled Foregut) showed much slower repression of Dnmt3b compared to the notochord or mesoderm lineages (6 fold vs. up to 19-fold down-regulation). Traceback kinetics showed contrastingly faster Dnmt3a repression in the Foregut compared to notochord or mesoderm (13-fold vs. ~8-fold at e7.25). Both Dnmt3a and Dnmt3b down-regulation toward ectoderm differentiation is delayed, consistent with the overall later initiation of transcriptional conversion of epiblast to ectoderm cell states. The data indicate that during a critical time window (i.e., E7.25) in which epiblast cells are acquiring their initial endoderm and mesoderm identities, DNMT3A/B are transcriptionally regulated asymmetrically. These unexpected trends motivated us to devise quantitative models for assessing the combined and independent contribution of the two DNA methyltransferases during the build-up of endoderm and mesoderm DNA methylation patterns in the differentiating epiblast.

### **MEEBs reconstitute the in-vivo meso-endo bifurcation**

To model DNA methylation during epiblast bifurcation we developed a standardized meso/endoderm embryoid bodies (MEEBs) assay. We exposed embryonic stem cells to a

short epigenetic reset stage using growth in 2i/LIF medium for 2-3 passages<sup>30</sup>. We then created embryoid bodies by aggregating cells in hanging drops<sup>31</sup> for 48h in serum supplemented medium and propagated the resulting MEEBs for up to 7 days. We sampled MEEBs every 24h for analysis using single cell RNA-seq (scRNA-seq)<sup>32</sup> and constructed a transcriptional Metacell<sup>33</sup> model from a total of 47,307 single cell profiles passing quality control (Fig. 1b-d, Extended Data Fig. 1a-d, Supplementary Fig. 1, Supplementary Table 1). Importantly, we could match MEEBs transcriptional states to matching in-vivo states from gastrulation atlases<sup>1,3</sup> with minimal bias (Extended Data Fig. 2a-d). We discovered that MEEB metacells mapped in a highly quantitative and precise fashion to respective in-vivo epiblast, primitive streak, endoderm and mesoderm states (Fig. 1e). Furthermore, temporal tracking of MEEBs at single cell resolution unveiled a spontaneous process of differentiation that followed closely previously characterized in-vivo temporal gene expression dynamics, with emergence of epiblast followed by primitive streak state and leading to meso-endo bifurcation.

All key embryo driving transcription factors were observed robustly in the model. MEEBs first exit the ESC naïve pluripotent program (marked by Klf4 and Nanog repression) and by day 2-3 show a fully activated epiblast program (marked by Utf1, Pou3f1). At these stages we observe massive expression of the epigenetic machinery, most notably DNA methyltransferases (Dnmt3b and Dnmt3a), but also epigenetic regulators linked with KRAB-domains zinc fingers (Trim28) and polycomb (Phc1, Cbx7) (Extended Data Fig. 3a). In day 4 the key PS transcription factors (e.g., Eomes) are induced and immediately following it we map spontaneous endoderm (Foxa2) and nascent mesoderm (Mesp1) bifurcation. Later stages (day 5-7) involve further differentiation of endoderm (Foxa1), extraembryonic mesoderm (Msx1/Hand1) and embryonic mesoderm (Foxc1). Out of these states we observe additional, more specialized differentiation toward cardiomyocytes (Mef2c) and hematoendothelial progenitors (Tal1). The only subpopulation of MEEB cells that could not be projected faithfully on the in-vivo atlas involved 4-7% of the cells in MEEB day 5-7, and maintained or regained expression of pluripotency TFs (e.g., Esrrb, but not Klf4) while also developing a transcriptional state correlated with the ES 2i states and/or primordial germ cell precursor signature (Klf2, Iftim3 and to a smaller extent Dppa3/Stella) (Extended Data Fig. 3b).

The initial diversification of MEEB transcriptional programs was self-organized and emerged despite the lack of clear global spatial organization as observed in models for embryonic axis formation<sup>34,35</sup>. These differentiation dynamics facilitate in-depth analysis of the impact of DNA methylation perturbations on epiblast, primitive streak, early mesoderm and early endoderm transcriptional programs, that we defined using specific, co-expressed gene sets (Extended Data Fig. 3c). In particular, the model showed asymmetric regulation of Dnmt3a and Dnmt3b during meso-endo bifurcation (Fig. 1f), similarly to the observation *in-vivo*.

### **Double knockout MEEBs show incomplete differentiation arrest**

It is widely assumed that in order to establish a pluripotent state and later embryonic differentiation, inner cell mass cells are reorganizing their epigenomic landscapes toward a unique “ground state”. Such ground state is known to be defined by global reduction in DNA methylation<sup>36</sup>, as well as by X activation<sup>37,38</sup>, redistribution of repressive histone marks<sup>39</sup>, but preservation of imprinting. Despite high resolution characterization of this epigenetic ground state *in-vivo*<sup>6</sup>, it is unclear what are the mechanistic roles of reduced DNA methylation in maintaining pluripotency (e.g., ESCs can be cultured successfully without it<sup>40</sup>). It is also unclear how the rapid re-methylation in the epiblast contribute to later exit from pluripotency. We therefore followed gene expression in MEEBs generated from ES Dnmt3a<sup>-/-</sup>; Dnmt3b<sup>-/-</sup> double knockout (DKO). We generated a Metacell transcriptional map and temporal model from 30,500 DKO single cells, which were processed similarly to the wild type (WT) counterparts. Initial annotation (Fig. 2a, b) showed DKO MEEBs establish the epiblast state, but fail to smoothly exit it toward massive differentiation as observed in the WT (Extended Data Fig. 4a-c). We computed an epiblast *program score* (Extended Data. 3c) using the expression of the 30 genes most correlated with the major epiblast TF Utf1 in the WT, and searched for genes whose metacell expression trend compared to this score was altered between WT and DKO MEEBs. Reciprocally to a previous study knocking out the demethylation TET system<sup>13</sup>, we noted marked increase in Lefty2 expression and decrease in Nodal expression in DKO cells (Fig. 2c), suggesting loss of methylation contributed to failure to activate nodal signaling. Lefty1 was more weakly induced in one mutant line but not the other (Extended Data Fig. 4d). Interestingly, we also observed an increase in DKO expression of Dppa3/Stella, Ifimt1 and Ifitm3<sup>41</sup> compared to the WT. To better characterize the switch

from normal in-vivo-like epiblast state to a Dppa3/Stella dominated program in DKO MEEBs, we computed a second gene program score using the 30 genes most correlated with Dppa3 in WT MEEBs (Extended Data Fig. 3c). We then observed a gradual decrease in the distribution of epiblast signatures over time until day 5, but later re-establishment of the program, together with increase in the Dppa3 signature (Fig. 2d, e, Extended Data Fig. 4e). In conclusion, a large fraction of the cells in DKO MEEBs are arrested in an epiblast state, with constitutively high expression of Lefty2 and gradual increase in the expression of Dppa3 and related genes.

While the disruption in smooth spontaneous germ layer formation in DKO MEEBs was expected, we also found unexpectedly that smaller DKO sub-populations managed to move toward differentiation and establish a primitive streak, early mesoderm or endoderm states (Fig. 2f). Careful comparison of the fidelity of these states in comparison to their WT counterparts (Fig. 2g), showed high consistency and only small expression changes (including lingering Lefty2 over-expression) in the PS and nascent mesoderm state. Interestingly, the endoderm state showed marked DKO over-expression of definitive/visceral endoderm markers, including Dab2, Ttr2 and Apoa1 (Fig. 2g). Another indication of DKO related de-repression of differentiation is the early appearance (from day 2) of Tal1 expressing hematoendothelial precursor cells (Fig. 2h). Similar analysis was done on triple knockout MEEBs (TKO: Dnmt1<sup>-/-</sup>; Dnmt3a<sup>-/-</sup>; Dnmt3b<sup>-/-</sup>) using 16682 single cell profiles, which like DKO showed an epiblast arrest followed by an even slower, but nevertheless discernible emergence of differentiation programs, including an extraembryonic endoderm state and enrichment of hematoendothelial precursors, in addition to emergence of a Sox1+ ectoderm-like state (Extended Data Fig. 5). Together this data showed that DNA methylation is important for enabling proper, high yield exit from the epiblast state, but still can be intrinsically dispensable for build-up of the initial gastrulation programs. It also suggests that methylation may be important for endoderm stability through repression of further definitive/visceral endoderm programs and that it is involved in the prevention of early Tal1-mediated hematoendothelial programs induction.

### **DNMT3A and DNMT3B knockouts perturb MEEB meso-endo programs**

We next constructed transcriptional manifolds and MEEB time series from 34,484 single cells from two independent lines of *Dnmt3a*<sup>-/-</sup> (Fig. 3a) and 34,514 single cells from two independent lines of *Dnmt3b*<sup>-/-</sup> (see methods) (Fig. 3b, Extended Data Fig. 6-7)<sup>42</sup>. Consistent with the reported mild in-vivo phenotypes, loss of either of the enzymes was well tolerated and gave rise to normal exit from the epiblast and formation of the initial germ-layer programs. But subsequent in-depth comparison of the transcriptional states established by *Dnmt3a*<sup>-/-</sup> and *Dnmt3b*<sup>-/-</sup> cells uncovered many quantitative differences. To facilitate unbiased comparison, we identified WT gene programs defining differentiation fates in addition to the *Utf1*/epiblast program (Extended Data Fig. 3c). We selected for each mutant line single cells with maximal expression of these gene program signatures. We then computed differential of expression of the selected cells between two independent pairs of *Dnmt3* mutants (Fig. 3c). This resulted in an effective screen for differential expression that was consistent between pairs (spearman rho=0.21-0.32, at least p < 10<sup>-5</sup>) for all differentiation programs and provided insight into the independent roles of DNMT3A and DNMT3B in the context of different gastrulation lineages. In the *Eomes/PS* program, we identified over expression for key endoderm factors (e.g. *Cer1*) in *Dnmt3a*<sup>-/-</sup>, and over expression for key mesoderm factors (e.g. *Mesp1*) in *Dnmt3b*<sup>-/-</sup>. Subsequently, in the *Foxa1/endoderm* program, *Dnmt3b*<sup>-/-</sup> showed over expression of mesoderm factors (*Msx1*), as well as induction in extra-embryonic endoderm genes (*Dab2*). In the *Dnmt3a*<sup>-/-</sup> *Mesp1/nascent mesoderm* program, we observed over expression of the retinoic acid synthesis gene *Aldh1a2* and the extra-embryonic mesoderm factor *Hand1*. Over expression of *Irx3*, *Ptn* and *Igfbp5* was detected in the *Dnmt3a*<sup>-/-</sup> *Foxc1/rostral mesoderm* program. Conversely, *Dnmt3b*<sup>-/-</sup> mesoderm programs showed over-expression of *Lefty2*. Transcriptional differences became intensified in the extra-embryonic mesoderm program – possibly accumulating intra-cellular and inter-cellular signaling effects. This data suggested that an endoderm differentiation bias and preference toward rostral programs is linked with loss of *Dnmt3a*, compared to loss of *Dnmt3b*. To follow up and further test this hypothesis, we quantified the fraction of endoderm and mesoderm cells across lines in replicates and showed a small but significant bias in the frequency of endoderm cells during initial PS differentiation in *Dnmt3a*<sup>-/-</sup> MEEBs (Fig. 3d). Taken together, we showed that while *Dnmt3a*<sup>-/-</sup> and *Dnmt3b*<sup>-/-</sup> may appear well balanced in their gastrulation dynamics at low resolution, higher resolution analysis uncovers specific regulatory function for the two enzymes, with impact on the expression of key mesoderm/endoderm TFs and

signaling agents, and consistent modulation in the endoderm vs. mesoderm differentiation balance.

We note that MEEBs mutant analysis is consistent with the in-vivo expression asymmetry of Dnmt3a/b in the endoderm and mesoderm. If Dnmt3a is maintained at higher level in newly differentiated mesoderm cells, it can assist in repressing endoderm genes in a way consistent with the Dnmt3a<sup>-/-</sup> overexpression of such genes we observed above. Likewise, if Dnmt3b is maintained at higher levels in new formed endoderm cells, it may participate in the repression of mesoderm genes as observed here. In both cases, Dnmits seems to modulate and fine-tune expression programs rather than inhibit or activate them completely. The mild in-vivo phenotypes of Dnmits independent mutants are consistent with an effective compensatory mechanism that tolerate the main effect of loss of either Dnmt3a or Dnmt3b, and can counter-act the associated transcriptional aberrations.

#### **DNMTs in-cis preferences drive epiblast methylation build-up**

We used a targeted post-bisulfite adaptor tagging (PBAT-capture) approach <sup>43</sup> (methods) to profile methylation in WT, Dnmt3a<sup>-/-</sup>, and Dnmt3b<sup>-/-</sup> MEEBs, during the initial setup of the epiblast program, before germ layer bifurcation (day 0 to 4). For control, we profiled matching ESCs grown in serum LIF (presenting maximal methylated state), DKO and TKO MEEBs (presenting unmethylated states). PBAT-capture probes were designed to target 50,000 loci that were selected to over-represent enhancers <sup>44</sup> (Extended Data Fig. 8a-h, Supplementary Table. 2). We reasoned that in the MEEB model, both independent and co-factor dependent DNMT3A/B specificity in the epiblast can be studied, since as shown above (Fig. 1, Fig. 3), up to day 4, all TFs and other putative co-factors are conserved between the in-vivo state and the mutant MEEB systems. Our data showed gradual increase in mean methylation from less than 30% to 80% at low CpG content sites in WT. Dnmt3b<sup>-/-</sup> showed similar average kinetics with some reduction at day 4, while Dnmt3a<sup>-/-</sup> showed slower methylation accumulation (Fig. 4a). Analysis of mutant methylation kinetics identified unexpectedly large number of loci with delayed methylation build-up that was specific to either Dnmt3a<sup>-/-</sup> or Dnmt3b<sup>-/-</sup> MEEBs (Fig. 4b-c). To understand the possible mechanisms underlying this specificity we performed sequence analysis around CpGs with Dnmt3a<sup>-/-</sup> and Dnmt3b<sup>-/-</sup> -dependent kinetics (Fig 4d-e, Extended Data Fig. 8i-j). This led to the detection of marked differences in the nucleotide and

dinucleotide distributions around the target CpGs, that we used to compute models predicting the specific loss of methylation in Dnmt3a<sup>-/-</sup> (model MEEB\_3a) Dnmt3b<sup>-/-</sup> (model MEEB\_3b), and to estimate difference in enzyme affinity (model MEEB\_3b/3a) from sequence alone (methods). Each model used simple regularized linear regression on dinucleotides in the 6bps surrounding each CpG to obtain high accuracy ( $R^2=0.41$  in cross validation for MEEB\_3b/3a, Extended Data Fig. 9c) that we further enhanced using a gradient boosting approach ( $R^2=0.49$ , Fig. 4f, compared to a maximal  $R^2 = 0.87$  that is possible given sequencing depth, based on resampled data, methods). Importantly, sequence context is changing methylation kinetics, but methylation accumulation is not inhibited at low affinity contexts of either enzymes (Fig. 4g). This gives rise to a locus-specific time delay in methylation levels through MEEB days 2-6, rather than to static and stable differentially methylated landscape. Most importantly, comparison of MEEB differential methylation and published data on in-vivo mutant embryos<sup>20,45</sup> reflected a highly consistent MEEB vs in-vivo impact on methylation. This showed that the in-vivo Dnmt3a/b differential methylation signal can be robustly predicted from the MEEB sequence model (Fig. 4h-i). On the other hand, comparison to published methylation profiles in MEFs<sup>18</sup> showed some of the differential methylation we observed is specific to the epiblast state (Extended Data Fig. 8k-l). Overall, these data provide evidence and a quantitative model for the kinetics of the methylation landscape in the differentiating epiblast, showing it to be quantitatively regulated by the activities DNMT3A and DNMT3B and their in-cis sequence affinities. It should be however noted that key regulatory sites, such as those marked with H3K4me3 or H3K27me3, are protected from this methylation dynamics, and that sequence-based estimation of methylation kinetics in the epiblast is only relevant in unprotected sites.

### Compensation of asymmetric DNMT3A/B preferences over strands

The DNMT3A/B sequence preference we observed in MEEB and in-vivo should be explicable by the combination of enzymes' de-novo methylation preferences and the effect of the methylation housekeeping machinery mediated by DNMT1 (Fig. 5a). These should together counteract the demethylation dynamics mediated by DNA replication and the Tet machinery. Importantly, while de-novo activities can be strand-specific, the housekeeping machinery can copy methylation from strand to strand. To separate these effects, we modeled a recently published study that profiled unmethylated (TKO) ES cells lacking the housekeeping

machinery, following reintroduction of either Dnmt3a or Dnmt3b<sup>17</sup>. We inferred sequence specificity models for each enzyme (models *TKOES\_3A*, *TKOES\_3B*), quantitatively generalizing the original study's enrichment of specific sequence contexts around DNMT3A or DNMT3B favoring CpGs (Fig. 5b-c). In marked contrast to the MEEB data, the inferred models were strongly strand asymmetric. But while DNMT3A specificities allowed some loci to be targeted specifically on both strands (Fig. 5d) due to partial symmetry of the sequence model, DNMT3B's sequence preferences disallowed symmetric strand preferences completely (Fig. 5e), such that high preference in one strand implied low preference on the other. This was reflected in our mutant MEEB models (Fig. 5f-g), showing preference in both strand is needed for maximal 3A mediated methylation, while preference in one of the strands is required for maximal 3B mediated methylation.

To combine all effects together, we inferred a (non-linear) model predicting MEEB differential methylation using only the strand-specific models inferred from the TKO-ES data (giving rise to model *MEEB\_strand*, methods). The resulting model used the maximum sequence specificity over the two strands (from models *TKOES\_3a*, and *TKOES\_3b*) as well as each strand's independent contributions (Fig. 5h). Remarkably, this reproduced almost perfectly the model we trained directly on MEEB data using dinucleotides (model *MEEB\_3b/3a*) (Fig. 5i). We therefore showed that epiblast methylation (in MEEBs, and in-vivo, Fig. 5j) is quantitatively explained by the combination of strand-specific *in-cis* sequence preferences for each enzyme, which are compensated by DNMT1 when renewing methylation between strands.

### **Replication linked turnover underlies methylation plasticity**

Given that methylation is known to reach maximal levels in the epiblast, prior to gastrulation, it is a-priori unclear if specific de-novo methylation via DNMT3A/B can have any impact within the differentiation process. In other words, if epiblast cells are already maximally methylated, the window of opportunity for DNMT3A/B mediated regulation may be closed. To better understand this, we sorted single cells from E7.5 mouse embryos and applied a modified single cell bisulfite sequencing protocol<sup>46,47</sup> to generate 2146 single cell methylation profiles at low coverage (Extended Data Fig. 9a-c). These were further grouped into subpopulations representing epiblast/ectoderm, mesoderm, endoderm and blood cells based on index

sorting with EPCAM and CXCR4 surface markers (Extended Data Fig. 9d-e). We used sequence coverage traces of early and late-replicating genomic domains for precise estimation of replication progress in single cells<sup>48</sup> (Extended Data Fig. 9f). When combining these traces with estimation of average methylation in early and late replicating domains we recovered a clear cell cycle trend (Fig. 6a). This trend was modeled using a principle curve to order single cells over G1, S and M phases. The methylation trend thus discovered was highly dynamic (Fig. 6b). In epiblast/ectoderm, methylation peaked at G1 with particularly high mean of 0.91 and 0.94 in early and late replicating domains respectively. It then decreased to 0.85 in early/mid S phase for early replicating domains and to 0.88 in mid/late S phase for late replicating domains. Similar trends were observed in mesoderm and endoderm single cells. These data showed a major lag in DNA methylation housekeeping following replication, in both early and late replicating domains, but in different cell-cycle timings. This lag must represent passive de-methylation that is continuously replenished by de-novo methylation, through either Dnmt3a/b or secondary Dnmt1 activity, demonstrating a potential window of opportunity for DNMT3A/B epigenetic regulation during gastrulation.

We next compared methylation in CpGs with sequence contexts favoring DNMT3B or DNMT3A (high/low model MEEB\_3b/3a score respectively) during the cell cycle (Fig. 6c). Ectoderm and endoderm methylation show significantly more preference for 3B favoring contexts than mesoderm, consistent with their higher DNMT3B / DNMT3A expression ratio (Extended Data Fig. 9g). To follow up on this observation we performed single cell bisulfite sequencing of 7398 cells from wild type and mutants MEEBs. We recovered a cell cycle methylation signature and methylation trend that was similar to the one observed in embryos (Fig. 6d-e, Extended Data Fig. 9h), with WT MEEB showing comparable methylation in CpGs with DNMT3A or DNMT3B favoring sequence contexts. For *Dnmt3a*<sup>-/-</sup> and *Dnmt3b*<sup>-/-</sup> MEEB we observed a consistent methylation gap correlated with sequence context throughout the cell cycle stages (Fig. 6f-g, Extended Data Fig. 9i). After normalizing for methylation peak level, we observed that the kinetics of re-methylation in S phase was faster in DNMT3A favoring sequences when only DNMT3A was active (i.e., in *Dnmt3b*<sup>-/-</sup>). When only DNMT3B was active (*Dnmt3a*<sup>-/-</sup>) we observed stronger reduction of methylation in mid-S-phase for DNMT3B favoring sequences. Taken together, we showed a methylation housekeeping lag is observed both in-vivo and in MEEBs. The de-novo methylation machinery can therefore replenish

partially methylated S-phase cells toward very high levels of up to 95% average methylation in G1. DNMT3A/B can compensate each other for ensuring proper re-methylation, but the kinetics of this process differ in early and late replicating domains and correlate with the sequence preference of the enzymes.

### **Compensation of DNMT3A/B preferences in CpG clusters**

The sequence preferences we inferred for DNMT3A/B represent a strong but ultra-local effect (~5bp around the affected CpG). Methylation effects on the larger scale of regulatory elements (typically 100s of bps) must involve multiple CpGs with variable sequence contexts. Indeed, we derived improved predictive power ( $R^2=0.54$ ) when adding mean enhancer methylation (excluding the targeted CpG) to the sequence-based methylation predictor (Fig. 7a). We note that the vast majority of enhancers elements are mixing CpGs with DNMT3A or DNMT3B favoring context (i.e. low and high MEEB\_3b/3a scores) rather than selecting groups of CpGs with common preference (Fig. 7b). Because of that, predicting mean enhancer methylation from sequence alone becomes less accurate as the number of CpGs in the enhancer increases (Fig. 7c). Mixing of DNMT3A and DNMT3B affinities in regulatory loci induce a powerful compensatory force that is decreasing differential methylation over whole enhancers elements, for the great majority of such elements, even when DNMT3A/B activity is unbalanced.

### **DNMT3A favoring CpGs are enriched in gastrulation enhancers**

Nevertheless, some enhancers cannot be fully compensated by slower methylation kinetics by the alternative enzyme, and remain hypo-methylated in *Dnmt3a*<sup>-/-</sup> MEEBs as late as MEEB day 6 (Fig. 7d). Such loci show remarkably high DNMT3A sequence affinity over all or most of their CpGs (Fig. 7e). Remarkably, enhancers showing high differential methylation between *Dnmt3* mutants are significantly enriched around the promoters of gene regulated during germ layer formation (Fig. 7f). Specific examples for enhancers with preference for DNMT3A include some key regulators of endoderm/mesoderm differentiation and function (e.g. *Foxa2*, *Msx1*) (Fig. 7g, Extended Data Fig. 10, Supplementary Table. 3-4). In summary, the affinity of DNMT3A/B to specific CpGs during DNA methylation build-up in the epiblast is blurred in most cases, when CpGs from two strands have different affinities and when enhancers consist of clustered CpGs with mixed preferences. But in some key enhancers, in particular around

important target gastrulation genes, we observe accumulation of pro-DNMT3A CpGs and significant, poorly compensated, *Dnmt3a*<sup>-/-</sup> dependent reduction in methylation. This effect is correlated (but can still not be causally linked) with poorer repression of mesoderm programs and induction of more endoderm in DNMT3A<sup>-/-</sup> MEEBs. Regardless of its potential functional impact, the model combining raw sequence preferences of the two *Dnmt3s*, with replication linked methylation turnover and asymmetric DNMT3A/B activity in mesoderm and endoderm can harmoniously explain how embryonic DNA methylation is being shaped up from few basic and well-defined mechanisms.

## DISCUSSION

Classical in-vitro analysis of the sequence specificity of the two mammalian de-novo methyltransferases, DNMT3A and DNMT3B<sup>4,16</sup> and more recently studies in methylation deprived mESC<sup>17</sup> showed clearly that the two factors methylate CpG dinucleotides with distinctive preferences for specific surrounding sequences. Here we asked whether the methylation preference of DNMT3A/B contribute to the build-up of the methylome in the epiblast and in the differentiated germ layers, using analysis of single cells from MEEB models and mouse embryos. According to our data, we observe major specificity in methylation preferences and kinetics. For example, in a set of 94516 captured CpGs from embryonic enhancer elements, 18.4% show significant differential methylation when knocking out DNMT3A or DNMT3B. But this remarkable, admittedly under-appreciated effect is not matched by similarly dramatic transcriptional and differentiation phenotypes. Classical knockout models, while showing overall methylation is critical for initiating gastrulation (also shown here in MEEB, Fig. 2), indicated that loss of each of the enzymes is of surprisingly mild effect, with post gastrulation lethality of *Dnmt3b*<sup>-/-</sup> and only post-natal lethality for *Dnmt3a*<sup>-/-</sup><sup>11</sup>. Indeed, using MEEBs to quantify precisely the fidelity of epiblast, early endoderm and mesoderm transcriptional programs, we show that cells can establish all of these programs with good precision even if one of the *Dnmt3s* is missing (Fig. 3). The conundrum of extremely high enzyme specificity but near-perfect compensatory capacity on epiblast, primitive streak and initial endoderm/mesoderm formation represents a gap in our understanding of methylation dynamics in early development. This gap also reflects on our lack of understanding of such dynamics and function in other tissues and developmental stages.

To fill this gap we combined published data from mESC<sup>17</sup> and from in-vivo bulk sequencing<sup>20,21,45</sup>, with our new single cell data from MEEBs and mouse embryos to synthesize a model that quantitatively explains how DNMT3A/B compensate each other in the epiblast. The model's starting point is defined by strand-specific sequence contexts of individual CpGs for each enzyme. This initiates the methylation process with a strong bias, and the model explains how a series of compensatory mechanisms balance such bias. First, the DNMT1 housekeeping methylation machinery methylates hemimethylated sites during replication, therefore essentially "copying" methylation from one strand to the other. For DNMT3B, this results in a strong compensatory force since its sequence preference is asymmetric and de-novo methylation that target a high affinity site at one strand can be copied to the opposite weak affinity strand by DNMT1 following replication. DNMT3A is characterized by symmetric sequence preferences, so weak sites are observed on opposite strands and are less effectively compensated by DNMT1. The second compensatory effect rely on mixing of CpGs with variable affinities to DNMT3A and DNMT3B in regulatory elements. Such mixing implies that when averaging the preferences of all CpGs in an enhancer, almost all element are neutral in their affinity. The third compensatory factor relies on time and turnover. Low-affinity CpGs (for either DNMT3A or DNMT3B) will be methylated at slower rates than high-affinity sites, but given sufficient time in the epiblast, methylation can reach high levels even in such sites. Methylation turnover contributes to this effect. As shown here by single cell analysis, the continuous turnover of DNA methylation during replication cycles in the epiblast<sup>46,49–52</sup>, slow down methylation accumulation, even for high-affinity sites.

As a result of these mechanisms, when both enzymes are functioning in the epiblast, most of the genome outside of CpG islands (which are protected from methylation completely) is becoming methylated homogenously. The kinetics of the process combines strand-specific de-novo DNMT3A or DNMT3B activity, the effect of DNMT1 copying between strands and the antagonistic effect of the turnover machineries. When knocking out either of the enzymes, the respective low-affinity CpGs accumulate methylation more slowly, but the net effect is initially mild given compensation by DNMT1 and nearby high affinity CpGs. This can explain all current observations on DNMT3A/B and epiblast methylation, leaving open however the question of their function later in gastrulation and the broad in-vivo post-gastrulation phenotypes of the enzymes.

Careful quantitative analysis of a gastrulation transcriptional flow model<sup>1</sup> show differential Dnmt3a/b control in the endoderm (low 3a, higher 3b), mesoderm (low 3b, higher 3a), and ectoderm (persisting high 3b/a) (Fig. 1a). This suggests unappreciated symmetry breaking in enzyme activity when exiting the epiblast program and initiating germ layer differentiation. Our MEEB models are reconstituting Dnmt3s differential transcriptional dynamics in wild type cells. MEEB single gene mutants allow quantification of transcriptional mis-regulation in early mesoderm programs (Dnmt3a<sup>-/-</sup> is de-repressing endoderm genes) and endoderm programs (Dnmt3b<sup>-/-</sup> is de-repressing mesoderm genes) (Fig. 3). The impact of these perturbations on differentiation rates in MEEBs is mild, but we do see significant bias toward mesoderm when knocking out Dnmt3b and toward endoderm when knocking out Dnmt3a. Together this leads to the hypothesis that bifurcation of primitive streak programs toward endoderm and mesoderm fates is supported by differential activity of DNMT3A/B which may help stabilize repression of genes that must be asymmetrically expressed between the germ-layers. Notably, our data show that even without Dnmt3a or Dnmt3b, the embryonic regulatory machinery can establish the mesoderm and endoderm program with reasonable precision. But since the remarkably robust nature of the gastrulation program relies on multiple backups for each regulatory mechanism, we suggest that partial tolerance to loss of one of the Dnmt3s does not imply their lack of function.

Given these observations of DNMT3A/B activities and emerging model of complex balancing forces shaping the methylome, it may not be immediately clear why the knockout of Dnmt3b leads to early embryonic lethality, while knocking out Dnmt3a is tolerated throughout organogenesis and until birth. Data on Dnmt3a/b expression in the different embryonic lineages suggest that the answer to this puzzle may involve the role of Dnmt3b in ectoderm differentiation, in which Dnmt3b is highly expressed in-vivo (Fig. 1a). However, since these lineages are not represented in our MEEB models, more follow-up is required in order to characterize this effect. But the present data already show clearly that both DNMT3A and DNMT3B participate in tuning regulation of specific gastrulation lineages, and that a notion of hierarchy of enzyme potency in which Dnmt3b is playing a more “important” role in gastrulation is imprecise.

Combining DNMT3A/B germ-layer asymmetry with their remarkable sequence affinities opens the way to uncovering a still poorly characterized layer of regulatory specificity facilitating gastrulation. Our methylation analysis in MEEB and in embryos suggests that for a small but potentially important group of enhancers, clusters of DNMT3A favoring CpGs may promote germ layer-specific methylation when DNMT3A activity is reduced in the endoderm. The observation that cell-cycle linked methylation loss is pervasively observed in early gastrulating lineages (Fig. 6) is important in that respect, since it shows methylation at these stages is still not entirely driven by simply copying the epiblast methylation model through DNMT1. In other words, DNMT3A/B are still "writing" methylation in E7.5 and can therefore still confer specificity.

Our proposed model for methylation dynamics and compensation of DNMT3A/B specificity in the epiblast is supported by multiple lines of evidence and by a robust quantitative model. On the other hand, much more work needs to be done to characterize the possible causal role of DNMT3A/B in supporting germ-layers differentiation. In particular, identifying those enhancers in which DNMT3A/B specificity is of a direct regulatory role is still an open challenge. It should be stressed that even for enhancers that encode clear DNMT3A/B methylation preferences, methylation alone is highly unlikely to deterministically define enhancer identity. One must consider in-cis preferences and complex interactions between additional layers specifying enhancer activity in each lineage, most importantly combinations of TFs<sup>53,54</sup>, the polycomb machinery and long-range chromosomal architectures<sup>55</sup>. The combination of in-vivo single cell expression atlases and extensive perturbation of epigenetic machineries in-vitro, with rich single cell profiling<sup>56,57</sup>, opens the way to the delineation of these regulatory layers. Ultimately, the new data will explain quantitatively how genomic sequences encode the build-up of epigenetic landscapes toward cell fate determination and commitment in the mammalian embryo.

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#### AUTHOR CONTRIBUTIONS STATEMENT

Z.M. and A.T. designed the experiments, Z.M. performed the experiments, A.T. designed the analysis. Z.M., A.T. and A.L analyzed the data with help from M.M, O.B.K and O.S. E.C. helped with automation of single cell PBAT protocol, M.Z. performed the mice embryos dissections, A.T. and Z.M wrote the manuscript with input from all authors.

#### COMPETING INTERESTS STATEMENT

The authors declare no competing interests.

#### FIGURE LEGENDS

##### **Fig. 1: Dnmt3a/b germ-layer expression asymmetry is modeled precisely in mesoderm-endoderm embryoid bodies (MEEBs)**

**a**, Kinetics of Dnmt3a/b repression over embryonic time (fold change compared to maximal levels in the epiblast plotted against embryonic time) in different cell type lineages inferred from a temporal gastrulation model<sup>1</sup>. The red line marks E7.25.

**b**, Expression levels heatmap of key transcription factors across metacells that were derived from WT MEEBs in eight time points. Color-coded bars represent metacell annotation based on projections over the in-vivo gastrulation atlas. Endo – Endoderm. Meso – Mesoderm. Epi – Epiblast. PS – primitive streak. Undef - undifferentiated cells.

**c**, Metacell 2D graph for the WT model shown in b. Cells – small points, Metacells – larger ovals. Both are colored by the cell type annotation color code. Lines are connecting related metacells.

**d**, Cells in each MEEB time point are projected separately over the MEEBs metacell 2D graph.

**e**, Gene expression ( $\log_2(\text{UMI frequency})$ ) of epiblast, primitive streak, nascent mesoderm and anterior primitive streak is compared between the MEEB model (X axis) and the in-vivo temporal gastrulation model (Y axis). Panels on the diagonal represent similar states with high quantitative match of MEEB and in-vivo transcription.

**f**, The average time (X axis) against fold repression of DNMT3A and DNMT3B (compared to maximal level in epiblast-like cells) for each MEEB metacell (points, color coded by annotated type). See panel A for the analogous in-vivo trends. Dashed line marks day 6.

**Fig. 2: Epiblast arrest in methylation deprived MEEBs.**

**a**, 2D Metacell graph derived from DKO MEEBs in eight time points. Annotation is performed by projection on the gastrulation atlas as done for WT metacells, with additional annotation of a persistent pluripotent state (Dppa3+/Klf4-).

**b**, Time series for the DKO experiments. DKO cells from each MEEB time point are projected on the metacell 2D graph shown in A.

**c**, Comparing epiblast gene program score (30 genes correlated with Utf1 in WT) to expression of select genes over WT and DKO metacells (points, color coded by cell type as in Fig. 1). Trend line (Lowess smoothed, dashed red) is determined based on the WT data.

**d**, Distribution of Utf1/Epiblast score over single cells density in WT (dashed gray) and two DKO lines (blue and cyan).

**e**, Similar to d, for a gene program correlated with Dppa3 expression.

**f**, Fraction of cells with gene program score above an activity threshold set by WT cells (Methods) is shown for two independent DKO lines (top and bottom rows, DKO1 and DKO2), and matched WT controls per time point.

**g**, Comparing pooled log2 mean gene expression for the 160 WT and DKO cells (or around 1M UMIs) with maximal Primitive streak, Nascent mesoderm and Endoderm gene program expression. Genes with top fold change are highlighted (only when q-value (chi-square, FDR corrected) is <0.05).

**h**, Similar to f, for hematopoietic gene program score.

**Fig. 3: DNMT3A and DNMT3B single knockout induce endoderm/mesoderm differentiation bias.**

**a, b**, Metacell 2D graph for  $Dnmt3a^{-/-}$  and  $Dnmt3b^{-/-}$  MEEBs.

**c**, Comparing differential expression of two independent pairs of  $Dnmt3a^{-/-}$  and  $Dnmt3b^{-/-}$  lines across five cell states. For each mutant line and gene program, expression of 160 single cell profiles with maximal gene program score was pooled. log2 expression for each mutant pair was subtracted. Color coding is based on the maximum q-value in the two comparisons.

Gene names are highlighted for genes with consistent effect. Correlation coefficient (Pearson) is quantifying the consistency of differential expression between the two independent mutant pairs.

**d**, Cumulative distribution of the Foxa1/endoderm gene program score over single cells sampled in MEEB day 4. Upper and lower panels show data from independent DNMT3A/DNMT3B mutant pairs. Shown are D statistic and p-value of a two-sided Kolmogorov-Smirnov test (for J1 p=2.29e-11, and p=2.03e-5 for N15).

**Fig. 4: In-cis specificity of DNMT3A/B methylation in the epiblast**

**a**, Mean methylation for high (>8%) and low (<3%) CpG content in selected loci over MEEB time, using PBAT-capture probes.

**b**, Sixty clusters heatmap of CpGs by methylation dynamics in developing MEEBs. Heatmap for depicts differential methylation between Dnmt3a and Dnmt3b knockout MEEBs in days 1-4. **c**, Heatmap show color-coded absolute methylation levels for the clusters in B in WT, Dnmt3a<sup>-/-</sup>, Dnmt3b<sup>-/-</sup>, DKO and TKO.

**d**, Heatmap for color coded positional dinucleotide weights for a model regressing Dnmt3b<sup>-/-</sup> and Dnmt3a<sup>-/-</sup> methylation difference from sequence. Positions are relative to the targeted CpG, with 0 indicating the pair of nucleotides immediately flanking the CpG on 5' and 3'.

**e**, Motif logos show preferred nucleotides around CpGs with slower methylation kinetics in DNMT3B (high score) or DNMT3A (low score). The core CpG is drawn in a fixed scale.

**f**, Performance of sequence-based prediction (Model MEEB\_3b/3a, X axis) for Dnmt3b<sup>-/-</sup>/Dnmt3a<sup>-/-</sup> methylation difference (Y axis), using a gradient boosting model on dinucleotides around the CpG.

**g**, Kinetics of CpG methylation over MEEB time, grouped by model MEEB\_3b/3a score and shown for WT and mutant MEEBs.

**h**, Left: showing matching between differential methylation of Dnmt3a and Dnmt3b knockouts in two conditions MEEB day 1-4 (X axis), and epiblast from E6.5 mouse embryos (Y axis). Right: comparing sequence-based predictions (model MEEB\_3b/3a) to epiblast mutant methylation difference. Shown are Pearson correlation coefficients ( $r$ ).

**i** Similar to h, using data on E8.5 embryos.

**Fig. 5: Integration of strand specific DNMT3A/B sequence preferences and housekeeping methylation predicts epiblast methylation trends**

- a**, Schematics diagram depicting de-novo strand-specific methylation with DNMT3A or DNMT3B preferences, which can be compensated by the Dnmt1 housekeeping machinery in a continuous cycle involving de-novo methylation and strand-to-strand copying during replication. The methylation gain mechanisms are counteracted by the dynamics of lossy methylation replication (with or without involvement of the TET machinery).
- b**, Heatmap depict dinucleotide model preferences for strand specific DNMT3A methylation preference, as inferred from data on TKO-ES cells with Dnmt3a re-introduction (model TKOES\_3a). X axis labels represent the position of the dinucleotide (XY) relative to the CpG (CG).
- c**, Similar to b, for Dnmt3b re-introduction data (model TKOES\_3b).
- d,e**, Color coded density map show the joint distribution of TKOES\_3a and TKOES\_3b model scores on plus and minus strands. Note lack of positions that match high Dnmt3b preference on both strands due to the enzyme's asymmetric preference and in contrast to Dnmt3a.
- f**, For 2-dimensional bins of plus and minus strand TKOES\_3a model scores we show the mean methylation in the MEEB model methylated by Dnmt1/Dnmt3a (Dnmt3b<sup>-/-</sup>)
- g**, Similar to f, for TKOES\_3b model and MEEB Dnmt3a<sup>-/-</sup> data.
- h**, We computed MEEB\_strand: a model predicting difference in MEEB Dnmt3b<sup>-/-</sup> and Dnmt3a<sup>-/-</sup> methylation using only the strand-specific TKOES\_3a and TKOES\_3b scores (panel b, c). Left: Mean Shapley values of the features used by the model are shown. Center: comparison of model score and methylation differences, Right: comparison of MEEB\_strand and the MEEB\_3b/3a models (Fig 4d-e).
- i**, Estimated effect of dinucleotides (encoded as “positon\_dinucleotide”) in the MEEB\_3b/3a and MEEB\_strand models.
- j**, Correlation of sequence-based prediction using MEEB\_strand and in-vivo epiblast differential Dnmt3b<sup>-/-</sup> vs Dnmt3b<sup>-/-</sup> methylation.

**Fig. 6: DNMT3A/B compensate replication dependent de-methylation during gastrulation.**

- a**, Early- and late- replicating domains are defined using encode ESC replichip (D3). Single cell methylation profiles from E7.5 mouse embryos were grouped based on EPCAM/CXCR4 markers staining to epiblast/ectoderm, mesoderm and endoderm subpopulations (Extended

Data Fig. 9d). For each single cell (points on the graph), we depict the coverage ratio on early and late domains (Y-axis), and the average methylation difference between early and late domains (X axis). Color coding represents the reconstructed cell cycle ordering.

**b**, Trends of cell cycle-dependent replication score (early vs late domain coverage, top), and average methylation in early and late domains (bottom).

**c**, Trends of cell cycle dependent methylation in CpGs with high vs. low model MEEB\_3b/3a scores. Gray lines show the ectoderm trends for reference.

**d**, Similar to a-c, showing data on WT MEEB day 5.

**e**, Similar to a,b, showing data on DNMT3A<sup>-/-</sup> and DNMT3B<sup>-/-</sup> MEEB day 5.

**f**, CpGs are grouped according to model MEEB\_3a (inferred by regression on the difference WT-Dnmt3a<sup>-/-</sup>). Methylation trends over the replication cycle are shown for MEEB Dnmt3b<sup>-/-</sup>.

**g**, Similar to f, by grouping according to model MEEB\_3b and showing data on Dnmt3a<sup>-/-</sup> MEEBs. See Extended Data Fig.9i for the normalized trends of both 3a and 3b.

### **Fig. 7: DNMT3A enhancer specificity matches expression asymmetry during gastrulation**

**a**, Performance of model MEEB\_3b/3a\_region predicting mutants' differential methylation from dinucleotides in addition the methylation of surrounding CpGs (methods).

**b**, Boxplot show distributions of mean CpG sequence score MEEB\_3b/3a for enhancers grouped by the number of CpGs in their sequence (n=145814, 131850, 113600, 97375, 85968 CpGs for enhancers with 2,3,4,5 and 6 CpGs). Shuffled controls are shown for reference. The middle line indicates the median, box limits represent quartiles, and whiskers are 1.5× the interquartile range.

**c**, Predictive power of a sequence model for average enhancer methylation for enhancers grouped by the number of their CpGs.

**d**, Comparing methylation of Dnmt3a<sup>-/-</sup> and Dnmt3b<sup>-/-</sup> MEEB day 6 using WGBS. Red lines represent over 25% methylation difference.

**e**, Distribution of model MEEB\_3b/3a score for CpGs which are hypo-methylated (over 30% difference) in Dnmt3a<sup>-/-</sup> in MEEB day 6.

**f**, Cumulative distribution of genomic distances from differential methylation (panel d) hotspots (difference > 0.3) and the nearest promoter out of 250 genes with highest expression change in an in-vivo gastrulation atlas (for 3a n=1561 methylation hotspots, 3b

n=14638, BG - Background n=531067. Exact p-values: A vs B: p= 0.001535, A vs background: p=1.477e-12, B vs background: p<2.2e-16. All tests are two-sided Kolmogorov-Smirnov).

**g**, For each depicted locus, the top graph shows mean regional methylation and marks one differentially methylated enhancer (green bar). We zoom on the enhancer hotspot region showing the CpGs' MEEB\_3b/a sequence score (middle panel) and the methylation trends of WT (black), DNMT3A<sup>-/-</sup> (magenta) and DNMT3B<sup>-/-</sup> (orange) MEEBs (bottom panel).

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## Methods (including supplementary methods)

### Cell culture

Mouse embryonic stem cells (mESCs) were maintained under standard conditions. Cells were grown on gamma irradiated primary mouse embryonic fibroblasts (iMEF) on 0.1% gelatin coated plates (G1393, Sigma) and DMEM (41965-039, Thermo Fisher Scientifics) containing 15% fetal bovine serum ESC grade (FBS), 100 µg/ml penicillin/streptomycin (03-033-1B, Biological Industries - Sartorius), 1 mM L Glutamine (03-020-1B, Biological Industries - Sartorius), 100 µM non-essential amino acids (01-340-1B, Biological Industries - Sartorius), 1mM Sodium pyruvate (03-042-1B, Biological Industries - Sartorius) 50 µM β-

mercaptoethanol (31350-010-1B, Biological Industries - Sartorius) and 20 ng/ml recombinant human LIF (Israel Structural Proteomics Center at Weizmann institute). Cells were fed with fresh medium every day and were split every 2 days. For the epigenetic reset, mESC were cultured in Neurobasal medium (Invitrogen 21103-049) and DMEM-F12 (WITHOUT HEPES) (BI 06-1170-50-1A) medium (1:1), supplemented with N2B27 (N2 and B27 supplement 17502048, 17504044 respectively, Invitrogen), 100 µg/ml penicillin/streptomycin, 1 mM L Glutamine, 100 µM non-essential amino acids, 1mM sodium pyruvate, 50 µM β-mercaptoethanol and 20 ng/ml recombinant human LIF, 2i (3 µM CHIR99021 and 1 µM PD0325901) (2128, Axon Medchem) for two to three passages. The mESCs lines that were used are J1 (SCRC1010, ATCC), DNMT3A<sup>-/-</sup> clone 6aa (AES0164), DNMT3B<sup>-/-</sup> clone 8bb (AES0165), Dnmt1<sup>-/-</sup> DNMT3A<sup>-/-</sup> DNMT3B<sup>-/-</sup> clone 19 (TKO) (AES0146) (Cell Bank Riken BioResource Research Center)<sup>40</sup>, DNMT3A<sup>-/-</sup> DNMT3B<sup>-/-</sup> clones 7aabb (DKO1) and 16aabb (DKO2) (kindly provided by Dr. Masaki Okano)<sup>11</sup>, Wild type, DNMT3A<sup>-/-</sup> and DNMT3B<sup>-/-</sup> knockout ES line, passages 3 or 5 in 2i/L, and were grown in our lab to reach to the same passage then were maintained in serum LIF (N15, kindly provided by Dr. Masaki Yagi)<sup>42</sup>. Mycoplasma detection tests were performed routinely to ensure mycoplasma free conditions using EZ PCR mycoplasma test kit (2070020, biological industries).

### **Embryoid bodies formation**

Embryoid bodies were generated by hanging drop protocol as previously described<sup>31</sup> with the following modification. Prior hanging drop production, mESCs were dissociated in to single cells using trypsin B 0.25% (03-052-1B, Biological Industries), and iMEF were depleted by 2 sequential re-plating on gelatin coated culture plate, each time for 20 min. Floating mESCs cells were gently collected, washed by PBS resuspended in differentiation media (containing 20% fetal bovine serum ESC grade (FBS), 100 µg/ml penicillin/streptomycin, 1 mM L Glutamine, 100 µM non-essential amino acids, 1mM Sodium pyruvate, 50 µM β-mercaptoethanol). Cells were passed through CellTrics 50 µm filter (04-004-2327, Sysmex) and were diluted in to concentration of 20 cells/µl. Embryoid bodies were established in 25 µl hanging drops on a cover of low-adherent bacterial culture dish, allowing 500 cells/drop to aggregate for 48 hours. After two days, 48-56 MEEBs were pooled into 8 ml differentiation media, in 10 cm low adherent, bacterial culture dish.

### **Embryos dissection**

Embryos were harvested from 15.5 week old pregnant C57BL/6JRccHsd or C57BL/6JOlaHsd females (obtained from Envigo) at E7.5. After dissection in PBS, pools of 5 embryos were collected in to low binding eppendorf tube and were dissociated by incubation in 30 µl trypsin B for 5 min at 37 °C combined with 3 pipetting steps using P1000 pipette. The trypsin was restored by adding 70 µl differentiation media. All animal experiments were approved by the Institutional Animal Care and Use Committee (IACUC). The animal experiment described here in was approved by Weizmann Institute IACUC #05710720.

### **Embryos and MEEBs dissociation and FACS**

At each studied time point samples of 48 to 144 MEEBs or samples of 4 to 9 embryos were collected for bulk or single cell protocols. For single cell assays, cells were dissociation by 0.25% trypsin, passed through 50 µm filter. Single cells sorting was performed on SORP-FACS Aria II sorter (BD Biosciences) using a 100 µm nozzle. 100,000 events were acquired, cells were gated for size and singlets using forward (FSC-A/W) and side scatter (SSC-A/W) and were sorted in to 384 well plates (Eppendorf twin.tec® PCR Plate 384, Cat 0030128508) . For germ layers proportion analysis and indexed single cell sort, single cells from dissociated embryos and MEEBs samples were incubated on ice for 25 min in 10% BSA/PBS, 1:100 Brilliant Violet 421™ anti-mouse CD184 (CXCR4) (BioLegend, BLG-146511 clone 276F12) and 1:100 APC rat anti mouse CD326 (Becton Dickinson Immunocytometry Systems, BD563478). Single cell sorting was done on index sorting protocol. Twelve wells in each plate were pre-defined as empty wells for negative control.

### **scRNA seq**

MARS Seq library preparation protocol was performed as previously described <sup>58</sup> with slight modifications as below. The final concentration of the RT primers was 2nM and set of 348 barcoded oligos was used, which allowed to pool the 384 well plate into VBLOCK KIT reservoir (Click bio) by centrifuge, later in the process. The step of Exonuclease I heat inactivation was removed from the protocol. The volumes of the first RT and Exonuclease I reaction mixes were scaled down to 1 and 0.5 µl respectively. Each reaction mix was dispensed by MANTIS<sup>R</sup> (FORMULATRIX). Sequencing, mapping and UMI extraction was performed as described below.

### Bisulfite conversion and PBAT library preparation

mESC and MEEBs were sampled at the relevant time points, dissociated by 0.25% trypsin, cells pellet was washed by PBS and DNA was purified using Quick-DNA Miniprep Plus Kit (Zymo D4068) following the manufacture instructions. Samples of 80 ng gDNA were suspended in 12 µl Tris pH 8 and bisulfate conversion was performed according to the EZ-96 DNA Methylation-Lightning MagPerp kit (D5046, Zymo) manufacture protocol with the following slight modifications. Mainly, half of the recommended amount of each reagent was used. CT reagent volume was reduced to 65 µl and 90 µl M-Binding buffer plus 10 µl MagBinding beads were added into each sample. Bisulfate converted DNA samples were eluted in 38 µl elution buffer and were subjected the slightly modified PBAT protocol<sup>43</sup>.

First strand synthesis was performed in a 50 µl reaction that contains 5 µl NEB buffer 2, 2 µl dNTPs (10 µM) and 4 µl PBAT1 (with or without barcode) oligo (4µM) ACACTTTCCCTACACGACGCTTCCGATCT-8bp BarcodI-NNNNNNNN (partial sequence of Illumine read 1 followed by 8bp barcode and 9 random bp) at 65 °C for 3 min followed by 4 min at 4 °C and pause break for adding 2 µl Klenow Fragment (3'→ 5' exo-) (M0212L, NEB). Graduate increase of temperature +1 °C/15 s to 37 °C for 90 min followed by heat inactivate of the enzyme at 70 °C for 10 min. Digesting and removing excess of oligoes was done by adding 1.5 µl exonuclease I (M0293L, NEB) and 1 µl of Shrimp Alkaline (M0371L,NEB) for 45 min at 37 °C. Following by DNA purification by 0.8X Agencourt Ampure XP beads (beads, A63881, Beckman Coulter) and elution in 38 µl. The second strand synthesis was performed similarly to the first strand synthesis using 4 µl PBAT2 oligo (4 µM). GTGACTGGAGTTCAGACGTGTGCTTCCGATCT 8bp Barcodell-NNNNNNNN (partial sequence of Illumine read 2 followed by 8bp barcode and 9 random bp), incubating at 95 °C for 45 s followed by 4 min at 4 °C and pause at 4 °C for adding 1.5 µl Klenow Fragment (3'→ 5' exo-) during incubation at 4 °C for 5 min, +1 °C/15 s to 37 °C, 37 °C for 90 min, 70 °C for 10 min, 1.5 µl of Exol and 1 µl of Shrimp Alkaline were add for 45 min at 37 °C followed by removing the excess of oligos by 0.8X beads and elution in 22 µl elution buffer. Tagged products were amplified in 12-14 PCR cycles using 25 µl Kapa HiFi Hot start ready mix kit (KK2601, KAPABIOSYSTEMS) (following the manufacture's protocol) and 3 µl (from 10 µM stock) of the following mixed PBAT PCR primers:

I. AATGATACGGCGACCACCGAGATCTACACTTTCCCTACACGACGCTTTC

CGATCT

II. CAAGCAGAAGACGGCATACGAGAT-6bp Index-GTGACTGGAGTCAGA

CGTGTG

Barcoded libraries were cleaned by 0.7X beads and eluted in 25 µl 10 mM Tris pH 8.

### In solution sequence capture

Pool of barcoded libraries (same molarity of each library), was concentrated by 0.7X beads to a volume of 10 µl and was subjected into Mybait capture reaction (MYcroarray Ann Arbor, Michigan, USA) <https://arborbiosci.com/genomics/targeted-sequencing/mybaits/mybaits-custom/>) according to the manufacture instructions with the following modifications. The amount of baits mix in the hybridization mix was changed to 2 µl and as a consequence the hybridization mix was in aliquot of 16 µl. The volume of the DNA library (125 ng to 2 µg DNA) in the blockers mix was changed to 10 µl and the captured libraries were washed 4 times for 10 min with washing buffer 2.2. Following amplification, the product was purify by 0.7X Agencourt Ampure XP beads, eluted in 10 µl elution buffer and was subjected to additional round of capture, four washes and 14 cycles of amplification. Libraries were pooled and sequenced on an Illumina Nextseq or Novaseq system using the 150 bp high output sequencing kits or 300 bp SP1 kits respectively.

### Bisulfite conversion and Single cell PBAT

Single cells were sorted into 2 µl lysis buffer (10 mM Tris HCl pH 7.4, 2% SDS and 10 µg proteinase K) in 384 well plate and were store at -20 °C until further processing. Cells were lysed at 65 °C for 30 min and were subjected in to sequential process, performed by Bravo Automated Liquid Handling Platform (Agilent) combining with the following modified scaled down version of EZ-96 DNA Methylation-Lightning MagPerp kit (D5046, Zymo). Purified bisulfate converted single strand DNA samples was subjected in to pre made single cell PBAT1 capture 384 well plate containing quintuplicate of 96 barcoded PBAT1 primers, using same PCR programs that were used above for PBAT library preparation with slight changes, 1 µl Klenow Fragment (3' → 5' exo-) reaction mix (0.045 µl M0212M, NEB, 0.1 µl NEB 2 (10X)

buffer, 0.855 µl water) followed by 1 µl Exonuclease reaction mix (0.45 µl Exonuclease I, 0.1 µl rSAP M0293L, M0371L, NEB respectively 0.1 µl Exo I (10X) buffer and 0.34 µl water) were added using mantis (Formulatix). Each 8 cells were Pooled into one well of 4 rows in 96 well plate) followed by removing the excess of oligos by 0.8X beads and elution in 19 µl Tris pH8 10 mM. Second strand synthesis was performed similarly to the PBAT bulk using 2 µl PBAT2 oligo (4 µM). After removing the excess of oligos by 0.8X and elution in 12.5 µl elution buffer Tagged products were amplified in 15-16 PCR cycles using 12.5 µl Kapa HiFi Hot start ready mix kit and 1 µl (10 µM) mixed PBAT PCR primers.

Each raw in the 96 well plate was pooled and clean by 0.7X beads. Libraries were pooled and sequences on an Illumina Nextseq or Novaseq system using the 150 bp high output sequencing kits or 300 bp SP1 kits, respectively.

### **ENCODE reference data processing**

We downloaded H3k4me1 tracks representing mouse embryonic tissues from ENCODE-phase3 (<https://www.encodeproject.org/>). We merged replicates and transformed coverage statistics into percentiles, using  $\log_2(1 - \text{coverage percentile})$  to score and compare H3k4me1 levels between conditions (for PBAT-capture probes design and for the analysis in Fig. 4). We extracted whole genome bisulfite sequencing data from ENCODE and used statistics on CpG methylation for matching embryonic tissues (Fig. 5).

### **PBAT- Capture baits design**

We selected regions for targeting by selecting genes showing high degree of transcriptional variance in E8.5 embryos and collecting loci that showed evidence for enhancer marking in at least one encode E10 tissue (facial prominence, forebrain, midbrain, hindbrain, limb), or in all the tissues at E14. We further restricted selected enhancers to those including at least one CpGs with partial methylation (between 20%-80%) in a new WGBS data we generated from E8.5 embryos. Our set of targeted regions was supplemented with 4080 regions showing a background distribution of CpG content and replication time. The complete set of targeted sites is available at [https://github.com/tanaylab/Dnmt3ab\\_MEEB](https://github.com/tanaylab/Dnmt3ab_MEEB).

Probe sequence designed was performed using cppd (version 0.1.0, <https://github.com/tanaylab/cppd>). Briefly, we selected probes that: a) have at most one

cytosine, b) are 60 bp in length and minimal TM of 54C, c) have at least 50bp distance to the nearest probe d) have no overly represented DNA 15-mer (motif that appears more than 10000 times in the genome), e) do not have a homopolymer of 8 bp, f) do not have >3bp reverse complementarity to between the prefix and suffix, g) are mapped uniquely to the genome and do not have any 14bp that is reverse complementing to subsequence of another probe. We designed two probes for each region, one for each strand. If the chosen probe had a CpG, the “C” base was replaced with “A” in order to avoid capture bias.

### Metacell analysis of MEEB datasets

We used the Metacell package <sup>33</sup> (Version 0.3.7, <https://github.com/tanaylab/metacell>) to analyze each of the MEEB datasets (WT, DNMT3A<sup>-/-</sup>, DNMT3B<sup>-/-</sup>, DKO, TKO) separately. The package was used as described before, with the following specific parametrization and controls. We first removed wells with less than 1000 UMIs. We then generated initial feature gene list using a metacell standard threshold on normalized variance ( $T_{vm}=0.1$ ). For each dataset we then generated 80 gene clusters which were analyzed manually for association with cell cycle or stress genes, and systematically by comparing distribution of expression in two or more replicate experiments. When comparing batches, we sampled single cells so as to match the number of cells per MEEB day in each experiment and sum up over their UMIs. In all cases, decisions on exclusion of a gene cluster from the feature gene set was made in a supervised fashion, but the genes filtered in the process were still included in all parts of the analysis except for the derivation of raw K-nn similarities in the Metacell algorithm. Metacell construction was then performed using the paramters  $Knn=80$ ,  $min\_mc\_size=15$  and  $Knn\_core=15$ . Complete lists of genes used as features and the derived metacell models are available from the supporting github repository ([https://github.com/tanaylab/DNMT3AB\\_MEEB](https://github.com/tanaylab/DNMT3AB_MEEB)).

For visualization purposes (and without affecting any aspect of the downstream analysis), we generated 2D projections of the metacell graphs. For simplifying the projected graphs we selected a small number of metacell-metacell links for supervised deletion, eliminating spurious links of rare and poorly annotated cell states, or links formed based on similarity in expression of specific transcriptional programs shared by different germ-layers in MEEB day 7. All supervised layout edits are documented by extended data figures showing heatmaps with the actual expression profiles of the cells within metacells involved in spurious links. It is

again important to clarify that 2D projections are used only for visualization and we have avoided any assumptions on implications of graph topology to dynamics (e.g. pseudo time, trajectories) since in our data time could be measured directly.

### **Metacell annotation using gastrulation atlas projection**

For re-analysis of the gastrulation atlas scRNA-seq, we used published filtered UMI tables, retaining only non-striped, non-doublet profiles from embryonic stage E6.5-E7.75 (a total of 59332 cells). We selected initial feature genes using metacell's normalized variance threshold on 0.1. Clustering of genes into 64 subsets and manual inspection of clusters, resulted in exclusion of cell cycle and stress genes (177 in total) retaining a total of 1624 genes from the initial feature list. Metacells were then generated using parameters Knn=100, min\_mc\_size=20, Knn\_core=30. This created 789 metacells over 57020 cells, with 2312 (3.9%) profiles classified as outliers. We annotated metacells by majority voting over the cell type/color annotation suggested in the original publication, maintaining maximum compatibility with the published reference.

To standardize the reference model, we computed the regularized expression profiles of 789 metacells describing the mouse gastrulation atlas as  $le_g^m = \log_2(10^{-5} + refu_g^m)$  where n is the total number of UMI per cell and  $refu_g^m = \sum_{i \in m} u_g^i / \sum_{i \in m} n^i$  is the frequency of gene g in metacell m. Atlas metacells were all classified into cell types defining  $t(m) \in types$ . For atlas projections we used the 1624 feature genes selected by the metacell package for the reference model construction, restricted to the 1463 genes that were unambiguously named between the MARS-seq and 10x pipelines. We note that over this large feature set we found that the effect of platform-specific biases on cell annotation to be low (validated using our in house MARS-seq in-vivo atlas, and a control MEEB 10X dataset experiment, data not shown).

Following the derivation of the reference model, annotation of metacells in any of the MEEB systems was approached as follows:

- 1) For each MEEB cell we found the maximally correlated reference metacell  $ref_i = argmax_m cor(le_g^m, u_i)$  where u is the umi vector of the cell i.

- 2) For each MEEB metacell  $m$  we counted the frequency of associated reference metacell types  $p_m^t = \frac{1}{|m|} \#_{i \in m} \{t(\text{ref}_i) = t\}$  and computed the *entropy* of this annotation  $h(m) = \sum_t p_m^t \log_2(p_m^t)$ .
3. Metacells with annotation entropy  $h(m)$  lower than 2 were annotated by the majority reference cell type. Other metacells were not annotated (color coded gray). Depiction of the annotation coherence using bar-graphs is provided in the extended data figures.
4. For each MEEB metacell we also pooled the expected reference umis  $u_{ref,m} = \sum_{i \in m} ref u_{ref(i)}$  and compared it to the observed umis frequencies of the MEEB metacell to generate the scatter plots in Extended Data Fig. 2e, and the correlation heatmaps shown in Extended Data Fig. 2,3,5,6.

### Gene program score and stratification

To score metacell or single cells in a comparable fashion, we derived gene programs from MEEB WT data by identifying groups of 30 genes with the top correlation (over metacell log umi frequency statistics – or  $le_g^m$  as defined above) to TF genes indicative of epiblast state (*Utf1*), Primitive streak (*Eomes*), Nascent Mesoderm (*Mesp1*), Endoderm (*Foxa1*), Extraembryonic mesoderm (*Hand1*), Rostral/Embryonic mesoderm (*Foxc1*) and hematoendothelial progenitors (*Tal1*). We also computed a gene program linked with delayed pluripotency using genes correlated with *Dppa3/Stella*. We removed from the gene programs genes that appeared in more than one list. We then computed a program score for each metacell (on either WT or mutant models) using summation over  $le_g^m$  values. The distribution per MEEB day (Fig. 2d-e) was computed by weighting the metacell program scores given the number of metacells' member cells per MEEB day. For each program we also determined a threshold score as the minimal score of a WT metacell associated with a matching cell type annotation (i.e. as described in Fig. 1). We then counted for each line and MEEB day the fraction of cells in metacells with score at least as high as the threshold to generate Fig. 2F.

To quantify differences in archetypical transcriptional states between mutants and WT, we computed a *single cell program score* by summing up  $\log_2(1 + 3u_g^i)$  from genes in the program in single cell profiles down-sampled to 3000 UMIs. We then pooled (non downsampled) UMIs from the 160 cells with top program scores in each condition or mutant

line to generate bulk profiles representing the most specific realization of the respective cell state in the given line/condition. Such bulk provided good quantitative resolution, based on over half a million UMIs each. Differential expression analysis (Fig. 2g, 3c) was done using a chi-square test and FDR correction to determine significance, and log fold change to determine intensity.

### **Processing and clustering of MEEB PBAT-Capture and WGBS data**

Raw PBAT sequencing were stripped of indices and random oligos, and were then mapped to the mm9 reference genome using an in-house script that is based on Bowtie2 (<https://github.com/tanaylab/bissli2>, Bowtie2 version 2.3.0) with the following parameters “--maxins 1000 -ga”. In cases where the two reads ends were not aligned concordantly, the reads were discarded. Reads that were mapped to the same genome coordinates were marked as duplicates and were used only once. Reads with mapping quality (MAPQ) below 30 or reads that had more than 3 non-converted C's in non-CpG content (CHH) were discarded. Individual CpG methylation level was then called for each read, discarding bases with base quality <20.

To identify groups of loci with specific methylation kinetics in MEEB day 1-4 we merged 67 methylation profiles by day and line (wt, 3a-/-, 3b-/-, tko), generating average methylation of 132052 captured CpGs with at least 10X coverage on at least 19 out of the 24 profiles analyzed. We then identified 15935 CpGs with mean methylation <= 5% across the profiles and removed them from our matrix.

To identify groups of loci with specific methylation kinetics in MEEB day 1-4, we generated average methylation profiles for 77541 captured CpGs with at least 20X coverage on at least 22 of the 24 profiles analyzed. The resulted matrix was clustered using an enhanced KMeans algorithm (Version 0.3.4, <https://github.com/tanaylab/tglkmeans>) using K=60 in order to define a range of quantitative methylation kinetics as shown in Extended Data Fig. 9.

### **DNMT3A/B MEEB sequence preference model (Fig. 4)**

For each of the 116117 CpGs represented in the MEEB methylation profiles we extracted the genomic sequences around the locus. We then computed the nucleotide frequencies in positions relative to the CpG. To facilitate refined modelling of the 3a/3b preferences we also

extracted for each CpG the matrix of nucleotide and dinucleotide (16 combinations) occurrence in positions -6 to -1 and +1 to +6. This binary sparse matrix was used for downstream regression tasks.

For each of the above CpGs we also computed the sum of average methylation in Dnmt3a<sup>-/-</sup> (**m3a**), Dnmt3b<sup>-/-</sup> (**m3a**) and wt (mwt) in time points 1,2,3 and 4. We inferred a linear model predicting *m3a-m3b* from the dinucleotide feature table using cross validated lasso-regularized linear regression with the glmnet R package (version 4.1.4, features shown in Fig. 4d). When regressing methylation, we ignore CpGs that were completely protected from methylation by filtering sites with mean methylation < 5%. In parallel we used gradient boosting to further improve regression accuracy, using R xgboost package (version 1.3.2.1) with max\_depth=4, gamma=0.1, eta=0.05 and nrounds=1750, following hyperparameter tuning. The resulted in the following models:

**MEEB\_3b**: regressing the difference between wt and 3b-/- methylation from dinucs.

**MEEB\_3a**: regressing the difference between wt and 3a-/- methylation from dinucs.

**MEEB\_3b/3a**: regressing the difference between 3a-/- and 3b-/- from dinucs (e.g. Fig. 4f).

Addition of regional enhancer methylation was done by computing the average methylation in putative enhancer regions (see below) that were covered by our profiles excluding the targeted CpG (punctured regional methylation), and then adding 3a/3b methylation difference to the dinucleotide frequencies and rerunning model training with similar hyperparameters (using 45056 CpG profiles with sufficient coverage and within enhancer context, Fig. 7a):

**MEEB\_3b/3a\_region**: regressing the difference between 3a-/- and 3b-/- from dinucleotides and punctured enhancer methylation.

In Extended Data Fig 8j we computed the nucleotide frequencies in positions relative to the CpG for each of the 60 MEEB methylation clusters. For visualization we wanted to highlight both nucleotide enrichment and anti-enrichment (since each cluster represent kinetics that is an outcome of the preferences of 3A and 3B either positively or negatively). Nucleotide height in the logos shown in Extended Data Fig. 9 were therefore defined as the log-enrichment scores -log2(p/0.25).

### **Strand specific 3a/3b sequence preference model.**

We downloaded Mallona et al Dnmt3a and Dnmt3b TKO data and modeled strand specific sequence preferences on 93967 Dnmt3a and Dnmt3b loci with sufficient coverage ( $>10$  in the plus strand for both), removing loci with average methylation (strand-symmetric) of less than 5% in WT ES cells. Using a linear model with L1 regularization on plus-strand dinucleotides (Fig. 5b,c ) we derived two models:

**TKOES\_3a** – regressing methylation in TKO ES cells with re-activation of Dnmt3a

**TKOES\_3b** – regressing methylation in TKO ES cells with re-activation of Dnmt3b

We used these models to compute plus and also minus strand (by reverse complementing dinucleotides and positions) scores for each enzyme (Fig. 5d-e).

To predict MEEB 3a/3b methylation using only the sequence preferences inferred in TKO ES cells, we trained a new gradient boosting model, with variables defining the plus and minus strand preferences of Dnmt3a and Dnmt3b (TKOES\_3a+, TKOES\_3a-, TKOES\_3b+, TKOES\_3b-), and the maximum between the two strands for each enzyme ( $\max(\text{TKOES\_3a+}, \text{TKOES\_3a-})$ ,  $\max(\text{TKOES\_3b+}, \text{TKOES\_3b-})$ ). This was done using xgboost (version 1.3.2.1) on these six variables with parameters `max_depth=4`, `gamma=0.1`, `eta=0.05` and `nrounds=1750`, giving rise to:

**MEEB\_strand** – regressing the difference between MEEB 3a/- and 3b/- using TKOES dinucleotide models.

To estimate the dinucleotide preferences implied by the combined strand model, applied a linear model on dinucleotides (using glmnet (version 4.1.4) with L1 regularization) to regress the predictions of the non-linear gradient boosting model, reporting coefficient of each dinucleotide at each position (including the “bridge” dinucleotide involving the 3' and 5' bases around the CpG) (Fig.5i)

### **Analysis of differential enhancer methylation (Fig. 7)**

We used H3K4me1 scores from encode (limb, liver, heart, midbrain, hindbrain, forebrain, stomach and kidney, E10.5 to E14.5) and H3K27ac scores from Xiang et al, (Nat Genet 2019) (ecto, meso, endo and ps, E7.5) to define enhancer regions as genomic intervals on which the

normalized coverage score (defined as  $-\log_2(1\text{-coverage\_percentile})$ ) is bigger than 7 for at least one tissue in at least one time point. We identified 588090 such putative enhancer intervals.

For MEEB day 6 differential methylation analysis (Fig. 7d), we generated average methylation of 9471151 CpGs smoothing over 250bp from each side of the CpG and requiring a coverage of at least 50 methylation calls over the smoothed data.

We then extracted 250 genes showing the highest fold enrichment (in all cases above 2-fold) in primitive streak, anterior primitive streak or nascent mesoderm compared to the entire model in the temporal gastrulation atlas (Mittnenzweig, Meishar et al). We identified the genomic loci of the TSSs of these genes and computed for each differentially methylated (or background) enhancer the distance to the nearest TSS in this group. Estimation of the cumulative distributions and KS statistics for these distances is reported in Fig. 7f.

### **Comparison of MEEB methylation to in-vivo RRBS data**

We downloaded E6 (GSE84236) and E8.5 (GSE60334) RRBS data from GEO, and identified CpGs that were represented in our PBAT-capture probe set and also covered by RRBS (using the methylation average reported by the original RRBS studies). Correlations of the in-vivo methylation data with the MEEB data and with the sequence model was then computed over CpGs that were covered at both 3a<sup>-/-</sup> and 3b<sup>-/-</sup> datasets.

### **Single cell methylation mapping and QC**

We used WGBS pipeline described above to generate 9544 single cells methylation profiles covered by at least 20k CpGs. Single cells with more than 2% of CHH (non-converted C's in non-CpG content) were discarded.

Since single cell PBAT was performed on FACS sorted plates, we used indices of EPCAM and CXCR4 to label each well (and thereby each single cell), as shown in Extended Data Fig. 9d-e.

### **Cell cycle phasing of single cell methylation profiles**

We used Encode Repli-seq data of mESC (D3, ENCF001JUO) for time of replication analysis. Loci with values below 0 were considered “late” and values above 0 were considered “early”.

We then computed for each single cell the total read coverage from “early” and “late” loci, and defined the ratio as  $\log_2(\text{early cov.} / \text{late cov.})$ . Average methylation was then computed by dividing the sum of all the methylated CpGs by the total methylation calls in “early” and “late” respectively, considering only CpGs with CpG content  $\leq 2\%$ . Cells with “early” or “late” coverage  $< 2000$  or total coverage  $< 20000$  were excluded.

We ordered single cells according to cell cycle by computing the principal curve of early late coverage ratio and methylation difference (Fig. 4c). We normalized the coverage ratio and methylation difference by dividing each variable with its standard deviation, and then used ‘principal\_curve’ from ‘princurve’ R package (version 2.1.6) with stretch=2 and smoother = “periodic\_lowess”. We used methylation dynamics to validate the direction of the cycle (i.e. clockwise or counter-clockwise).

Smoothed trends in Fig. 4 were computed using ‘loess’ with span=0.2. To account for the cyclic structure we concatenated two copies of the trends, smoothed it, and removed the first and last halves of the derived trends, thereby eliminating the effects of the margins.

We defined CpGs with lowest 10% of a/b score as DNMT3A-pro and top 10% as DNMT3B-pro. We then computed average methylation of DNMT3A-pro and DNMT3B-pro CpGs for each single cell, again separating “early” and “late” loci.

## DATA AND CODE AVAILABILITY

Data is deposited GEO 199806. Analysis code and processed tables are available in github [https://github.com/tanaylab/Dnmt3ab\\_MEEB](https://github.com/tanaylab/Dnmt3ab_MEEB).

## Extended data

### Extended Data Fig. 1: MEEB models for epiblast and meso-endoderm bifurcation

**a**, Correlation between single cell umi count in the wt dataset (down-sampled profiles) is shown for genes excluded from the metacell features list. Exclusion is based on prior annotation of cell cycle and stress genes, and on quantification of the batch-to-batch differential expression of gene clusters.

**b**, For each of 10 gene programs identified in a, the total UMI per cell per time point and replicate is shown using standard boxplots. Labeling of conditions specify MEEB day and line. The middle line indicates the median, box limits represent quartiles, and whiskers are  $1.5 \times$  the interquartile range.

- c**, 2D projection of J1 and N15 cells (see methods) from replicate experiments on different MEEB days. Shown is a partial subset of the batches with overlapping MEEB days, focusing on day 4,5,6 in which the critical stages of germ layer formation are observed.
- d**, Distribution of annotated cell type/states over time.

**Extended Data Fig. 2: Comparison of WT MEEB to in-vivo gastrulation atlases**

- a**, Shown are color coded expression level of key transcription factors over metacells (columns) that were derived from the Pijuan-Sala et al gastrulation atlas data set. Lower colored labels are based on the annotation in the original analysis.
- b**, Shown are metacells (colored ovals) projection in 2D using the metacell 2D graph projection, illustrating the reference in-vivo atlas we used for initial annotation of MEEB models.
- c**, Each cell in the MEEB data set was tested for correlation with each metacell profile in the atlas, deriving a putative cell type annotation from the best matching atlas state. Shown are the distribution of annotations in each MEEB metacell (bottom), and the entropy of this annotation, which we use to threshold the decision on MEEB metacell cell type annotation.
- d**, For each MEEB metacell we compared the MEEB UMI distribution to a distribution derived by pooling atlas RNA according to the best matching atlas metacell for each MEEB single cell (methods). Shown is the correlation between MEEB and pooled atlas RNAs for each metacell.
- e**, Scatter plots compare the absolute expression ( $\log_2$  Umi frequency) in MEEB metacells and the expression expected given projection on the MARS-seq temporal mouse gastrulation atlas. Good quantitative matching is observed for multiple genes, suggesting the combinatorial transcriptional state in MEEB cells is highly similar to the in-vivo state. Genes showing imperfect scaling of expression in a subset of the metacells represent in-vivo/in-vitro differences that must be considered carefully. Note increased Dnmt3b expression in gut and increased Dnmt3a expression in mesenchyme, accentuating the trends observed in vivo (Fig. 1a).

**Extended Data Fig. 3: MEEB transcriptional programs**

- a**, 2D projections highlight gene expression distributions for key epigenetic factors and additional TFs.
- b**, For each ESC or epiblast metacell (ovals color coded by annotation) we computed the mean MEEB day over all grouped cells (X axis), which is compared to  $\log_2$  metacell enrichment (Y

axis) for select genes. Focusing on representative genes that are activated or de-activated in the Dppa3+/Klf4- cell population compared to epiblasts or ESCs.

**c**, Inferred gene programs for downstream quantitative analysis. Each bar graph shows the top correlated gene to one TF (excluding genes appearing in more than one list), defining eight programs covering the key stages of epiblast formation and differentiation in the MEEB model.

#### **Extended Data Fig. 4: DKO MEEB expression atlas**

**a**, Annotation breakdown per time point.

**b**, TF gene expression levels

**c**, 2D gene expression projection for key genes are depicted for the DKO MEEB atlas.

**d**, DKO cells were grouped according to the log<sub>2</sub> total expression of the epiblast gene program (X axis), and the mean expression (log<sub>2</sub> RNA frequency) in each bin is shown for Lefty1,2 and Nodal (Y axis). Controls (matched J1 line) are shown in gray.

**e**, Comparing pooled gene expression for 160 DKO single cells with the top Utf1/Epiblast score and 160 single cells with the top Dppa3 program score. Genes with top fold change are highlighted (but only when q-value (chi-square, FDR corrected) is <0.05).

#### **Extended Data Fig. 5: TKO MEEB expression atlas**

**a**, TKO metacell 2D map. **b**, time series. **c**, annotation breakdown per time point. **d**, 2D gene expression projection for key genes are depicted for a TKO MEEB atlas.

**e**, Each point is a metacell, color coded by annotated type and showing mean MEEB time (X axis) vs. expression of genes linked with activation of a Sox1/definitive ectoderm gene program (Y axis).

#### **Extended Data Fig. 6: DNMT3A-/- MEEBs expression atlas**

**a**, TF heat map for MEEB DNMT3A-/- . **b**, Gene modules representative genes projected on DNMT3A -/- MEEB. **c** time series for the Dnmt3a<sup>-/-</sup> MEEB dataset.

#### **Extended Data Fig. 7: DNMT3B-/- MEEBs expression atlas**

**a**, TF heat map for MEEB DNMT3B-/. **b**, Gene modules representative genes projected on DNMT3B -/- MEEB. **c**, time series for the DNMT3B<sup>-/-</sup> MEEB dataset.

**d**, Distribution cell type/state frequencies per time, shown for the two single enzyme mutants.

#### **Extended Data Fig. 8: Quantification of MEEB methylation**

- a**, Cumulative distribution of genome-wide CpG coverage on mouse embryo E8.5 bulk data that was generated to assist with selection of PBAT-capture probes. Dashed line represents the mean CpG coverage.
- b**, Breakdown of designed methylation probes by genomic context.
- c**, Distribution of E8.5 methylation on selected probes (Designed), compared to the genomic distribution (Other).
- d**, Coverage distribution of selected CpGs (n=92501) per MEEB genetic background and MEEB time. The middle line indicates the median, box limits represent quartiles, and whiskers are 1.5× the interquartile range.
- e, f**, Number of methylation calls in MEEB methylation profiles mixing capture and WGBS datasets, or including WGBS data alone. Blue – methylation calls from on-target sequences.
- g**, Average methylation as a function of time, shown based only on probes designed to cover low CpG content loci without any known association to epigenetic activity.
- h**, Global rate of inferred CHH methylation in the different experiments. Note that CHH methylation can be called due to sequencing errors at some basal level, but the overall trend here is consistent with increase in off-target CpG methylation and with the increase in background CpG methylation.
- i**, Quantification of select clusters (from Fig. 4) methylation dynamics in WT (blue), Dnmt3a<sup>-/-</sup> (magenta) and Dnmt3b<sup>-/-</sup> (yellow) MEEBs. Shown is average methylation in days 1-4 for each cluster. Number of CpGs in each cluster: 1: 1179, 9: 5459, 19: 2023, 24: 1573, 30: 1295, 32: 2810, 40: 1837, 44: 1755, 53: 1606, 60: 1660.
- j**, Nucleotide enrichment and anti-enrichment logos around CpGs in the clusters highlighted in panel (i). Logos positive values show enrichment and negative value show anti-enrichments (methods). The core CpG is drawn in fixed scale for reference.
- k**, Comparison of MEEB methylation trends in X-linked loci. In the context of the epiblast (MEEB model, or in-vivo), X-linked trends are indistinguishable from autosomes.
- l**, Focus on loci identified as differentially methylated by Yagi et al. 2020 Shown are methylation distributions from Dnmt3a<sup>-/-</sup>, Dnmt3b<sup>-/-</sup> and WT in MEEB (d0-d6), E6 epiblast (epi, Smith et al., 2017) and in the Yagi et al., 2020 data. n = 427 3a favoring DMRs, and 343 3b favoring DMRs. The middle line indicates the median, box limits represent quartiles, and whiskers are 1.5× the interquartile range.

**Extended Data Fig. 9: Single cell methylation in-vivo and in MEEBs**

**a**, Number of single cells assayed from embryo E7.5 and MEEB at day5.

**b**, Distribution of estimated unconverted C in CHH contexts over single cells.

**c**, Distribution of the total number of methylation calls per cell. Note that our analysis aimed at a large sample of single cells with low coverage per-cell. Number of cells was 2217 for d5\_3a, 2197 for d5\_3b, 2984 for d5\_wt and 2146 for e7.5. The middle line indicates the median, box limits represent quartiles, and whiskers are  $1.5 \times$  the interquartile range.

**d,e**, Scatter plot show distribution of CXCR4 and EPCAM levels in RNA (metacells from a gastrulation scRNA-seq manifold (left), points, color coded by cell type as in S7) and from FACS indices (on cells sorted from E7.5 embryos). Gating on EPCAM/CXCR4 is allowing (in-silico) identification of Epiblast, endoderm and mesoderm sub-populations. Blood cells were shown to have low EPCAM and low CXCR4 levels and were gated separately.

Mean methylation analysis allows further separation of extraembryonic cells (right, Green points).

**f**, Comparing total read coverage over early and late replication domains across single cells. Color coding represents the inferred cell cycle ordering, which is based on the early/late coverage ratio as well as the early/late methylation difference (Fig. 6, not shown in this panel).

**g**, CpGs grouped according to their model (MEEB\_3b/3a) sequence-based score, and according to their replication time (early or late). Box plot shows distribution of the computed differences in average methylation of CpGs with high (3b favoring) and low (3a favoring) scores, for each single cell ( $n=199$  for ectoderm, 356 for mesoderm and 25 for endoderm). Single cells were grouped according to their germ layer (using index sorting as in D, color coded) and according to their inferred cell cycle phase (start, mid and end). The middle line indicates the median, box limits represent quartiles, and whiskers are  $1.5 \times$  the interquartile range. Distributions are compared using 2-sided Kolmogorov-Smirnov statistics ( $**** = p < 0.0001$ ,  $*** = p < 0.001$ ,  $** = p < 0.01$ ,  $* = p < 0.05$ ).

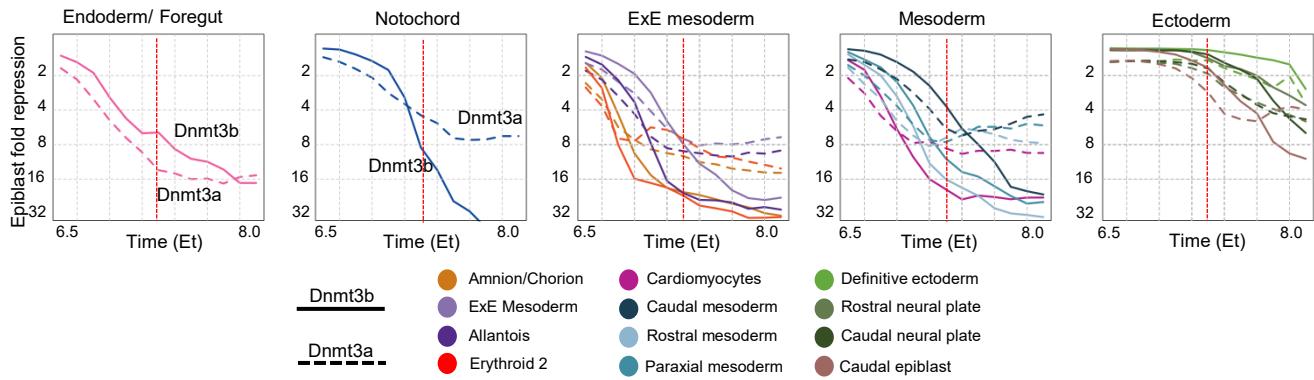
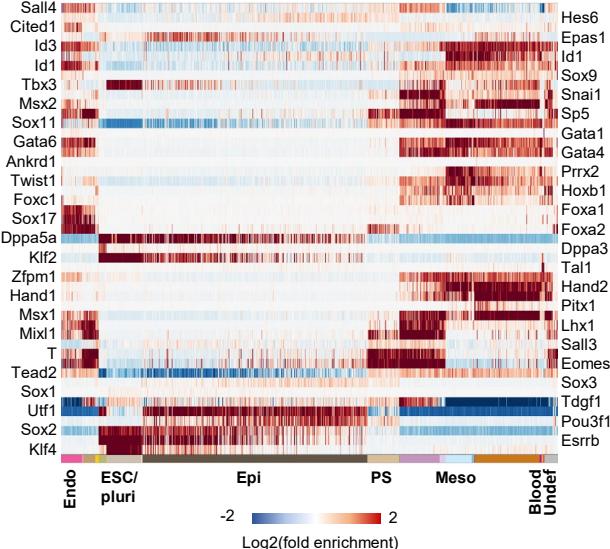
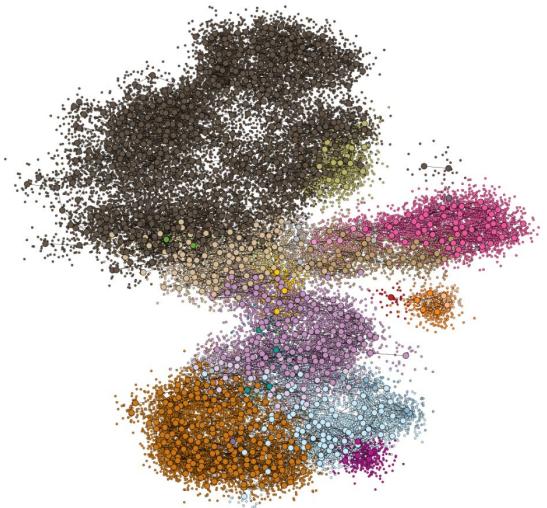
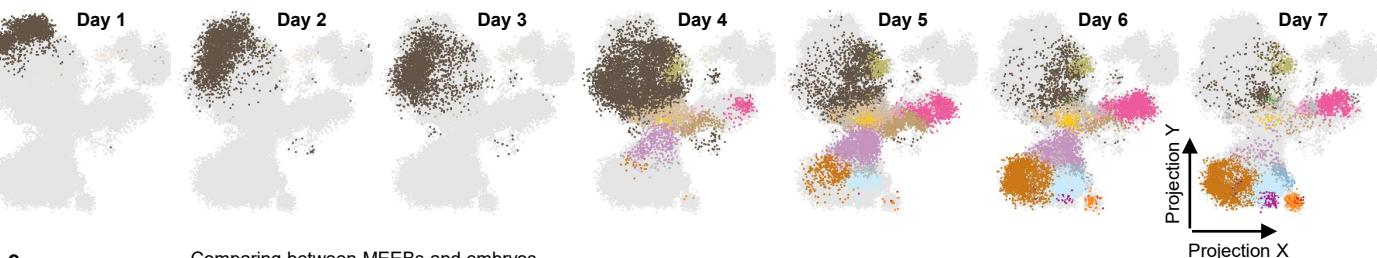
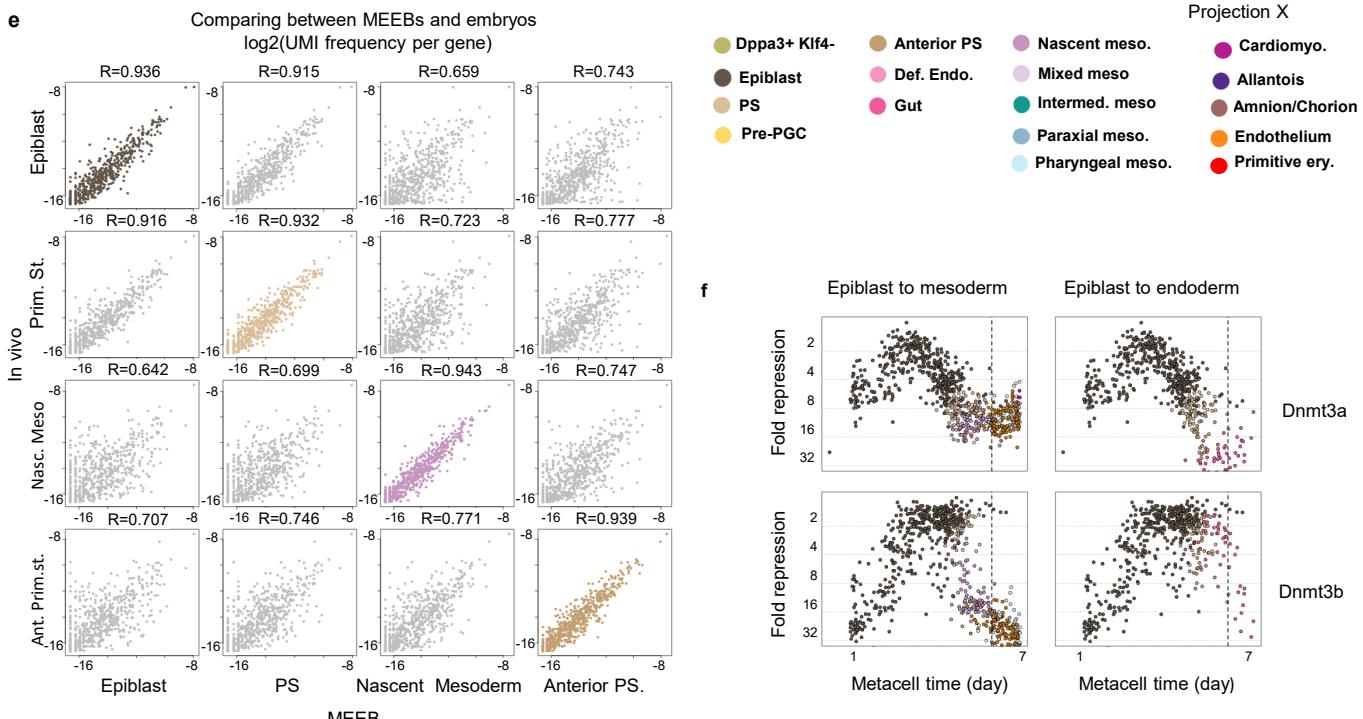
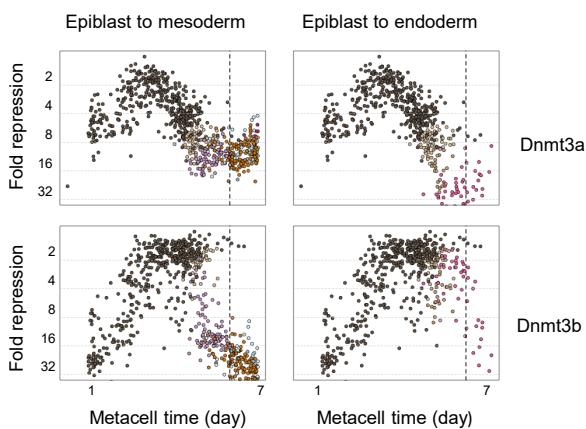
**h**, Phased cell cycle ordering for additional batches of single cell data from WT and mutant MEEBs.

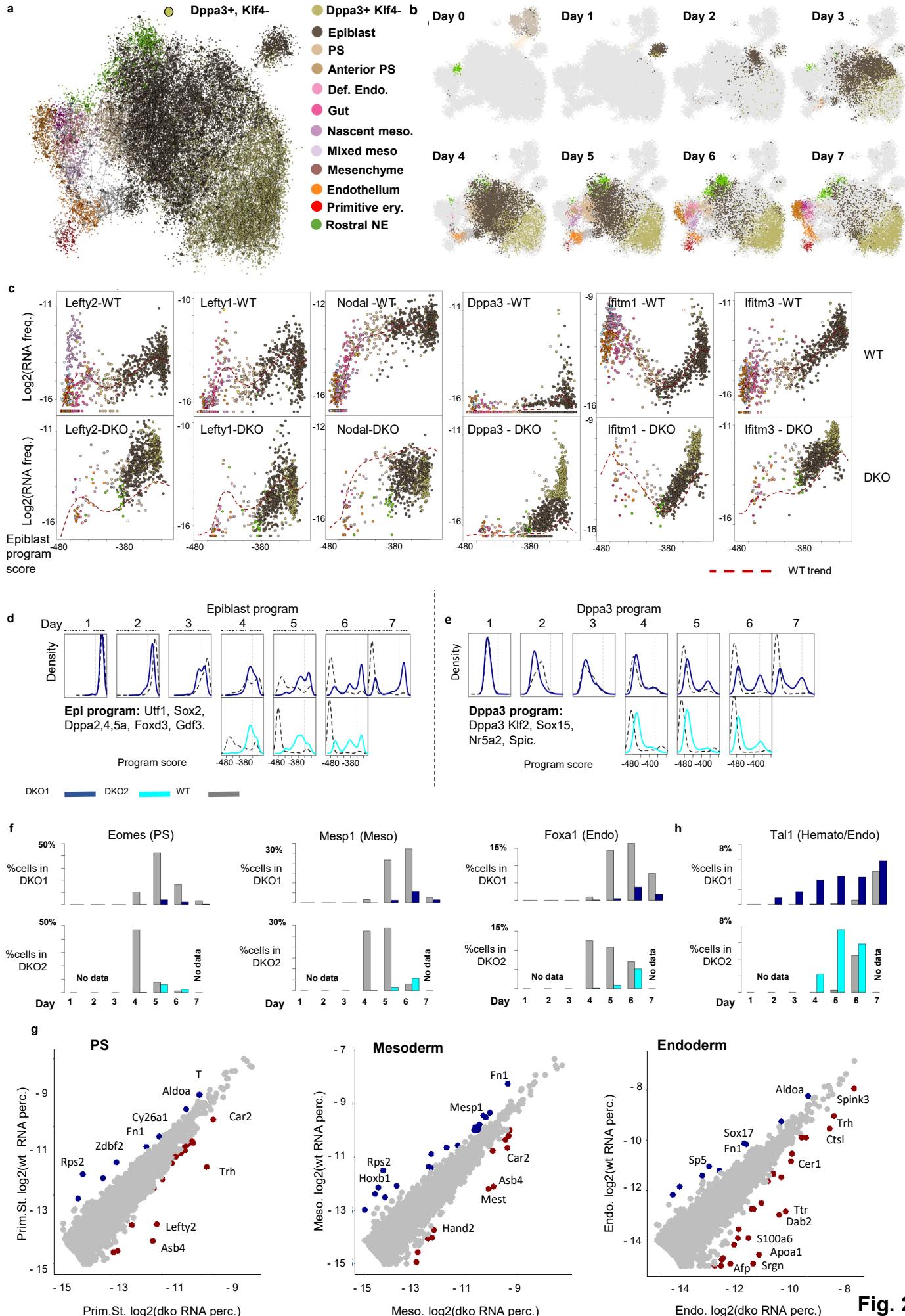
**i**, Cell cycle trends are computed for loci with high/low sequence preferences in early and late replicating domains (as in Fig. 6), but here we are normalizing values to the maximum level across the replication cycle in each group, to allow comparison of the relative trends. Top: sequence model MEEB\_3b/3a (regressing mutant difference), and methylation data is from WT MEEBs. Middle: sequence model is MEEB\_3a (regression WT-Dnmt3a<sup>-/-</sup>) and methylation data is from Dnmt3b<sup>-/-</sup> MEEBs. Bottom: sequence model is MEEB\_3b and

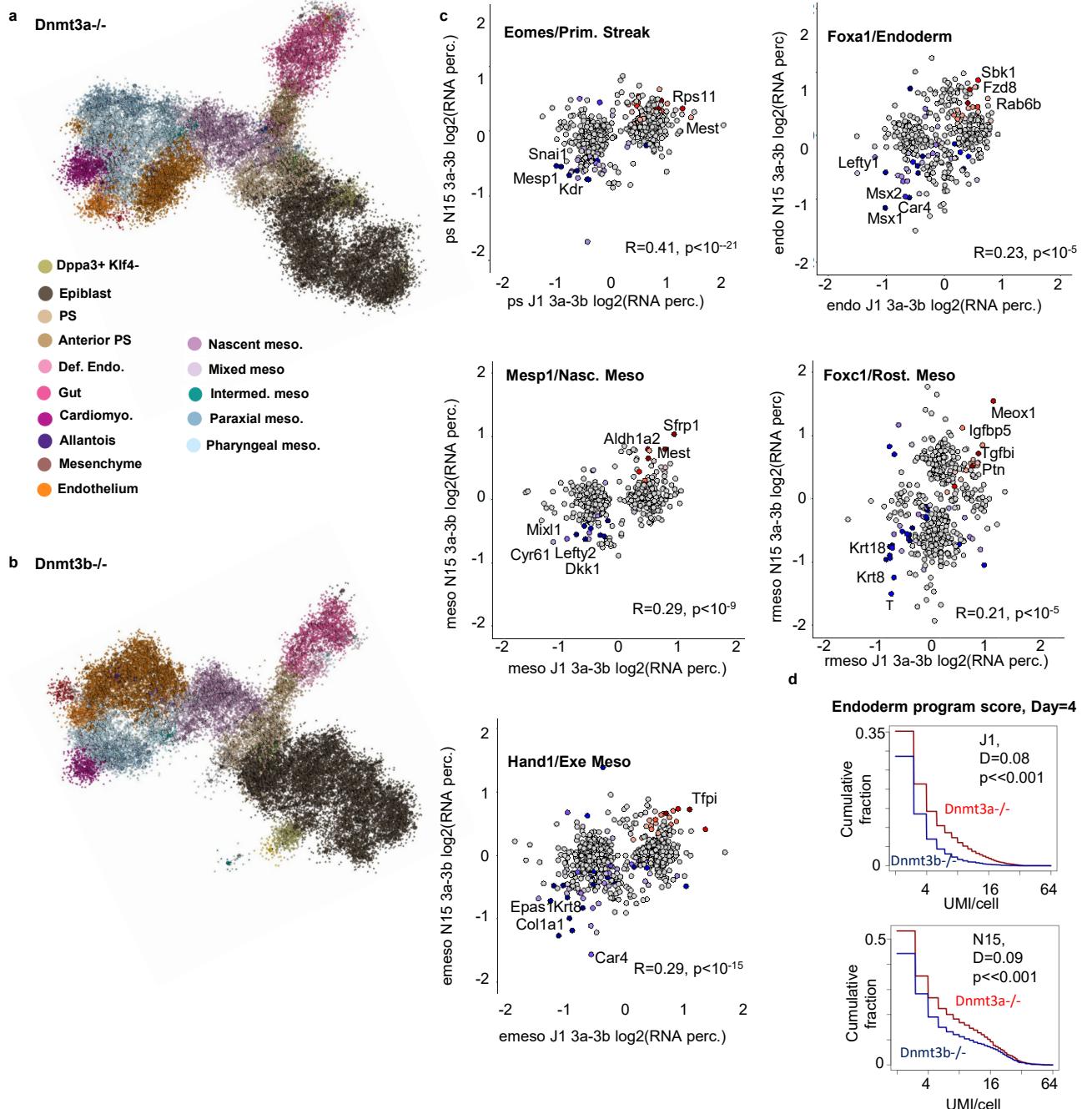
methylation is from Dnmt3a<sup>-/-</sup>. We note the slower re-methylation for low-affinity sites in the middle panel, and deeper reduction in methylation for high affinity sites in the lower panel.

**Extended Data Fig. 10: DNMT3A and germ layer specific methylation preferences at enhancers**

Additional hotspots around key gastrulation genes similar to Fig. 7g.

**a****b****c****d****e****f****Fig. 1**





**Fig. 3**

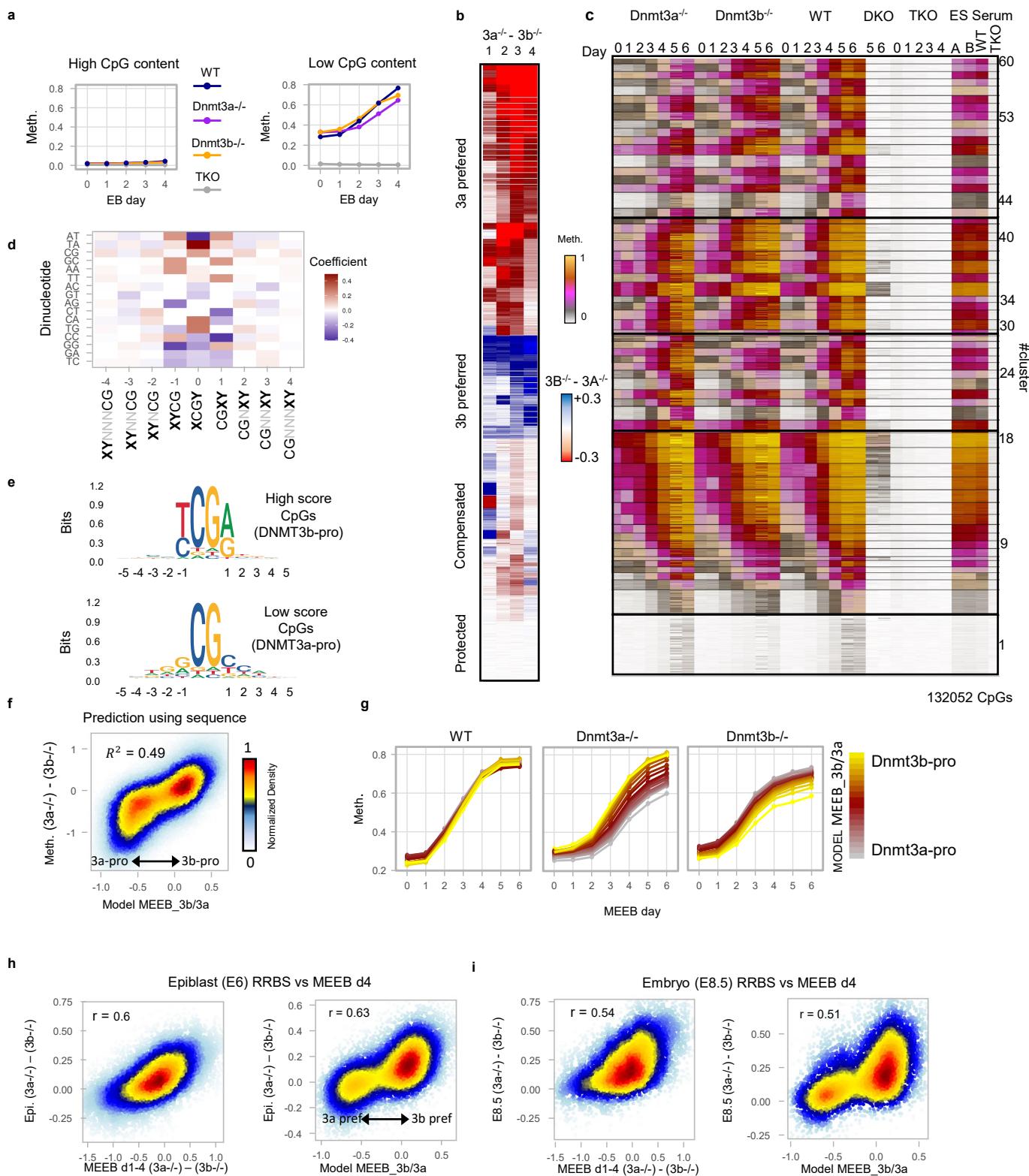
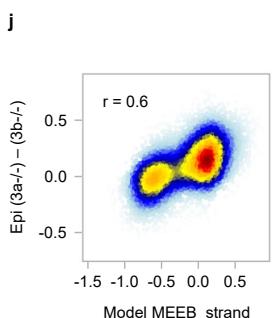
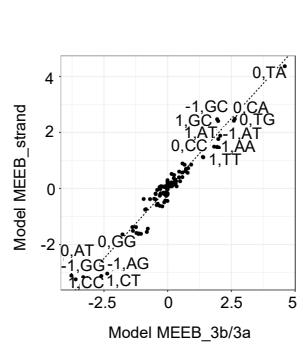
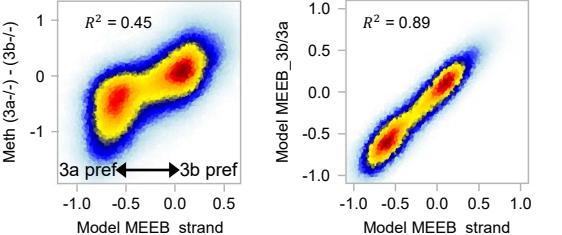
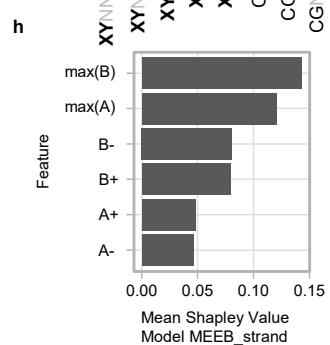
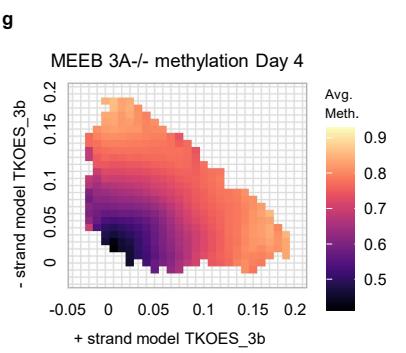
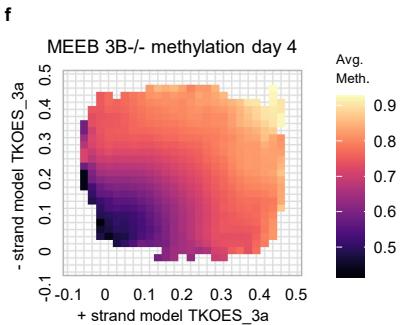
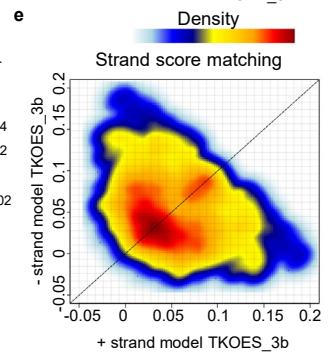
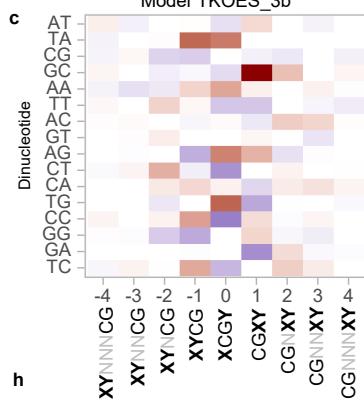
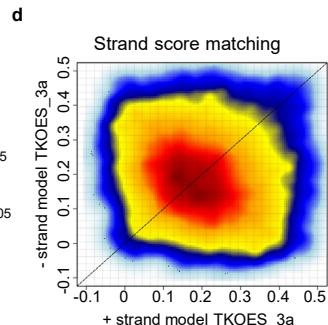
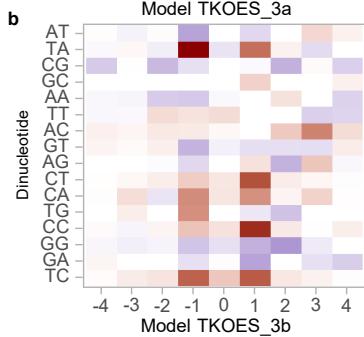
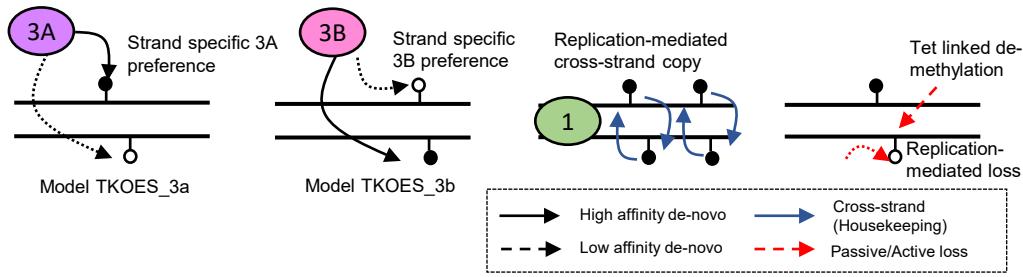


Fig. 4

a

**Fig. 5**

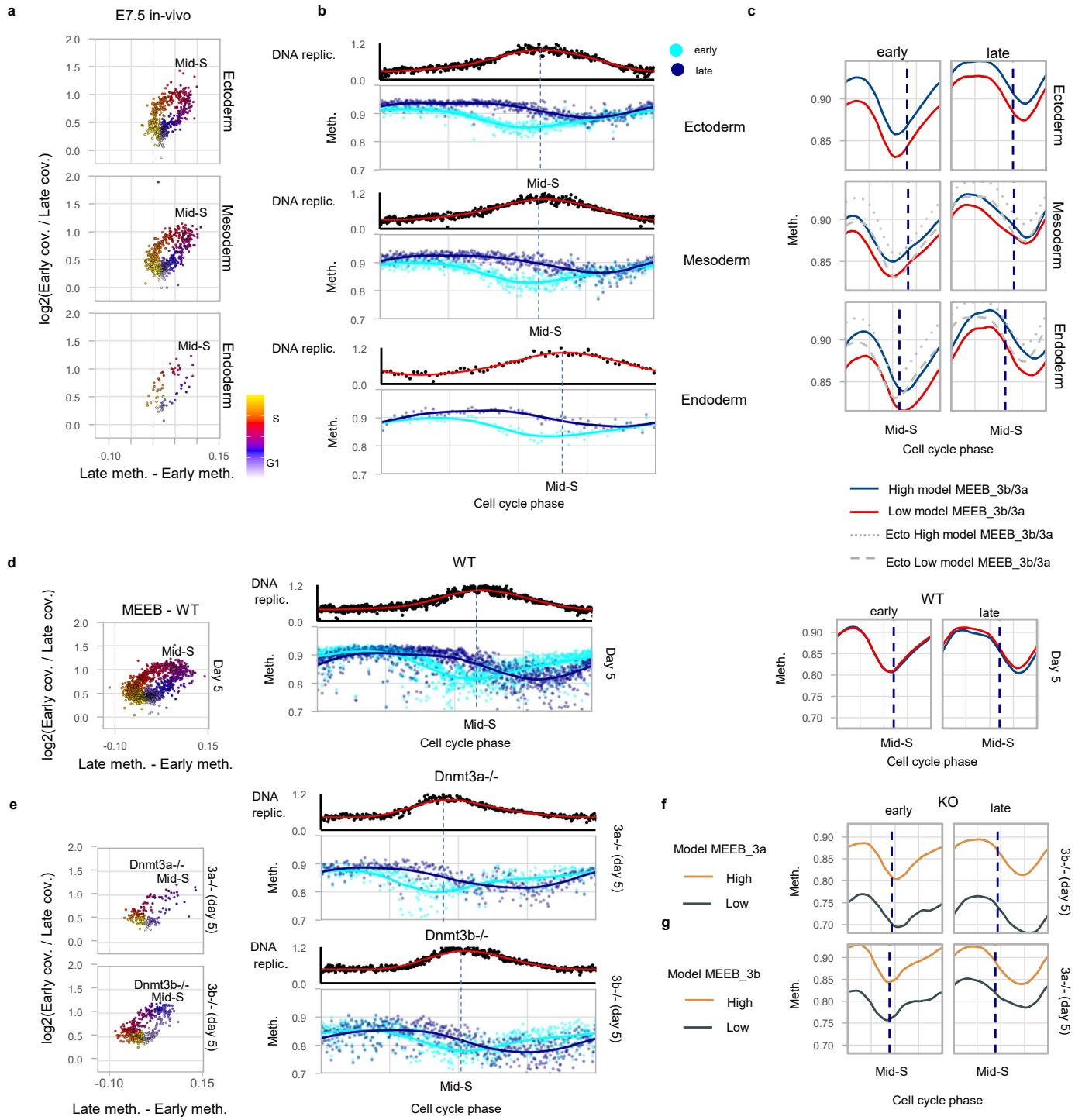


Fig. 6

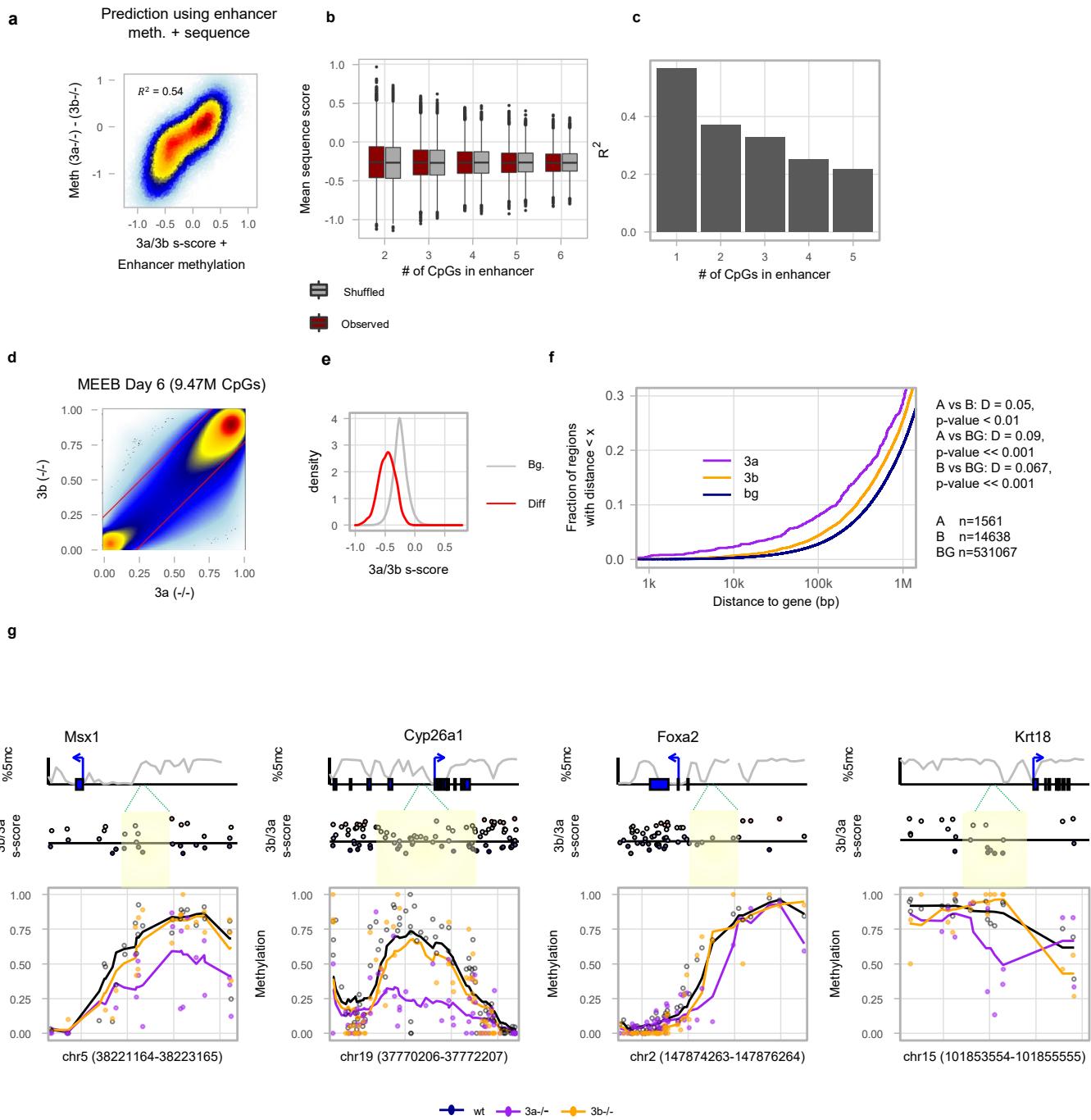
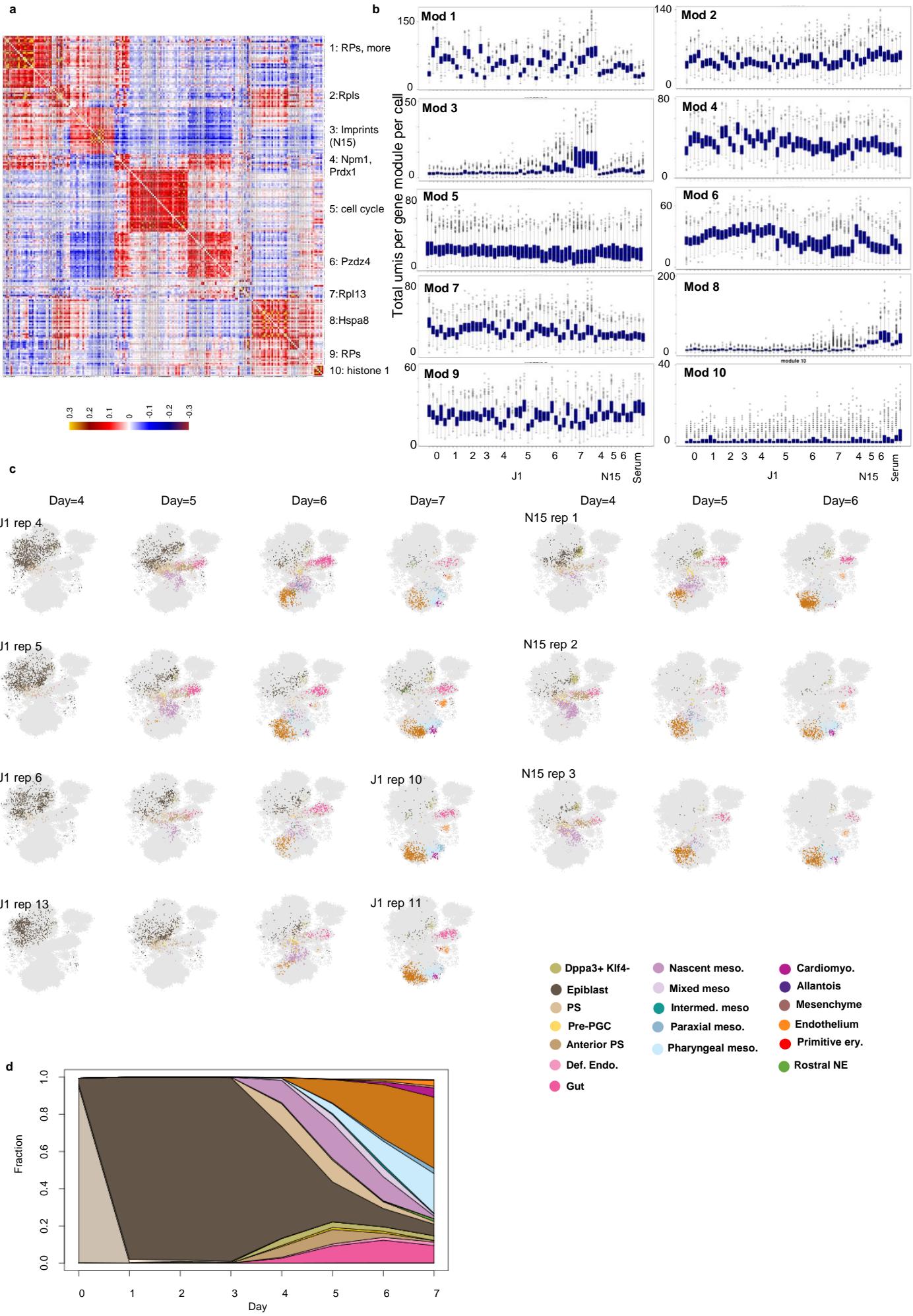
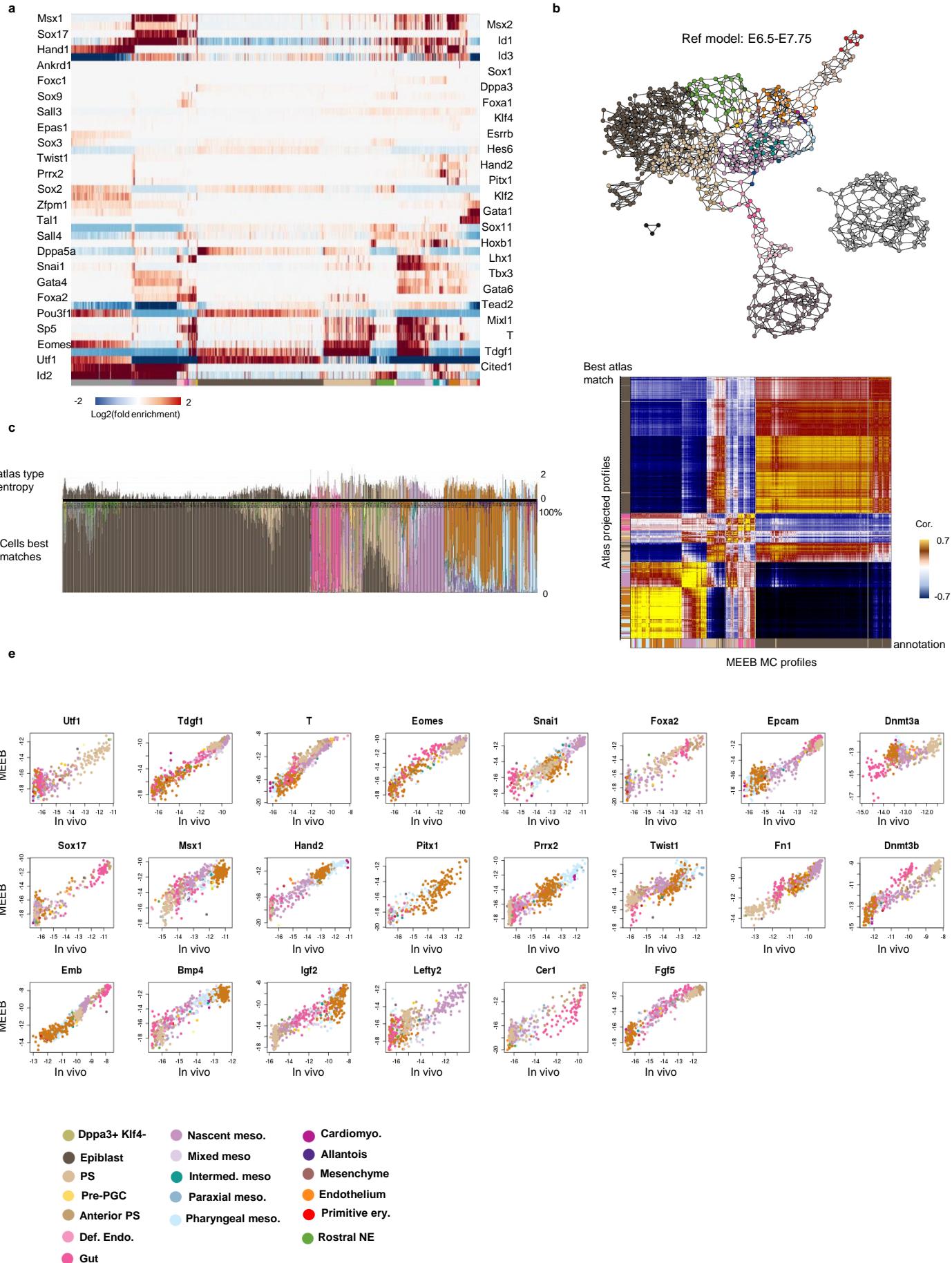
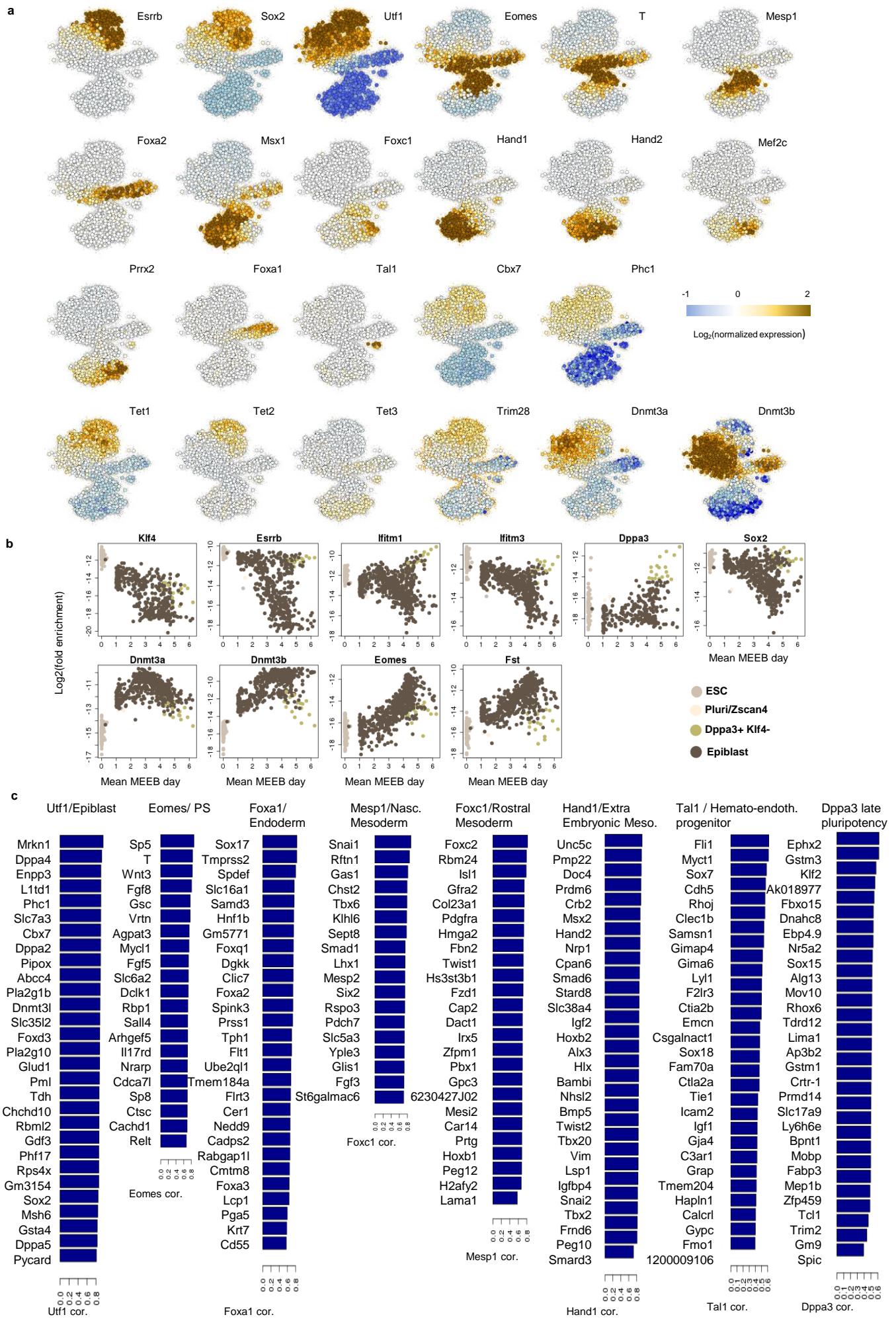


Fig. 7

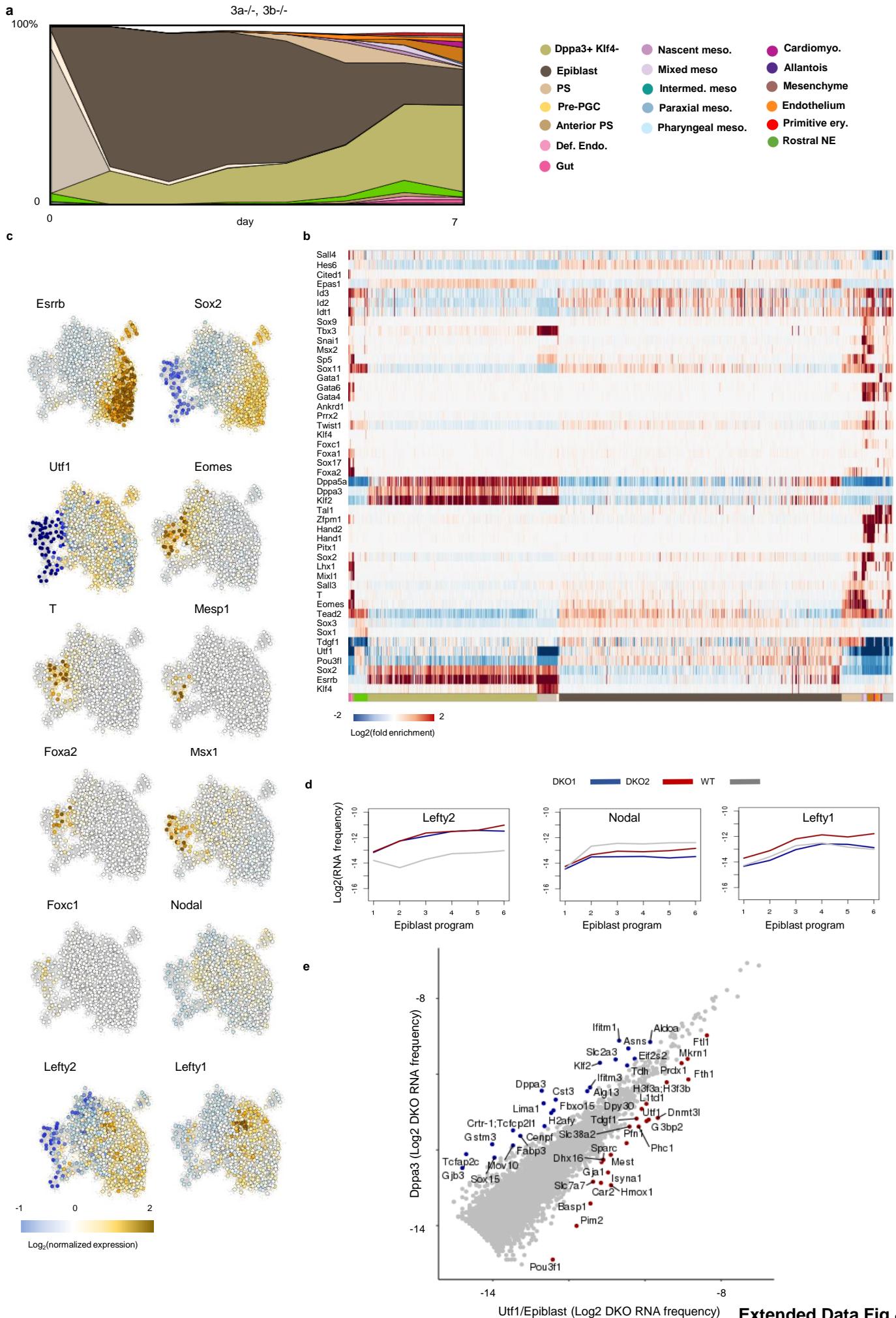


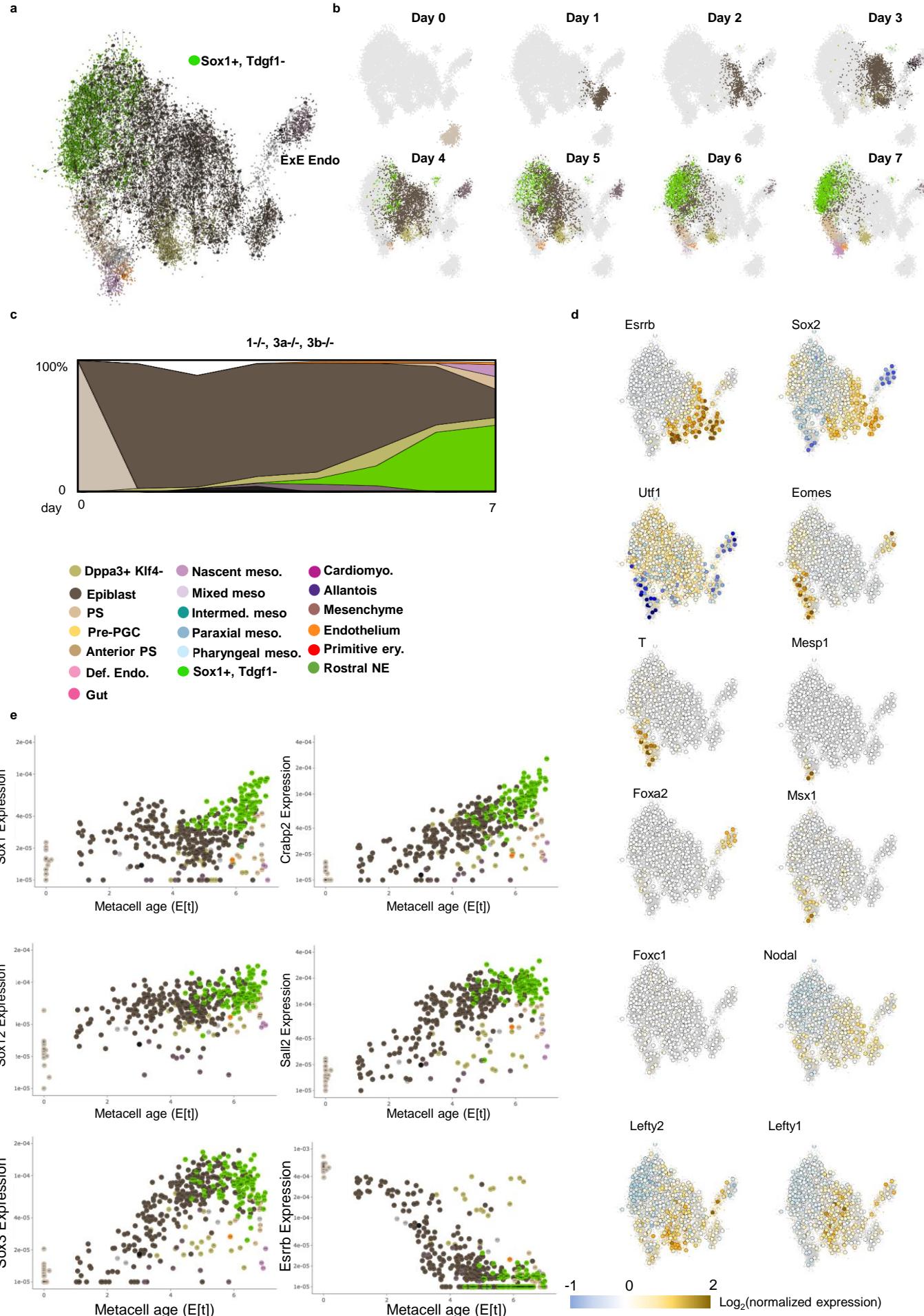


Extended Data Fig.2

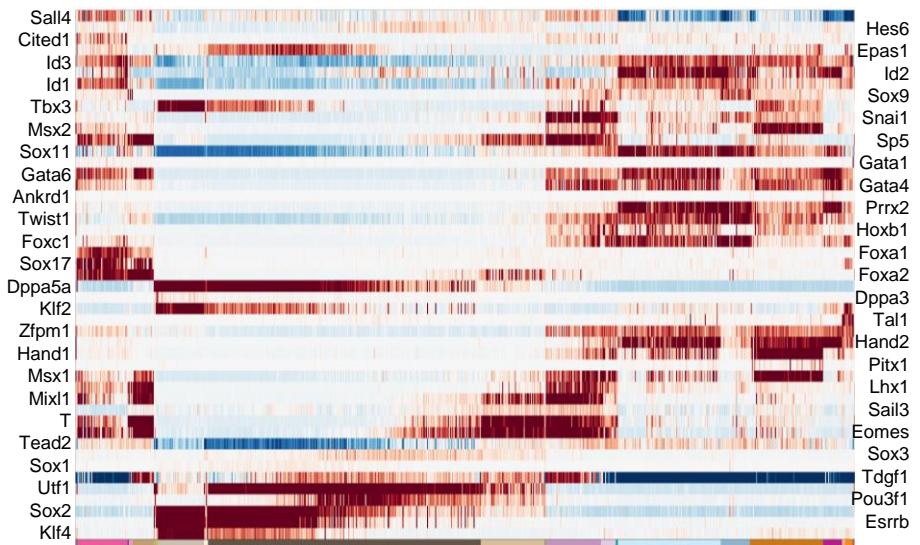
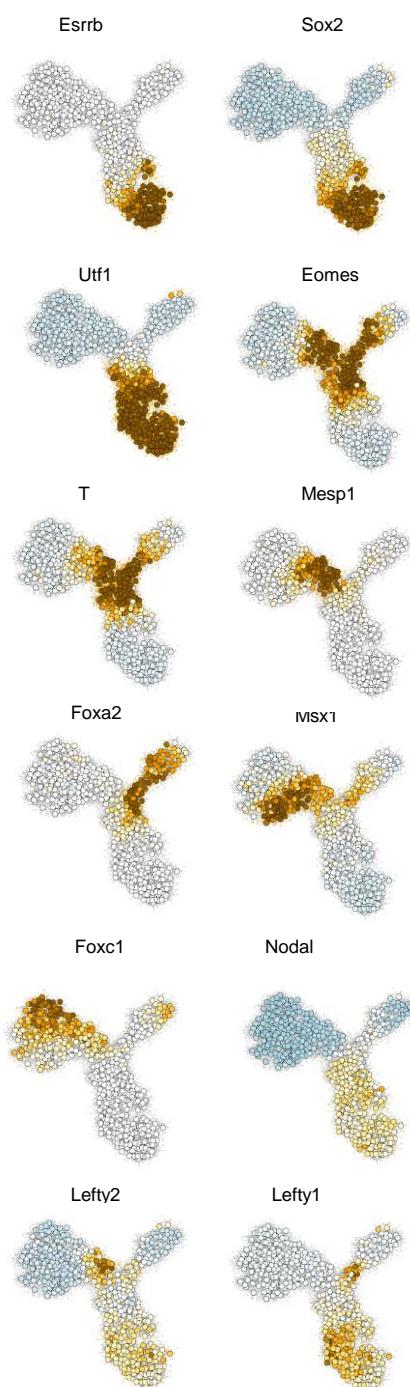


Extended Data Fig.3





Extended Data Fig.5

**a****b****c**

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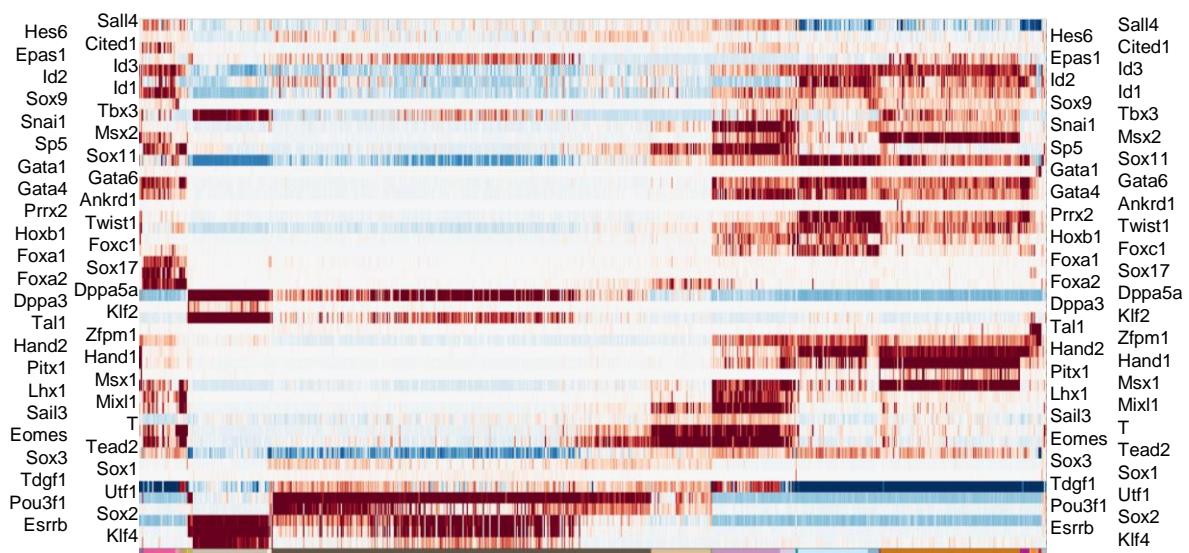
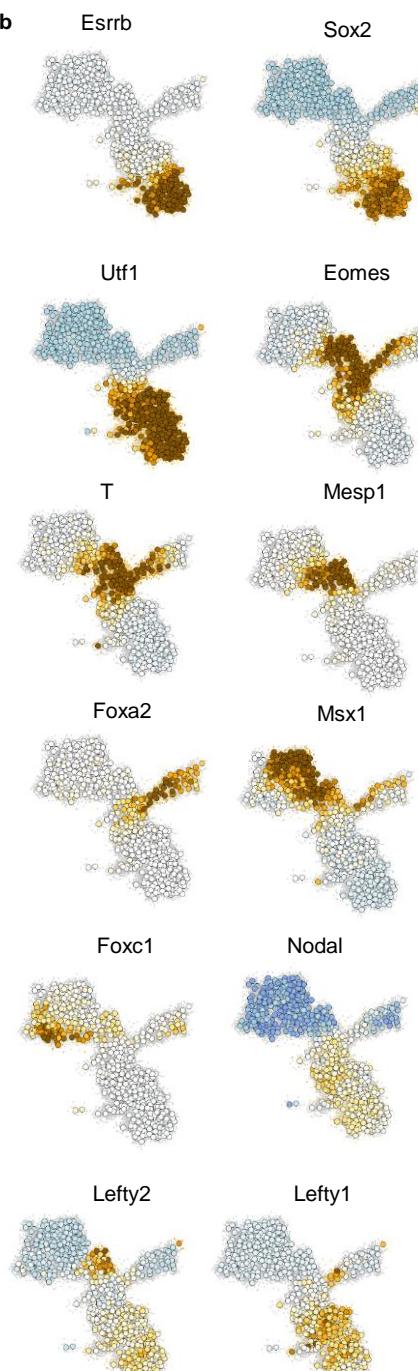
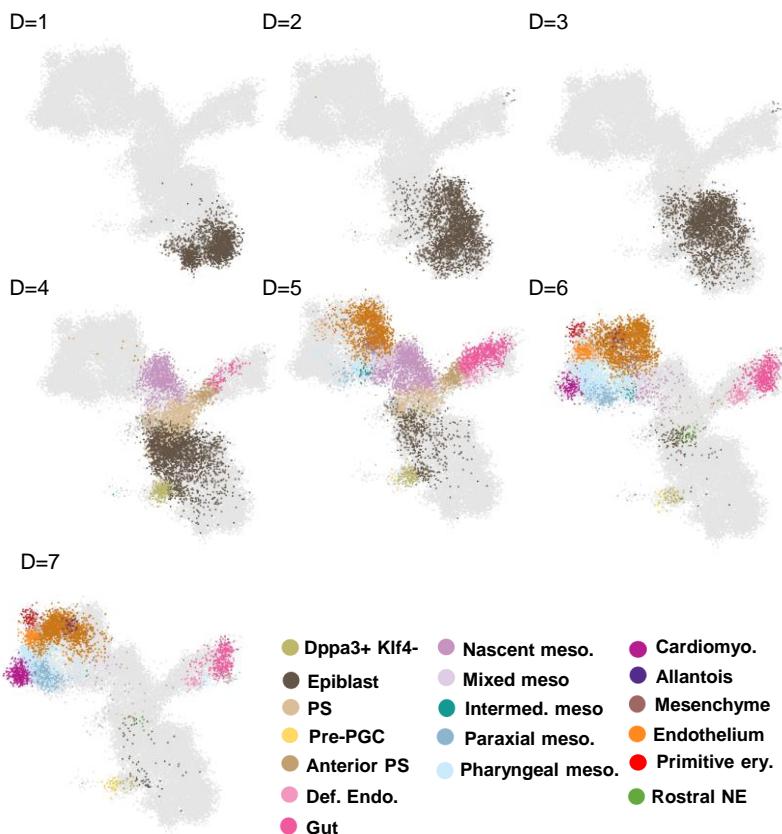
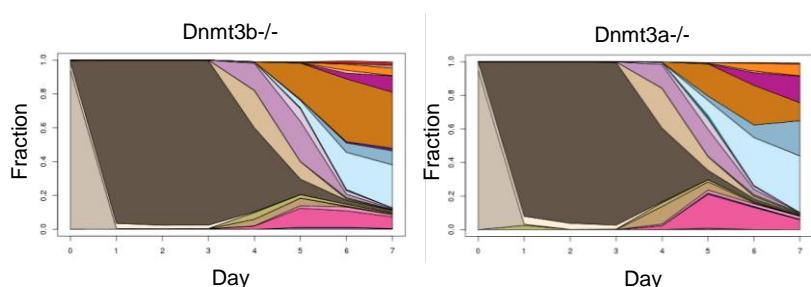
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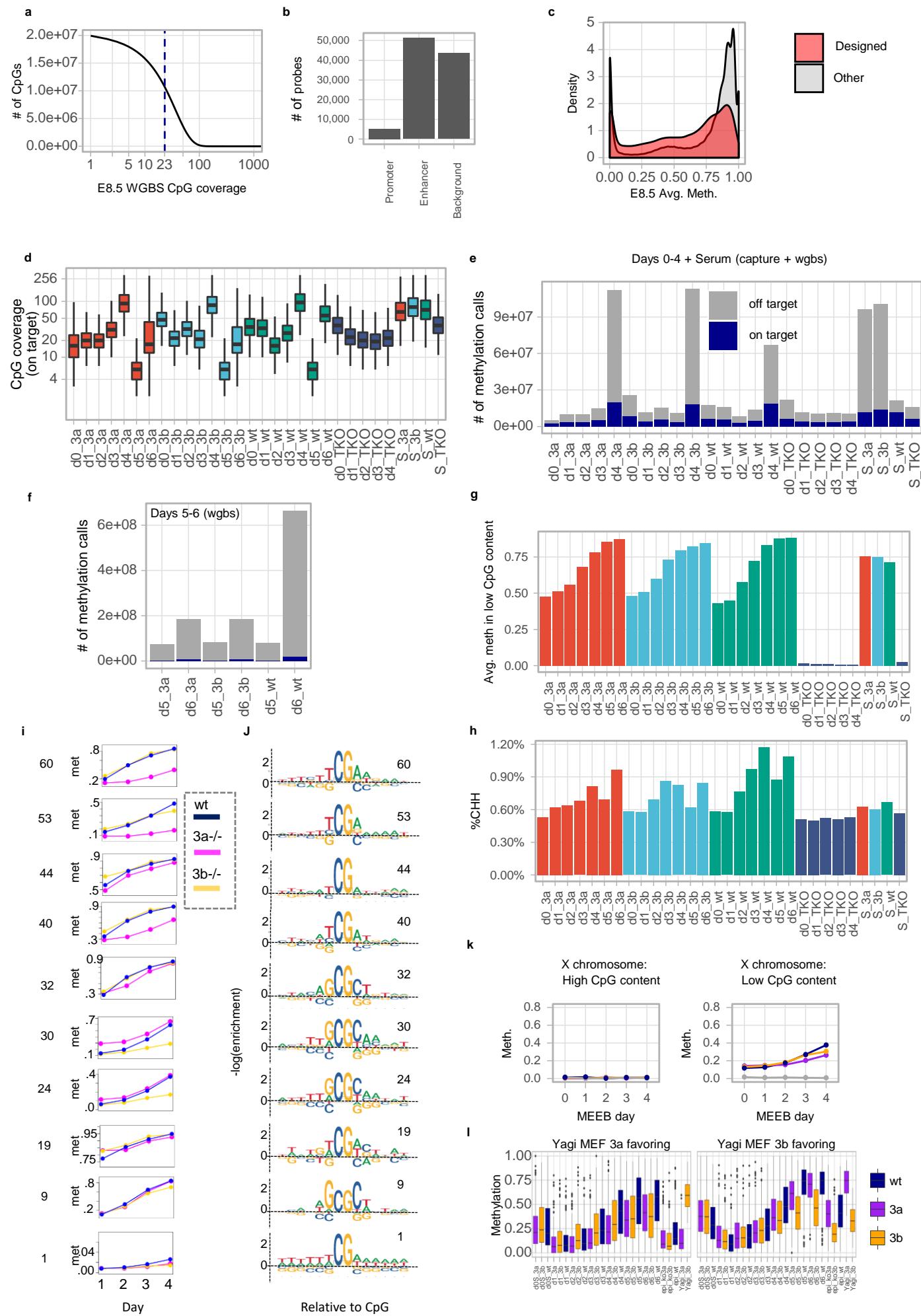
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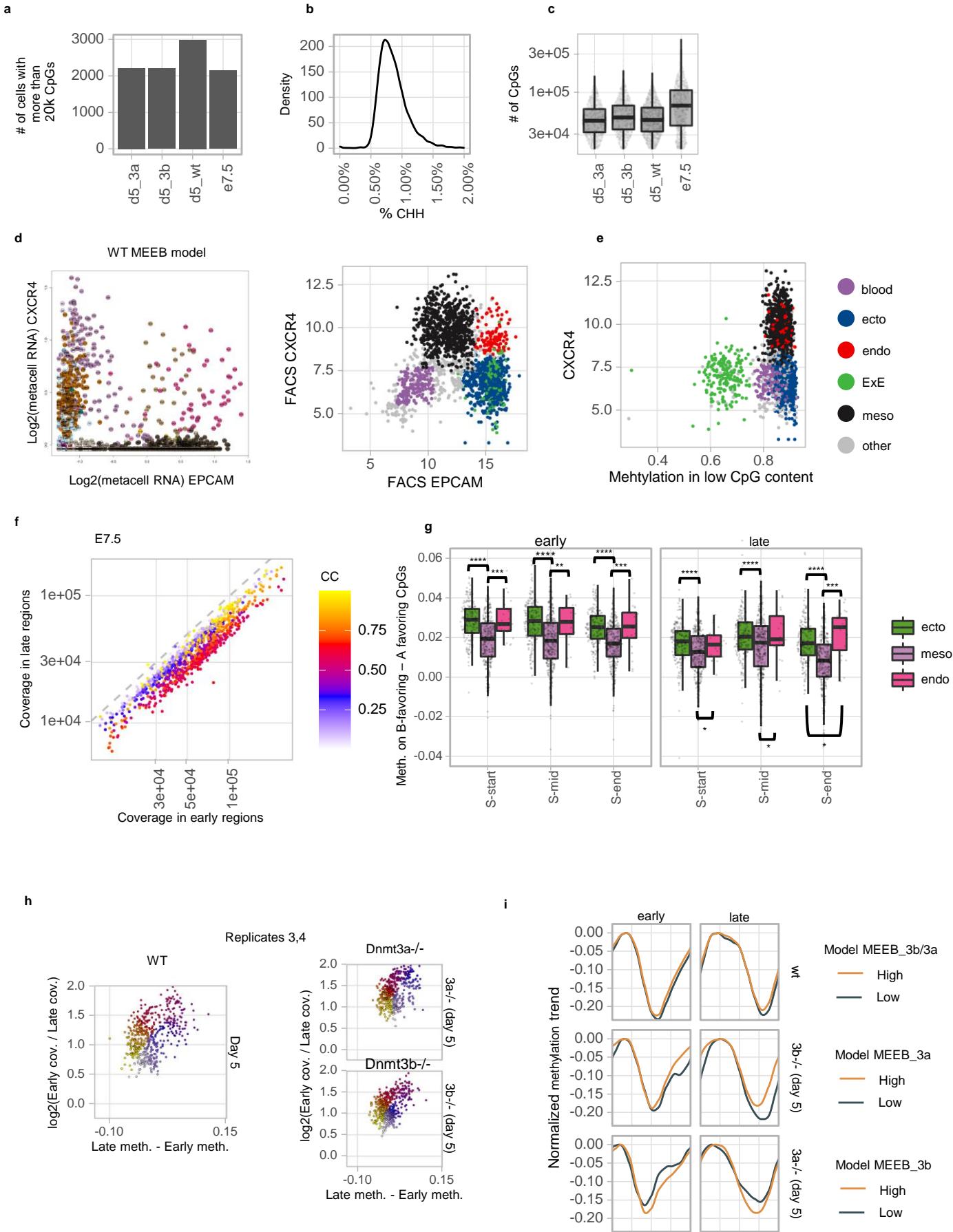
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- PS      ● Intermed. meso      ● Mesenchyme
- Pre-PGC      ● Paraxial meso      ● Endothelium
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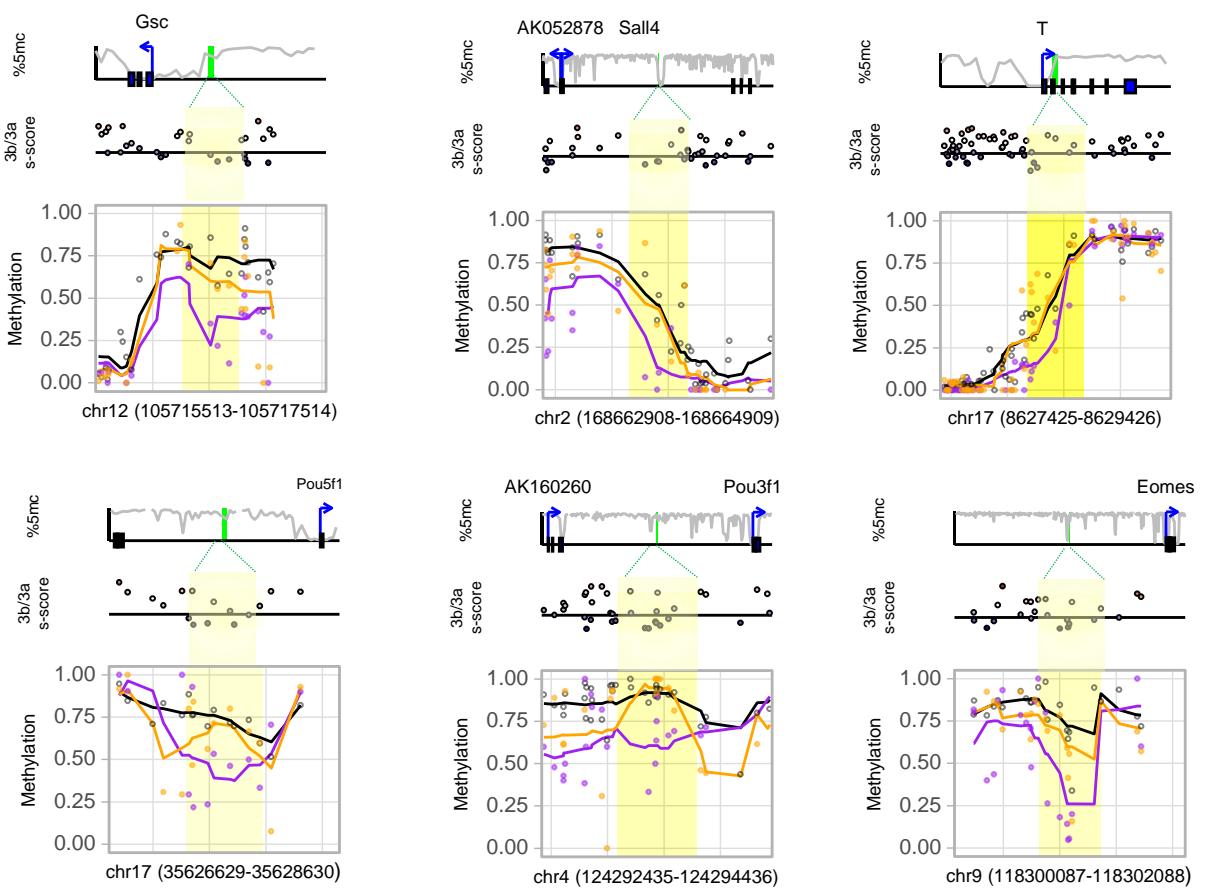
**Extended Data Fig.6**

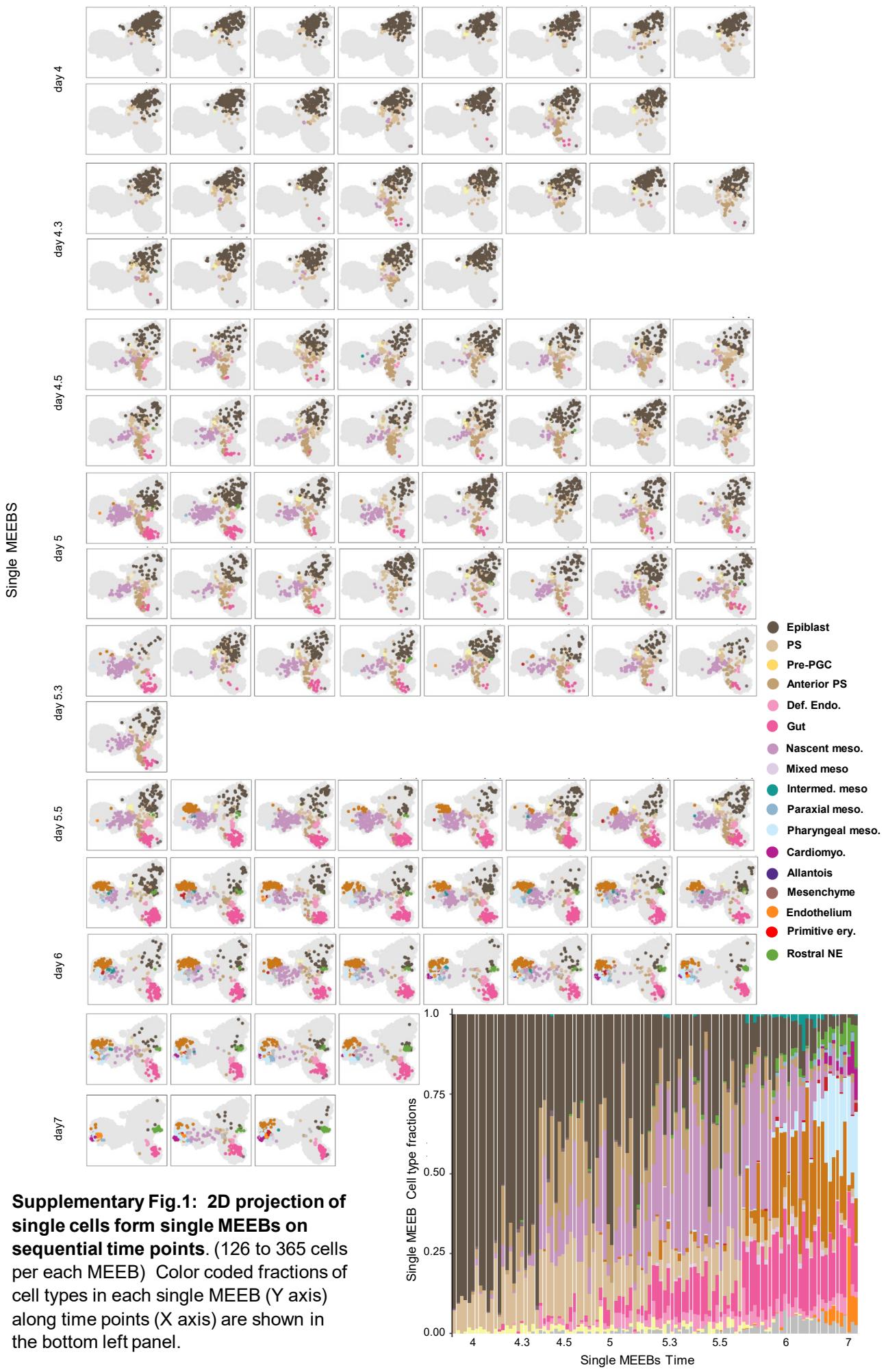
**a****b****c****d**



Extended Data Fig.8







**Table S1: MARS-seq plates.** For each amplification batch the table specifies: the basic line, EB\_day and replicate number, in addition to the median number of UMIs per cell and the total number of cells that passed QC (note that 12 of the wells are always used as empty well negative controls)

amp_batch_id	line	EB_day	rep	type	umi_med	n_qc_cell
ABZM00171	J1	0	1	wt	4763	365
ABZM00172	J1	0	1	wt	5101	358
ABZM00173	J1	0	1	wt	4893	274
ABZM00177	J1	5	1	wt	5477	363
ABZM00178	J1	5	1	wt	5389.5	370
ABZM00179	J1	5	1	wt	7569	351
ABZM00180	J1	5	1	wt	6216.5	368
ABZM00185	J1	7	1	wt	7904.5	368
ABZM00186	J1	7	1	wt	5027.5	370
ABZM00187	J1	7	1	wt	4819	365
ABZM00188	J1	7	1	wt	4637	327
ABZM00212	J1	2	2	wt	6200.5	370
ABZM00213	J1	2	2	wt	5927	370
ABZM00240	J1	1	3	wt	5016.5	368
ABZM00241	J1	1	3	wt	5243.5	372
ABZM00242	J1	2	3	wt	9447	360
ABZM00243	J1	2	3	wt	6422	361
ABZM00258	J1	3	3	wt	7612.5	364
ABZM00259	J1	3	3	wt	6224.5	360
ABZM00341	J1	4	3	wt	8186	366
ABZM00342	J1	4	3	wt	8218.5	344
ABZM00343	J1	4	3	wt	9413.5	340
ABZM00363	J1	6	3	wt	2804	352
ABZM00364	J1	6	3	wt	3488	354
ABZM00365	J1	6	3	wt	2660	344
ABZM00414	J1	7	4	wt	3197	347
ABZM00415	J1	7	4	wt	2551	335
ABZM00533	J1	4	4	wt	5915	361
ABZM00534	J1	4	4	wt	5338	371
ABZM00535	J1	4	4	wt	5580	369
ABZM00539	J1	5	4	wt	6345.5	354
ABZM00540	J1	5	4	wt	5102	361
ABZM00541	J1	5	4	wt	5982	345
ABZM00542	J1	5	4	wt	9458	350
ABZM00547	J1	6	4	wt	8621	360
ABZM00548	J1	6	4	wt	7640	365
ABZM00549	J1	6	4	wt	6991	366
ABZM00550	J1	6	4	wt	5350.5	360

ABZM00555	J1	7	4 wt	4810	352
ABZM00556	J1	7	4 wt	4589	359
ABZM00557	J1	7	4 wt	5307.5	354
ABZM00558	J1	7	4 wt	5714	353
ABZM00563	J1	4	5 wt	5337	363
ABZM00564	J1	4	5 wt	6043	366
ABZM00565	J1	4	5 wt	5896	365
ABZM00575	J1	5	5 wt	3535	362
ABZM00576	J1	5	5 wt	3417	366
ABZM00577	J1	5	5 wt	3324	366
ABZM00587	J1	6	5 wt	5114.5	368
ABZM00588	J1	6	5 wt	3090	351
ABZM00589	J1	6	5 wt	3679	355
ABZM00599	J1	7	5 wt	5701	363
ABZM00600	J1	7	5 wt	4323	357
ABZM00601	J1	7	5 wt	5754.5	362
ABZM00602	J1	7	5 wt	3714	366
ABZM00615	J1	4	6 wt	4051	356
ABZM00616	J1	4	6 wt	4450	364
ABZM00621	J1	5	6 wt	5470	369
ABZM00622	J1	5	6 wt	6513.5	370
ABZM00633	J1	6	6 wt	4323	358
ABZM00634	J1	6	6 wt	3726.5	348
ABZM00655	J1	6	7 wt	4610	365
ABZM00656	J1	6	7 wt	4260.5	358
ABZM00704	J1	4	8 wt	4824.5	362
ABZM00705	J1	4	8 wt	5588	363
ABZM00742	J1	3	9 wt	4058	363
ABZM00743	J1	3	9 wt	3975	360
ABZM00744	J1	3	9 wt	5068.5	362
ABZM00751	J1	4	9 wt	4632	369
ABZM00752	J1	4	9 wt	4305	366
ABZM00753	J1	4	9 wt	5551	364
ABZM00760	J1	5	9 wt	8215.5	368
ABZM00761	J1	5	9 wt	9722	367
ABZM00776	J1	0	10 wt	4683	345
ABZM00777	J1	0	10 wt	8669.5	356
ABZM00778	J1	0	11 wt	4759	345
ABZM00779	J1	0	11 wt	5982	360
ABZM00784	J1	1	10 wt	2989.5	340
ABZM00785	J1	1	10 wt	4672	348
ABZM00786	J1	1	11 wt	6985.5	358
ABZM00787	J1	1	11 wt	7354	360
ABZM00788	J1	2	10 wt	3032	355

ABZM00789	J1	2	10 wt	3663	349
ABZM00790	J1	2	11 wt	3192.5	336
ABZM00791	J1	2	11 wt	3985.5	354
ABZM00792	J1	3	10 wt	4649	353
ABZM00793	J1	3	10 wt	3712.5	354
ABZM00794	J1	7	11 wt	4574.5	366
ABZM00795	J1	7	11 wt	3486.5	356
ABZM00796	J1	7	10 wt	3751	347
ABZM00797	J1	6	10 wt	3916	345
ABZM00798	J1	6	11 wt	4857	346
ABZM00799	J1	6	11 wt	2735	333
ABZM00800	J1	7	10 wt	3985	359
ABZM00801	J1	7	10 wt	3819	359
ABZM00802	J1	7	11 wt	3645	365
ABZM00803	J1	7	11 wt	6736.5	40
ABZM00804	J1	0	12 wt	6155	343
ABZM00805	J1	0	12 wt	3282	345
ABZM00872	J1	4	13 wt	3418	339
ABZM00873	J1	4	13 wt	4623	345
ABZM00874	J1	5	13 wt	4660.5	356
ABZM00875	J1	5	13 wt	4522	362
ABZM00876	J1	6	13 wt	6036.5	370
ABZM00877	J1	6	13 wt	4508.5	366
ABZM00880	N15S	6	1 wt	2376.5	268
ABZM00881	N15S	6	1 wt	3220	357
ABZM00882	N15S	6	1 wt	2646	362
ABZM00883	N15S	5	1 wt	2878	348
ABZM00884	N15S	4	1 wt	3385	355
ABZM00885	N15S	4	1 wt	2677	347
ABZM00886	N15S	5	1 wt	5726	365
ABZM00887	N15S	5	1 wt	5024.5	356
ABZM00896	N15	4	1 wt	3573	361
ABZM00897	N15	4	1 wt	4453.5	368
ABZM00902	N15	5	1 wt	3807	340
ABZM00903	N15	5	1 wt	6775	363
ABZM00904	N15	5	1 wt	4815	341
ABZM00913	N15	6	1 wt	3656	353
ABZM00914	N15	6	1 wt	4624	351
ABZM00915	N15	6	1 wt	5674	345
ABZM00922	J1	0	14 wt	5770.5	370
ABZM00923	J1	0	14 wt	5571.5	372
ABZM00926	J1	1	14 wt	6763	367
ABZM00927	J1	1	14 wt	7403	372
ABZM00928	N15	4	2 wt	7068	363

ABZM00929	N15	4	2 wt	6667.5	356
ABZM00934	N15	5	2 wt	2835	347
ABZM00935	N15	5	2 wt	2837	331
ABZM00940	N15	6	2 wt	4288	359
ABZM00941	N15	6	2 wt	2286	329
ABZM00946	N15	4	3 wt	5044	361
ABZM00947	N15	4	3 wt	3084	349
ABZM00952	N15	5	3 wt	2414	318
ABZM00953	N15	5	3 wt	3023	306
ABZM00958	N15	6	3 wt	3876.5	344
ABZM00959	N15	6	3 wt	2667.5	336
ABZM00964	N15	4	2 wt	3999	357
ABZM00383	J1	1	1 3a	4340	361
ABZM00384	J1	1	1 3a	6817	371
ABZM00389	J1	2	1 3a	5925	372
ABZM00390	J1	2	1 3a	3970	355
ABZM00395	J1	3	1 3a	5612	363
ABZM00396	J1	3	1 3a	4450	368
ABZM00403	J1	0	1 3a	3677	359
ABZM00404	J1	0	1 3a	3036	360
ABZM00405	J1	4	1 3a	4794	357
ABZM00406	J1	4	1 3a	5281	365
ABZM00407	J1	4	1 3a	4521.5	356
ABZM00418	J1	7	1 3a	2663	320
ABZM00419	J1	7	1 3a	1889	291
ABZM00420	J1	7	1 3a	2421.5	312
ABZM00421	J1	7	1 3a	2407.5	328
ABZM00438	J1	4	2 3a	5178.5	370
ABZM00439	J1	4	2 3a	4602	367
ABZM00440	J1	4	2 3a	9132.5	368
ABZM00441	J1	5	2 3a	5910	369
ABZM00442	J1	5	2 3a	5543.5	370
ABZM00443	J1	5	2 3a	7460	370
ABZM00444	J1	6	2 3a	5262	369
ABZM00445	J1	6	2 3a	5025.5	368
ABZM00446	J1	6	2 3a	6147	367
ABZM00478	J1	4	3 3a	8970	371
ABZM00479	J1	4	3 3a	5869	370
ABZM00480	J1	4	3 3a	6715	371
ABZM00481	J1	5	3 3a	4644	365
ABZM00482	J1	5	3 3a	10697.5	372
ABZM00483	J1	5	3 3a	6970	365
ABZM00484	J1	6	3 3a	5184.5	364
ABZM00485	J1	6	3 3a	4743	366

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ABZM00487	J1	7	3 3a	6937.5	370
ABZM00488	J1	7	3 3a	3359	363
ABZM00489	J1	7	3 3a	4473	356
ABZM00500	J1	4	3 3a	7579	371
ABZM00501	J1	5	3 3a	4867	367
ABZM00502	J1	6	3 3a	6014	361
ABZM00503	J1	7	3 3a	6105	360
ABZM00504	J1	7	3 3a	5607	343
ABZM00566	J1	4	4 3a	6072	359
ABZM00567	J1	4	4 3a	7222.5	370
ABZM00568	J1	4	4 3a	5461.5	370
ABZM00578	J1	5	4 3a	4382	365
ABZM00579	J1	5	4 3a	3429.5	362
ABZM00580	J1	5	4 3a	3445	362
ABZM00590	J1	6	4 3a	3249	354
ABZM00591	J1	6	4 3a	4320	350
ABZM00592	J1	6	4 3a	2870	333
ABZM00603	J1	7	4 3a	3505	348
ABZM00604	J1	7	4 3a	4859	359
ABZM00605	J1	7	4 3a	4710	350
ABZM00606	J1	7	4 3a	3012	332
ABZM00829	J1	0	5 3a	5179	371
ABZM00830	J1	0	5 3a	6835.5	356
ABZM00833	J1	1	5 3a	5682	366
ABZM00834	J1	1	5 3a	11164	371
ABZM00837	J1	2	5 3a	5159	350
ABZM00840	J1	2	5 3a	7223.5	366
ABZM00841	J1	2	5 3a	9038	369
ABZM00844	J1	0	5 3a	5770	361
ABZM00845	J1	0	5 3a	6018	367
ABZM00848	J1	1	5 3a	6781	372
ABZM00849	J1	1	5 3a	10602	371
ABZM00852	J1	2	5 3a	9369	367
ABZM00853	J1	2	5 3a	6529	369
ABZM00856	J1	3	5 3a	4374	369
ABZM00857	J1	3	5 3a	4042	365
ABZM00860	J1	4	5 3a	6349	369
ABZM00861	J1	4	5 3a	9123.5	370
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ABZM00865	J1	6	5 3a	4021	351
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ABZM00889	N15S	5	1 3a	2258	240
ABZM00890	N15S	6	1 3a	2111	287

ABZM00891	N15S	6	1 3a	3326	318
ABZM00898	N15	4	1 3a	3522	347
ABZM00899	N15	4	1 3a	4172	356
ABZM00905	N15	5	1 3a	6192	365
ABZM00906	N15	5	1 3a	5029	357
ABZM00907	N15	5	1 3a	9127	352
ABZM00916	N15	6	1 3a	4903	357
ABZM00917	N15	6	1 3a	5503.5	360
ABZM00918	N15	6	1 3a	5577	359
ABZM00930	N15	4	2 3a	3812	362
ABZM00931	N15	4	2 3a	4230	333
ABZM00936	N15	5	2 3a	5198	345
ABZM00937	N15	5	2 3a	5053	354
ABZM00942	N15	6	2 3a	2352	311
ABZM00943	N15	6	2 3a	2317	286
ABZM00948	N15	4	3 3a	4309	361
ABZM00949	N15	4	3 3a	3328	352
ABZM00954	N15	5	3 3a	3540	246
ABZM00955	N15	5	3 3a	4952.5	292
ABZM00960	N15	6	3 3a	2157	302
ABZM00961	N15	6	3 3a	1850.5	286
ABZM00965	N15	4	2 3a	2653	345
ABZM00284	J1	0	1 3b	3374	369
ABZM00285	J1	0	1 3b	5667	369
ABZM00286	J1	0	1 3b	6566	357
ABZM00287	J1	0	1 3b	3925	362
ABZM00288	J1	3	1 3b	5277	315
ABZM00289	J1	3	1 3b	5552.5	310
ABZM00290	J1	3	1 3b	5899	265
ABZM00291	J1	3	1 3b	10670	175
ABZM00292	J1	5	1 3b	8862	366
ABZM00293	J1	5	1 3b	8321	366
ABZM00294	J1	5	1 3b	12251	369
ABZM00295	J1	5	1 3b	10785	370
ABZM00296	J1	7	1 3b	4101	351
ABZM00297	J1	7	1 3b	5082	353
ABZM00298	J1	7	1 3b	4010	347
ABZM00299	J1	7	1 3b	5495	351
ABZM00300	J1	7	1 3b	5629	359
ABZM00301	J1	7	1 3b	5448	348
ABZM00385	J1	1	2 3b	4986	369
ABZM00386	J1	1	2 3b	4089	357
ABZM00391	J1	2	2 3b	5146	349
ABZM00392	J1	2	2 3b	3935	361

ABZM00397	J1	3	2 3b	6704.5	370
ABZM00398	J1	3	2 3b	8528.5	368
ABZM00399	J1	3	2 3b	5387	369
ABZM00408	J1	4	2 3b	4303	361
ABZM00409	J1	4	2 3b	5390	363
ABZM00410	J1	4	2 3b	7840.5	360
ABZM00422	J1	7	2 3b	2354	308
ABZM00423	J1	7	2 3b	1681	275
ABZM00514	J1	4	3 3b	6210	371
ABZM00515	J1	4	3 3b	5850.5	370
ABZM00516	J1	4	3 3b	6079	370
ABZM00517	J1	5	3 3b	5023	369
ABZM00518	J1	5	3 3b	5252	368
ABZM00519	J1	5	3 3b	7258	369
ABZM00524	J1	6	3 3b	5103	344
ABZM00525	J1	6	3 3b	5808.5	368
ABZM00526	J1	6	3 3b	5636.5	352
ABZM00530	J1	7	3 3b	4706.5	370
ABZM00531	J1	7	3 3b	4921	366
ABZM00532	J1	7	3 3b	5312	367
ABZM00569	J1	4	4 3b	6554	370
ABZM00570	J1	4	4 3b	6008.5	372
ABZM00571	J1	4	4 3b	5874	369
ABZM00581	J1	5	4 3b	6876	372
ABZM00582	J1	5	4 3b	6154	371
ABZM00583	J1	5	4 3b	4029.5	364
ABZM00593	J1	6	4 3b	5500	364
ABZM00594	J1	6	4 3b	3382	362
ABZM00595	J1	6	4 3b	4364	347
ABZM00607	J1	7	4 3b	3556	349
ABZM00608	J1	7	4 3b	4224	355
ABZM00609	J1	7	4 3b	3363	343
ABZM00610	J1	7	4 3b	2854	347
ABZM00831	J1	0	5 3b	4449	365
ABZM00832	J1	0	5 3b	7406	365
ABZM00835	J1	1	5 3b	5738	369
ABZM00836	J1	1	5 3b	7619	367
ABZM00838	J1	2	5 3b	10897	370
ABZM00839	J1	2	5 3b	8531	367
ABZM00842	J1	2	5 3b	8272	360
ABZM00843	J1	2	5 3b	9516.5	366
ABZM00846	J1	0	5 3b	7489	367
ABZM00847	J1	0	5 3b	4394	362
ABZM00850	J1	1	5 3b	7036	369

ABZM00851	J1	1	5 3b	10136	369
ABZM00854	J1	2	5 3b	6909	370
ABZM00855	J1	2	5 3b	7611	371
ABZM00858	J1	3	5 3b	9186	368
ABZM00859	J1	3	5 3b	3965	353
ABZM00862	J1	4	5 3b	7415	371
ABZM00863	J1	4	5 3b	3515	366
ABZM00866	J1	6	5 3b	4525.5	356
ABZM00867	J1	6	5 3b	3232	346
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ABZM00894	N15S	6	1 3b	3869	321
ABZM00895	N15S	6	1 3b	3166	299
ABZM00900	N15	4	1 3b	3433	352
ABZM00901	N15	4	1 3b	3915.5	348
ABZM00908	N15	5	1 3b	4303.5	332
ABZM00909	N15	5	1 3b	8869	367
ABZM00910	N15	5	1 3b	4685	359
ABZM00919	N15	6	1 3b	9083	369
ABZM00920	N15	6	1 3b	2662.5	318
ABZM00921	N15	6	1 3b	6151	364
ABZM00932	N15	4	2 3b	6832	336
ABZM00933	N15	4	2 3b	6217	325
ABZM00938	N15	5	2 3b	5844	347
ABZM00939	N15	5	2 3b	3926	350
ABZM00944	N15	6	2 3b	2720	295
ABZM00945	N15	6	2 3b	2968	247
ABZM00950	N15	4	3 3b	5659	366
ABZM00951	N15	4	3 3b	3073	355
ABZM00956	N15	5	3 3b	2526.5	272
ABZM00957	N15	5	3 3b	2174	267
ABZM00962	N15	6	3 3b	2496.5	304
ABZM00963	N15	6	3 3b	1842.5	256
ABZM00447	DKO	4	1 3ab	5993	367
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ABZM00451	DKO	5	1 3ab	5413.5	368
ABZM00452	DKO	5	1 3ab	6042	366
ABZM00453	DKO	6	1 3ab	6040	367
ABZM00454	DKO	6	1 3ab	7598	365
ABZM00455	DKO	6	1 3ab	5651.5	366
ABZM00456	DKO	0	2 3ab	7715.5	356
ABZM00457	DKO	0	2 3ab	7281.5	356

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ABZM00462	DKO	4	2 3ab	11000	369
ABZM00463	DKO	4	2 3ab	9548	368
ABZM00464	DKO	4	2 3ab	7754	372
ABZM00465	DKO	5	2 3ab	7226	371
ABZM00466	DKO	5	2 3ab	13999	371
ABZM00467	DKO	5	2 3ab	5961.5	370
ABZM00468	DKO	5	2 3ab	10504.5	372
ABZM00469	DKO	6	2 3ab	4979	368
ABZM00470	DKO	6	2 3ab	7237	368
ABZM00471	DKO	6	2 3ab	5438	368
ABZM00472	DKO	6	2 3ab	5195	371
ABZM00473	DKO	7	2 3ab	4967	368
ABZM00474	DKO	7	2 3ab	5159	368
ABZM00475	DKO	7	2 3ab	5741	366
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ABZM00492	DKO	1	2 3ab	5364	370
ABZM00493	DKO	2	2 3ab	6212	361
ABZM00494	DKO	2	2 3ab	4848	369
ABZM00495	DKO	6	2 3ab	7680.5	372
ABZM00505	DKO	7	1 3ab	5516.5	370
ABZM00506	DKO	7	1 3ab	10107	371
ABZM00507	DKO	7	1 3ab	7426.5	368
ABZM00572	DKO	4	3 3ab	5285.5	368
ABZM00573	DKO	4	3 3ab	7199	367
ABZM00574	DKO	4	3 3ab	4925	369
ABZM00584	DKO	5	3 3ab	5242	366
ABZM00585	DKO	5	3 3ab	4297	367
ABZM00586	DKO	5	3 3ab	3366	370
ABZM00596	DKO	6	3 3ab	8661	369
ABZM00597	DKO	6	3 3ab	7229	368
ABZM00598	DKO	6	3 3ab	5687	361
ABZM00611	DKO	7	3 3ab	6579.5	370
ABZM00612	DKO	7	3 3ab	5980	368
ABZM00613	DKO	7	3 3ab	6739	371
ABZM00614	DKO	7	3 3ab	3899	367
ABZM00617	DKO	4	6 3ab	4836	368
ABZM00618	DKO	4	6 3ab	5227	365
ABZM00625	DKO	5	6 3ab	6444	365
ABZM00626	DKO	5	6 3ab	5301	369

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ABZM00638	DKO	6	6 3ab	4626	354
ABZM00745	DKO	3	9 3ab	6316	368
ABZM00746	DKO	3	9 3ab	6206	369
ABZM00747	DKO	3	9 3ab	4991	363
ABZM00748	DKO16	3	9 3ab	7271	366
ABZM00749	DKO16	3	9 3ab	5540.5	368
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ABZM00754	DKO	4	9 3ab	4035	367
ABZM00755	DKO	4	9 3ab	5892.5	370
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ABZM00759	DKO16	4	9 3ab	5488	359
ABZM00765	DKO	5	9 3ab	6119	352
ABZM00766	DKO	5	9 3ab	6232	353
ABZM00770	DKO16	5	9 3ab	4599.5	352
ABZM00771	DKO16	5	9 3ab	5059.5	354
ABZM00775	DKO16	5	9 3ab	12592	371
ABZM00809	DKO16	0	1 3ab	5797	336
ABZM00810	DKO16	0	1 3ab	3278	325
ABZM00811	DKO16	3	1 3ab	7911	371
ABZM00812	DKO16	3	1 3ab	6756	371
ABZM00813	DKO16	4	1 3ab	5976	369
ABZM00814	DKO16	4	1 3ab	6105	369
ABZM00815	DKO16	5	1 3ab	8561	371
ABZM00816	DKO16	5	1 3ab	6628	368
ABZM00817	DKO16	6	1 3ab	6670	367
ABZM00818	DKO16	6	1 3ab	5340	370
ABZM00819	DKO16	7	1 3ab	6074	369
ABZM00820	DKO16	7	1 3ab	4461	362
ABZM00821	DKO16	7	1 3ab	9625.5	372
ABZM00318	J1	0	1 TKO	6959.5	372
ABZM00319	J1	0	1 TKO	4782	371
ABZM00320	J1	3	1 TKO	11557	371
ABZM00321	J1	3	1 TKO	7248	371
ABZM00322	J1	3	1 TKO	8107	366
ABZM00323	J1	5	1 TKO	12147	372
ABZM00324	J1	5	1 TKO	10962.5	372
ABZM00325	J1	5	1 TKO	5579	371
ABZM00326	J1	5	1 TKO	4378	365
ABZM00327	J1	7	1 TKO	4396	363
ABZM00328	J1	7	1 TKO	4207	368
ABZM00329	J1	7	1 TKO	4016.5	366

ABZM00330	J1	7	1 TKO	4304.5	368
ABZM00387	J1	1	1 TKO	4903	345
ABZM00388	J1	1	1 TKO	4616	356
ABZM00393	J1	2	1 TKO	5980.5	356
ABZM00394	J1	2	1 TKO	3644	362
ABZM00400	J1	3	1 TKO	4499.5	372
ABZM00401	J1	3	1 TKO	4766	371
ABZM00402	J1	3	1 TKO	3702	367
ABZM00411	J1	4	1 TKO	4783	352
ABZM00412	J1	4	1 TKO	4353	366
ABZM00413	J1	4	1 TKO	4131	354
ABZM00424	J1	7	1 TKO	4644	363
ABZM00425	J1	7	1 TKO	2576.5	354
ABZM00508	J1	4	2 TKO	6165	372
ABZM00509	J1	4	2 TKO	5960.5	372
ABZM00510	J1	4	2 TKO	5623	372
ABZM00511	J1	5	2 TKO	5676	371
ABZM00512	J1	5	2 TKO	5720	365
ABZM00513	J1	5	2 TKO	6374	367
ABZM00520	J1	6	2 TKO	5121	367
ABZM00521	J1	6	2 TKO	5736	368
ABZM00522	J1	6	2 TKO	6635.5	368
ABZM00523	J1	6	2 TKO	6590	366
ABZM00527	J1	7	2 TKO	6236	369
ABZM00528	J1	7	2 TKO	6655	369
ABZM00529	J1	7	2 TKO	5765.5	364
ABZM00619	J1	4	6 TKO	5111	369
ABZM00620	J1	4	6 TKO	5520	371
ABZM00629	J1	5	6 TKO	5526	365
ABZM00630	J1	5	6 TKO	4021	360
ABZM00641	J1	6	6 TKO	1941	263
ABZM00642	J1	6	6 TKO	3135	352
ABZM00700	J1	6	7 TKO	2877	346
ABZM00701	J1	6	7 TKO	2863	352

**Table S2: Methylation experiments table.** Each row contains the information of a single experiment. ‘type’ column indicates if the experiment was done in bulk or single cell. The statistics shown for single cell experiments are average over cells. Cells and samples with CHH > 2% were discarded and are not shown here.

samp_id	day	line	sort	type	n_cells	capture	total_reads	mapped_reads	uniq_frac	meth_calls	cpg_num	CHH	CHG	CpG
d0_ko3a.1 d0		3a/-	all	bulk	V1	14681004	6258604	0.244565312	1997966	1535846	0.00579	0	0.400754	
d0_ko3a.2 d0		3a/-	all	bulk	V1	7068378	3441495	0.59268106	2772033	560004	0.004764	0	0.340249	
d0_ko3b.1 d0		3b/-	all	bulk	V1	81246600	44804162	0.358617108	19610442	7054440	0.005232	0	0.41834	
d0_ko3b.2 d0		3b/-	all	bulk	V1	14277409	6395708	0.990152146	6256639	5085617	0.006405	0	0.424775	
d0_tko.1 d0		TKO	all	bulk	V1	55565048	29760513	0.435961396	15709635	6233690	0.004996	0	0.016712	
d0_tko.2 d0		TKO	all	bulk	V1	14169898	6527950	0.990549563	6356491	5223097	0.005236	0	0.016302	
d0_wt.1 d0		wt	all	bulk	V1	53634491	29252731	0.39466947	13906634	5307048	0.006247	0	0.371183	
d0_wt.2 d0		wt	all	bulk	V1	9514508	4071384	0.989685073	3669722	3263988	0.005426	0	0.38487	
d0S_ko3a. d0S		3a/-	all	bulk	V1	62143537	35013910	0.282686699	12390968	5227550	0.007127	0	0.697083	
d0S_ko3a. d0S		3a/-	all	wgbs	56186314	14606378	0.980552061	21500191	11633044	0.006362	0	0.685626		
d0S_ko3a. d0S		3a/-	all	wgbs	47898753	12994176	0.980932171	19067244	10922798	0.006229	0	0.683011		
d0S_ko3a. d0S		3a/-	all	wgbs	50023391	13369083	0.980739236	18924819	11038325	0.006268	0	0.690185		
d0S_ko3a. d0S		3a/-	all	wgbs	46892991	12848530	0.979863058	17920801	10781323	0.006744	0	0.692577		
d0S_ko3a. d0S		3a/-	all	bulk	V1	3742425	1805120	0.636240469	1494844	396071	0.005891	0	0.559216	
d0S_ko3a. d0S		3a/-	all	bulk	V1	3667145	1677108	0.627222498	1370630	381676	0.00557	0	0.562148	
d0S_ko3a. d0S		3a/-	all	bulk	V1	5645436	2789882	0.534657056	1950171	456948	0.006106	0	0.561586	
d0S_ko3a. d0S		3a/-	all	bulk	V1	5600968	2671225	0.520804307	1821054	463586	0.005946	0	0.567591	
d0S_ko3b. d0S		3b/-	all	bulk	V1	67080332	37384958	0.310361712	14122942	5551400	0.007611	0	0.720721	
d0S_ko3b. d0S		3b/-	all	wgbs	66925159	16831183	0.97173133	22554376	12123120	0.005441	0	0.685545		
d0S_ko3b. d0S		3b/-	all	wgbs	71735504	20060338	0.978269074	28872647	13628167	0.006123	0	0.680594		
d0S_ko3b. d0S		3b/-	all	wgbs	70113090	18316432	0.978994906	26933185	13085396	0.006231	0	0.680384		
d0S_ko3b. d0S		3b/-	all	bulk	V1	5181109	2665446	0.46242841	1557888	440650	0.005055	0	0.579538	
d0S_ko3b. d0S		3b/-	all	bulk	V1	17158870	8423798	0.566921985	3211508	577244	0.006068	0	0.563612	
d0S_ko3b. d0S		3b/-	all	bulk	V1	16734306	8460728	0.61113919	3501416	586180	0.005749	0	0.568034	
d0S_tko.1 d0S		TKO	all	bulk	V1	65869842	37900999	0.306867008	15669178	5792244	0.005662	0	0.021241	
d0S_wt.1 d0S		wt	all	bulk	V1	82526331	49404521	0.214007353	13627405	4521500	0.008064	0	0.6602	
d0S_wt.2 d0S		wt	all	bulk	V1	4809102	2415489	0.553437096	1776354	436137	0.006205	0	0.551076	
d0S_wt.3 d0S		wt	all	bulk	V1	4885176	2345371	0.57594531	1719499	423899	0.007082	0	0.562802	
d0S_wt.4 d0S		wt	all	bulk	V1	5259013	2644200	0.577998047	2013623	457019	0.005813	0	0.562714	
d0S_wt.5 d0S		wt	all	bulk	V1	5745820	2868675	0.576610974	2172087	485117	0.006088	0	0.558551	
d1_ko3a.1 d1		3a/-	all	bulk	V1	59997553	34114404	0.234682069	9972366	4685545	0.006201	0	0.441969	
d1_ko3b.1 d1		3b/-	all	bulk	V1	64524844	35097473	0.276336502	11546018	5520928	0.005754	0	0.438476	
d1_tko.1 d1		TKO	all	bulk	V1	48282762	26470698	0.360791577	11805579	5613704	0.00498	0	0.011251	
d1_wt.1 d1		wt	all	bulk	V1	72500375	40534252	0.320555165	16115257	6570084	0.00574	0	0.392167	
d2_ko3a.1 d2		3a/-	all	bulk	V1	49030907	26618739	0.29968802	9685860	4709610	0.006415	0	0.48026	
d2_ko3b.1 d2		3b/-	all	bulk	V1	65524864	36873837	0.334229854	15220458	6213541	0.006921	0	0.523084	
d2_tko.1 d2		TKO	all	bulk	V1	40372384	21141295	0.405003436	10420259	5136350	0.005197	0	0.009249	
d2_wt.1 d2		wt	all	bulk	V1	46854560	25873305	0.278301198	8629911	4537014	0.007639	0	0.49672	
d3_ko3a.1 d3		3a/-	all	bulk	V1	61490473	34915132	0.345560131	14821752	6365801	0.0068	0	0.591843	
d3_ko3b.1 d3		3b/-	all	bulk	V1	45320288	25596350	0.345025146	10767119	5136246	0.008632	0	0.638364	
d3_tko.1 d3		TKO	all	bulk	V1	51034425	28918690	0.305349532	10910231	5452683	0.005129	0	0.007386	
d3_wt.1 d3		wt	all	bulk	V1	57126827	32237605	0.346938693	13410266	6030001	0.009738	0	0.635147	
d4_ko3a.1 d4		3a/-	all	bulk	V1	45679376	27120894	0.26595766	9240500	3864026	0.007657	0	0.657564	
d4_ko3a.1 d4		3a/-	all	bulk	V2	57249673	23292360	0.977817079	20219186	11808041	0.008474	0	0.731851	
d4_ko3a.1 d4		3a/-	all	bulk	V2	28961648	15866323	0.167633244	3394228	712691	0.00773	0	0.651614	
d4_ko3a.1 d4		3a/-	all	bulk	V2	31936481	17531365	0.171751278	4007448	751418	0.006907	0	0.638325	
d4_ko3a.2 d4		3a/-	all	wgbs	58902715	15036776	0.979132766	21179029	11794413	0.007917	0	0.718319		
d4_ko3a.3 d4		3a/-	all	wgbs	40018168	8746368	0.980342464	11526670	8244419	0.009043	0	0.726962		
d4_ko3a.4 d4		3a/-	all	wgbs	37410980	9273682	0.980360897	12187187	8452696	0.009819	0	0.714908		
d4_ko3a.5 d4		3a/-	all	wgbs	53873177	13989876	0.980315794	19515295	11336594	0.008449	0	0.719247		
d4_ko3a.6 d4		3a/-	all	bulk	V1	13747342	6716473	0.404871488	3573009	664957	0.006798	0	0.598517	
d4_ko3a.7 d4		3a/-	all	bulk	V1	11154853	5278144	0.379238161	2558399	574710	0.008322	0	0.617505	
d4_ko3a.8 d4		3a/-	all	bulk	V1	6992799	3391695	0.418282018	1774518	447907	0.008958	0	0.594716	
d4_ko3a.9 d4		3a/-	all	bulk	V1	10895726	5491398	0.425671113	3091328	588041	0.007547	0	0.600536	
d4_ko3b.1 d4		3b/-	all	bulk	V1	49683480	29128837	0.262616654	9627580	4471595	0.008845	0	0.682881	
d4_ko3b.1 d4		3b/-	all	bulk	V2	76030370	32504246	0.9735561	29724484	13960238	0.008479	0	0.732143	
d4_ko3b.1 d4		3b/-	all	bulk	V2	36657300	20253219	0.148015405	3897299	785434	0.007939	0	0.666701	
d4_ko3b.1 d4		3b/-	all	bulk	V2	24587992	13300317	0.158953739	2689429	630494	0.008797	0	0.670574	
d4_ko3b.2 d4		3b/-	all	wgbs	21943385	7986924	0.980447446	11096719	7991183	0.008527	0	0.717972		
d4_ko3b.3 d4		3b/-	all	wgbs	24645792	7799017	0.9810215	10712740	7759903	0.008586	0	0.714696		
d4_ko3b.4 d4		3b/-	all	wgbs	46232554	12810162	0.978099132	17720797	10724239	0.008583	0	0.719613		
d4_ko3b.5 d4		3b/-	all	wgbs	40930250	12662239	0.979436183	17769594	10669170	0.008558	0	0.716178		
d4_ko3b.6 d4		3b/-	all	bulk	V1	9929208	5109596	0.323688002	2240255	539091	0.007227	0	0.617132	
d4_ko3b.7 d4		3b/-	all	bulk	V1	8658297	4261411	0.364726318	2044183	521610	0.007729	0	0.616941	
d4_ko3b.8 d4		3b/-	all	bulk	V1	11894515	5790180	0.392633377	2952428	581713	0.007953	0	0.620817	
d4_ko3b.9 d4		3b/-	all	bulk	V1	10748724	5334975	0.423328772	2962452	560907	0.007682	0	0.617522	
d4_tko.1 d4		TKO	all	bulk	V1	58754335	33369550	0.249282294	10339428	4562750	0.005264	0	0.006597	
d4_wt.1 d4		wt	all	bulk	V1	64030422	37804543	0.289807445	13586062	5557108	0.011828	0	0.733854	
d4_wt.2 d4		wt	all	bulk	V1	9392898	4731076	0.418057734	2610512	553536	0.010567	0	0.681572	
d4_wt.3 d4		wt	all	bulk	V1	9121688	4628668	0.424177803	2577071	544096	0.011034	0	0.674627	
d4_wt.4 d4		wt	all	bulk	V1	12757039	6158809	0.393825187	3154000	623919	0.010699	0	0.675906	

d4_wt.5	d4	wt	all	bulk	V1	12895577	6252616	0.36821361	3022594	632282	0.01038	0	0.67025
d4_wt.6	d4	wt	all	bulk	V2	114231256	43643736	0.971904122	36478357	15310885	0.014256	0	0.783914
d4_wt.7	d4	wt	all	bulk	V2	29259554	15399007	0.138377277	2570665	644847	0.013468	0	0.724819
d4_wt.8	d4	wt	all	bulk	V2	20331027	11433829	0.195640728	2928314	570450	0.011651	0	0.720874
d5_3a/-s d5	3a/-	CXCR4-EPC	sc	372 wgb	105082.1962	35939.38172	0.740470148	47021.40054	47021.40054	0.007564	0	0.666747	
d5_3a/-s d5	3a/-	CXCR4+EP	sc	372 wgb	80943.01075	25167.36828	0.745400248	33470.5457	33470.5457	0.007128	0	0.685997	
d5_3a/-s d5	3a/-	index	sc	371 wgb	76818.56065	19917.07278	0.593381764	35716.469	35716.469	0.009549	0	0.565449	
d5_3a/-s d5	3a/-	index	sc	370 wgb	73161.71892	24034.0027	0.580993552	44710.15135	44710.15135	0.00968	0	0.570033	
d5_3a/-s d5	3a/-	index	sc	371 wgb	73360.46092	24937.50135	0.613905586	46440.00809	46440.00809	0.008971	0	0.584953	
d5_3a/-s d5	3a/-	index	sc	371 wgb	117221.0566	32876.48248	0.541263447	52741.09704	52741.09704	0.008032	0	0.553246	
d5_3a/-s d5	3a/-	index	sc	368 wgb	104836.1549	27783.72826	0.704512916	55626.38587	55626.38587	0.008269	0	0.577755	
d5_3b/-s d5	3b/-	CXCR4-EPC	sc	372 wgb	151182.836	40185.05108	0.862207293	65598.88172	65598.88172	0.006511	0	0.628962	
d5_3b/-s d5	3b/-	CXCR4+EP	sc	372 wgb	144265.9274	39302.56183	0.85339692	62759.13441	62759.13441	0.006214	0	0.636219	
d5_3b/-s d5	3b/-	index	sc	363 wgb	71838.13499	20723.73003	0.565299452	35893.41047	35893.41047	0.007985	0	0.602234	
d5_3b/-s d5	3b/-	index	sc	366 wgb	68903.97268	21885.17213	0.57081222	37111.07377	37111.07377	0.007334	0	0.606533	
d5_3b/-s d5	3b/-	index	sc	369 wgb	56023.8103	17969.94309	0.656712669	35956.73442	35956.73442	0.007619	0	0.570588	
d5_3b/-s d5	3b/-	index	sc	371 wgb	110005.1267	30782.26685	0.574776126	50041.70081	50041.70081	0.007123	0	0.549802	
d5_3b/-s d5	3b/-	index	sc	368 wgb	113129.7527	25881.25815	0.701703942	51500.04348	51500.04348	0.007106	0	0.545074	
d5_ko3a.1 d5	3a/-	CXCR4-EPC	bulk	wgb	125494983	29889618	0.966956169	49116013	16382400	0.007088	0	0.765655	
d5_ko3a.2 d5	3a/-	CXCR4+EP	bulk	wgb	60167802	15109902	0.974205132	24885143	12877415	0.006809	0	0.782228	
d5_ko3b.1 d5	3b/-	CXCR4-EPC	bulk	wgb	111904419	30839888	0.958413574	51863716	16506566	0.006869	0	0.739379	
d5_ko3b.2 d5	3b/-	CXCR4+EP	bulk	wgb	73597579	17876561	0.972046796	28905989	13880622	0.00548	0	0.742008	
d5_wt.1	d5	wt	CXCR4-EPC	bulk	wgb	103290764	24839177	0.965538989	40379966	15547754	0.00943	0	0.78948
d5_wt.2	d5	wt	CXCR4+EP	bulk	wgb	92809983	23029247	0.970089014	38559262	15332107	0.008125	0	0.810561
d5_wt.sc1 d5	wt	CXCR4-EPC	sc	371 wgb	184386.6092	64262	0.735573108	38555.9407	38555.9407	0.010191	0	0.680582	
d5_wt.sc2 d5	wt	CXCR4+EP	sc	372 wgb	189895.9543	72632.51075	0.770254189	44311.43548	44311.43548	0.008811	0	0.707005	
d5_wt.sc3 d5	wt	index	sc	366 wgb	198620.9372	75732.0082	0.769614635	60317.61749	60317.61749	0.011738	0	0.680812	
d5_wt.sc4 d5	wt	index	sc	351 wgb	218609.6296	82515.17664	0.741034824	61281.82051	61281.82051	0.012774	0	0.677405	
d5_wt.sc5 d5	wt	index	sc	372 wgb	133310.6478	33810.60753	0.633333685	51426.57527	51426.57527	0.010411	0	0.652474	
d5_wt.sc6 d5	wt	index	sc	370 wgb	211184.1324	20874.98378	0.738736704	39328.33784	39328.33784	0.010268	0	0.635853	
d5_wt.sc7 d5	wt	index	sc	372 wgb	103745.4274	33962.3871	0.451884026	46888.65323	46888.65323	0.009845	0	0.586369	
d5_wt.sc8 d5	wt	index	sc	367 wgb	87842.46866	24287.56676	0.548411044	39752.62125	39752.62125	0.009805	0	0.559672	
d5_wt.sc9 d5	wt	index	sc	369 wgb	118782.2547	34057.70461	0.488784496	47975.53117	47975.53117	0.010627	0	0.577058	
d6_ko3a.1 d6	3a/-	CXCR4-EPC	bulk	wgb	307411435	89459193	0.660681788	60780957	17027124	0.010067	0	0.794078	
d6_ko3a.2 d6	3a/-	CXCR4+EP	bulk	wgb	357190645	98436944	0.682960688	69634370	17296564	0.009159	0	0.789478	
d6_ko3a.3 d6	3a/-	CXCR4+EP	bulk	wgb	291344326	88580527	0.603873378	52496533	16474691	0.009699	0	0.80026	
d6_ko3b.1 d6	3b/-	CXCR4-EPC	bulk	wgb	294794755	70851508	0.789468245	57820566	16823166	0.008654	0	0.760273	
d6_ko3b.2 d6	3b/-	CXCR4+EP	bulk	wgb	261147603	67482241	0.785092683	52512458	16535000	0.00831	0	0.759762	
d6_ko3b.3 d6	3b/-	CXCR4+EP	bulk	wgb	378992859	86081350	0.812019707	74050421	17648662	0.008374	0	0.767791	
d6_wt.1	d6	wt	all	bulk	wgb	535523818	226131463	0.905908337	196652860	19369566	0.009305	0	0.817477
d6_wt.2	d6	wt	all	bulk	wgb	478207590	196628333	0.915235871	163622109	19344893	0.007723	0	0.770951
d6_wt.3	d6	wt	all	bulk	wgb	225347462	97985012	0.888021563	82826353	18387276	0.01574	0	0.791038
d6_wt.4	d6	wt	CXCR4-EPC	bulk	wgb	278332659	80273913	0.77609321	64604077	17207446	0.010812	0	0.797702
d6_wt.5	d6	wt	CXCR4+EP	bulk	wgb	370284156	99532106	0.682618104	75585621	17342788	0.009678	0	0.824798
d6_wt.6	d6	wt	CXCR4+EP	bulk	wgb	348341325	99868758	0.762153056	80105329	17928427	0.011994	0	0.830198
e7.5_mou e7.5	mouse	index	sc	354 wgb	382822.1102	129440.5311	0.714706203	105854.8785	105854.8785	0.00845	0	0.708526	
e7.5_mou e7.5	mouse	index	sc	370 wgb	214182.5135	90508.77297	0.799468642	78781.1	78781.1	0.008025	0	0.689058	
e7.5_mou e7.5	mouse	index	sc	370 wgb	269061.5432	112276.3622	0.863203979	65791.20811	65791.20811	0.007737	0	0.681305	
e7.5_mou e7.5	mouse	index	sc	369 wgb	405697.3117	178653.897	0.682608235	89338.07046	89338.07046	0.007691	0	0.668365	
e7.5_mou e7.5	mouse	index	sc	369 wgb	340035.7236	151555.607	0.766286667	103908.1626	103908.1626	0.007813	0	0.682579	
e7.5_mou e7.5	mouse	index	sc	372 wgb	48051.90323	6889.048387	0.90822526	17403.65054	17403.65054	0.008189	0	0.609306	
e7.5_mou e7.5	mouse	index	sc	372 wgb	54237.14247	4934.094086	0.89791782	14544.46774	14544.46774	0.007143	0	0.559021	
e7.5_mou e7.5	mouse	index	sc	368 wgb	61959.73913	4298.331522	0.904015029	12751.77174	12751.77174	0.007648	0	0.565555	
e7.5_mou e7.5	mouse	index	sc	369 wgb	44278.27371	8957.831978	0.859066609	25058.97561	25058.97561	0.008251	0	0.572781	

**Table S3: DNMT3A\_DMRs. Regions with preference for DNMT3A**

chrom	start	end	ko3a	ko3a.cov	ko3b	ko3b.cov	wt	wt.cov	ab_score
chr1	12856026	12856579	0.530769	130	0.734694	98	0.788889	450	-0.43328
chr1	12982972	12983473	0.291667	408	0.30083	482	0.411179	1306	-0.48454
chr1	13117514	13118055	0.288079	302	0.396166	313	0.42069	1160	-0.40925
chr1	13350890	13351391	0.729167	96	0.915094	106	0.895442	373	-0.54607
chr1	13524846	13525376	0.764228	246	0.939252	214	0.887484	791	-0.50096
chr1	14495784	14496427	0.204698	298	0.35625	320	0.346847	888	-0.42626
chr1	14497465	14498563	0.382979	282	0.615599	359	0.684114	1089	-0.44538
chr1	14907781	14908427	0.550725	138	0.734513	113	0.779545	440	-0.33553
chr1	21042568	21043129	0.771784	241	0.916318	239	0.927711	664	-0.6414
chr1	21070030	21070537	0.423077	182	0.561321	212	0.689956	687	-0.37967
chr1	23308754	23309379	0.366337	101	0.538462	169	0.534574	376	-0.33811
chr1	23917260	23917761	0.703704	108	0.914894	94	0.884498	329	-0.5774
chr1	23941254	23941755	0.791045	201	0.781609	174	0.882789	674	-0.44071
chr1	32288072	32288597	0.644737	76	0.880734	109	0.822981	322	-0.51121
chr1	33771028	33771791	0.436975	119	0.587838	148	0.7041	561	-0.28798
chr1	33949620	33950329	0.492462	199	0.628415	183	0.70091	769	-0.59222
chr1	34165321	34165845	0.528846	104	0.712	125	0.634921	504	-0.54297
chr1	34696274	34696775	0.746293	1214	0.884116	1001	0.905618	1780	-0.72203
chr1	34909387	34909888	0.737226	548	0.851759	398	0.881851	821	-0.45415
chr1	36322197	36322698	0.769231	91	0.925532	94	0.888889	297	-0.64557
chr1	38677249	38677758	0.551402	107	0.848684	152	0.770115	435	-0.28748
chr1	39705971	39706573	0.649682	157	0.657895	152	0.775439	570	-0.2955
chr1	39942097	39942614	0.627551	196	0.652941	170	0.75	528	-0.72131
chr1	43959678	43960381	0.590164	61	0.909091	55	0.860577	208	-0.68777
chr1	45559543	45560316	0.340206	194	0.625668	187	0.723785	782	-0.34604
chr1	45981409	45981910	0.591837	98	0.675676	111	0.760291	413	-0.12579
chr1	52655173	52655674	0.636364	165	0.741758	182	0.862709	539	-0.4403
chr1	58087612	58088113	0.481675	191	0.502618	191	0.663029	733	-0.46551
chr1	59373075	59373626	0.391892	148	0.629139	151	0.711002	609	-0.46308
chr1	59474505	59475006	0.52809	89	0.758621	87	0.665517	290	-0.37718
chr1	59532278	59532779	0.571429	56	0.758621	58	0.760417	192	-0.50216
chr1	59648341	59649118	0.53012	249	0.605263	266	0.631922	921	-0.48507
chr1	59845731	59846430	0.632479	117	0.877193	171	0.888268	537	-0.58356
chr1	63228807	63229312	0.538462	117	0.778947	95	0.817143	350	-0.50307
chr1	67033989	67034636	0.655172	116	0.830409	171	0.793761	577	-0.45777
chr1	69734964	69735604	0.169014	355	0.235149	404	0.322759	725	-0.47235
chr1	72860668	72861169	0.348371	399	0.415282	301	0.549935	771	-0.66369
chr1	74827444	74827945	0.433735	83	0.631068	103	0.692708	384	-0.59605
chr1	74839437	74839938	0.466926	257	0.699346	306	0.698643	1032	-0.46825
chr1	74850596	74851097	0.433099	284	0.535714	308	0.605905	779	-0.49013
chr1	75357544	75358045	0.234491	806	0.209977	862	0.349112	2873	-0.43813
chr1	75395661	75396179	0.195313	128	0.409836	122	0.439926	541	-0.36896
chr1	75454112	75454613	0.144	250	0.434375	320	0.507549	861	-0.46822

chr1	75455885	75456386	0.417969	256	0.543544	333	0.627263	939	-0.29908
chr1	75464776	75465277	0.543956	182	0.653465	202	0.702791	609	-0.56765
chr1	75503340	75503841	0.530945	307	0.714715	333	0.644252	922	-0.71264
chr1	78195440	78196539	0.468665	367	0.5925	400	0.629223	1184	-0.32699
chr1	78206748	78207516	0.549729	553	0.773305	472	0.782752	1519	-0.33703
chr1	87818415	87818916	0.800664	301	0.917098	193	0.915764	831	-0.65577
chr1	89079070	89079701	0.780749	187	0.790816	196	0.893617	611	-0.40873
chr1	89748789	89749290	0.516667	120	0.466019	103	0.766082	342	-0.41648
chr1	91084892	91085573	0.682692	104	0.842105	95	0.91573	356	-0.64815
chr1	91821494	91821995	0.57377	305	0.763819	199	0.806738	564	-0.52797
chr1	91837319	91837820	0.248254	1289	0.399727	733	0.411705	1982	-0.5611
chr1	91888104	91888605	0.4225	400	0.413534	266	0.577493	1013	-0.60565
chr1	92031036	92031537	0.635417	192	0.759398	133	0.839161	572	-0.48892
chr1	92486915	92487416	0.593985	133	0.686567	134	0.662736	424	-0.36202
chr1	1.21E+08	1.21E+08	0.705882	136	0.828767	146	0.759223	515	-0.51531
chr1	1.21E+08	1.21E+08	0.621849	119	0.84058	138	0.849188	431	-0.41129
chr1	1.21E+08	1.21E+08	0.455172	145	0.595745	141	0.588235	544	-0.59229
chr1	1.22E+08	1.22E+08	0.669355	124	0.71223	139	0.741667	480	-0.45752
chr1	1.22E+08	1.22E+08	0.256148	488	0.57109	422	0.472535	1511	-0.2511
chr1	1.22E+08	1.22E+08	0.301754	285	0.620209	287	0.645583	917	-0.25114
chr1	1.22E+08	1.22E+08	0.302885	416	0.522857	350	0.590531	1563	-0.27521
chr1	1.23E+08	1.23E+08	0.243292	559	0.391365	718	0.437332	1859	-0.28139
chr1	1.23E+08	1.23E+08	0.615	200	0.837438	203	0.875136	921	-0.3956
chr1	1.23E+08	1.23E+08	0.393617	188	0.481481	243	0.535475	747	-0.31028
chr1	1.27E+08	1.27E+08	0.351852	54	0.626667	75	0.664122	262	-0.45614
chr1	1.34E+08	1.34E+08	0.301158	259	0.506803	294	0.566279	860	-0.3841
chr1	1.34E+08	1.34E+08	0.660494	162	0.78125	160	0.801504	665	-0.61201
chr1	1.35E+08	1.35E+08	0.56213	169	0.662921	178	0.704374	663	-0.54609
chr1	1.35E+08	1.35E+08	0.574074	162	0.907801	141	0.876	500	-0.64122
chr1	1.35E+08	1.35E+08	0.51087	92	0.794643	112	0.71134	388	-0.50542
chr1	1.37E+08	1.37E+08	0.587879	165	0.759358	187	0.761035	657	-0.81204
chr1	1.39E+08	1.39E+08	0.373016	126	0.666667	129	0.713131	495	-0.60376
chr1	1.53E+08	1.53E+08	0.768116	138	0.905983	117	0.869478	498	-0.43049
chr1	1.54E+08	1.54E+08	0.567686	229	0.738462	195	0.713568	597	-0.3223
chr1	1.55E+08	1.55E+08	0.612717	173	0.627586	145	0.721724	557	-0.45524
chr1	1.55E+08	1.55E+08	0.541096	146	0.705882	136	0.783981	412	-0.44886
chr1	1.55E+08	1.55E+08	0.550847	236	0.7713	223	0.725728	824	-0.24543
chr1	1.57E+08	1.57E+08	0.212121	231	0.315068	219	0.353791	831	-0.55467
chr1	1.57E+08	1.57E+08	0.297561	205	0.531469	143	0.536661	641	-0.35377
chr1	1.61E+08	1.61E+08	0.681818	88	0.923077	143	0.907652	379	-0.5767
chr1	1.63E+08	1.63E+08	0.649485	194	0.919492	236	0.907879	825	-0.5378
chr1	1.65E+08	1.65E+08	0.346341	205	0.51087	184	0.540154	909	-0.6033
chr1	1.68E+08	1.68E+08	0.72449	98	0.890411	146	0.830287	383	-0.51444
chr1	1.68E+08	1.68E+08	0.593301	209	0.833333	204	0.845378	595	-0.68687
chr1	1.69E+08	1.69E+08	0.730871	379	0.745989	374	0.808173	881	-0.63088
chr1	1.7E+08	1.7E+08	0.37931	435	0.624041	391	0.673653	1002	-0.5324
chr1	1.7E+08	1.7E+08	0.757576	132	0.930818	159	0.922631	517	-0.44641

chr1	1.71E+08	1.71E+08	0.697531	162	0.850515	194	0.858144	571	-0.52868
chr1	1.73E+08	1.73E+08	0.695652	115	0.810811	148	0.863118	526	-0.50738
chr1	1.74E+08	1.74E+08	0.534031	191	0.697318	261	0.808664	831	-0.41013
chr1	1.78E+08	1.78E+08	0.3	230	0.40293	273	0.434682	865	-0.41573
chr1	1.83E+08	1.83E+08	0.577236	615	0.855956	361	0.858847	1006	-0.46231
chr1	1.83E+08	1.83E+08	0.792135	534	0.872958	551	0.879017	1058	-0.81299
chr1	1.83E+08	1.83E+08	0.857143	336	0.980159	252	0.927476	717	-0.85543
chr1	1.83E+08	1.83E+08	0.631746	315	0.803828	209	0.780715	643	-0.61617
chr1	1.84E+08	1.84E+08	0.45	120	0.746667	75	0.812834	187	-0.74941
chr1	1.87E+08	1.87E+08	0.416667	252	0.640167	239	0.730594	657	-0.79332
chr1	1.89E+08	1.89E+08	0.626984	126	0.811594	138	0.884259	432	-0.41647
chr1	1.92E+08	1.92E+08	0.466814	452	0.599532	427	0.697711	1267	-0.57204
chr10	6084403	6084904	0.739884	173	0.846154	143	0.880357	560	-0.28313
chr10	6402742	6403243	0.558824	102	0.614907	161	0.71831	497	-0.49828
chr10	8837427	8838140	0.542056	214	0.769608	204	0.875676	740	-0.56662
chr10	12294676	12295177	0.632653	147	0.865385	156	0.903226	496	-0.3581
chr10	12638675	12639176	0.463415	82	0.625	88	0.792683	328	-0.84867
chr10	12643297	12643978	0.569231	130	0.704348	115	0.748858	438	-0.60427
chr10	12716132	12716644	0.436019	211	0.71564	211	0.7408	625	-0.6665
chr10	18150090	18150591	0.644898	245	0.700893	224	0.788551	856	-0.66042
chr10	19075773	19076412	0.198444	257	0.387454	271	0.56286	867	-0.55421
chr10	19077445	19077946	0.209169	349	0.273775	347	0.347749	1133	-0.31952
chr10	20808835	20809746	0.73384	263	0.931373	204	0.878173	788	-0.41335
chr10	21213485	21214016	0.571429	210	0.675127	197	0.740597	771	-0.47122
chr10	21509139	21509640	0.709544	241	0.92278	259	0.888889	747	-0.58991
chr10	21611100	21611601	0.49505	101	0.654676	139	0.752759	453	-0.35481
chr10	24720530	24721326	0.598291	234	0.777385	283	0.87748	857	-0.52229
chr10	38892245	38892746	0.634146	205	0.71179	229	0.753281	762	-0.36303
chr10	40902066	40902676	0.497512	201	0.719101	267	0.790968	775	-0.41478
chr10	42660393	42660914	0.640625	320	0.837912	364	0.836412	1137	-0.51705
chr10	42661080	42661941	0.595833	240	0.823529	238	0.879059	893	-0.4749
chr10	43269858	43270359	0.75	176	0.885057	174	0.922601	646	-0.56863
chr10	43724786	43725494	0.161725	371	0.243553	349	0.28093	1463	-0.27468
chr10	50613179	50613924	0.160207	387	0.297468	474	0.286048	1713	-0.33891
chr10	59371656	59372157	0.4	185	0.463878	263	0.469649	939	-0.58286
chr10	59373755	59374353	0.148855	262	0.294521	292	0.34564	1273	-0.56176
chr10	59387273	59388002	0.505155	194	0.7343	207	0.686528	772	-0.45629
chr10	59419685	59420186	0.217532	308	0.298462	325	0.383162	1164	-0.66191
chr10	59578739	59579536	0.439306	173	0.683908	174	0.65088	739	-0.59309
chr10	59920560	59921234	0.576389	144	0.816456	158	0.831502	546	-0.52531
chr10	60294919	60295420	0.394089	203	0.550725	207	0.622423	776	-0.48891
chr10	60297105	60297669	0.509202	326	0.598886	359	0.643092	1216	-0.33544
chr10	60533511	60534012	0.54878	82	0.835294	85	0.842105	361	-0.71001
chr10	60675036	60675696	0.296943	229	0.390947	243	0.50904	719	-0.28443
chr10	60736540	60737141	0.175676	518	0.250929	538	0.246465	1485	-0.3078
chr10	60856940	60857441	0.165891	645	0.317172	495	0.367677	990	-0.60687
chr10	60867926	60868639	0.451737	259	0.538136	236	0.603896	770	-0.45722

chr10	61590727	61591387	0.445071	2658	0.667732	1878	0.708854	3919	-0.42869
chr10	61592174	61592890	0.279503	483	0.48556	554	0.584211	1520	-0.36986
chr10	61637172	61637681	0.890017	591	0.851786	560	0.897864	1077	-0.49482
chr10	61980609	61981110	0.76009	446	0.735897	390	0.861979	768	-0.87664
chr10	62364435	62364936	0.465278	144	0.66879	157	0.640426	470	-0.54377
chr10	66377826	66378795	0.743719	199	0.90625	224	0.900253	792	-0.34187
chr10	66590526	66591102	0.44086	279	0.51087	276	0.561366	937	-0.32179
chr10	72422539	72423040	0.57037	135	0.787037	108	0.876356	461	-0.67004
chr10	75489846	75490374	0.509202	163	0.547945	146	0.740219	639	-0.4503
chr10	76653345	76653877	0.457627	354	0.381579	304	0.62894	698	-0.67385
chr10	77031086	77031587	0.786207	725	0.874363	589	0.893953	1075	-0.67773
chr10	77145592	77146093	0.708609	151	0.891089	101	0.887246	541	-0.69496
chr10	77261035	77261536	0.677596	183	0.885135	148	0.878205	312	-0.79554
chr10	77324410	77325569	0.440476	252	0.781726	197	0.821494	549	-0.67326
chr10	77928051	77928552	0.212389	226	0.223629	237	0.334252	1089	-0.48999
chr10	79327273	79327774	0.818681	182	0.696203	237	0.842377	774	-0.8578
chr10	79512499	79513000	0.335766	137	0.434109	129	0.54811	582	-0.47284
chr10	79678781	79679282	0.592593	270	0.793578	218	0.880682	528	-0.52063
chr10	79961446	79961986	0.411531	503	0.575829	422	0.748052	770	-0.78525
chr10	80270678	80271434	0.413348	929	0.60689	1132	0.726529	2812	-0.38624
chr10	80389089	80389590	0.761261	444	0.806604	424	0.89651	831	-0.55896
chr10	80401446	80401961	0.359801	403	0.423469	392	0.571571	1006	-0.57624
chr10	80480536	80481037	0.41337	733	0.287695	577	0.551351	1110	-0.26686
chr10	82232276	82232777	0.447619	105	0.685393	89	0.652406	374	-0.37137
chr10	82271739	82272244	0.585185	135	0.687179	195	0.768224	535	-0.58376
chr10	84321408	84321909	0.460465	215	0.493671	237	0.594624	930	-0.3746
chr10	86245281	86246025	0.50495	101	0.777778	117	0.782418	455	-0.57794
chr10	93370344	93370845	0.525926	135	0.75	136	0.771127	568	-0.35044
chr10	95148308	95148809	0.427481	131	0.640719	167	0.632759	580	-0.42435
chr10	98748769	98749528	0.351648	364	0.377011	435	0.593819	1359	-0.42056
chr10	1.07E+08	1.07E+08	0.380734	218	0.590308	227	0.710905	972	-0.45474
chr10	1.08E+08	1.08E+08	0.333333	117	0.553398	103	0.696629	356	-0.2265
chr10	1.1E+08	1.1E+08	0.458498	253	0.635452	299	0.675241	933	-0.29382
chr10	1.11E+08	1.11E+08	0.555184	299	0.860465	344	0.896646	1103	-0.51383
chr10	1.14E+08	1.14E+08	0.72549	204	0.956522	184	0.915042	718	-0.59055
chr10	1.17E+08	1.17E+08	0.3125	128	0.457447	188	0.630178	676	-0.29726
chr10	1.22E+08	1.22E+08	0.72	100	0.867769	121	0.864368	435	-0.72503
chr10	1.25E+08	1.25E+08	0.268966	145	0.496599	147	0.563258	577	-0.4088
chr10	1.27E+08	1.27E+08	0.477064	218	0.5	222	0.727154	766	-0.47677
chr10	1.27E+08	1.27E+08	0.555957	277	0.59375	288	0.595078	894	-0.38152
chr10	1.27E+08	1.27E+08	0.239496	238	0.352584	329	0.434091	880	-0.54188
chr10	1.27E+08	1.27E+08	0.405286	227	0.407563	238	0.538547	895	-0.62984
chr10	1.27E+08	1.27E+08	0.275862	319	0.47861	374	0.529207	1147	-0.65149
chr10	1.28E+08	1.28E+08	0.228571	175	0.310185	216	0.434884	860	-0.53781
chr10	1.28E+08	1.28E+08	0.606667	150	0.724138	145	0.731219	599	-0.50341
chr10	1.28E+08	1.28E+08	0.170787	445	0.188442	398	0.336409	1192	-0.4973
chr11	4155963	4156789	0.739535	215	0.906542	214	0.915335	626	-0.54627

chr11	5639783	5640394	0.613445	119	0.737288	118	0.834499	429	-0.4019
chr11	5678079	5678580	0.728682	129	0.836957	92	0.873995	373	-0.57193
chr11	5713610	5714111	0.713483	178	0.787356	174	0.864502	893	-0.65545
chr11	11733309	11733871	0.540741	135	0.806931	202	0.845821	694	-0.45103
chr11	16156812	16157422	0.078534	382	0.147692	325	0.176976	1164	-0.56538
chr11	16651457	16651958	0.182648	219	0.30837	227	0.341463	820	-0.45759
chr11	18775889	18776393	0.157143	280	0.320755	265	0.331498	908	-0.5182
chr11	18915043	18915757	0.022133	497	0.103211	436	0.081081	1776	-0.34412
chr11	19835469	19836140	0.558824	102	0.854701	117	0.838542	384	-0.33615
chr11	22845666	22846169	0.736111	144	0.917197	157	0.857595	632	-0.52298
chr11	32604367	32604928	0.641304	92	0.858407	113	0.799511	409	-0.61717
chr11	33607167	33607703	0.447368	114	0.633588	131	0.720174	461	-0.80417
chr11	34212400	34212984	0.734807	181	0.877193	171	0.867925	636	-0.53391
chr11	35791849	35792350	0.483221	149	0.693252	163	0.791916	668	-0.41093
chr11	44425462	44426440	0.120939	554	0.346801	594	0.387835	2055	-0.36577
chr11	44434361	44435285	0.119534	343	0.377672	421	0.390386	1373	-0.32157
chr11	44445172	44445673	0.625	128	0.693252	163	0.754601	489	-0.55205
chr11	44514626	44515127	0.676692	133	0.834483	145	0.785199	554	-0.18904
chr11	47193032	47193533	0.434211	228	0.455026	189	0.661891	698	-0.34281
chr11	48587661	48588192	0.428571	189	0.539474	152	0.597716	788	-0.52276
chr11	51493305	51493806	0.737179	156	0.880597	134	0.928322	572	-0.57691
chr11	51815618	51816119	0.505495	182	0.669421	121	0.714579	487	-0.41832
chr11	52113755	52114297	0.633508	191	0.753846	195	0.82825	623	-0.39968
chr11	52183612	52184146	0.481818	110	0.674603	126	0.737569	362	-0.54303
chr11	52348769	52349286	0.742515	167	0.906367	267	0.874659	734	-0.51757
chr11	53558046	53558620	0.653061	98	0.810526	95	0.839437	355	-0.51592
chr11	55384201	55384747	0.455556	90	0.54878	82	0.59824	341	-0.25956
chr11	57601917	57602490	0.526316	76	0.753086	81	0.8	275	-0.3937
chr11	57774168	57774669	0.59	200	0.803681	163	0.770492	732	-0.28512
chr11	57829649	57830150	0.488798	491	0.572165	388	0.735577	832	-0.29138
chr11	57832181	57832694	0.450382	262	0.75	140	0.739011	364	-0.72916
chr11	57834550	57835051	0.554455	202	0.523585	212	0.776995	426	-0.62375
chr11	57846903	57847590	0.523179	151	0.797297	148	0.68231	277	-0.59678
chr11	57888327	57888868	0.777778	126	0.927007	137	0.907579	541	-0.56741
chr11	58615664	58616165	0.316239	117	0.528736	87	0.545455	396	-0.573
chr11	60235854	60236355	0.455882	68	0.545455	77	0.718045	266	-0.83054
chr11	60817590	60818091	0.534483	116	0.78	100	0.701099	455	-0.72385
chr11	61429683	61430224	0.554286	175	0.572917	192	0.765458	938	-0.26363
chr11	62734703	62735204	0.273273	333	0.35443	316	0.508333	960	-0.56032
chr11	66719693	66720253	0.288462	312	0.483444	302	0.419574	1175	-0.59955
chr11	67739748	67740249	0.319444	144	0.469388	147	0.418312	557	-0.46499
chr11	68724617	68725118	0.674419	172	0.825472	212	0.877637	711	-0.47565
chr11	68878018	68878677	0.352459	122	0.573913	115	0.639566	369	-0.38072
chr11	69035192	69035693	0.676923	195	0.872093	172	0.884977	426	-0.84092
chr11	69185327	69185828	0.653299	773	0.803432	641	0.862105	1929	-0.61008
chr11	69241597	69242116	0.564417	163	0.634328	134	0.752161	347	-0.29039
chr11	69422901	69423420	0.496599	147	0.706294	143	0.741201	483	-0.67432

chr11	69522628	69523129	0.233898	295	0.372294	231	0.516807	476	-0.55227
chr11	75106081	75106602	0.72973	259	0.873016	189	0.907029	882	-0.55631
chr11	75286771	75287523	0.551181	127	0.832168	143	0.851923	520	-0.47779
chr11	77604918	77605545	0.423077	208	0.543478	184	0.659062	789	-0.6968
chr11	78009379	78009880	0.690141	142	0.852941	102	0.864286	420	-0.48473
chr11	78640604	78641136	0.232558	258	0.281106	217	0.351889	1006	-0.51046
chr11	78790453	78791114	0.525316	158	0.775194	129	0.777365	539	-0.3963
chr11	81401828	81402329	0.431373	357	0.565079	315	0.616406	1280	-0.27706
chr11	84454319	84454820	0.817073	164	0.935484	155	0.913793	464	-0.474
chr11	84973739	84974240	0.630952	84	0.851351	74	0.88015	267	-0.64443
chr11	85706098	85706618	0.610169	118	0.882883	111	0.861856	485	-0.35669
chr11	87394195	87394696	0.778443	167	0.872093	172	0.864697	643	-0.40818
chr11	89116143	89116680	0.761658	193	0.874372	199	0.819149	470	-0.43725
chr11	94594255	94594851	0.570213	235	0.590909	198	0.686493	807	-0.32733
chr11	94851390	94851891	0.086294	197	0.237288	177	0.260163	615	-0.43289
chr11	94947900	94948401	0.526882	93	0.773333	75	0.811594	276	-0.45493
chr11	95072510	95073011	0.633803	213	0.746835	158	0.81198	601	-0.68126
chr11	95085869	95086538	0.423611	288	0.680365	219	0.703466	779	-0.56574
chr11	95179539	95180040	0.784314	255	0.873096	197	0.907873	597	-0.66525
chr11	95193312	95193892	0.537313	67	0.810345	58	0.866667	270	-0.50145
chr11	95573219	95573903	0.102222	450	0.276316	304	0.278677	1421	-0.52971
chr11	95693296	95693985	0.468852	915	0.616695	587	0.706649	1534	-0.46354
chr11	95889617	95890118	0.616279	172	0.822857	175	0.840671	477	-0.40304
chr11	96033573	96034074	0.492537	201	0.596708	243	0.71547	724	-0.31787
chr11	96039774	96040447	0.435644	404	0.606684	389	0.707634	1310	-0.51899
chr11	96063254	96063805	0.269461	167	0.335443	158	0.442244	606	-0.27149
chr11	96066023	96066524	0.455882	136	0.589744	156	0.707581	554	-0.2005
chr11	96115261	96115826	0.26087	138	0.530172	232	0.655914	465	-0.41518
chr11	96122356	96122903	0.117155	478	0.211302	407	0.226097	1663	-0.42802
chr11	96130514	96131183	0.243451	649	0.437848	539	0.524494	1878	-0.43655
chr11	96148889	96149390	0.275862	174	0.365639	227	0.41033	697	-0.44777
chr11	96175607	96176108	0.358079	916	0.44994	829	0.53114	2280	-0.21275
chr11	96185207	96185708	0.233333	120	0.511364	88	0.487952	332	-0.4555
chr11	96209219	96210045	0.558824	238	0.807692	260	0.768335	859	-0.43824
chr11	96596720	96597221	0.140097	207	0.307292	192	0.388439	865	-0.37336
chr11	96722121	96722622	0.188144	388	0.340659	364	0.423623	1126	-0.3679
chr11	96847466	96847967	0.548077	104	0.792308	130	0.87957	465	-0.36081
chr11	96946531	96947032	0.774096	332	0.800562	356	0.842105	1007	-0.40729
chr11	96987348	96988049	0.579439	214	0.503817	262	0.658228	790	-0.54003
chr11	97284633	97285134	0.679104	268	0.857651	281	0.889023	829	-0.54229
chr11	97371653	97372154	0.724138	232	0.940541	185	0.896707	668	-0.63358
chr11	97658899	97660137	0.306757	740	0.570423	710	0.564918	1887	-0.40302
chr11	97848183	97848814	0.155496	373	0.15443	395	0.231975	1276	-0.35876
chr11	97917990	97918491	0.633803	213	0.760638	188	0.754829	673	-0.41884
chr11	98270862	98271363	0.405063	158	0.630769	130	0.567164	469	-0.29492
chr11	98606766	98607267	0.526316	285	0.560166	241	0.719665	478	-0.63271
chr11	98611655	98612156	0.676322	794	0.801196	669	0.900464	1507	-0.52583

chr11	98637562	98638079	0.310484	248	0.48374	246	0.571627	719	-0.40839
chr11	98643535	98644036	0.157082	1165	0.228113	811	0.321128	2021	-0.46845
chr11	98924242	98924743	0.517483	286	0.74	250	0.794355	744	-0.72814
chr11	99003648	99004149	0.557861	1253	0.788079	1057	0.869631	1979	-0.56024
chr11	1E+08	1E+08	0.640845	142	0.841727	139	0.839237	367	-0.61745
chr11	1E+08	1E+08	0.571782	404	0.455206	413	0.595876	1455	-0.591
chr11	1.01E+08	1.01E+08	0.648148	162	0.80315	127	0.9	360	-0.5003
chr11	1.01E+08	1.01E+08	0.607018	285	0.676724	232	0.800582	687	-0.37792
chr11	1.01E+08	1.01E+08	0.374233	163	0.46875	128	0.448718	624	-0.68269
chr11	1.02E+08	1.02E+08	0.604317	139	0.758065	124	0.793269	416	-0.38257
chr11	1.02E+08	1.02E+08	0.558719	281	0.702439	205	0.812349	826	-0.46903
chr11	1.02E+08	1.02E+08	0.814471	539	0.9163	454	0.92851	1161	-0.43695
chr11	1.02E+08	1.02E+08	0.373034	445	0.535627	407	0.659558	1313	-0.49987
chr11	1.02E+08	1.02E+08	0.494949	99	0.686047	172	0.773913	460	-0.44408
chr11	1.02E+08	1.02E+08	0.56338	284	0.626087	230	0.670702	826	-0.47067
chr11	1.03E+08	1.03E+08	0.701493	201	0.836364	220	0.840183	657	-0.60304
chr11	1.03E+08	1.03E+08	0.611979	384	0.73028	393	0.737759	1205	-0.48001
chr11	1.05E+08	1.05E+08	0.684615	130	0.810606	132	0.867273	550	-0.58937
chr11	1.05E+08	1.05E+08	0.54386	171	0.716667	180	0.788873	701	-0.64957
chr11	1.05E+08	1.05E+08	0.768595	242	0.803448	290	0.88111	757	-0.55774
chr11	1.07E+08	1.07E+08	0.264151	159	0.483871	217	0.587629	776	-0.56063
chr11	1.07E+08	1.07E+08	0.639535	86	0.851852	108	0.863128	358	-0.414
chr11	1.09E+08	1.09E+08	0.625	168	0.817708	192	0.854133	617	-0.58815
chr11	1.14E+08	1.14E+08	0.458647	133	0.551282	156	0.531092	595	-0.26513
chr11	1.14E+08	1.14E+08	0.626374	91	0.826087	92	0.871622	296	-0.59156
chr11	1.15E+08	1.15E+08	0.490358	363	0.549296	284	0.495868	847	-0.65284
chr11	1.16E+08	1.16E+08	0.521531	209	0.621053	190	0.715488	594	-0.52543
chr11	1.16E+08	1.16E+08	0.695291	1444	0.813131	1188	0.841379	2320	-0.43541
chr11	1.17E+08	1.17E+08	0.8	210	0.928177	181	0.892617	596	-0.56857
chr11	1.17E+08	1.17E+08	0.711149	592	0.722944	462	0.867514	1102	-0.61895
chr11	1.17E+08	1.17E+08	0.633452	281	0.798319	238	0.7414	843	-0.41552
chr11	1.17E+08	1.17E+08	0.334008	494	0.555804	448	0.714945	1084	-0.51348
chr11	1.17E+08	1.17E+08	0.315155	1907	0.470548	1460	0.529495	3543	-0.50288
chr11	1.17E+08	1.17E+08	0.583333	144	0.76875	160	0.738382	581	-0.46445
chr11	1.17E+08	1.17E+08	0.554585	687	0.722662	631	0.768595	1331	-0.49042
chr11	1.17E+08	1.17E+08	0.383495	206	0.455253	257	0.56015	798	-0.46155
chr11	1.17E+08	1.17E+08	0.682039	412	0.780405	296	0.837838	925	-0.53391
chr11	1.17E+08	1.17E+08	0.35376	359	0.475524	286	0.665888	856	-0.60581
chr11	1.17E+08	1.17E+08	0.620525	419	0.828125	384	0.805395	1038	-0.3337
chr11	1.18E+08	1.18E+08	0.619632	163	0.852071	169	0.857143	455	-0.63674
chr11	1.19E+08	1.19E+08	0.569482	367	0.788506	435	0.841837	1568	-0.42485
chr11	1.19E+08	1.19E+08	0.507109	211	0.672986	211	0.71777	574	-0.44516
chr11	1.21E+08	1.21E+08	0.727273	165	0.858108	148	0.863366	505	-0.66119
chr12	3548454	3549131	0.55814	129	0.810127	158	0.845471	563	-0.49286
chr12	4179165	4179679	0.64186	215	0.711538	208	0.74189	709	-0.60305
chr12	8527935	8528436	0.209877	81	0.482993	147	0.62037	432	-0.66457
chr12	12789334	12790062	0.544974	189	0.783654	208	0.74928	694	-0.30219

chr12	12828285	12828918	0.5625	240	0.696203	237	0.757062	885	-0.63731
chr12	12935314	12936281	0.553846	130	0.788321	137	0.861538	455	-0.37737
chr12	12937273	12937795	0.695313	128	0.903509	114	0.899029	515	-0.56041
chr12	15611072	15611639	0.653846	104	0.806122	98	0.713499	363	-0.4468
chr12	17054424	17054925	0.48	75	0.688312	77	0.653696	257	-0.21581
chr12	17699075	17699576	0.16	300	0.169675	277	0.238599	1228	-0.48828
chr12	25779079	25779859	0.243478	115	0.527638	199	0.65767	704	-0.37776
chr12	25781952	25783169	0.255365	466	0.501124	445	0.558317	1569	-0.36532
chr12	27766267	27766938	0.505495	182	0.634286	175	0.70991	555	-0.54594
chr12	30053717	30054218	0.649485	97	0.658915	129	0.75	348	-0.43723
chr12	50479032	50479533	0.412698	126	0.783333	120	0.664557	474	-0.64071
chr12	50491590	50492091	0.266187	278	0.316964	224	0.339825	1027	-0.32168
chr12	53802102	53802619	0.391566	166	0.506667	225	0.698856	787	-0.69323
chr12	55176736	55177243	0.492958	71	0.738095	84	0.678378	370	-0.15519
chr12	55646585	55647137	0.524138	145	0.621739	230	0.691574	629	-0.33345
chr12	57711911	57712598	0.253289	304	0.335244	349	0.364865	1184	-0.30073
chr12	57819184	57819873	0.387097	124	0.552	125	0.636364	594	-0.39724
chr12	70543152	70543653	0.689655	87	0.890756	119	0.744382	356	-0.47779
chr12	72212659	72213160	0.193772	289	0.22561	328	0.393258	1068	-0.63185
chr12	73870734	73871235	0.575	80	0.883333	60	0.848101	237	-0.75527
chr12	73935112	73935613	0.573944	284	0.646226	212	0.742754	552	-0.39363
chr12	74038715	74039359	0.378947	285	0.597345	226	0.668357	986	-0.31833
chr12	74041613	74042137	0.203279	305	0.355685	343	0.397914	1342	-0.2585
chr12	76410015	76410516	0.301994	351	0.309091	495	0.474453	1370	-0.41499
chr12	77631514	77632123	0.412214	131	0.591195	159	0.659044	481	-0.52987
chr12	77941817	77942318	0.73384	263	0.66065	277	0.764973	1102	-0.60872
chr12	78298443	78298944	0.557522	113	0.73494	83	0.818824	425	-0.39124
chr12	81319171	81319672	0.670455	88	0.825581	86	0.79	400	-0.51251
chr12	85745523	85746054	0.5	80	0.723684	76	0.8125	320	-0.49145
chr12	86703357	86703858	0.689655	87	0.892473	93	0.848739	357	-0.42403
chr12	86785505	86786006	0.346386	664	0.556714	767	0.70566	1325	-0.61272
chr12	86880796	86881328	0.664384	438	0.59306	317	0.79952	833	-0.43185
chr12	86886150	86886651	0.817204	279	0.917323	254	0.875	544	-0.48206
chr12	88109089	88109830	0.285714	168	0.53	200	0.513846	975	-0.30545
chr12	88112325	88112826	0.402913	206	0.443478	230	0.603912	818	-0.63872
chr12	88145132	88145633	0.451429	175	0.676329	207	0.75	596	-0.56669
chr12	88173293	88173915	0.469274	358	0.638462	390	0.706748	1630	-0.34876
chr12	88282465	88282966	0.517857	112	0.689076	119	0.751121	446	-0.38465
chr12	88318172	88319055	0.504425	339	0.723558	416	0.785485	1557	-0.41415
chr12	88750211	88750819	0.722581	155	0.88764	178	0.880192	626	-0.42021
chr12	1.05E+08	1.05E+08	0.333333	183	0.51	200	0.529655	725	-0.51685
chr12	1.06E+08	1.06E+08	0.405292	718	0.58714	591	0.733165	1188	-0.43245
chr12	1.07E+08	1.07E+08	0.364341	129	0.443478	115	0.49577	591	-0.49904
chr12	1.08E+08	1.08E+08	0.442308	260	0.511962	209	0.566486	925	-0.44643
chr12	1.12E+08	1.12E+08	0.322957	771	0.544753	648	0.58209	1474	-0.61313
chr12	1.12E+08	1.12E+08	0.596639	238	0.650538	186	0.697586	787	-0.62421
chr12	1.13E+08	1.13E+08	0.819005	221	0.883408	223	0.913771	777	-0.56271

chr12	1.13E+08	1.13E+08	0.46473	241	0.667954	259	0.612305	1024	-0.61658
chr12	1.14E+08	1.14E+08	0.538012	171	0.683168	202	0.777038	601	-0.6564
chr12	1.2E+08	1.2E+08	0.380597	268	0.595092	326	0.697479	952	-0.28266
chr13	5823437	5823938	0.674419	129	0.792593	135	0.821826	449	-0.52728
chr13	12451888	12452389	0.572727	110	0.68	100	0.666667	402	-0.70574
chr13	15111652	15112210	0.734375	192	0.923977	171	0.871547	724	-0.37872
chr13	18224658	18225177	0.720588	68	0.8875	80	0.854671	289	-0.38654
chr13	22020866	22021394	0.084034	119	0.245614	114	0.232416	327	-0.37548
chr13	23400157	23400736	0.458716	109	0.538462	169	0.546642	536	-0.17152
chr13	24084795	24085468	0.426667	75	0.797872	94	0.797571	247	-0.62495
chr13	28866407	28867174	0.309091	165	0.530201	149	0.707361	557	-0.52222
chr13	28873932	28874497	0.32967	364	0.509235	379	0.637363	819	-0.44897
chr13	28979248	28979778	0.187611	565	0.210016	619	0.352041	1372	-0.35271
chr13	31720269	31720883	0.139073	302	0.252778	360	0.287459	1228	-0.19605
chr13	34026392	34026997	0.537313	67	0.898305	59	0.828	250	-0.56994
chr13	34742130	34742818	0.47931	290	0.72	200	0.779564	871	-0.57236
chr13	36821598	36822493	0.510204	294	0.73747	419	0.666147	1282	-0.36035
chr13	36822545	36823218	0.329377	337	0.536341	399	0.538462	1274	-0.22185
chr13	37640494	37640995	0.736264	91	0.838384	99	0.853234	402	-0.51526
chr13	40802221	40802731	0.286822	129	0.440559	143	0.42029	483	-0.43073
chr13	40806411	40806912	0.238095	63	0.658228	79	0.632716	324	-0.36758
chr13	40834755	40835256	0.513514	370	0.740113	354	0.756168	1378	-0.17147
chr13	43277391	43278058	0.537445	227	0.696035	227	0.715818	746	-0.35577
chr13	43294493	43294994	0.593333	150	0.739645	169	0.800296	676	-0.62112
chr13	44659721	44660222	0.454148	229	0.666667	231	0.674497	894	-0.34879
chr13	44863461	44863962	0.669725	109	0.873786	103	0.888218	331	-0.652
chr13	51663127	51663950	0.089939	656	0.216942	484	0.222542	2431	-0.38236
chr13	52070486	52071259	0.577982	218	0.787356	174	0.796221	741	-0.45805
chr13	53379544	53380045	0.095238	273	0.207317	164	0.192982	855	-0.45201
chr13	53755092	53755777	0.787671	146	0.925373	134	0.889764	635	-0.50706
chr13	54210582	54211155	0.71134	194	0.913265	196	0.893333	675	-0.5473
chr13	55595509	55596040	0.273469	490	0.402685	298	0.478981	785	-0.76732
chr13	56357787	56358288	0.604878	205	0.616162	198	0.755844	770	-0.47757
chr13	58571531	58572060	0.417391	230	0.605128	195	0.663252	781	-0.49298
chr13	63133460	63133961	0.744444	90	0.890244	82	0.91	300	-0.60531
chr13	63252539	63253054	0.684211	152	0.789474	114	0.747475	495	-0.53576
chr13	63290957	63291657	0.576271	118	0.77907	86	0.816327	245	-0.52059
chr13	69620017	69620518	0.488889	180	0.582888	187	0.752809	801	-0.27813
chr13	70793598	70794166	0.712963	108	0.888889	108	0.808451	355	-0.09383
chr13	72095263	72096086	0.173993	546	0.374294	708	0.348645	1698	-0.28288
chr13	72774343	72774844	0.561224	294	0.575893	224	0.627826	575	-0.47773
chr13	73401557	73402454	0.393711	795	0.644752	867	0.676024	2636	-0.27003
chr13	78723712	78724213	0.720307	261	0.757322	239	0.856566	495	-0.56341
chr13	83859933	83860471	0.282895	456	0.418552	442	0.395742	1597	-0.33055
chr13	83861568	83862148	0.199005	201	0.300353	283	0.37666	1054	-0.29398
chr13	93252021	93252682	0.669492	118	0.913462	104	0.88	400	-0.69398
chr13	95056219	95056720	0.555556	180	0.820628	223	0.820064	628	-0.41329

chr13	95416595	95417125	0.607143	84	0.83	100	0.713568	398	-0.35667
chr13	95639508	95640802	0.345238	420	0.560229	523	0.649941	1694	-0.35696
chr13	95651355	95651856	0.544444	90	0.75641	78	0.751553	322	-0.46533
chr13	95654374	95655092	0.123188	414	0.28169	568	0.307339	1526	-0.38344
chr13	96318660	96319219	0.542308	260	0.592025	326	0.805755	973	-0.45906
chr13	96367865	96368707	0.599156	237	0.834746	236	0.853828	862	-0.30509
chr13	96780795	96781296	0.471264	87	0.642857	98	0.795745	470	-0.57736
chr13	98208157	98208733	0.369099	233	0.611111	180	0.736566	763	-0.42792
chr13	98211247	98211985	0.53125	128	0.857143	168	0.854545	605	-0.37393
chr13	99138216	99138717	0.442105	95	0.67619	105	0.755287	331	-0.57772
chr13	1E+08	1E+08	0.130137	292	0.338028	213	0.33843	981	-0.63366
chr13	1.02E+08	1.02E+08	0.6375	80	0.771429	70	0.812749	251	-0.61042
chr13	1.09E+08	1.09E+08	0.684211	95	0.947917	96	0.887255	408	-0.47018
chr13	1.1E+08	1.1E+08	0.62963	108	0.834711	121	0.757642	458	-0.49835
chr13	1.1E+08	1.1E+08	0.596639	238	0.669492	236	0.68272	706	-0.44639
chr13	1.15E+08	1.15E+08	0.578947	152	0.669291	127	0.728606	409	-0.48642
chr13	1.15E+08	1.15E+08	0.846535	404	0.902703	370	0.941822	911	-0.58352
chr13	1.17E+08	1.17E+08	0.139535	258	0.206557	305	0.292661	1131	-0.53011
chr13	1.17E+08	1.17E+08	0.649351	77	0.798319	119	0.808743	366	-0.26709
chr13	1.17E+08	1.18E+08	0.231818	220	0.466667	210	0.444934	908	-0.38805
chr13	1.18E+08	1.18E+08	0.632124	193	0.796813	251	0.833124	797	-0.40124
chr13	1.19E+08	1.19E+08	0.768657	134	0.921569	153	0.867232	354	-0.60838
chr14	11957750	11958251	0.560241	166	0.678082	146	0.874214	477	-0.56372
chr14	11993155	11993660	0.189394	132	0.398438	128	0.561024	508	-0.14774
chr14	12535612	12536354	0.465517	174	0.706468	201	0.616667	600	-0.4892
chr14	12596123	12596859	0.635802	162	0.8375	160	0.855721	603	-0.42346
chr14	13171831	13172558	0.258741	143	0.42953	149	0.529817	436	-0.43586
chr14	13174209	13175526	0.202899	897	0.453446	827	0.429441	2792	-0.32148
chr14	13183132	13183821	0.684588	279	0.875969	258	0.85641	780	-0.32985
chr14	20805270	20805863	0.430769	195	0.613333	225	0.707355	639	-0.59556
chr14	22812466	22813069	0.218182	165	0.351759	199	0.483713	614	-0.27611
chr14	26217072	26217573	0.335526	152	0.433498	203	0.570513	468	-0.60774
chr14	26404835	26405336	0.454301	372	0.586563	387	0.781359	1148	-0.61493
chr14	31702064	31702565	0.723881	134	0.767442	172	0.791667	576	-0.4708
chr14	35577940	35578453	0.75	176	0.835556	225	0.889717	671	-0.18916
chr14	41678114	41678615	0.609195	87	0.719512	82	0.652866	314	-0.67149
chr14	44694578	44695079	0.564356	101	0.650794	126	0.804009	449	-0.31783
chr14	49240603	49241143	0.614458	166	0.91716	169	0.92429	317	-0.64062
chr14	49272161	49272662	0.269006	342	0.304636	302	0.415991	863	-0.43081
chr14	49323602	49324103	0.656051	471	0.844612	399	0.833977	1036	-0.58119
chr14	49342827	49343328	0.663492	630	0.324903	514	0.733473	953	-0.28842
chr14	56380128	56380629	0.455587	349	0.521739	322	0.645191	1071	-0.45917
chr14	57919571	57920072	0.657143	140	0.785714	140	0.842536	489	-0.55275
chr14	58026738	58027239	0.511494	174	0.607383	298	0.628205	780	-0.37182
chr14	58161487	58161988	0.577428	762	0.351449	552	0.635969	2302	-0.40303
chr14	59694738	59695239	0.445274	402	0.705394	482	0.781737	1347	-0.46004
chr14	61704257	61704834	0.80791	177	0.87013	154	0.899648	568	-0.55987

chr14	62304327	62304842	0.083558	371	0.186916	428	0.2073	1452	-0.39054
chr14	63584465	63585066	0.42	200	0.614583	192	0.742049	849	-0.30412
chr14	63704372	63704975	0.527778	144	0.842697	89	0.873563	261	-0.67434
chr14	63858049	63858591	0.554054	148	0.659259	135	0.694789	403	-0.6704
chr14	63862530	63863075	0.186709	316	0.412214	262	0.486436	1069	-0.2484
chr14	63875512	63876013	0.522337	291	0.732456	228	0.826016	615	-0.49092
chr14	67255492	67256356	0.323484	643	0.372287	599	0.493075	2166	-0.46063
chr14	68668379	68668880	0.402174	184	0.554545	220	0.68256	797	-0.22102
chr14	75434692	75435207	0.56746	252	0.701493	201	0.781991	633	-0.63335
chr14	76647252	76647753	0.710692	159	0.868421	152	0.823713	641	-0.41256
chr14	76912925	76913426	0.448276	203	0.508876	169	0.559043	669	-0.34033
chr14	76998965	76999783	0.384615	156	0.633484	221	0.715026	579	-0.42328
chr14	77058321	77058834	0.626374	182	0.826271	236	0.827048	769	-0.60533
chr14	79675751	79676252	0.720588	204	0.780269	223	0.774799	746	-0.34622
chr14	79701714	79702215	0.156915	376	0.326471	340	0.320066	1206	-0.50456
chr14	99723802	99724424	0.639456	147	0.748201	139	0.740219	639	-0.3641
chr14	1.05E+08	1.05E+08	0.095588	272	0.145749	247	0.21618	754	-0.33724
chr14	1.06E+08	1.06E+08	0.144928	69	0.386667	75	0.299296	284	-0.58202
chr14	1.19E+08	1.19E+08	0.498039	255	0.632911	158	0.637155	689	-0.422
chr14	1.19E+08	1.19E+08	0.405405	148	0.341772	158	0.517321	433	-0.46594
chr14	1.22E+08	1.22E+08	0.533333	105	0.779817	109	0.787234	376	-0.42984
chr14	1.23E+08	1.23E+08	0.196203	158	0.426554	354	0.595745	658	-0.42814
chr14	1.23E+08	1.23E+08	0.048246	228	0.209677	186	0.271907	776	-0.20541
chr14	1.23E+08	1.23E+08	0.313084	214	0.611111	234	0.692994	785	-0.284
chr14	1.23E+08	1.23E+08	0.198312	474	0.432323	495	0.490218	1789	-0.38144
chr14	1.23E+08	1.23E+08	0.553571	112	0.617021	141	0.727459	488	-0.37259
chr15	6834264	6834824	0.666667	150	0.801205	166	0.813758	596	-0.37196
chr15	8051624	8052127	0.531579	190	0.71345	171	0.519527	845	-0.53658
chr15	28111282	28111846	0.448905	274	0.618868	265	0.721212	825	-0.23981
chr15	31240068	31240685	0.56962	79	0.735294	136	0.802041	490	-0.61035
chr15	35281964	35282465	0.338983	59	0.683333	60	0.673077	156	-0.70657
chr15	36741937	36742464	0.535	200	0.721649	194	0.74198	717	-0.48367
chr15	37719641	37720142	0.798246	114	0.990826	109	0.926282	312	-0.54636
chr15	37996394	37996895	0.591549	71	0.795699	93	0.754266	293	-0.66126
chr15	38127757	38128258	0.361702	188	0.512438	201	0.666193	704	-0.47694
chr15	38788723	38789224	0.698413	126	0.849057	159	0.848552	449	-0.1567
chr15	39945126	39945627	0.543307	127	0.656	125	0.773707	464	-0.43905
chr15	41622312	41622978	0.40566	106	0.603306	121	0.718954	459	-0.5205
chr15	48622729	48623230	0.440367	218	0.620087	229	0.698068	828	-0.46434
chr15	51634045	51634782	0.768519	108	0.893443	122	0.869023	481	-0.58695
chr15	54928984	54929766	0.597701	87	0.895833	96	0.86747	415	-0.40566
chr15	54974234	54974765	0.490741	108	0.788462	104	0.776081	393	-0.59908
chr15	57808233	57808734	0.242991	321	0.317343	271	0.412698	1134	-0.3205
chr15	58976993	58977626	0.537102	283	0.727554	323	0.812896	946	-0.49323
chr15	59035468	59036012	0.63245	302	0.72093	258	0.840438	821	-0.48978
chr15	61927614	61928115	0.606061	99	0.897959	147	0.771712	403	-0.56209
chr15	61949782	61950283	0.75	120	0.784483	116	0.81	500	-0.46697

chr15	66116539	66117040	0.145	200	0.340314	191	0.382309	667	-0.52978
chr15	75510242	75510792	0.673797	374	0.758065	434	0.809322	1416	-0.62842
chr15	75574031	75574733	0.653465	202	0.841026	195	0.869626	721	-0.69733
chr15	75708066	75708567	0.590909	66	0.852941	68	0.787072	263	-0.62777
chr15	76807069	76807570	0.643678	87	0.875	96	0.892019	426	-0.47431
chr15	76980052	76980553	0.65736	394	0.870091	331	0.872449	588	-0.41392
chr15	77186103	77186614	0.465909	88	0.811321	106	0.644377	329	-0.42652
chr15	77677399	77678019	0.643836	146	0.759398	133	0.79602	402	-0.72938
chr15	77734485	77734986	0.535519	183	0.691429	175	0.711201	741	-0.44076
chr15	78665491	78665992	0.472222	180	0.725	160	0.744722	521	-0.34068
chr15	78874020	78874683	0.316614	319	0.447853	326	0.356944	1440	-0.63094
chr15	79845526	79846223	0.301653	242	0.403042	263	0.451546	970	-0.52134
chr15	79893220	79893721	0.621495	214	0.771863	263	0.802083	864	-0.67057
chr15	79896472	79897180	0.322581	124	0.491803	122	0.528474	439	-0.62399
chr15	81879157	81879658	0.59375	64	0.8625	80	0.871287	303	-0.76263
chr15	82045620	82046121	0.647059	136	0.833333	156	0.836224	519	-0.41492
chr15	82759611	82760112	0.481481	162	0.606452	155	0.755319	564	-0.57222
chr15	83580259	83580897	0.527919	197	0.727273	275	0.824879	828	-0.40524
chr15	83898655	83899202	0.520737	217	0.594714	227	0.768953	831	-0.43669
chr15	96373849	96374368	0.222222	180	0.438596	171	0.529965	851	-0.29446
chr15	96956284	96956833	0.568306	183	0.681592	201	0.863184	804	-0.68757
chr15	97586513	97587030	0.768212	151	0.730496	141	0.877506	449	-0.83302
chr15	97633424	97633959	0.480769	208	0.541063	207	0.688047	686	-0.50339
chr15	97670169	97670729	0.608108	370	0.791506	259	0.795699	744	-0.64054
chr15	98010366	98010989	0.304659	279	0.402439	246	0.509317	805	-0.50619
chr15	98341512	98342052	0.53629	248	0.657061	347	0.820016	1239	-0.46531
chr15	98723152	98723816	0.55615	187	0.75	212	0.830346	837	-0.5022
chr15	98883294	98883881	0.384615	195	0.45509	167	0.559829	702	-0.65184
chr15	98884772	98885294	0.371429	70	0.677778	90	0.650655	458	-0.33472
chr15	98926182	98926825	0.197581	248	0.378378	185	0.43757	889	-0.48084
chr15	98957868	98958369	0.05	220	0.140449	178	0.116705	874	-0.18919
chr15	99119311	99119955	0.80531	113	0.915033	153	0.927798	554	-0.65731
chr15	99546980	99547481	0.714286	140	0.827869	122	0.854098	610	-0.24577
chr15	99723161	99723737	0.785276	163	0.827068	133	0.888889	531	-0.37862
chr15	1.01E+08	1.01E+08	0.633333	600	0.669643	448	0.801605	1371	-0.36816
chr15	1.01E+08	1.01E+08	0.446886	1092	0.673887	831	0.759018	1996	-0.30626
chr15	1.01E+08	1.01E+08	0.448052	462	0.666667	411	0.706655	1142	-0.31176
chr15	1.01E+08	1.01E+08	0.543046	151	0.623596	178	0.738562	612	-0.52403
chr15	1.01E+08	1.01E+08	0.261959	439	0.404432	361	0.486676	713	-0.59332
chr15	1.02E+08	1.02E+08	0.698864	176	0.931034	203	0.899083	763	-0.60855
chr15	1.02E+08	1.02E+08	0.50639	626	0.541485	458	0.643002	1479	-0.64794
chr15	1.02E+08	1.02E+08	0.326901	881	0.535144	626	0.61194	1608	-0.26425
chr15	1.02E+08	1.02E+08	0.629921	254	0.764977	217	0.800659	607	-0.68907
chr15	1.03E+08	1.03E+08	0.205825	515	0.261658	386	0.355505	1744	-0.41897
chr15	1.03E+08	1.03E+08	0.542169	332	0.81194	335	0.847791	1222	-0.37033
chr15	1.03E+08	1.03E+08	0.434673	398	0.584856	383	0.753721	1478	-0.492
chr15	1.03E+08	1.03E+08	0.360976	205	0.521053	190	0.610561	909	-0.35098

chr15	1.03E+08	1.03E+08	0.230769	221	0.215054	279	0.352539	1024	-0.47824
chr15	1.03E+08	1.03E+08	0.666667	102	0.861538	130	0.889493	552	-0.33596
chr15	1.03E+08	1.03E+08	0.580189	424	0.683871	465	0.770279	1541	-0.55345
chr15	1.03E+08	1.03E+08	0.330677	502	0.453571	560	0.636121	1877	-0.34958
chr16	8730612	8731113	0.528571	70	0.915254	59	0.813433	268	-0.59746
chr16	8734116	8734623	0.649635	137	0.860335	179	0.785714	504	-0.85848
chr16	10991696	10992197	0.357895	190	0.387283	173	0.531014	661	-0.47293
chr16	13753914	13754479	0.155313	367	0.263699	292	0.369838	1114	-0.60715
chr16	17051965	17052466	0.689531	277	0.825073	343	0.895695	1208	-0.45211
chr16	17074727	17075228	0.674242	132	0.90099	101	0.866397	494	-0.71576
chr16	17251435	17251936	0.589744	78	0.92	75	0.84	275	-0.60511
chr16	17252564	17253065	0.546667	150	0.708791	182	0.674617	587	-0.78896
chr16	17488756	17489257	0.462617	214	0.532407	216	0.65184	652	-0.47484
chr16	20443639	20444140	0.513699	146	0.668874	151	0.813913	575	-0.7314
chr16	21247363	21247988	0.210526	247	0.326446	242	0.375619	1009	-0.28235
chr16	21389492	21390189	0.533898	118	0.834711	121	0.812121	495	-0.31846
chr16	21984394	21984895	0.737288	236	0.834746	236	0.903005	732	-0.75141
chr16	28493068	28493569	0.737705	122	0.880952	126	0.868932	412	-0.53368
chr16	29681780	29682380	0.573964	338	0.657371	251	0.791196	886	-0.5853
chr16	29871544	29872045	0.677632	152	0.823529	136	0.871429	490	-0.79553
chr16	30511697	30512240	0.576744	215	0.690722	194	0.766942	605	-0.5884
chr16	31906390	31906891	0.511706	299	0.618297	317	0.715686	1020	-0.52602
chr16	32813884	32814500	0.431034	174	0.606557	183	0.69078	705	-0.54616
chr16	33336364	33336865	0.767442	129	0.929688	128	0.930314	574	-0.4877
chr16	35586843	35587592	0.487179	117	0.775	120	0.655319	470	-0.55184
chr16	36878862	36879432	0.776786	112	0.892086	139	0.913866	476	-0.45207
chr16	38110187	38110702	0.679537	259	0.909836	244	0.854286	700	-0.38308
chr16	38168783	38169571	0.66055	436	0.873754	301	0.882567	826	-0.72529
chr16	38342338	38342909	0.418033	122	0.528926	121	0.561587	479	-0.46957
chr16	38383707	38384428	0.851675	418	0.925414	362	0.914081	838	-0.70098
chr16	38741682	38742183	0.182203	472	0.203091	453	0.228818	1853	-0.24625
chr16	42444681	42445246	0.491525	118	0.570423	142	0.71068	515	-0.68069
chr16	45844901	45845438	0.169192	396	0.261589	302	0.26774	1367	-0.49842
chr16	50380146	50380647	0.724138	87	0.904255	94	0.871795	351	-0.45345
chr16	55823035	55823729	0.277344	256	0.5	290	0.666667	870	-0.41151
chr16	64873110	64873929	0.173599	553	0.400458	437	0.242806	1668	-0.32849
chr16	72687004	72687509	0.554054	74	0.681159	69	0.710963	301	-0.48682
chr16	78427322	78427823	0.646259	147	0.786517	178	0.866795	518	-0.48405
chr16	91228121	91228938	0.107004	514	0.267983	709	0.274038	2080	-0.39396
chr16	91908029	91908587	0.820513	273	0.787456	287	0.878218	1010	-0.26467
chr16	92610712	92611262	0.760684	234	0.909091	242	0.863061	869	-0.47624
chr16	95218179	95218680	0.567347	245	0.6	280	0.666667	915	-0.56895
chr17	5885763	5886277	0.728	125	0.795455	132	0.848592	568	-0.39604
chr17	7385486	7385987	0.730205	341	0.7375	320	0.832694	1303	-0.62977
chr17	8498409	8499137	0.412869	373	0.75493	355	0.802009	697	-0.74479
chr17	8590539	8591073	0.707792	154	0.946565	131	0.940774	439	-0.66799
chr17	8606478	8607414	0.321596	426	0.436585	410	0.56205	1112	-0.59706

chr17	8628175	8628676	0.385827	254	0.462633	281	0.444831	1151	-0.4942
chr17	9958007	9958508	0.260274	146	0.483333	180	0.607397	703	-0.53421
chr17	14304100	14304864	0.586777	121	0.850746	134	0.877551	490	-0.51935
chr17	15343728	15344375	0.51938	129	0.548611	144	0.587879	660	-0.36299
chr17	23675664	23676325	0.455882	204	0.619512	205	0.687793	852	-0.30964
chr17	24671961	24672501	0.672131	122	0.8	110	0.834016	488	-0.45877
chr17	24677475	24677983	0.613861	101	0.838384	99	0.815642	358	-0.57481
chr17	25958119	25958620	0.653846	104	0.834646	127	0.822115	416	-0.91377
chr17	26846296	26846833	0.790698	129	0.821053	190	0.86558	491	-0.77996
chr17	26973697	26974492	0.509615	312	0.765472	307	0.846154	1092	-0.29548
chr17	26977159	26977937	0.314587	569	0.436728	648	0.475334	1946	-0.1107
chr17	26978685	26979186	0.286385	213	0.328889	225	0.345044	797	-0.36512
chr17	27455680	27456181	0.754941	253	0.782772	267	0.856818	880	-0.49113
chr17	27738633	27739134	0.704663	193	0.845411	207	0.794479	652	-0.31473
chr17	27843417	27843944	0.729107	347	0.804945	364	0.866055	1090	-0.31761
chr17	28368402	28368903	0.617486	366	0.682353	340	0.78903	948	-0.43919
chr17	28692633	28693143	0.64	75	0.797753	89	0.882143	280	-0.56729
chr17	28936458	28936959	0.428571	147	0.448529	136	0.642599	554	-0.34404
chr17	28980614	28981115	0.75	96	0.894309	123	0.904192	334	-0.41169
chr17	29068401	29068902	0.67451	255	0.778523	298	0.889381	904	-0.5492
chr17	29160788	29161289	0.465347	303	0.601246	321	0.673358	1096	-0.45874
chr17	29216434	29216935	0.562724	279	0.768657	268	0.75374	869	-0.55006
chr17	29594914	29595492	0.623656	186	0.783133	166	0.842434	641	-0.38446
chr17	32249875	32250376	0.192308	312	0.306878	378	0.378698	1183	-0.45923
chr17	34340477	34340988	0.55914	186	0.718615	231	0.807074	622	-0.38623
chr17	34402447	34402948	0.377522	347	0.397403	385	0.560699	1145	-0.14365
chr17	34765478	34766088	0.247423	194	0.303318	211	0.403156	697	-0.52423
chr17	35213803	35214461	0.397661	171	0.614173	254	0.586926	719	-0.45992
chr17	35458219	35458739	0.374677	387	0.495671	462	0.549716	1408	-0.52172
chr17	35627288	35627970	0.508982	167	0.577143	175	0.688103	622	-0.45919
chr17	35671982	35672483	0.537736	106	0.730435	115	0.747059	340	-0.34612
chr17	35710381	35710882	0.594937	79	0.850467	107	0.872928	362	-0.33983
chr17	35847740	35848362	0.804781	251	0.825726	241	0.852229	785	-0.65855
chr17	43295502	43296013	0.607843	306	0.819923	261	0.825362	899	-0.43449
chr17	43705975	43706712	0.226667	150	0.391892	222	0.384892	556	-0.31952
chr17	44473573	44474326	0.669643	112	0.897638	127	0.893401	394	-0.74981
chr17	45906647	45907168	0.681818	110	0.864	125	0.870824	449	-0.70911
chr17	47565752	47566265	0.575163	153	0.630435	184	0.626623	616	-0.55466
chr17	47660688	47661197	0.683938	193	0.798701	154	0.824	750	-0.24697
chr17	48754671	48755172	0.550336	149	0.535948	153	0.681655	556	-0.45326
chr17	56441710	56442237	0.437198	414	0.613527	414	0.752466	1115	-0.41876
chr17	56802907	56803471	0.514774	643	0.546248	573	0.670366	1532	-0.69822
chr17	64426551	64427318	0.659091	88	0.948718	78	0.964968	314	-0.49896
chr17	66807582	66808083	0.631285	179	0.828221	163	0.781588	554	-0.29621
chr17	71129698	71130786	0.184874	238	0.486842	228	0.599428	699	-0.62614
chr17	71340687	71341188	0.326087	230	0.397059	204	0.478873	781	-0.60316
chr17	71835911	71836418	0.681034	116	0.780952	105	0.766667	450	-0.40614

chr17	73239270	73239984	0.735772	246	0.85283	265	0.741972	872	-0.26351
chr17	74671633	74672134	0.631399	293	0.701389	288	0.814601	1041	-0.55992
chr17	75853518	75854019	0.6	50	0.921569	51	0.856481	216	-0.35382
chr17	79020394	79020923	0.493151	73	0.72449	98	0.670951	389	-0.58968
chr17	79149894	79150742	0.46875	160	0.738255	149	0.748527	509	-0.71614
chr17	80462700	80463201	0.4375	128	0.587838	148	0.751634	765	-0.40027
chr17	80527580	80528115	0.322275	211	0.48	200	0.519767	860	-0.44052
chr17	83521942	83522443	0.63	300	0.739766	342	0.785217	1150	-0.27066
chr17	83613022	83613523	0.05	60	0.269231	104	0.243011	465	-0.28313
chr17	85864777	85865285	0.42487	193	0.477987	159	0.547847	836	-0.29324
chr17	85883500	85884001	0.597938	97	0.820313	128	0.826577	444	-0.49485
chr17	85888135	85888658	0.246154	195	0.414141	198	0.604054	740	-0.44278
chr17	86008526	86009260	0.098121	479	0.125523	478	0.1795	2000	-0.43123
chr17	88332288	88332789	0.587021	339	0.707641	301	0.776699	618	-0.69405
chr17	88669587	88670104	0.64	100	0.82	100	0.883168	505	-0.41292
chr18	7002716	7003270	0.155894	526	0.113903	597	0.184022	1815	-0.34529
chr18	9211304	9211828	0.091346	208	0.220974	267	0.205298	906	-0.51571
chr18	12661954	12662455	0.564286	140	0.808511	141	0.78972	428	-0.45008
chr18	15219434	15220183	0.322835	254	0.411215	214	0.472924	831	-0.3633
chr18	21118808	21119382	0.631841	201	0.697531	162	0.759202	652	-0.30373
chr18	24347390	24348076	0.666667	96	0.887755	98	0.893671	395	-0.3952
chr18	34261319	34261820	0.472973	148	0.666667	150	0.825316	395	-0.47984
chr18	34943587	34944143	0.534091	88	0.776786	112	0.77193	399	-0.60484
chr18	35904656	35905157	0.7	90	0.87069	116	0.84252	381	-0.5502
chr18	35992644	35993293	0.194872	195	0.428571	182	0.452888	658	-0.43957
chr18	35996890	35997391	0.635193	233	0.777778	288	0.761053	950	-0.38237
chr18	36009813	36010314	0.548387	217	0.626126	222	0.81715	793	-0.67195
chr18	36091716	36092217	0.6	90	0.780488	82	0.823671	414	-0.57374
chr18	38257561	38258262	0.360731	1095	0.586797	818	0.605939	1987	-0.54157
chr18	38332928	38333727	0.292056	428	0.405751	313	0.53348	911	-0.30457
chr18	38367369	38368144	0.543536	379	0.627551	392	0.740494	1052	-0.45429
chr18	38535621	38536122	0.736559	372	0.805825	309	0.805639	993	-0.55052
chr18	38731550	38732399	0.411202	732	0.683969	655	0.744695	1508	-0.44753
chr18	38808557	38809358	0.768657	268	0.868293	205	0.88642	810	-0.45443
chr18	43367826	43368327	0.489051	137	0.507463	134	0.660377	530	-0.25905
chr18	47524521	47525072	0.373333	75	0.719298	57	0.721519	237	-0.5353
chr18	60963307	60964024	0.483051	118	0.736842	133	0.80593	371	-0.54405
chr18	61133340	61133841	0.79932	294	0.913333	300	0.901667	600	-0.61533
chr18	61847892	61848421	0.7	150	0.932584	178	0.869403	536	-0.52426
chr18	61907821	61908322	0.772947	207	0.882155	297	0.886414	898	-0.56884
chr18	64174123	64174624	0.49	100	0.729167	96	0.748555	346	-0.57503
chr18	65901376	65901877	0.550459	109	0.716667	120	0.706114	507	-0.38747
chr18	67766278	67766956	0.34375	128	0.690608	181	0.665865	416	-0.51935
chr18	67771501	67772002	0.617886	123	0.598039	102	0.711828	465	-0.31412
chr18	74225296	74225797	0.067308	312	0.228782	271	0.234411	866	-0.46873
chr18	75424294	75424827	0.814516	248	0.854077	233	0.886792	583	-0.52173
chr18	75490483	75491523	0.369775	622	0.645161	527	0.679739	1530	-0.39997

chr18	75503540	75504329	0.362069	232	0.615176	369	0.666354	1067	-0.43472
chr18	81187346	81187864	0.574713	174	0.830882	136	0.848214	448	-0.36923
chr18	82994499	82995000	0.539535	215	0.705314	207	0.804372	915	-0.53171
chr18	83072178	83072679	0.201183	169	0.329843	191	0.37541	610	-0.27284
chr18	83085974	83086646	0.356061	132	0.531915	141	0.54955	555	-0.22163
chr19	4182350	4182851	0.560748	107	0.736434	129	0.760766	418	-0.52345
chr19	4207691	4208192	0.630208	192	0.698492	199	0.791367	695	-0.23443
chr19	4721410	4721940	0.342857	210	0.387931	232	0.503429	729	-0.57273
chr19	5060002	5060748	0.385321	109	0.606838	117	0.732432	370	-0.52255
chr19	5405604	5406338	0.27027	222	0.295918	294	0.41691	1029	-0.39814
chr19	5818527	5819058	0.545455	121	0.7343	207	0.736538	520	-0.33164
chr19	6529723	6530354	0.519856	277	0.61039	231	0.695755	848	-0.64165
chr19	6614922	6615423	0.826816	179	0.819383	227	0.888102	706	-0.76788
chr19	7140397	7140939	0.6	225	0.779661	236	0.788599	842	-0.51642
chr19	8779475	8779976	0.590164	61	0.878378	74	0.907631	249	-0.60254
chr19	9998869	9999739	0.512295	244	0.851964	331	0.876428	963	-0.5799
chr19	10634533	10635059	0.26506	83	0.58209	67	0.596045	354	-0.69765
chr19	16016871	16017421	0.609649	228	0.673611	144	0.67344	689	-0.55194
chr19	17434498	17434999	0.604167	240	0.838057	247	0.816804	726	-0.30123
chr19	24296294	24296795	0.715789	190	0.620818	269	0.805405	555	-0.50732
chr19	24325375	24325939	0.440678	118	0.65035	143	0.836272	397	-0.47204
chr19	25638315	25638816	0.73029	241	0.870833	240	0.888889	837	-0.65507
chr19	26822628	26823425	0.297491	279	0.480427	281	0.422105	950	-0.30466
chr19	30092456	30093055	0.758621	174	0.77551	196	0.858633	863	-0.52525
chr19	36893749	36894250	0.612245	98	0.848485	99	0.834215	567	-0.5466
chr19	37312006	37312507	0.55814	129	0.581006	179	0.789223	631	-0.57891
chr19	37731105	37731606	0.532338	201	0.668293	205	0.730827	665	-0.37996
chr19	37733174	37733677	0.365385	52	0.651515	66	0.793103	232	-0.30273
chr19	37770689	37771723	0.168525	807	0.298982	786	0.362911	3133	-0.38934
chr19	37953536	37954037	0.572414	435	0.549878	411	0.705882	765	-0.40833
chr19	37958444	37958945	0.632353	68	0.85567	97	0.864111	287	-0.38312
chr19	38199655	38200156	0.334426	305	0.335526	304	0.354788	1274	-0.47382
chr19	38347876	38348377	0.693122	189	0.781955	133	0.849485	485	-0.3391
chr19	40588656	40589254	0.102857	350	0.12297	431	0.198551	1380	-0.39972
chr19	41086914	41087660	0.327103	107	0.486301	146	0.596774	434	-0.49524
chr19	43459920	43460604	0.145221	544	0.281145	594	0.226482	2243	-0.31707
chr19	43683608	43684248	0.31694	183	0.497238	181	0.51229	773	-0.47452
chr19	44320604	44321552	0.365979	194	0.594488	254	0.609209	847	-0.32216
chr19	44339681	44340338	0.393939	132	0.566176	136	0.603306	484	-0.53138
chr19	44483144	44483685	0.145729	199	0.306667	150	0.294721	682	-0.62133
chr19	44592302	44593005	0.563291	158	0.748571	175	0.770893	694	-0.50951
chr19	44815083	44815597	0.086466	266	0.115625	320	0.132212	1248	-0.50724
chr19	44816825	44817407	0.171296	216	0.399209	253	0.350663	981	-0.48601
chr19	45298829	45299811	0.444043	554	0.644699	698	0.733418	2352	-0.49199
chr19	45374954	45375455	0.436047	344	0.571429	308	0.655963	1090	-0.31126
chr19	46480709	46481214	0.660131	153	0.818182	143	0.753226	620	-0.62699
chr19	48888565	48889258	0.691489	94	0.867188	128	0.868512	289	-0.44523

chr19	53381178	53381696	0.53617	235	0.685619	299	0.845087	865	-0.50356
chr19	53498560	53499195	0.523918	439	0.622605	522	0.797524	1373	-0.53517
chr19	53523585	53524160	0.766234	308	0.798956	383	0.817653	1031	-0.58274
chr19	53748551	53749052	0.437751	249	0.441176	204	0.516564	815	-0.49797
chr19	53752197	53752918	0.34058	414	0.482222	450	0.512853	1595	-0.30259
chr19	53965151	53965830	0.576087	184	0.676471	136	0.823755	522	-0.51572
chr19	54244632	54245133	0.720588	68	0.928571	70	0.891374	313	-0.5204
chr19	58856025	58856526	0.739583	96	0.876289	97	0.90625	288	-0.45194
chr19	59536325	59537311	0.327684	531	0.560074	541	0.682606	1903	-0.39326
chr19	59542760	59543403	0.291737	593	0.38704	571	0.550272	2019	-0.35696
chr19	60546047	60546564	0.276316	76	0.584615	65	0.457364	129	-0.65271
chr2	3716817	3717329	0.425121	207	0.569061	181	0.668	750	-0.30349
chr2	4040791	4041292	0.5	74	0.855072	69	0.762963	270	-0.49892
chr2	4383198	4384019	0.413793	145	0.664557	158	0.73854	589	-0.40857
chr2	5019127	5019647	0.536364	110	0.78022	91	0.859956	457	-0.48635
chr2	6242457	6242964	0.328767	146	0.557522	113	0.64	525	-0.43092
chr2	9797314	9797922	0.326733	101	0.793478	92	0.7825	400	-0.53032
chr2	9818031	9818862	0.323129	294	0.449883	429	0.487956	1453	-0.47965
chr2	9819635	9820136	0.58209	67	0.793103	87	0.815182	303	-0.55719
chr2	12933530	12934031	0.257576	132	0.307692	143	0.420082	488	-0.80672
chr2	13198490	13198991	0.790055	181	0.844037	218	0.897401	731	-0.63256
chr2	13930456	13930987	0.652174	115	0.807018	114	0.87108	287	-0.50192
chr2	17960583	17961084	0.239264	163	0.407258	248	0.544118	952	-0.35399
chr2	18508157	18508658	0.254386	114	0.51634	153	0.40106	566	-0.28299
chr2	19474538	19475071	0.280303	132	0.521008	119	0.563805	431	-0.39289
chr2	25325098	25325763	0.626168	107	0.831776	107	0.797674	430	-0.28953
chr2	26482917	26483462	0.324607	191	0.404651	215	0.506831	732	-0.48351
chr2	27347466	27348124	0.447368	114	0.795918	98	0.893805	226	-0.63482
chr2	30326486	30327226	0.086514	393	0.228571	420	0.173802	1565	-0.30497
chr2	30401343	30401844	0.509434	318	0.752577	291	0.855034	745	-0.40314
chr2	30555959	30556460	0.3625	160	0.583942	137	0.726688	311	-0.60522
chr2	30570946	30571624	0.705479	146	0.88	175	0.914966	588	-0.4324
chr2	30640384	30641185	0.257813	1024	0.373041	957	0.374797	2460	-0.37985
chr2	30684150	30684651	0.192683	410	0.290909	330	0.239567	1294	-0.47496
chr2	30740859	30741360	0.589786	607	0.686508	504	0.817121	1028	-0.85429
chr2	30987948	30988553	0.588235	102	0.868613	137	0.837905	401	-0.61454
chr2	31094439	31094972	0.36971	449	0.582	500	0.652335	1349	-0.54044
chr2	31097626	31098285	0.506494	154	0.601064	188	0.73508	687	-0.74788
chr2	31100012	31100513	0.660714	168	0.798658	149	0.861032	698	-0.37095
chr2	31115375	31115876	0.327731	119	0.536765	136	0.593385	514	-0.77732
chr2	31702684	31703185	0.463878	263	0.634783	345	0.654749	895	-0.44761
chr2	32010226	32010899	0.369863	146	0.465753	146	0.581015	611	-0.34161
chr2	32014132	32014697	0.553571	168	0.747619	210	0.725309	648	-0.54691
chr2	33435037	33435703	0.46281	121	0.673913	184	0.736765	680	-0.57117
chr2	36057327	36057828	0.570248	242	0.535055	271	0.728337	854	-0.52506
chr2	37623467	37624190	0.455446	101	0.622951	122	0.660088	456	-0.06812
chr2	37649968	37650482	0.729592	196	0.775862	174	0.859838	742	-0.81734

chr2	38544841	38545453	0.290102	293	0.317221	331	0.412308	975	-0.54248
chr2	38787941	38788442	0.164336	286	0.26616	263	0.340686	816	-0.53386
chr2	52551843	52552344	0.734177	79	0.922078	77	0.924	250	-0.79906
chr2	52786524	52787147	0.610778	167	0.677632	152	0.756272	558	-0.37865
chr2	58558933	58559434	0.633333	60	0.931034	58	0.902439	246	-0.74902
chr2	64315229	64315938	0.361111	72	0.644737	76	0.814433	194	-0.48571
chr2	65879582	65880337	0.492386	197	0.628713	202	0.722334	994	-0.38173
chr2	69640835	69641589	0.50885	226	0.733564	289	0.764875	1042	-0.56071
chr2	70295831	70296506	0.665789	380	0.831126	302	0.880542	812	-0.45776
chr2	70358016	70358753	0.387387	111	0.677778	90	0.763699	292	-0.56606
chr2	70498574	70499091	0.364162	173	0.487654	162	0.554636	604	-0.42613
chr2	71371161	71371712	0.374502	251	0.420074	269	0.461911	827	-0.23849
chr2	71376278	71376782	0.255411	231	0.343612	227	0.511182	626	-0.37497
chr2	72337915	72338451	0.536	125	0.628931	159	0.736667	600	-0.51117
chr2	72345293	72345794	0.72028	143	0.871622	148	0.873267	505	-0.53531
chr2	72457812	72458347	0.322581	155	0.477273	176	0.677198	728	-0.52742
chr2	74512185	74512766	0.513684	475	0.721649	582	0.742952	1809	-0.27608
chr2	74562421	74563135	0.587719	114	0.89916	119	0.877863	393	-0.30549
chr2	74567302	74567803	0.567164	67	0.782051	78	0.798479	263	-0.31525
chr2	74586183	74586855	0.594714	227	0.776744	215	0.813582	751	-0.3708
chr2	74590313	74590835	0.123418	632	0.153846	559	0.153386	2171	-0.37243
chr2	75591457	75591958	0.552632	76	0.829787	94	0.742857	245	-0.558
chr2	77165569	77166070	0.773333	75	0.951807	83	0.907186	334	-0.30823
chr2	77356563	77357068	0.668874	151	0.792553	188	0.853157	681	-0.52903
chr2	79294907	79295628	0.255533	497	0.434066	546	0.481581	1493	-0.35763
chr2	79300250	79300799	0.573099	342	0.794721	341	0.811608	1051	-0.46566
chr2	84629720	84630304	0.581699	153	0.613333	150	0.790323	558	-0.5517
chr2	84889170	84889671	0.398148	108	0.516129	124	0.63789	417	-0.58542
chr2	86205936	86206588	0.186667	75	0.651685	89	0.37535	357	-0.26164
chr2	90889063	90889564	0.605839	137	0.7	150	0.839768	518	-0.79541
chr2	93485150	93485664	0.517588	199	0.706612	242	0.750299	837	-0.23167
chr2	93748187	93748688	0.707006	157	0.734513	113	0.839583	480	-0.64314
chr2	1.05E+08	1.05E+08	0.248634	366	0.52766	470	0.629787	1410	-0.35849
chr2	1.05E+08	1.05E+08	0.282511	223	0.520619	194	0.496036	883	-0.28538
chr2	1.06E+08	1.06E+08	0.378571	420	0.631791	497	0.766304	1472	-0.22655
chr2	1.06E+08	1.06E+08	0.319149	282	0.547893	261	0.562814	995	-0.34058
chr2	1.06E+08	1.06E+08	0.143689	515	0.456294	572	0.51919	1876	-0.291
chr2	1.06E+08	1.06E+08	0.261682	107	0.559633	109	0.546713	289	-0.47254
chr2	1.13E+08	1.13E+08	0.106729	431	0.158683	334	0.136905	1344	-0.21524
chr2	1.16E+08	1.16E+08	0.433566	143	0.567901	162	0.643103	580	-0.41753
chr2	1.16E+08	1.16E+08	0.117647	221	0.372093	215	0.381308	1070	-0.28436
chr2	1.16E+08	1.16E+08	0.294643	224	0.537313	268	0.657572	733	-0.35545
chr2	1.16E+08	1.16E+08	0.355932	118	0.610169	118	0.679724	434	-0.41816
chr2	1.17E+08	1.17E+08	0.719512	164	0.896226	106	0.903743	561	-0.4208
chr2	1.18E+08	1.18E+08	0.52	100	0.745614	114	0.857143	392	-0.59887
chr2	1.2E+08	1.2E+08	0.623853	109	0.885714	105	0.873303	442	-0.73324
chr2	1.28E+08	1.28E+08	0.324675	154	0.388158	152	0.522346	716	-0.44792

chr2	1.28E+08	1.28E+08	0.382979	141	0.651007	149	0.755068	592	-0.49231
chr2	1.29E+08	1.29E+08	0.062257	257	0.095057	263	0.083672	1231	-0.19393
chr2	1.32E+08	1.32E+08	0.441315	213	0.582569	218	0.660996	823	-0.42379
chr2	1.47E+08	1.47E+08	0.177596	366	0.328612	353	0.401764	1247	-0.48946
chr2	1.47E+08	1.47E+08	0.152542	531	0.361446	415	0.401419	1973	-0.33506
chr2	1.47E+08	1.47E+08	0.206897	290	0.372727	330	0.405676	1198	-0.17404
chr2	1.48E+08	1.48E+08	0.211503	539	0.235714	420	0.31455	1189	-0.48766
chr2	1.52E+08	1.52E+08	0.448925	372	0.632353	272	0.687737	791	-0.56939
chr2	1.53E+08	1.53E+08	0.66041	586	0.735556	450	0.8054	1074	-0.60012
chr2	1.53E+08	1.53E+08	0.885965	456	0.87594	266	0.890411	511	-0.76925
chr2	1.53E+08	1.53E+08	0.623656	186	0.770833	144	0.780967	662	-0.25695
chr2	1.53E+08	1.53E+08	0.554217	166	0.846154	156	0.9	600	-0.50159
chr2	1.53E+08	1.53E+08	0.389831	177	0.490909	165	0.572592	737	-0.49771
chr2	1.53E+08	1.53E+08	0.455939	261	0.669091	275	0.665158	1105	-0.35621
chr2	1.53E+08	1.53E+08	0.519685	127	0.752381	105	0.726786	560	-0.62072
chr2	1.53E+08	1.53E+08	0.466667	90	0.674699	83	0.821818	275	-0.42001
chr2	1.54E+08	1.54E+08	0.412844	109	0.630435	92	0.674312	436	-0.46429
chr2	1.54E+08	1.54E+08	0.757062	177	0.940678	118	0.849638	552	-0.47694
chr2	1.54E+08	1.54E+08	0.076923	338	0.127962	422	0.151811	1436	-0.46221
chr2	1.56E+08	1.56E+08	0.27907	86	0.496183	131	0.442308	364	-0.34992
chr2	1.57E+08	1.57E+08	0.451389	432	0.643917	337	0.74104	865	-0.59233
chr2	1.57E+08	1.57E+08	0.585495	1696	0.919963	2149	0.48881	6211	-0.2756
chr2	1.58E+08	1.58E+08	0.100571	875	0.143337	893	0.250112	2223	-0.37013
chr2	1.59E+08	1.59E+08	0.348993	149	0.626866	134	0.623853	436	-0.76726
chr2	1.61E+08	1.61E+08	0.241573	178	0.416216	185	0.435185	756	-0.53494
chr2	1.65E+08	1.65E+08	0.369811	265	0.558704	247	0.670236	934	-0.52276
chr2	1.65E+08	1.65E+08	0.466418	268	0.605691	246	0.59846	909	-0.68876
chr2	1.65E+08	1.65E+08	0.684848	165	0.801471	136	0.807273	550	-0.38497
chr2	1.67E+08	1.67E+08	0.503597	139	0.706667	150	0.813022	599	-0.5828
chr2	1.67E+08	1.67E+08	0.65896	173	0.88172	186	0.889594	788	-0.5948
chr2	1.68E+08	1.68E+08	0.704974	583	0.80663	362	0.777643	823	-0.3846
chr2	1.68E+08	1.68E+08	0.84669	574	0.759551	445	0.897698	1173	-0.54564
chr2	1.68E+08	1.68E+08	0.468439	301	0.569697	330	0.692308	988	-0.42187
chr2	1.68E+08	1.68E+08	0.788296	581	0.756637	452	0.861171	922	-0.89637
chr2	1.68E+08	1.68E+08	0.40636	283	0.401606	249	0.47302	871	-0.41637
chr2	1.69E+08	1.69E+08	0.173516	219	0.255507	227	0.286765	816	-0.40831
chr2	1.69E+08	1.69E+08	0.343629	259	0.416268	209	0.570629	715	-0.45678
chr2	1.7E+08	1.7E+08	0.628788	132	0.730496	141	0.80566	530	-0.5738
chr2	1.7E+08	1.7E+08	0.449275	276	0.44586	157	0.601081	925	-0.3534
chr2	1.72E+08	1.72E+08	0.59176	267	0.786957	230	0.854875	882	-0.58552
chr2	1.72E+08	1.72E+08	0.59434	212	0.762332	223	0.73746	937	-0.41623
chr2	1.73E+08	1.73E+08	0.76	525	0.89486	428	0.898488	926	-0.31109
chr2	1.73E+08	1.73E+08	0.505133	487	0.617336	473	0.697586	787	-0.47294
chr2	1.73E+08	1.73E+08	0.712674	1152	0.853365	832	0.902484	1610	-0.65333
chr2	1.78E+08	1.78E+08	0.707602	171	0.911765	170	0.866438	584	-0.54751
chr2	1.8E+08	1.8E+08	0.602339	171	0.687117	163	0.739067	686	-0.57947
chr2	1.8E+08	1.8E+08	0.623932	117	0.8	115	0.84186	430	-0.91445

chr2	1.81E+08	1.81E+08	0.426386	523	0.428571	364	0.642317	794	-0.43672
chr2	1.81E+08	1.81E+08	0.614286	140	0.679389	131	0.748792	414	-0.52202
chr2	1.81E+08	1.81E+08	0.26	600	0.254279	409	0.364253	1768	-0.54335
chr3	5210563	5211209	0.241379	319	0.477807	383	0.694047	1327	-0.47906
chr3	5213947	5214695	0.443548	124	0.664234	137	0.693299	388	-0.41132
chr3	9345792	9346688	0.401617	371	0.643068	339	0.581498	1135	-0.24959
chr3	10367772	10368273	0.301282	156	0.470199	151	0.504244	589	-0.55317
chr3	17689972	17690477	0.244094	254	0.538095	210	0.650572	787	-0.32072
chr3	17695435	17696317	0.357759	232	0.701754	285	0.623923	1045	-0.42232
chr3	18961897	18962497	0.265537	177	0.408602	186	0.623886	561	-0.42159
chr3	22019489	22019990	0.544218	147	0.769231	130	0.787276	503	-0.49268
chr3	30404286	30404862	0.525714	175	0.737327	217	0.838554	830	-0.20716
chr3	30410731	30411505	0.292208	154	0.538813	219	0.567568	851	-0.25981
chr3	31039727	31040228	0.709459	148	0.887097	124	0.879342	547	-0.43277
chr3	34540137	34540914	0.167442	430	0.242424	528	0.338274	1889	-0.3697
chr3	34560535	34561741	0.117949	585	0.3625	720	0.510385	2600	-0.27578
chr3	34565483	34566212	0.336364	110	0.678899	109	0.647841	301	-0.45571
chr3	34654843	34655344	0.323636	550	0.429112	529	0.615005	1013	-0.65332
chr3	34848270	34848771	0.6	195	0.563291	158	0.793956	364	-0.5875
chr3	35241272	35241846	0.648084	287	0.846154	208	0.878345	411	-0.43774
chr3	40431507	40432217	0.491525	236	0.705263	190	0.732782	726	-0.33761
chr3	40548156	40548694	0.237736	265	0.325949	316	0.403738	1070	-0.48659
chr3	40849206	40849740	0.781818	110	0.945946	111	0.914127	361	-0.31513
chr3	41158062	41158612	0.689655	116	0.892157	102	0.870079	508	-0.35127
chr3	45179177	45179678	0.092199	141	0.209302	172	0.261206	647	-0.4303
chr3	51161213	51162146	0.296954	394	0.463007	419	0.504041	1361	-0.33997
chr3	52062359	52062894	0.516129	186	0.649533	214	0.714968	628	-0.40646
chr3	52218821	52219705	0.62766	188	0.921212	165	0.864336	715	-0.25903
chr3	56242104	56242609	0.666667	96	0.884615	104	0.923684	380	-0.35943
chr3	65239341	65239842	0.767442	129	0.817518	137	0.887265	479	-0.38732
chr3	65469366	65469935	0.106	500	0.194296	561	0.225	2120	-0.39049
chr3	65674530	65675031	0.439791	191	0.479798	198	0.620596	738	-0.34139
chr3	65732148	65732724	0.700787	127	0.823529	136	0.879098	488	-0.59242
chr3	66776493	66777118	0.193833	227	0.361217	263	0.359102	802	-0.39935
chr3	86975263	86975776	0.557522	113	0.774194	124	0.753521	426	-0.39947
chr3	87749443	87749944	0.492228	193	0.668712	163	0.836812	527	-0.55713
chr3	87776323	87777058	0.325243	206	0.570755	212	0.641485	781	-0.18929
chr3	87941289	87941931	0.469274	179	0.568306	183	0.648368	674	-0.42997
chr3	87943400	87944152	0.270208	433	0.372654	373	0.474432	1408	-0.28414
chr3	87954703	87955204	0.282258	124	0.287425	167	0.461216	477	-0.54702
chr3	89142713	89143280	0.344961	258	0.483755	277	0.577922	924	-0.3282
chr3	89592717	89593218	0.492669	341	0.700637	314	0.787133	1057	-0.578
chr3	89666872	89667373	0.619048	63	0.912621	103	0.794521	292	-0.32401
chr3	90249532	90250033	0.209091	110	0.367816	174	0.456942	569	-0.69319
chr3	90252275	90252776	0.416	125	0.682119	151	0.67019	473	-0.59858
chr3	94172335	94172905	0.720779	154	0.812121	165	0.890681	558	-0.49577
chr3	94625559	94626060	0.104072	221	0.247967	246	0.265467	889	-0.3352

chr3	94963222	94963723	0.267123	146	0.369697	165	0.40836	622	-0.38747
chr3	95117911	95118598	0.303704	405	0.362069	348	0.495582	1358	-0.44454
chr3	95706909	95707650	0.367021	188	0.555556	207	0.594183	722	-0.55521
chr3	95985768	95986297	0.459677	124	0.617486	183	0.753597	556	-0.64615
chr3	96137534	96138072	0.261084	1015	0.434211	912	0.59493	3708	-0.42578
chr3	96138994	96139616	0.514778	406	0.702233	403	0.823908	1397	-0.31462
chr3	96229486	96229987	0.604938	162	0.789116	147	0.893574	498	-0.1259
chr3	96300668	96301231	0.170426	399	0.231481	324	0.276434	1447	-0.29676
chr3	96350769	96351270	0.262857	175	0.375	216	0.510417	672	-0.40461
chr3	96618846	96619347	0.654412	136	0.896552	116	0.898824	425	-0.54698
chr3	99039863	99040457	0.410596	151	0.669065	139	0.654723	614	-0.34993
chr3	99053390	99053944	0.338028	284	0.553125	320	0.629703	1010	-0.26424
chr3	99056021	99056687	0.506667	225	0.781893	243	0.802508	638	-0.25501
chr3	99059495	99060036	0.574074	108	0.765152	132	0.854806	489	-0.26951
chr3	1.01E+08	1.01E+08	0.705	200	0.890244	164	0.891207	671	-0.6327
chr3	1.05E+08	1.05E+08	0.290909	165	0.337209	172	0.348195	471	-0.30816
chr3	1.07E+08	1.07E+08	0.630872	149	0.691275	149	0.680532	601	-0.20154
chr3	1.08E+08	1.08E+08	0.66443	149	0.768362	177	0.852041	588	-0.55742
chr3	1.08E+08	1.08E+08	0.176734	447	0.290043	462	0.334099	1742	-0.26931
chr3	1.09E+08	1.09E+08	0.612069	232	0.830116	259	0.849252	869	-0.43046
chr3	1.15E+08	1.15E+08	0.467857	280	0.663755	229	0.730464	883	-0.42659
chr3	1.16E+08	1.16E+08	0.651163	86	0.890411	73	0.738255	298	-0.63204
chr3	1.21E+08	1.21E+08	0.583333	84	0.890909	110	0.819307	404	-0.5787
chr3	1.21E+08	1.21E+08	0.559441	143	0.737864	206	0.855714	700	-0.53817
chr3	1.21E+08	1.21E+08	0.677632	152	0.783069	189	0.870523	726	-0.46368
chr3	1.27E+08	1.27E+08	0.700508	197	0.918367	147	0.89198	611	-0.39955
chr3	1.29E+08	1.29E+08	0.459893	187	0.537037	216	0.709318	719	-0.31193
chr3	1.29E+08	1.29E+08	0.351145	131	0.434783	115	0.517308	520	-0.38093
chr3	1.29E+08	1.29E+08	0.47929	169	0.715084	179	0.755357	560	-0.38809
chr3	1.36E+08	1.36E+08	0.347594	187	0.479675	246	0.551938	645	-0.55147
chr3	1.42E+08	1.42E+08	0.515539	547	0.657556	622	0.783699	957	-0.28314
chr3	1.44E+08	1.44E+08	0.491071	112	0.744	125	0.793103	377	-0.46506
chr3	1.44E+08	1.44E+08	0.586957	92	0.698795	83	0.811258	302	-0.58275
chr3	1.44E+08	1.44E+08	0.252033	123	0.27027	148	0.39399	599	-0.45986
chr3	1.45E+08	1.45E+08	0.178667	375	0.3241	361	0.30927	1219	-0.51308
chr3	1.49E+08	1.49E+08	0.298077	104	0.406504	123	0.61809	398	-0.54236
chr3	1.49E+08	1.49E+08	0.689655	87	0.810526	95	0.791667	432	-0.34418
chr3	1.49E+08	1.49E+08	0.679487	156	0.847059	170	0.899676	618	-0.40884
chr3	1.6E+08	1.6E+08	0.189873	79	0.417266	139	0.491651	539	-0.25769
chr4	8836795	8837296	0.145	200	0.353535	198	0.419872	624	-0.4752
chr4	8847242	8847804	0.679389	131	0.896825	126	0.880299	401	-0.56993
chr4	8853747	8854248	0.494318	176	0.735294	170	0.750433	577	-0.55791
chr4	8858451	8858952	0.675926	108	0.865979	97	0.857143	476	-0.64712
chr4	9062218	9062771	0.372881	177	0.550562	178	0.635193	699	-0.33273
chr4	10889757	10890263	0.655914	93	0.807018	114	0.796804	438	-0.32656
chr4	10971871	10972396	0.318182	88	0.611765	85	0.52459	366	-0.37441
chr4	22059768	22060269	0.641667	120	0.820225	178	0.879928	558	-0.40166

chr4	32024884	32025529	0.207273	275	0.169444	360	0.291071	1120	-0.34398
chr4	32334920	32335421	0.445783	166	0.462264	212	0.488688	663	-0.17626
chr4	32337222	32337855	0.336538	208	0.61674	227	0.668646	842	-0.46066
chr4	40733549	40734050	0.77551	245	0.875	208	0.88269	699	-0.38998
chr4	41596586	41597087	0.716049	162	0.939597	149	0.932056	574	-0.70953
chr4	41643791	41644535	0.300448	223	0.447154	246	0.562282	859	-0.27557
chr4	43840424	43840925	0.4375	80	0.732143	56	0.760331	242	-0.67242
chr4	45749166	45749667	0.700297	337	0.833333	240	0.886394	757	-0.67177
chr4	45882563	45883254	0.346278	618	0.485075	536	0.706034	1160	-0.42538
chr4	46384523	46385024	0.506977	215	0.759804	204	0.738494	478	-0.62155
chr4	55528206	55528892	0.24734	376	0.334218	377	0.368913	1499	-0.46235
chr4	56878909	56879410	0.6	95	0.818182	110	0.866983	421	-0.45861
chr4	56964438	56965088	0.798387	124	0.949275	138	0.880208	576	-0.79475
chr4	59049210	59049728	0.468254	252	0.643443	244	0.62949	1058	-0.3053
chr4	59331647	59332148	0.743421	152	0.861842	152	0.896797	562	-0.71699
chr4	61870060	61870561	0.101604	187	0.214634	205	0.274336	678	-0.52522
chr4	62322583	62323084	0.370079	127	0.625	96	0.557143	350	-0.54293
chr4	73659900	73660509	0.164009	439	0.265193	362	0.371974	1363	-0.45167
chr4	82188666	82189167	0.485981	107	0.696078	102	0.724311	399	-0.51252
chr4	83160899	83161400	0.613333	150	0.800885	226	0.894422	502	-0.52738
chr4	86508191	86508870	0.287234	94	0.645669	127	0.603604	333	-0.69502
chr4	87014891	87015392	0.414286	210	0.520833	192	0.677019	644	-0.51839
chr4	88918288	88918909	0.438298	235	0.700893	224	0.77327	838	-0.32422
chr4	88937801	88938388	0.495238	105	0.745763	118	0.789063	384	-0.62267
chr4	96258268	96258769	0.113208	106	0.27907	129	0.324478	527	-0.55549
chr4	97420735	97421246	0.506276	239	0.7125	240	0.787571	885	-0.43092
chr4	98471078	98472102	0.676923	260	0.875	208	0.856308	856	-0.45618
chr4	99229454	99229955	0.345455	55	0.696429	56	0.834225	187	-0.54073
chr4	99328346	99329752	0.220674	1364	0.513761	1308	0.691086	3590	-0.33801
chr4	1.08E+08	1.08E+08	0.675926	108	0.65625	128	0.790419	501	-0.3888
chr4	1.08E+08	1.08E+08	0.517094	234	0.680934	257	0.784217	811	-0.61096
chr4	1.15E+08	1.15E+08	0.301676	179	0.456853	197	0.613251	649	-0.37837
chr4	1.16E+08	1.16E+08	0.309859	355	0.482673	404	0.488121	1389	-0.46062
chr4	1.16E+08	1.16E+08	0.172297	296	0.276596	329	0.265686	1020	-0.286
chr4	1.16E+08	1.16E+08	0.224806	387	0.257062	354	0.329588	1602	-0.52243
chr4	1.17E+08	1.17E+08	0.5625	112	0.791139	158	0.800789	507	-0.63141
chr4	1.17E+08	1.17E+08	0.572519	131	0.759398	133	0.785595	597	-0.60847
chr4	1.18E+08	1.18E+08	0.443478	115	0.579832	119	0.642276	615	-0.34722
chr4	1.18E+08	1.18E+08	0.738095	84	0.903509	114	0.937158	366	-0.48096
chr4	1.18E+08	1.18E+08	0.568966	58	0.877193	57	0.858491	212	-0.42136
chr4	1.19E+08	1.19E+08	0.472222	72	0.62963	81	0.735974	303	-0.47943
chr4	1.19E+08	1.19E+08	0.402878	139	0.56875	160	0.456811	602	-0.4433
chr4	1.2E+08	1.2E+08	0.672414	116	0.792079	101	0.843602	422	-0.5205
chr4	1.23E+08	1.23E+08	0.728155	103	0.816514	109	0.893462	413	-0.69092
chr4	1.24E+08	1.24E+08	0.534247	73	0.72973	74	0.836601	306	-0.57038
chr4	1.24E+08	1.24E+08	0.655814	215	0.769565	230	0.872973	740	-0.49365
chr4	1.24E+08	1.24E+08	0.10084	238	0.173729	236	0.335556	900	-0.59527

chr4	1.25E+08	1.25E+08	0.736486	148	0.816	125	0.765957	564	-0.69236
chr4	1.25E+08	1.25E+08	0.22549	204	0.472973	222	0.619835	847	-0.45239
chr4	1.29E+08	1.29E+08	0.622951	183	0.565445	191	0.663435	722	-0.38532
chr4	1.29E+08	1.29E+08	0.672727	110	0.77027	148	0.737903	496	-0.71097
chr4	1.29E+08	1.29E+08	0.324022	179	0.431694	183	0.485294	748	-0.28415
chr4	1.29E+08	1.29E+08	0.443636	275	0.574286	350	0.749248	997	-0.40086
chr4	1.33E+08	1.33E+08	0.541126	231	0.76087	230	0.736767	699	-0.27807
chr4	1.33E+08	1.33E+08	0.254181	299	0.412	250	0.319044	1213	-0.48126
chr4	1.33E+08	1.33E+08	0.592105	76	0.826446	121	0.839394	330	-0.46746
chr4	1.33E+08	1.33E+08	0.606667	150	0.757764	161	0.819048	525	-0.50223
chr4	1.33E+08	1.33E+08	0.522388	67	0.804878	82	0.793003	343	-0.30476
chr4	1.33E+08	1.33E+08	0.330986	142	0.379032	124	0.408492	683	-0.24534
chr4	1.33E+08	1.33E+08	0.577465	71	0.794118	68	0.783019	318	-0.42692
chr4	1.34E+08	1.34E+08	0.578358	268	0.641732	254	0.733129	978	-0.43756
chr4	1.34E+08	1.34E+08	0.138249	217	0.325792	221	0.358804	903	-0.15692
chr4	1.34E+08	1.34E+08	0.1	80	0.283186	113	0.355658	433	-0.44935
chr4	1.35E+08	1.35E+08	0.748428	159	0.809917	121	0.860233	601	-0.39293
chr4	1.35E+08	1.35E+08	0.4	290	0.561905	315	0.498525	1356	-0.46975
chr4	1.35E+08	1.35E+08	0.416185	173	0.454545	220	0.51843	841	-0.48509
chr4	1.35E+08	1.35E+08	0.709497	179	0.873362	229	0.869873	707	-0.7019
chr4	1.36E+08	1.36E+08	0.764706	102	0.966292	89	0.857143	210	-0.416
chr4	1.36E+08	1.36E+08	0.443836	365	0.670927	313	0.755958	1049	-0.42011
chr4	1.36E+08	1.36E+08	0.461538	182	0.78453	181	0.881029	622	-0.48708
chr4	1.36E+08	1.36E+08	0.451613	310	0.722772	202	0.820896	536	-0.60989
chr4	1.37E+08	1.37E+08	0.218182	110	0.375887	141	0.455253	514	-0.62614
chr4	1.38E+08	1.38E+08	0.61194	134	0.796748	123	0.836207	580	-0.66988
chr4	1.38E+08	1.38E+08	0.669643	112	0.872881	118	0.812195	410	-0.57647
chr4	1.38E+08	1.38E+08	0.806349	315	0.862454	269	0.91607	977	-0.65828
chr4	1.38E+08	1.38E+08	0.402878	139	0.666667	141	0.726103	544	-0.46451
chr4	1.39E+08	1.39E+08	0.705479	146	0.814815	189	0.864198	567	-0.54508
chr4	1.4E+08	1.4E+08	0.638587	368	0.681319	364	0.755382	1022	-0.37938
chr4	1.41E+08	1.41E+08	0.488372	172	0.643357	143	0.580198	505	-0.24938
chr4	1.41E+08	1.41E+08	0.682243	107	0.839416	137	0.821121	464	-0.55317
chr4	1.41E+08	1.41E+08	0.511905	84	0.739726	73	0.781609	348	-0.73043
chr4	1.43E+08	1.43E+08	0.488722	133	0.585938	128	0.718412	554	-0.43063
chr4	1.48E+08	1.48E+08	0.4375	256	0.45	200	0.583565	718	-0.47543
chr4	1.48E+08	1.48E+08	0.610063	159	0.84466	103	0.835381	407	-0.43015
chr4	1.48E+08	1.48E+08	0.346505	329	0.415686	255	0.468644	1180	-0.6861
chr4	1.48E+08	1.48E+08	0.686047	172	0.864198	162	0.833333	678	-0.3322
chr4	1.48E+08	1.48E+08	0.711409	298	0.8583	247	0.915179	896	-0.62033
chr4	1.49E+08	1.49E+08	0.510703	327	0.662551	243	0.7914	1093	-0.46723
chr4	1.49E+08	1.49E+08	0.583732	209	0.807692	156	0.865269	668	-0.30114
chr4	1.49E+08	1.49E+08	0.735043	117	0.85	100	0.858382	346	-0.52513
chr4	1.5E+08	1.5E+08	0.570533	319	0.683706	313	0.772487	1134	-0.28309
chr4	1.5E+08	1.5E+08	0.666667	105	0.833333	114	0.830435	460	-0.60823
chr4	1.5E+08	1.5E+08	0.326667	150	0.5	90	0.575	400	-0.26109
chr4	1.51E+08	1.51E+08	0.659483	232	0.744898	196	0.860435	781	-0.61119

chr4	1.52E+08	1.52E+08	0.63	200	0.767241	116	0.822076	607	-0.74719
chr4	1.52E+08	1.52E+08	0.623967	242	0.798206	223	0.87125	800	-0.57284
chr4	1.53E+08	1.53E+08	0.690909	110	0.868132	91	0.895062	324	-0.55564
chr4	1.54E+08	1.54E+08	0.35942	345	0.393293	328	0.45384	1159	-0.39611
chr5	8997507	8998085	0.236842	266	0.328947	304	0.252809	1246	-0.47027
chr5	21291538	21292236	0.2	195	0.304348	230	0.3879	843	-0.45775
chr5	23869570	23870142	0.748031	127	0.886364	176	0.894737	437	-0.61901
chr5	24237809	24238310	0.545852	229	0.756757	222	0.835616	876	-0.58001
chr5	25174018	25174792	0.514286	175	0.6	155	0.631667	600	-0.55893
chr5	28486321	28487043	0.319372	191	0.618834	223	0.619327	683	-0.23518
chr5	28488967	28489557	0.289617	366	0.403125	320	0.487402	1270	-0.42737
chr5	29798063	29798564	0.213068	352	0.339523	377	0.456221	1302	-0.37067
chr5	29799152	29799864	0.142105	380	0.374718	443	0.468915	1512	-0.35021
chr5	29802105	29802606	0.336538	104	0.568345	139	0.604119	437	-0.44656
chr5	29811287	29811799	0.212121	297	0.358268	254	0.503409	880	-0.54951
chr5	30137251	30137752	0.46988	83	0.705128	78	0.724138	319	-0.70737
chr5	30438790	30439291	0.729927	137	0.962617	107	0.934726	383	-0.56317
chr5	31762443	31762981	0.744186	86	0.949495	99	0.925806	310	-0.54067
chr5	32645955	32646456	0.774194	124	0.966387	119	0.896296	405	-0.63133
chr5	33360073	33360574	0.648936	94	0.837838	74	0.791946	298	-0.38699
chr5	33385749	33386250	0.723881	134	0.859155	142	0.909664	476	-0.63057
chr5	34670053	34670580	0.354108	353	0.345455	330	0.543643	1054	-0.36001
chr5	38109314	38109815	0.613953	215	0.654088	159	0.711111	405	-0.61835
chr5	38221914	38222415	0.421053	266	0.658009	231	0.688564	822	-0.41426
chr5	38222493	38223086	0.455696	316	0.683735	332	0.747644	955	-0.37891
chr5	38224163	38224799	0.240143	279	0.540179	224	0.523592	657	-0.45869
chr5	39165410	39166090	0.682028	217	0.823077	130	0.900151	661	-0.63289
chr5	42147219	42147850	0.193717	191	0.296875	192	0.351433	663	-0.24345
chr5	44053326	44053831	0.538889	180	0.72028	143	0.777592	598	-0.51094
chr5	53860557	53861160	0.401674	239	0.594595	222	0.643282	841	-0.477
chr5	53993238	53993916	0.642857	154	0.925234	107	0.81761	636	-0.49083
chr5	54061708	54062554	0.459184	294	0.612319	276	0.652948	899	-0.3093
chr5	64549664	64550412	0.218254	252	0.232044	362	0.288868	1042	-0.3239
chr5	65450776	65451334	0.635659	129	0.68	125	0.766827	416	-0.73386
chr5	66974151	66974716	0.815972	288	0.927954	347	0.903299	879	-0.53073
chr5	67486438	67486939	0.136471	425	0.368831	385	0.443535	1222	-0.39805
chr5	67488314	67488815	0.152	500	0.215457	427	0.30532	1654	-0.4108
chr5	67489200	67490293	0.185083	724	0.381481	810	0.454545	2486	-0.3265
chr5	67491695	67492795	0.304217	664	0.592217	591	0.720823	1945	-0.3914
chr5	72047358	72047859	0.597403	77	0.793814	97	0.82622	328	-0.53069
chr5	73287560	73288061	0.630573	157	0.8	170	0.824348	575	-0.56738
chr5	77566760	77567261	0.603604	222	0.807692	182	0.86087	690	-0.58473
chr5	92827607	92828179	0.386243	189	0.553957	139	0.593066	548	-0.50998
chr5	93553048	93553623	0.732919	161	0.873239	142	0.91684	481	-0.78512
chr5	99466503	99467056	0.222222	522	0.213447	937	0.305726	2113	-0.42074
chr5	99716701	99717202	0.671053	76	0.8125	96	0.778098	347	-0.4418
chr5	1.02E+08	1.02E+08	0.336735	196	0.517442	172	0.522222	720	-0.46184

chr5	1.03E+08	1.03E+08	0.544503	191	0.600939	213	0.726115	628	-0.57177
chr5	1.05E+08	1.05E+08	0.350365	274	0.535032	314	0.642342	1110	-0.55241
chr5	1.07E+08	1.07E+08	0.55802	586	0.828711	613	0.882298	2124	-0.23563
chr5	1.07E+08	1.07E+08	0.373297	367	0.614085	355	0.706749	1289	-0.23446
chr5	1.07E+08	1.07E+08	0.370861	151	0.489209	139	0.501053	475	-0.31454
chr5	1.08E+08	1.08E+08	0.329032	465	0.414458	415	0.590585	1402	-0.38359
chr5	1.12E+08	1.12E+08	0.766667	360	0.882206	399	0.872646	1115	-0.52341
chr5	1.12E+08	1.12E+08	0.124402	627	0.233933	778	0.221526	2713	-0.32339
chr5	1.14E+08	1.14E+08	0.5125	480	0.460526	532	0.65889	1586	-0.63988
chr5	1.14E+08	1.14E+08	0.594872	195	0.769565	230	0.822667	750	-0.49526
chr5	1.16E+08	1.16E+08	0.294606	241	0.31982	222	0.493552	853	-0.43906
chr5	1.17E+08	1.17E+08	0.666667	96	0.747826	115	0.804878	369	-0.6747
chr5	1.17E+08	1.17E+08	0.602564	156	0.636986	146	0.764805	591	-0.53394
chr5	1.17E+08	1.17E+08	0.325203	123	0.511111	135	0.627002	437	-0.35798
chr5	1.19E+08	1.19E+08	0.514056	249	0.392739	303	0.622201	1027	-0.43496
chr5	1.19E+08	1.19E+08	0.614943	174	0.796875	192	0.799397	663	-0.49967
chr5	1.2E+08	1.2E+08	0.117925	212	0.333333	210	0.30692	896	-0.37525
chr5	1.2E+08	1.2E+08	0.144981	538	0.427027	555	0.445545	1414	-0.38944
chr5	1.2E+08	1.2E+08	0.449379	2094	0.411829	1843	0.693568	3296	-0.42174
chr5	1.21E+08	1.21E+08	0.244499	409	0.306818	352	0.320057	1406	-0.5187
chr5	1.21E+08	1.21E+08	0.248555	346	0.215347	404	0.318325	1266	-0.31011
chr5	1.21E+08	1.21E+08	0.751295	193	0.900383	261	0.902069	725	-0.60445
chr5	1.23E+08	1.23E+08	0.488506	174	0.677966	177	0.610951	694	-0.54782
chr5	1.23E+08	1.23E+08	0.230769	247	0.237013	308	0.349524	1050	-0.65949
chr5	1.23E+08	1.24E+08	0.384106	302	0.468944	322	0.527778	1224	-0.47439
chr5	1.25E+08	1.25E+08	0.605634	142	0.7	190	0.822368	760	-0.51102
chr5	1.26E+08	1.26E+08	0.664	125	0.789474	152	0.819957	461	-0.41441
chr5	1.26E+08	1.26E+08	0.657459	181	0.534483	232	0.765739	683	-0.49408
chr5	1.28E+08	1.28E+08	0.223881	268	0.375912	274	0.346766	943	-0.43593
chr5	1.28E+08	1.28E+08	0.486486	111	0.597701	87	0.808108	370	-0.36399
chr5	1.3E+08	1.3E+08	0.595041	121	0.732143	112	0.839674	368	-0.36638
chr5	1.32E+08	1.32E+08	0.606557	122	0.774775	111	0.8434	447	-0.46619
chr5	1.34E+08	1.34E+08	0.685714	245	0.762376	202	0.893617	564	-0.64529
chr5	1.35E+08	1.35E+08	0.535714	280	0.691318	311	0.76501	966	-0.42908
chr5	1.35E+08	1.35E+08	0.74026	154	0.816176	136	0.892938	439	-0.67217
chr5	1.35E+08	1.35E+08	0.802548	157	0.930435	115	0.860095	629	-0.52863
chr5	1.36E+08	1.36E+08	0.771429	210	0.878049	246	0.881871	855	-0.58004
chr5	1.36E+08	1.36E+08	0.837209	258	0.912698	252	0.919355	930	-0.5552
chr5	1.36E+08	1.36E+08	0.451613	217	0.707424	229	0.731495	689	-0.58945
chr5	1.38E+08	1.38E+08	0.338462	65	0.602273	88	0.634812	293	-0.1542
chr5	1.41E+08	1.41E+08	0.518325	191	0.681034	232	0.797082	754	-0.4535
chr5	1.42E+08	1.42E+08	0.481752	137	0.593548	155	0.698556	554	-0.65896
chr5	1.44E+08	1.44E+08	0.635762	151	0.820359	167	0.763293	583	-0.48917
chr5	1.45E+08	1.45E+08	0.528662	157	0.646067	178	0.666055	545	-0.37168
chr5	1.45E+08	1.45E+08	0.484663	163	0.560694	173	0.651633	643	-0.54971
chr5	1.45E+08	1.45E+08	0.26506	249	0.22314	242	0.363725	1020	-0.40253
chr5	1.46E+08	1.46E+08	0.613065	199	0.664634	164	0.731055	673	-0.41678

chr5	1.46E+08	1.46E+08	0.404959	121	0.625	192	0.56314	586	-0.43601
chr5	1.48E+08	1.48E+08	0.506912	217	0.590698	215	0.684669	574	-0.80573
chr5	1.48E+08	1.48E+08	0.276923	390	0.583979	387	0.670963	1474	-0.31279
chr5	1.48E+08	1.48E+08	0.659824	682	0.875536	699	0.89214	1743	-0.52234
chr5	1.48E+08	1.48E+08	0.480418	383	0.592896	366	0.629741	1002	-0.35307
chr5	1.48E+08	1.48E+08	0.682493	337	0.698182	275	0.762065	891	-0.35872
chr5	1.48E+08	1.48E+08	0.252747	455	0.612756	439	0.661398	1645	-0.32065
chr6	4551635	4552155	0.072093	430	0.15864	353	0.161017	1652	-0.3138
chr6	4603089	4603629	0.478705	587	0.636054	588	0.772368	1643	-0.40549
chr6	5056920	5057421	0.80597	469	0.928947	380	0.924528	795	-0.64219
chr6	5206296	5206797	0.333333	162	0.394737	152	0.585333	750	-0.56137
chr6	6804583	6805084	0.396135	207	0.558704	247	0.660508	866	-0.56976
chr6	6905119	6905852	0.121535	469	0.164216	408	0.141917	2128	-0.25181
chr6	11743046	11743651	0.597826	184	0.746377	138	0.767986	556	-0.50576
chr6	12212938	12213439	0.617801	191	0.782609	161	0.810707	523	-0.49505
chr6	14847538	14848116	0.417112	187	0.612121	165	0.642265	724	-0.4152
chr6	14848763	14849314	0.216561	314	0.348649	370	0.433892	1074	-0.5225
chr6	28152775	28153276	0.596859	191	0.681159	207	0.839695	524	-0.61961
chr6	28720444	28720964	0.453704	108	0.540541	111	0.711409	447	-0.60975
chr6	29130125	29130714	0.270492	122	0.529762	168	0.590708	452	-0.39635
chr6	29384645	29385170	0.065421	107	0.263889	144	0.218509	389	-0.44141
chr6	29934378	29934986	0.27933	179	0.280335	239	0.455128	624	-0.53699
chr6	30158391	30158931	0.680851	141	0.821192	151	0.839479	461	-0.58529
chr6	31169618	31170119	0.203488	172	0.337963	216	0.41522	749	-0.41905
chr6	39219990	39220491	0.542254	142	0.801047	191	0.859964	557	-0.40253
chr6	39372535	39373036	0.449495	198	0.626794	209	0.696011	727	-0.64488
chr6	42298370	42298871	0.465649	131	0.50625	160	0.612378	614	-0.36873
chr6	42328962	42329529	0.690647	139	0.911392	158	0.901079	556	-0.31723
chr6	48387282	48387783	0.491453	234	0.643902	205	0.617778	675	-0.45114
chr6	50175548	50176051	0.597403	77	0.822917	96	0.738462	260	-0.45271
chr6	51757809	51758402	0.660819	171	0.856436	202	0.888579	718	-0.49789
chr6	52102334	52102835	0.5	122	0.606667	150	0.728137	526	-0.34419
chr6	52119380	52119881	0.390374	187	0.514151	212	0.565163	798	-0.36281
chr6	52129654	52130406	0.416667	288	0.627962	422	0.731771	1152	-0.36409
chr6	52139108	52139609	0.59375	96	0.83871	93	0.79403	335	-0.48801
chr6	52169700	52170601	0.512881	427	0.768116	483	0.800968	1653	-0.28525
chr6	52189301	52189802	0.240175	229	0.384848	330	0.375582	1073	-0.30394
chr6	52262122	52262871	0.105528	199	0.297753	178	0.330484	702	-0.16856
chr6	52792846	52793347	0.751553	161	0.873239	142	0.871036	473	-0.51758
chr6	52910349	52910850	0.778802	217	0.859813	214	0.905512	635	-0.70594
chr6	54765612	54766123	0.483696	184	0.625731	171	0.673684	570	-0.59459
chr6	64086393	64087116	0.607143	140	0.860656	122	0.894118	595	-0.54619
chr6	66978136	66978660	0.712644	87	0.935185	108	0.938272	324	-0.60543
chr6	66978965	66979645	0.649254	134	0.727273	143	0.792237	438	-0.40404
chr6	67178196	67178726	0.241107	253	0.38191	199	0.340378	899	-0.41775
chr6	67215056	67215557	0.666667	102	0.867347	98	0.902703	370	-0.65692
chr6	83016283	83017050	0.547739	199	0.695279	233	0.732006	653	-0.70189

chr6	83021594	83022095	0.227273	176	0.465438	217	0.426471	748	-0.44526
chr6	83654679	83655180	0.657658	111	0.816514	109	0.819527	338	-0.50258
chr6	83663908	83664496	0.244224	303	0.537162	296	0.657321	963	-0.32951
chr6	85845539	85846289	0.422018	218	0.509091	220	0.691375	742	-0.55125
chr6	86143749	86144250	0.459677	124	0.574194	155	0.726166	493	-0.5512
chr6	86160811	86161318	0.52027	148	0.678261	115	0.846336	423	-0.50254
chr6	86446971	86447480	0.246269	134	0.340278	144	0.433468	496	-0.28444
chr6	86535815	86536316	0.605634	142	0.722222	144	0.808458	402	-0.45432
chr6	88885425	88885926	0.449275	69	0.764706	68	0.719512	246	-0.34798
chr6	90400336	90401003	0.518987	158	0.654639	194	0.696203	632	-0.50866
chr6	92195103	92195604	0.320632	1076	0.313568	995	0.438644	1858	-0.44976
chr6	92894656	92895157	0.416667	84	0.602151	93	0.691932	409	-0.46075
chr6	94722925	94723608	0.356481	216	0.470046	217	0.506667	825	-0.26334
chr6	97260639	97261140	0.497354	189	0.557823	147	0.731298	655	-0.27866
chr6	97565632	97566172	0.301724	232	0.4125	240	0.476306	823	-0.47883
chr6	97690789	97691290	0.55942	345	0.683849	291	0.72227	1163	-0.52587
chr6	99641409	99641944	0.268382	272	0.353659	246	0.362085	1055	-0.48077
chr6	1E+08	1E+08	0.574074	162	0.701493	134	0.730871	379	-0.81545
chr6	1E+08	1E+08	0.509434	106	0.768595	121	0.71564	422	-0.41315
chr6	1E+08	1E+08	0.488172	465	0.68	300	0.759162	1146	-0.33547
chr6	1E+08	1E+08	0.581699	153	0.718182	110	0.765172	379	-0.73627
chr6	1E+08	1E+08	0.775665	263	0.861386	202	0.874138	580	-0.71813
chr6	1E+08	1E+08	0.59375	160	0.759259	162	0.818314	688	-0.47908
chr6	1.09E+08	1.09E+08	0.682243	107	0.778761	113	0.832258	465	-0.63564
chr6	1.13E+08	1.13E+08	0.519774	177	0.57971	207	0.632964	722	-0.62045
chr6	1.14E+08	1.14E+08	0.507143	140	0.75	124	0.725314	557	-0.57732
chr6	1.15E+08	1.15E+08	0.3125	32	0.461538	13	0.706395	344	-0.34712
chr6	1.15E+08	1.15E+08	0.474359	312	0.680934	257	0.82238	1126	-0.53656
chr6	1.19E+08	1.19E+08	0.710227	176	0.851613	155	0.903268	765	-0.54614
chr6	1.19E+08	1.19E+08	0.334821	224	0.455	200	0.620887	699	-0.58188
chr6	1.19E+08	1.19E+08	0.416667	120	0.664234	137	0.694	500	-0.46078
chr6	1.2E+08	1.2E+08	0.447619	105	0.571429	112	0.608137	467	-0.46523
chr6	1.2E+08	1.2E+08	0.551913	183	0.706731	208	0.732493	714	-0.59656
chr6	1.23E+08	1.23E+08	0.756757	222	0.778261	230	0.798271	694	-0.47192
chr6	1.23E+08	1.23E+08	0.416894	367	0.513158	456	0.705653	1026	-0.57474
chr6	1.23E+08	1.23E+08	0.585366	656	0.722736	541	0.80726	1157	-0.59407
chr6	1.23E+08	1.23E+08	0.551724	609	0.646667	600	0.73913	1288	-0.59207
chr6	1.25E+08	1.25E+08	0.402256	266	0.524017	229	0.509645	985	-0.46983
chr6	1.25E+08	1.25E+08	0.325843	89	0.542056	107	0.635802	324	-0.59427
chr6	1.25E+08	1.25E+08	0.272727	319	0.487719	285	0.516652	1171	-0.30134
chr6	1.26E+08	1.26E+08	0.424731	186	0.561404	171	0.579193	644	-0.44444
chr6	1.26E+08	1.26E+08	0.446602	206	0.649718	177	0.607717	622	-0.38115
chr6	1.27E+08	1.27E+08	0.485714	140	0.604278	187	0.744409	626	-0.34118
chr6	1.31E+08	1.31E+08	0.285461	564	0.39531	597	0.456372	1891	-0.22955
chr6	1.31E+08	1.31E+08	0.121339	478	0.226141	482	0.253957	1390	-0.39439
chr6	1.34E+08	1.34E+08	0.745614	228	0.700637	157	0.817156	443	-0.53474
chr6	1.35E+08	1.35E+08	0.533333	90	0.819149	94	0.890052	191	-0.41995

chr6	1.35E+08	1.35E+08	0.722543	346	0.849498	299	0.897799	636	-0.31854
chr6	1.37E+08	1.37E+08	0.637255	102	0.824074	108	0.73102	461	-0.5501
chr6	1.41E+08	1.41E+08	0.76	125	0.89781	137	0.904762	399	-0.49343
chr6	1.43E+08	1.43E+08	0.652174	92	0.714286	112	0.730769	260	-0.47416
chr6	1.45E+08	1.45E+08	0.537879	132	0.701389	144	0.78169	426	-0.51034
chr6	1.49E+08	1.49E+08	0.824176	273	0.924623	199	0.932455	607	-0.42032
chr7	3263890	3264432	0.583732	209	0.634021	194	0.795217	669	-0.67822
chr7	3368770	3369333	0.624277	173	0.778571	140	0.824138	580	-0.3639
chr7	3454344	3454845	0.728111	217	0.89071	183	0.837307	713	-0.51721
chr7	4850116	4850729	0.650307	163	0.677885	208	0.764881	672	-0.50724
chr7	4884029	4884540	0.686275	102	0.761905	84	0.874652	359	-0.7214
chr7	13595902	13596403	0.213198	197	0.290323	186	0.408805	795	-0.38277
chr7	16519063	16519564	0.680233	172	0.713115	244	0.86115	713	-0.61508
chr7	16886311	16886876	0.521739	69	0.811594	69	0.831169	231	-0.47524
chr7	17486940	17487814	0.476471	170	0.697561	205	0.691304	690	-0.49799
chr7	19457909	19458692	0.220588	136	0.442308	104	0.533333	525	-0.41397
chr7	19533868	19534369	0.5625	128	0.716814	113	0.713376	628	-0.50192
chr7	19704011	19704537	0.199667	601	0.181501	573	0.295444	2261	-0.38536
chr7	19753485	19753986	0.622785	790	0.652968	657	0.800162	1236	-0.32367
chr7	20050554	20051113	0.470697	2167	0.529904	1672	0.638845	3187	-0.3616
chr7	20338714	20339219	0.674627	335	0.719457	221	0.81351	681	-0.35981
chr7	20410746	20411247	0.541787	347	0.682927	246	0.778078	739	-0.39615
chr7	25377284	25377785	0.77512	209	0.894366	142	0.9	360	-0.76763
chr7	28873623	28874124	0.609524	105	0.728477	151	0.824348	575	-0.66436
chr7	29126898	29127399	0.623377	154	0.816667	180	0.801075	558	-0.34211
chr7	30016074	30016756	0.625	192	0.86911	191	0.867807	643	-0.49044
chr7	30074806	30075579	0.291759	449	0.432323	495	0.520557	1581	-0.53142
chr7	30093575	30094076	0.219731	223	0.306034	232	0.389744	780	-0.63648
chr7	31854322	31854853	0.683582	335	0.931129	363	0.925251	1097	-0.37054
chr7	35379099	35379690	0.561644	146	0.698113	159	0.776488	689	-0.17861
chr7	35634205	35634765	0.507538	199	0.466165	266	0.578771	895	-0.37694
chr7	35902001	35902502	0.466321	193	0.531073	177	0.612329	730	-0.48192
chr7	36018698	36019199	0.328571	280	0.520408	294	0.536443	1029	-0.34226
chr7	37311055	37311556	0.674699	83	0.842975	121	0.887097	310	-0.59661
chr7	37476247	37477108	0.413223	363	0.644562	377	0.71544	1114	-0.31066
chr7	38409917	38410548	0.173184	179	0.30303	165	0.341812	629	-0.37171
chr7	46800281	46800810	0.164773	176	0.264865	185	0.296081	689	-0.45399
chr7	51605564	51606077	0.679325	237	0.734756	328	0.863799	1116	-0.45398
chr7	52419827	52420454	0.34507	142	0.623894	226	0.562147	708	-0.5467
chr7	52595525	52596026	0.226453	499	0.338947	475	0.303354	1968	-0.34304
chr7	52770621	52771381	0.421712	479	0.713362	464	0.724342	1520	-0.42371
chr7	52787110	52787611	0.630435	138	0.641509	159	0.752418	517	-0.53995
chr7	52809030	52809531	0.606667	150	0.812121	165	0.751524	656	-0.59466
chr7	52995149	52995883	0.266667	90	0.526316	133	0.475066	381	-0.60246
chr7	53268390	53268891	0.204082	98	0.471831	142	0.497925	482	-0.30976
chr7	54090154	54090704	0.643979	191	0.790323	186	0.872671	644	-0.46243
chr7	56559863	56560632	0.243827	324	0.39899	396	0.45915	1224	-0.39682

chr7	56893652	56894444	0.125436	287	0.343396	265	0.339	1000	-0.20416
chr7	56894512	56895464	0.095571	429	0.374486	486	0.408834	1766	-0.26967
chr7	56895734	56896346	0.15508	187	0.386792	212	0.529412	663	-0.41249
chr7	56917969	56918470	0.435065	154	0.568627	204	0.668421	570	-0.59414
chr7	56942981	56943512	0.319372	191	0.397516	161	0.548561	556	-0.68422
chr7	72210036	72210656	0.44586	157	0.5	212	0.550442	565	-0.54584
chr7	75421503	75422004	0.270042	237	0.376518	247	0.407643	942	-0.4404
chr7	77477460	77478828	0.313025	476	0.570806	459	0.5932	1647	-0.22565
chr7	77479047	77479548	0.422727	220	0.463333	300	0.645248	747	-0.29199
chr7	77491623	77494012	0.315113	933	0.637525	1018	0.672934	2819	-0.25983
chr7	77510550	77511129	0.128302	265	0.214022	271	0.228019	1035	-0.36092
chr7	77512565	77513174	0.41573	178	0.50495	202	0.511864	590	-0.25118
chr7	86535153	86535654	0.526316	114	0.694656	131	0.742529	435	-0.61895
chr7	86751426	86752025	0.46134	388	0.535411	353	0.671736	789	-0.2999
chr7	86873645	86874179	0.276786	224	0.390244	164	0.43544	728	-0.27785
chr7	87166999	87167500	0.772222	180	0.923077	156	0.907449	443	-0.51356
chr7	87844365	87844866	0.658915	129	0.812903	155	0.90273	586	-0.39569
chr7	97178674	97179175	0.748792	207	0.936842	190	0.915171	613	-0.47387
chr7	99328596	99329097	0.539419	241	0.659306	317	0.693195	867	-0.55491
chr7	1.07E+08	1.07E+08	0.723881	134	0.85567	97	0.862573	342	-0.50492
chr7	1.07E+08	1.07E+08	0.526316	95	0.86	100	0.806962	316	-0.77346
chr7	1.08E+08	1.08E+08	0.537313	134	0.630872	149	0.800373	536	-0.40516
chr7	1.09E+08	1.09E+08	0.572917	192	0.787097	155	0.796875	640	-0.46886
chr7	1.19E+08	1.19E+08	0.328502	207	0.355422	332	0.443515	956	-0.39807
chr7	1.2E+08	1.2E+08	0.647321	224	0.802395	167	0.833871	620	-0.34762
chr7	1.2E+08	1.2E+08	0.590674	193	0.653333	150	0.683507	673	-0.20538
chr7	1.2E+08	1.2E+08	0.69403	134	0.670103	97	0.718504	508	-0.48229
chr7	1.2E+08	1.2E+08	0.528926	363	0.682266	406	0.70258	1318	-0.32115
chr7	1.21E+08	1.21E+08	0.541096	146	0.720183	218	0.770227	618	-0.39665
chr7	1.23E+08	1.23E+08	0.219917	241	0.403922	255	0.451319	1099	-0.35445
chr7	1.3E+08	1.3E+08	0.116279	129	0.259259	108	0.273885	471	-0.72463
chr7	1.33E+08	1.33E+08	0.769231	78	0.974359	78	0.897351	302	-0.42124
chr7	1.35E+08	1.35E+08	0.333333	279	0.373494	249	0.470135	1038	-0.4652
chr7	1.38E+08	1.38E+08	0.774194	124	0.892308	130	0.886562	573	-0.45263
chr7	1.38E+08	1.38E+08	0.460784	102	0.561983	121	0.711688	385	-0.60254
chr7	1.39E+08	1.39E+08	0.427083	96	0.671642	134	0.724221	417	-0.59344
chr7	1.39E+08	1.39E+08	0.527473	91	0.754237	118	0.739234	418	-0.65254
chr7	1.4E+08	1.4E+08	0.404255	141	0.666667	171	0.71979	571	-0.5482
chr7	1.41E+08	1.41E+08	0.691358	81	0.892157	102	0.885609	271	-0.42353
chr7	1.42E+08	1.42E+08	0.283582	402	0.324324	481	0.353496	1273	-0.40744
chr7	1.44E+08	1.44E+08	0.183333	240	0.288525	305	0.389229	817	-0.53769
chr7	1.48E+08	1.48E+08	0.482143	224	0.633508	191	0.751908	524	-0.69081
chr7	1.48E+08	1.48E+08	0.435115	131	0.577778	135	0.610687	393	-0.57709
chr7	1.48E+08	1.48E+08	0.574545	550	0.677824	478	0.772298	953	-0.66586
chr7	1.48E+08	1.48E+08	0.337449	243	0.36747	332	0.490779	976	-0.55348
chr7	1.5E+08	1.5E+08	0.290909	165	0.420765	183	0.375546	687	-0.65496
chr7	1.51E+08	1.51E+08	0.402344	256	0.539735	302	0.661417	889	-0.59838

chr7	1.51E+08	1.51E+08	0.576577	111	0.819149	94	0.821429	392	-0.6234
chr7	1.52E+08	1.52E+08	0.546512	86	0.693069	101	0.719403	335	-0.36903
chr8	4413252	4413900	0.492754	138	0.765152	132	0.776493	519	-0.52843
chr8	4612127	4612875	0.357143	168	0.5	116	0.560938	640	-0.14319
chr8	8490523	8491024	0.594872	195	0.793103	174	0.808696	575	-0.52656
chr8	8985451	8985980	0.607143	308	0.761765	340	0.868309	1177	-0.46056
chr8	8992293	8992804	0.375758	165	0.486631	187	0.603448	638	-0.20464
chr8	8995506	8996007	0.622449	98	0.886179	123	0.889101	523	-0.44062
chr8	10007612	10008113	0.196581	234	0.236842	190	0.327009	896	-0.30317
chr8	10946811	10947333	0.624	375	0.66881	311	0.802299	870	-0.43914
chr8	11479833	11480334	0.19802	202	0.394366	213	0.418938	697	-0.37654
chr8	11645809	11646310	0.324675	77	0.524752	101	0.74212	349	-0.63658
chr8	12393884	12394423	0.329787	188	0.410526	190	0.427515	676	-0.22487
chr8	12398312	12398813	0.221374	131	0.439759	166	0.411992	517	-0.29281
chr8	12402162	12402761	0.397004	534	0.562852	533	0.653719	1210	-0.28606
chr8	12485351	12485852	0.708861	316	0.814465	318	0.837237	854	-0.55012
chr8	26478407	26479061	0.473469	245	0.634921	252	0.703742	962	-0.27696
chr8	27104977	27105478	0.452381	168	0.512821	156	0.631751	611	-0.37612
chr8	28269756	28270534	0.174757	206	0.413265	196	0.402576	621	-0.50871
chr8	28343001	28343502	0.774648	142	0.933333	165	0.876812	414	-0.69236
chr8	33901780	33902361	0.646465	99	0.764706	119	0.749311	363	-0.33833
chr8	34494420	34494921	0.555556	90	0.851852	81	0.809392	362	-0.38005
chr8	34626872	34627467	0.413994	343	0.521978	364	0.598297	1292	-0.50506
chr8	35102482	35102983	0.101449	138	0.386139	101	0.375839	447	-0.8087
chr8	42219790	42220353	0.329545	264	0.350649	231	0.430733	859	-0.42301
chr8	46195370	46195973	0.590717	237	0.761682	214	0.775591	762	-0.37846
chr8	47085715	47086216	0.189189	555	0.310811	444	0.364565	1665	-0.40081
chr8	47772886	47773387	0.639175	194	0.836066	183	0.834739	593	-0.34232
chr8	49093999	49094954	0.612732	377	0.84399	391	0.89622	1561	-0.43767
chr8	49861395	49862005	0.615	200	0.722449	245	0.760112	717	-0.57563
chr8	49902503	49903015	0.547368	190	0.739884	173	0.778563	849	-0.3661
chr8	59818707	59819208	0.391304	138	0.608392	143	0.731369	577	-0.69003
chr8	63620898	63621399	0.6	125	0.745763	118	0.850117	427	-0.67037
chr8	67172148	67172649	0.178947	285	0.291262	206	0.326757	811	-0.33172
chr8	67445510	67446011	0.569182	318	0.827004	237	0.90107	748	-0.57109
chr8	72674486	72674987	0.451977	177	0.466981	212	0.590604	745	-0.34434
chr8	72721209	72721710	0.603604	111	0.792453	106	0.773171	410	-0.56968
chr8	73010622	73011123	0.265823	237	0.384354	294	0.510093	1288	-0.56693
chr8	73334303	73334804	0.674009	227	0.776596	188	0.787105	822	-0.89765
chr8	74036603	74037104	0.68	200	0.873016	189	0.870324	802	-0.60867
chr8	74210831	74211332	0.330049	406	0.546729	428	0.540972	1379	-0.44204
chr8	80637803	80638403	0.545455	143	0.620155	129	0.786645	614	-0.5261
chr8	80674964	80675465	0.666667	147	0.867089	158	0.905429	571	-0.15159
chr8	80676217	80676921	0.530303	132	0.846939	98	0.860194	515	-0.36892
chr8	80677103	80677732	0.607143	84	0.825581	86	0.865672	335	-0.47405
chr8	81540022	81540542	0.717241	145	0.810345	116	0.894737	475	-0.46323
chr8	86307420	86308127	0.162712	295	0.309701	268	0.300551	1088	-0.42434

chr8	86918865	86919425	0.634328	134	0.738854	157	0.720706	623	-0.32175
chr8	87226055	87226556	0.587065	201	0.67234	235	0.771987	614	-0.42958
chr8	87264339	87264840	0.625	88	0.688525	122	0.831395	344	-0.40646
chr8	87267265	87267994	0.529412	238	0.814947	281	0.830857	875	-0.38016
chr8	87322230	87322923	0.226824	507	0.285974	549	0.348769	1706	-0.61019
chr8	87505606	87506251	0.717949	195	0.843434	198	0.877958	803	-0.30043
chr8	90500924	90501463	0.732919	161	0.922156	167	0.886293	642	-0.46737
chr8	91132846	91133595	0.614213	197	0.802198	182	0.836305	617	-0.35941
chr8	91474083	91474584	0.417582	273	0.516949	236	0.592205	1052	-0.3134
chr8	91475099	91475602	0.813397	209	0.886364	176	0.782051	702	-0.45061
chr8	92089024	92089525	0.702532	158	0.721429	140	0.704415	521	-0.5414
chr8	93375938	93376465	0.322034	59	0.614035	57	0.485106	235	-0.40963
chr8	93421005	93421585	0.477941	136	0.821782	101	0.858676	559	-0.36292
chr8	93854045	93854707	0.562937	286	0.863071	241	0.824473	997	-0.42232
chr8	94018881	94019382	0.341463	123	0.383178	107	0.554054	370	-0.5533
chr8	94327308	94328055	0.1875	496	0.32716	486	0.392545	1717	-0.22648
chr8	94390759	94391495	0.455285	123	0.760417	96	0.65859	454	-0.51161
chr8	94887915	94888438	0.343602	422	0.428954	373	0.607756	1573	-0.16509
chr8	96678469	96678970	0.621951	82	0.776596	94	0.805158	349	-0.37737
chr8	98220049	98220550	0.62963	162	0.79375	160	0.840467	514	-0.44828
chr8	1.07E+08	1.07E+08	0.387879	165	0.485232	237	0.602426	742	-0.43289
chr8	1.09E+08	1.09E+08	0.304813	187	0.379888	179	0.453608	776	-0.57716
chr8	1.11E+08	1.11E+08	0.643791	306	0.707237	304	0.817035	951	-0.2561
chr8	1.11E+08	1.11E+08	0.103139	223	0.308696	230	0.368697	952	-0.37692
chr8	1.12E+08	1.12E+08	0.598425	254	0.737013	308	0.757009	856	-0.50157
chr8	1.14E+08	1.14E+08	0.685315	143	0.889764	127	0.890295	474	-0.6372
chr8	1.14E+08	1.14E+08	0.567568	111	0.78125	128	0.846715	548	-0.66207
chr8	1.2E+08	1.2E+08	0.620253	158	0.655172	203	0.756388	587	-0.61937
chr8	1.22E+08	1.22E+08	0.410596	151	0.593939	165	0.648374	492	-0.44407
chr8	1.23E+08	1.23E+08	0.597682	604	0.772829	449	0.779579	1851	-0.3836
chr8	1.23E+08	1.23E+08	0.485477	241	0.704762	210	0.65544	772	-0.59098
chr8	1.23E+08	1.23E+08	0.283465	127	0.529412	102	0.572165	388	-0.54921
chr8	1.23E+08	1.23E+08	0.68932	206	0.852381	210	0.899183	734	-0.60679
chr8	1.24E+08	1.24E+08	0.626609	233	0.792373	236	0.839068	901	-0.59306
chr8	1.24E+08	1.24E+08	0.53125	320	0.566116	242	0.678125	960	-0.31819
chr8	1.24E+08	1.24E+08	0.798214	560	0.753846	520	0.87884	1172	-0.30258
chr8	1.25E+08	1.25E+08	0.578947	95	0.757576	99	0.747881	472	-0.41704
chr8	1.25E+08	1.25E+08	0.387657	1037	0.542069	725	0.637068	1937	-0.55838
chr8	1.25E+08	1.25E+08	0.707042	355	0.790476	315	0.851466	1057	-0.52018
chr8	1.26E+08	1.26E+08	0.292398	171	0.431034	174	0.591525	590	-0.45705
chr8	1.29E+08	1.29E+08	0.536723	177	0.692308	117	0.839583	480	-0.54345
chr9	7762468	7762969	0.30625	160	0.448819	127	0.561243	547	-0.54064
chr9	13694579	13695080	0.536364	110	0.642857	126	0.709007	433	-0.47397
chr9	18278208	18278709	0.086207	406	0.185811	296	0.198391	1492	-0.48424
chr9	20666584	20667085	0.565789	152	0.61745	149	0.686534	453	-0.44458
chr9	20834703	20835204	0.290389	489	0.429066	578	0.576646	1944	-0.39329
chr9	21000175	21000916	0.585492	193	0.709184	196	0.795332	557	-0.70849

chr9	21851913	21852414	0.805128	195	0.909091	154	0.848855	655	-0.36252
chr9	24582592	24583538	0.371951	492	0.560748	428	0.550253	1781	-0.35277
chr9	24585979	24586484	0.239344	305	0.366906	278	0.372646	1009	-0.22176
chr9	28376649	28377265	0.709677	124	0.819355	155	0.866279	516	-0.48745
chr9	31702453	31703023	0.621469	177	0.828194	227	0.91492	811	-0.57959
chr9	37015043	37015544	0.174074	270	0.267081	322	0.298446	1223	-0.17279
chr9	37336969	37337511	0.413223	121	0.548872	133	0.627787	583	-0.1944
chr9	40578235	40578855	0.440678	118	0.738095	84	0.600671	298	-0.29452
chr9	41390350	41390851	0.626984	126	0.811765	85	0.757009	428	-0.40514
chr9	41931031	41931532	0.354037	161	0.530864	162	0.630137	584	-0.39055
chr9	43943952	43944459	0.747191	178	0.775281	178	0.815878	592	-0.51305
chr9	44945151	44945785	0.58871	124	0.761538	130	0.797727	440	-0.49975
chr9	45240394	45240954	0.654867	226	0.770909	275	0.846029	617	-0.62751
chr9	46227353	46227854	0.56962	79	0.824324	74	0.845324	278	-0.4966
chr9	46247017	46247563	0.619469	113	0.730159	126	0.821862	494	-0.44952
chr9	46551718	46552458	0.598837	172	0.776699	103	0.670918	392	-0.35194
chr9	48457968	48458469	0.510417	192	0.667954	259	0.723457	810	-0.44955
chr9	50512827	50513457	0.696203	79	0.865169	89	0.849693	326	-0.57203
chr9	54433519	54434020	0.096154	260	0.182648	219	0.145285	1177	-0.40565
chr9	54583686	54584187	0.131148	122	0.304	125	0.415094	530	-0.48266
chr9	56383515	56384118	0.631818	220	0.648276	145	0.761317	729	-0.42098
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chr9	56758052	56758553	0.582609	115	0.537815	119	0.713675	468	-0.45996
chr9	57147472	57147973	0.738739	111	0.948529	136	0.923963	434	-0.88504
chr9	57400720	57401562	0.106494	385	0.292754	345	0.27931	1450	-0.35504
chr9	58048011	58048512	0.414286	140	0.644068	177	0.663918	485	-0.26441
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chr9	60560218	60560719	0.1175	800	0.14098	837	0.176244	2332	-0.61853
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chr9	1.08E+08	1.08E+08	0.574803	127	0.663793	116	0.64486	428	-0.65105
chr9	1.1E+08	1.1E+08	0.694915	118	0.88961	154	0.897862	421	-0.54732
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chr9	1.17E+08	1.17E+08	0.413793	87	0.46789	109	0.64723	343	-0.62542
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chrX	11574985	11575889	0.333333	189	0.540179	224	0.603797	790	-0.30278
chrX	11578049	11578557	0.204301	279	0.431034	290	0.606776	974	-0.20615
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chrX	33736269	33737097	0.238806	134	0.593985	133	0.503906	512	-0.36931
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chrX	55172312	55172945	0.293233	133	0.493671	158	0.642857	448	-0.32995
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chrX	1.08E+08	1.08E+08	0.244344	221	0.447154	246	0.438137	687	-0.3905
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**CG contentGC contentgeneSymbolance to gene**

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0.009394	0.485909	Fbxw11;ml	61492
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0.013485	0.459394	Fam196b	-1837
0.013719	0.472231	Wwc1	1240
0.025545	0.490818	Ebf1;Ebf4	-5195
0.023349	0.570718	Ebf1;Ebf4	2725
0.013223	0.431074	Ebf1;Ebf4	13536
0.015868	0.42843	Ebf1;Ebf4	82990
0.019669	0.487107	Sgcd	-228
0.015207	0.419339	Gnb2l1	-25669
0.011405	0.482314	0610009Bz	8329
0.014215	0.403967	Cdkl3	-1603
0.018512	0.457521	Tcf7	-17239
0.010579	0.46281	Vdac1	8995
0.017025	0.524628	9530068Ec	138839
0.007692	0.5	Il5	23750
0.00876	0.476694	Glra1	36544
0.011667	0.461212	AK007998	12428
0.01405	0.492727	Larp1	-47896
0.008926	0.489917	Larp1	7083
0.008264	0.470083	Larp1	9615
0.004463	0.459835	Larp1	11984
0.005325	0.481039	Larp1	24337
0.015606	0.464242	Cnot8	-28786
0.014545	0.479504	Fam183b	-202
0.007438	0.40876	4933439F1	5207
0.010083	0.546446	Kcnj12	-17974
0.020455	0.564848	Epn2	-36530
0.026612	0.543802	AK043365	0
0.025175	0.501958	Pirt	-5239
0.013388	0.472066	Usp43	-4093
0.017355	0.446942	Rpl26	9480
0.011429	0.488442	2310047M	4741
0.006116	0.545785	Gucy2e	14830
0.02281	0.558017	Chd3	-2399
0.007273	0.439091	Kdm6b	-14422
0.01157	0.433884	Atp1b2	-3439

0.005785	0.494876	BC096441;	-13028
0.018788	0.483788	AK217047	-7348
0.0125	0.442045	Tlcd2	5190
0.013287	0.520559	Myo18a	-9258
0.00876	0.488264	Proca1	2485
0.020992	0.465455	1810012P1	507
0.010649	0.523896	Lgals9	7311
0.027438	0.490083	1700071K0	-14787
0.007603	0.506446	AK018946	79113
0.007273	0.420826	1700125H:	-9665
0.010909	0.486212	Tbx4	2533
0.017025	0.553719	Sept4	0
0.018788	0.475303	Nog	47192
0.013147	0.498042	Gm11545	27644
0.01124	0.469256	Ppp1r9b	-634
0.009256	0.517355	Itga3	-9785
0.010744	0.561322	Tac4	-49831
0.014026	0.560649	Tac4	-36304
0.013058	0.450083	Myst2	-7979
0.008182	0.463788	Fam117a	-4439
0.029576	0.480606	AK027957	164
0.016606	0.550182	Phospho1	7482
0.008926	0.516364	Gip	3758
0.016529	0.521818	Hoxb13	-21600
0.025584	0.46	Hoxb13	-15227
0.014545	0.466212	AK078606	-962
0.015207	0.392397	AK078606	1255
0.01697	0.483333	AK078566	2178
0.024545	0.460758	Mir196a-1	-3574
0.036883	0.483507	Hoxb9	-1460
0.017851	0.53686	Hoxb7	929
0.052893	0.514711	Mir10a	-2370
0.008099	0.482645	Hoxb3	767
0.017861	0.470695	Hoxb2	-2900
0.020331	0.444298	AK008491	11502
0.019669	0.52562	Mir152	10414
0.010248	0.539669	Sp2	-8464
0.019008	0.509752	Osbpl7	18336
0.009576	0.529212	Tbx21	-10703
0.013554	0.509421	DQ716032	7713
0.012231	0.422479	Arhgap23	20267
0.027762	0.479301	Lasp1	-848
0.022857	0.543377	Plxdc1	-423
0.017851	0.481818	Stac2	-3214
0.017521	0.514711	Erbb2	-2434
0.00562	0.453223	Thra	3579
0.015868	0.583306	Thra	-2447

0.016033	0.50281	Nr1d1	-1006
0.020331	0.524132	Nr1d1	-6979
0.013884	0.516859	Tns4	11911
0.024628	0.532727	Ccr7	12241
0.008252	0.491329	Krt19	-4113
0.020699	0.513147	Fkbp10	368
0.01124	0.424298	Tubg2	-12502
0.012159	0.445	Cntd1	3167
0.010568	0.493295	Aarsd1	22227
0.011736	0.471405	Arl4d	24568
0.017576	0.493182	Etv4	-28603
0.016033	0.503306	AK076700	-25151
0.020087	0.540346	Sost	1415
0.011901	0.528099	Sost	-1155
0.017483	0.52993	AK144330	1002
0.014215	0.483306	Adam11	-26152
0.017326	0.527059	Plcd3	5686
0.015152	0.486545	Efcab3	-33001
0.014091	0.522424	Mettl2	26843
0.010769	0.498322	Mrc2	2179
0.014545	0.51157	Tex2	-26369
0.009091	0.451901	Nol11	-13468
0.017686	0.518678	Axin2	-26427
0.017841	0.50125	Cdc42ep4	-1983
0.010744	0.492066	4932435O:	-27953
0.015207	0.532397	Slc9a3r1	1944
0.012231	0.57405	Cdk3	2863
0.015909	0.48625	Rnf157	-10093
0.01124	0.549256	Gm11744	6915
0.014545	0.514711	Mxra7	15135
0.018831	0.531558	Mgat5b	-29259
0.014825	0.526154	Mgat5b	-18449
0.022879	0.540379	Mgat5b	19938
0.014215	0.488264	Mgat5b	23464
0.010519	0.472208	Sec14l1	4342
0.015207	0.580992	Sept9	-22936
0.015041	0.544298	Sept9	-6482
0.011016	0.50139	Sept9	34367
0.019669	0.451405	Sept9	53131
0.011818	0.503788	Tnrc6c	-23800
0.026477	0.520227	Gaa	-8765
0.013788	0.532576	Mir1932	3996
0.009587	0.557686	Stra13	1558
0.010649	0.521429	Dtnb	-23259
0.012727	0.560661	Adcy3	45012
0.013223	0.480331	AK050516	9928
0.012273	0.496705	Mycn	157359

0.017143	0.51961	Mycn	118503
0.009364	0.467091	Mycn	11140
0.012893	0.47719	Mycn	9626
0.011667	0.457121	Trib2	211951
0.008099	0.503306	2410004P(	-35891
0.017686	0.50843	Hpcal1	1455
0.025882	0.434545	Id2	1097
0.0272	0.470764	Id2	-995
0.014286	0.465974	AK044503;	78559
0.012066	0.540826	Myt1l	-159030
0.012727	0.42281	Foxg1	-4336
0.019174	0.441322	3110039M	0
0.02	0.49405	Akap6	1732
0.015537	0.461322	AK018924	3135
0.015909	0.447879	Mir1892	99861
0.021429	0.503636	Nkx2-9	1672
0.021939	0.44497	Pax9	22558
0.012562	0.473884	AK039829	32880
0.02314	0.515537	Tomm20l	244
0.009917	0.486446	Ppm1a	8536
0.013388	0.455372	Ppm1a	50442
0.029351	0.500649	Six6	-1572
0.022645	0.519339	4930447C(	0
0.02314	0.411736	Rhoj	715
0.012727	0.475804	Plekhg3	-2423
0.018843	0.455537	Fntb	3363
0.009091	0.470909	Fut8	-40167
0.007934	0.521157	Actn1	41685
0.012879	0.391818	Entpd5	-3715
0.007273	0.447769	Tmed10	-11487
0.02314	0.481488	Fos	-28844
0.012576	0.510455	Jdp2	-58726
0.007769	0.454215	Jdp2	-53403
0.019773	0.537727	Gm6772	33770
0.016694	0.480331	Gm6772	37006
0.010083	0.527603	Gm6772	69813
0.028052	0.527532	6430527G:	51848
0.011736	0.40595	Kiaa1737	-5026
0.024593	0.512823	Zdhhc22	10570
0.012448	0.492028	Sptlc2	-21031
0.01297	0.46097	Ppp4r4	-656
0.015372	0.456364	Gsc	-4817
0.020661	0.499835	Vrk1	216208
0.01961	0.474545	1700121N:	137090
0.011345	0.496946	Dio3	3527
0.013223	0.470083	Dync1h1	-1985
0.010744	0.479174	AK080484	-18156

0.019008	0.509091	BC115444	44076
0.012562	0.555372	Pld4	-13073
0.032159	0.458409	Sp8	-5165
0.011736	0.456529	AK006031	33399
0.012066	0.492397	Actn2	-18889
0.017424	0.484091	AK085253	-23739
0.013554	0.563636	Pou6f2	39209
0.010083	0.451901	Zfp184	-15568
0.017576	0.46	Vmn1r223	59050
0.007515	0.455394	Scgn	-1712
0.013182	0.451477	BC025054	108271
0.011515	0.465455	BC025054	100948
0.020455	0.453788	AK012007	-2027
0.018601	0.512727	Foxf2	2584
0.008951	0.428671	AK004186	-903
0.014909	0.499394	1300014I0	1731
0.022871	0.541818	Nrn1	3829
0.026424	0.478545	Nrn1	3104
0.010083	0.488595	AK155516	7268
0.014545	0.483306	Tcfap2a	17824
0.012893	0.454711	Tcfap2a	13643
0.023967	0.481322	Tcfap2a	-4466
0.01297	0.498667	Tbc1d7	-10617
0.013058	0.494545	Tbc1d7	-27719
0.020661	0.472066	AK006512	124625
0.008264	0.451736	Jarid2	36743
0.02877	0.46877	Shc3	-674
0.015722	0.559786	AK029587	120777
0.018512	0.46843	Ror2	1432
0.012364	0.469455	AK020556	-20530
0.012448	0.515944	Sfxn1	43368
0.006446	0.558017	Dbn1	-6072
0.015702	0.511405	Neurog1	-4263
0.014697	0.468636	Rmi1	65104
0.008099	0.440331	2010111I0	17074
0.01197	0.512576	apo	-88296
0.010061	0.446667	apo	-49693
0.021983	0.462975	Papd7	52223
0.00965	0.516643	BC018507	-17086
0.042567	0.48107	Irx1	5084
0.012727	0.377355	Irx2	7917
0.039043	0.517321	Irx4	3612
0.009421	0.419174	AK051417	381664
0.036667	0.454849	C130071C	-7239
0.029091	0.476061	C130071C	-5562
0.011688	0.464935	Fam151b	1303
0.015537	0.468926	Scamp1	-433

0.013485	0.52803	AK079595	173
0.022761	0.455354	Otp	-4779
0.011074	0.438843	Otp	5773
0.028	0.449333	Otp	8792
0.020455	0.454091	F2rl1	-23465
0.022323	0.490808	F2r	19680
0.014876	0.469587	Sv2c	-25990
0.010152	0.484394	BC065997	3232
0.015795	0.485795	BC065997	6322
0.013388	0.392727	Foxd1	14016
0.018312	0.434805	AK135852	209
0.008926	0.434711	Pik3r1	248788
0.012727	0.449091	Zswim6	-13384
0.015455	0.433636	Pde4d	-56618
0.024463	0.376033	Pde4d	-1220
0.012308	0.390909	Arl15	82156
0.013719	0.47124	Arl15	100466
0.021061	0.49197	Isl1;isl1-be	15839
0.014215	0.405455	Isl1;isl1-be	-1720
0.024	0.485576	Parp8	167836
0.017091	0.489697	Emb	-12099
0.026096	0.476471	AK143952	370
0.012727	0.426612	Fhit	0
0.018843	0.467273	Fhit	885
0.013864	0.470909	Ptprg	149545
0.015114	0.486818	Ptprg	210056
0.014432	0.485	Fezf2	5799
0.035488	0.490572	Fezf2	2831
0.018182	0.444242	Fezf2	-4753
0.013007	0.454825	Gng2	-8799
0.015524	0.454825	Zfp503	-3643
0.012727	0.534711	AK146230	-43553
0.019008	0.524463	4931406H:	-953
0.01405	0.533058	Itih4	2386
0.019848	0.483485	Grid1	-54868
0.008264	0.460496	Sh2d4b	-10478
0.031074	0.579835	Ear3	14026
0.005124	0.403967	Otx2	41403
0.018347	0.453884	Otx2	9884
0.023306	0.527438	Otx2os1	34639
0.006612	0.430248	Otx2os1	53864
0.017355	0.548099	Ltb4r2	0
0.009587	0.506777	Cryl1	97247
0.01719	0.458678	Cryl1	-9418
0.026612	0.486446	Il17d	17821
0.031736	0.507107	1700129C(	66490
0.011212	0.485909	Tnfrsf19	-38565

0.02876	0.431405	Dleu2	-3117
0.017063	0.527972	Defb48	18280
0.005594	0.488531	Defb30	-35575
0.007121	0.484545	Gata4	5505
0.022576	0.437727	Gata4	1021
0.010744	0.497686	Gata4	-11415
0.034641	0.542871	Adra1a	1397
0.019339	0.485289	Nefl	-33060
0.014848	0.51803	5031414D:	18858
0.013388	0.48281	AK013627	-3515
0.019174	0.503141	Tsc22d1	8608
0.014439	0.508877	Serp2	-42269
0.019174	0.493719	1700108F1	-18540
0.016198	0.539174	1190002H:	25189
0.022479	0.500331	1190002H:	-272
0.010629	0.486993	Klf5	25892
0.025315	0.405035	Rnf219	623
0.010744	0.401322	Spry2	36018
0.02	0.49124	AK039417	-10726
0.012066	0.441488	Abcc4	-6548
0.010909	0.451736	Ubac2	-12472
0.025175	0.447832	AK011684	3310
0.020165	0.461653	AK011684	2015
0.015372	0.504793	Zic2	8202
0.022975	0.551074	Zic2	8906
0.020455	0.368485	Zic2	14174
0.014242	0.454394	Osmr	-9951
0.02562	0.493554	Gm1943;W	-2415
0.024697	0.487727	Dnahc5	-21674
0.018042	0.506853	Ankrd33b	56828
0.008926	0.468099	Vps13b	-18835
0.017273	0.433788	Ywhaz	-17644
0.012066	0.481322	Ncald	1612
0.009421	0.444298	Ubr5	11712
0.014215	0.512066	Odf1	-20699
0.011074	0.460661	AK134270	-18555
0.011405	0.427438	BC048765	-48525
0.012208	0.438182	Oxr1	1251
0.020496	0.411901	Csmd3	304
0.010227	0.454659	Eif3h	62224
0.009091	0.480321	Dscc1	-6951
0.012727	0.415	Deptor	9243
0.016694	0.51124	Fam83a	-8723
0.012078	0.458442	Mtss1;mKI	-63412
0.02303	0.472121	DQ560483	49473
0.011736	0.498512	Pvt1	-10587
0.01157	0.508099	Pvt1	11079

0.015372	0.454711	Kcnq3	745
0.021667	0.52197	Top1mt	-1022
0.010182	0.523515	Mafa	3618
0.007603	0.426281	Gsdmd	15297
0.010248	0.46843	1110038F1	28010
0.006777	0.440661	Rbfox2;Rbi	3688
0.015207	0.472893	BC100417	14825
0.008571	0.502987	Myh9	-4854
0.012066	0.531901	Txn2	24411
0.012397	0.558843	Cdc42ep1	-7084
0.015455	0.484545	Galr3	1705
0.013697	0.560606	Pdgfb	-288
0.015702	0.570579	Snord83b	15287
0.008727	0.49903	Snord83b	11828
0.006116	0.48314	Nhp2l1	-1129
0.01719	0.524297	Tnfrsf13c	8644
0.011901	0.568099	Tcf20	-17047
0.019441	0.513427	Scube1	-24808
0.021667	0.568788	Efcab6	-2876
0.030909	0.407576	Scaf11	-82575
0.017273	0.510606	Slc38a4	-69897
0.007934	0.54562	Rapgef3	11066
0.013333	0.499848	HDAC7	-8548
0.01	0.535455	Hdac7	4003
0.015944	0.455524	AI836003	12129
0.024242	0.465909	AK217757	7476
0.017013	0.483247	Dhh	5154
0.013147	0.565035	Prph	-1723
0.015868	0.579008	Prph	-310
0.010649	0.477013	Dnajc22	-3089
0.019174	0.38876	Spats2	592
0.00987	0.465974	Fam186b	-1700
0.016033	0.516529	Gpd1	-542
0.016364	0.471212	Lima1	-17274
0.020909	0.541948	Ankrd33	-30806
0.01697	0.558424	Ankrd33	-23075
0.013636	0.530649	Ankrd33	-21292
0.01686	0.464463	AK039268	-14749
0.009752	0.498678	Nr4a1	-19393
0.014026	0.511818	Krt18	-3747
0.011636	0.533333	Rarg	-3919
0.019339	0.463636	Aaas	-5880
0.008264	0.456198	Sp1	-9683
0.03405	0.513554	Calcoco1	-25330
0.030455	0.468182	Hoxc13	-2310
0.033554	0.52314	AK035706	-2132
0.02314	0.466446	Hoxc10	-3751

0.01972	0.42979	Mir196a-2	-1031
0.017576	0.484394	Hoxc4	0
0.031736	0.520331	Hoxc4	-6912
0.036364	0.499301	Hoxc4	26201
0.006777	0.470083	Usp7	7321
0.013223	0.508926	Usp7	3811
0.011405	0.463471	Litaf	1016
0.023485	0.471061	Pla2g10	-23236
0.021322	0.551901	Ypel1	-17937
0.009421	0.507934	Ypel1	4323
0.009091	0.496364	Hic2	17755
0.010083	0.519835	Hic2	18884
0.013058	0.461818	Aifm3	-446
0.010909	0.447273	Abcc5	-17172
0.024476	0.475524	Ephb3	30473
0.011515	0.508606	Vps8;mKIA	-33001
0.018182	0.486116	Liph	10719
0.009752	0.468264	Fgf12	-47755
0.017343	0.439161	Opa1	102360
0.01124	0.504132	AK144120	60398
0.017727	0.452879	Tmem44	38423
0.020331	0.558347	Pigz	-27045
0.01049	0.468112	mKIAA022	10505
0.01157	0.493554	AK160141	43947
0.011591	0.471932	Sema5b	45395
0.011515	0.411061	Golgb1	3574
0.015455	0.446667	BC031361	-20841
0.012086	0.430588	Gsk3b	24437
0.014965	0.417622	4932425I2	-392
0.007879	0.448364	Popdc2	21448
0.024959	0.442645	B4galtn4	-193
0.016818	0.484242	Gap43	-103917
0.02562	0.470579	Phldb2	-410
0.012397	0.393884	Bbx	-49040
0.021576	0.426788	Nfkbbz	-784
0.031444	0.453476	Cggbp1	21199
0.013554	0.429091	Robo1;Rok	23610
0.018512	0.432066	Btg3	-49896
0.035829	0.469091	Olig2	2326
0.018788	0.430909	maa-13	-3616
0.019848	0.513636	Runx1	86307
0.024298	0.510248	Kcnj6	622
0.015868	0.509587	Snx9	44383
0.016529	0.542314	Rps6ka2	11022
0.006061	0.498061	AK015714	4807
0.009242	0.510303	T2	1045
0.014455	0.525545	T2	16984

0.019669	0.538678	T	887
0.02281	0.422314	AK019626	10223
0.010568	0.525795	Dact2	35973
0.012078	0.496364	Gm10510	147049
0.01961	0.432857	Zfp213	24867
0.012879	0.514848	Rab26	-1269
0.011405	0.447273	Rab26	-6783
0.010579	0.425124	Wdr24	-1951
0.011515	0.480303	A930001N	-5761
0.022781	0.515187	Nkx2-5	4017
0.030568	0.516136	Nkx2-5	572
0.01438	0.492066	Nkx2-5	-175
0.012562	0.540165	DQ718216	0
0.016033	0.479008	Nudt3	21262
0.023471	0.502479	Pacsin1	568
0.017851	0.482645	Ppard	-795
0.011405	0.483636	Clps	4515
0.016364	0.406116	Brpf3	-1111
0.009917	0.473058	Pnpla1	-14240
0.016694	0.5	Pxt1	10304
0.021322	0.455207	Sfrs3;Srsf3	-8315
0.016529	0.483471	LOC100491	-528
0.01303	0.529394	Pim1	-32497
0.021653	0.496364	BC048393	0
0.013719	0.543802	Tap2	-435
0.020496	0.458843	H2-Ab1	748
0.016084	0.508951	Prrt1	-542
0.016623	0.564805	Ly6g6e	0
0.022314	0.591405	Gm8909;H	716
0.011273	0.500485	Pou5f1	-15013
0.007438	0.465785	Psors1c2	1836
0.00876	0.493223	2300002M	5951
0.012987	0.489091	Ddr1	-6196
0.020165	0.478512	AK053296;	-262
0.015568	0.472955	Pla2g7	575
0.009545	0.460568	Clic5	99518
0.011364	0.536061	AK080425	2503
0.017025	0.541488	AI661453	-7322
0.015868	0.495702	AK088937	-3714
0.01124	0.493058	Unc5cl	153170
0.016694	0.521488	Uhrf1	-522
0.014697	0.527727	Ranbp3	-9208
0.00875	0.400114	Fert2	139230
0.011736	0.456529	1110012J1	-8492
0.013676	0.49415	AK082862	24612
0.014215	0.447438	Myl12b	-831
0.012562	0.466116	Smchd1	-11228

0.02303	0.507273	Lbh	-27660
0.020826	0.56	Memo1	22068
0.01438	0.423636	Rasgrp3	-10858
0.012879	0.476364	Vit	47124
0.037071	0.54596	Strn	-13994
0.023471	0.444628	Hnrpll	-1026
0.022121	0.436667	Galm	769
0.026612	0.51124	Pkdcc	-92179
0.02	0.542479	Pkdcc	-1099
0.027769	0.556033	Six3	-147662
0.015207	0.451405	Six3	-128946
0.017273	0.442879	Six3	-124289
0.029773	0.465114	Six3	-3687
0.007769	0.499504	Msh6	-41600
0.021515	0.452121	AK007204	34571
0.026818	0.475909	Mkx	1506
0.018678	0.465455	Fzd8	-1025
0.012397	0.464959	Lama3	-252
0.017727	0.443636	Kctd1	1907
0.013485	0.448788	Rnf125	-590
0.010424	0.429939	Galnt1	-15768
0.01124	0.437355	Epb4.1l4a	-94459
0.011667	0.485455	Kdm3b;mK	6925
0.009091	0.468099	Tmem173	-4448
0.015974	0.494156	Cxxc5	3172
0.019174	0.596364	Cxxc5	7418
0.017851	0.559669	Cxxc5	-4030
0.010579	0.515041	AK021191	18930
0.018667	0.551515	Arap3	-98999
0.011979	0.5	Pcdh1	23732
0.017727	0.532955	Pcdh1	1271
0.012562	0.436694	Gnpda1	-36974
0.019251	0.490588	Spry4	28522
0.009519	0.535294	9630014M	47369
0.014711	0.415207	Stk32a	475
0.011515	0.399849	Sema6a	3449
0.010424	0.483394	Cd74	0
0.00876	0.503967	Camk2a	10132
0.012879	0.544091	Il17b	303
0.018678	0.490248	1500015A(	21777
0.011901	0.489917	St8sia3	-239388
0.013388	0.491901	5330437l0	43454
0.023394	0.438545	Spire1	3487
0.01438	0.407603	Spire1	-1057
0.02	0.443471	AK036329	539
0.010152	0.504848	AK008334	32155
0.019835	0.549917	AK008334	-33500

0.019572	0.509626	Smad7	-22689
0.011364	0.437424	Sall3	-4029
0.015868	0.453388	AK015395	-30285
0.017851	0.444959	Zfp516	-7591
0.016234	0.423766	Zfp516	1950
0.009091	0.513554	Tbc1d10c	2680
0.011901	0.517355	Rad9	-6088
0.015868	0.561322	Spnb3	9002
0.009333	0.546909	Cd248	-7329
0.017697	0.468	4930481A:	-535
0.012121	0.55803	Malat1	-15856
0.016494	0.518571	Slc22a12	11194
0.014215	0.520331	Slc22a12	-71852
0.013485	0.577424	Macrod1	9139
0.006942	0.477521	Slc3a2	7416
0.017778	0.485354	Incenp	-24846
0.009091	0.424394	Tmem216	-3805
0.014394	0.420152	Psat1	-17356
0.019835	0.448595	Gcnt1	-3341
0.014215	0.419339	Tjp2	2720
0.011061	0.446818	Tjp2	-25859
0.015702	0.497851	Dmrt3	-46210
0.021604	0.419037	Smarca2	0
0.019021	0.427972	NIRF;Uhrf2	-11947
0.014876	0.422479	Tnks2	-14471
0.015537	0.463802	DQ693081	19387
0.016529	0.405124	Cyp26c1	-28563
0.008926	0.469256	Cyp26c1	-26492
0.039421	0.543471	Cyp26a1	-574
0.010909	0.45405	mKIAA120	60470
0.010248	0.506116	mKIAA120	55562
0.021488	0.438512	Rbp4	0
0.012562	0.43124	AK035873;	8573
0.018462	0.451189	Sorbs1	-354
0.012273	0.446364	AK082813	644
0.034788	0.448364	Hps2	2196
0.018881	0.454545	Nkx2-3	-2566
0.017182	0.468	Scd3	8299
0.013506	0.464156	Scd3	27376
0.012879	0.475758	Scd1	-945
0.013576	0.551879	Wnt8b	24340
0.03157	0.529421	Pax2	-16286
0.023916	0.519301	Pax2	-14476
0.031082	0.539913	Lbx1	9914
0.017025	0.484463	Btrc;Fbxw1	-62768
0.015372	0.532727	Sufu	9301
0.026788	0.514303	Sorcs3	608050

0.023967	0.495207	Mxi1	-3299
0.020559	0.483497	5830416P1	26797
0.021538	0.526154	5830416P1	1832
0.014711	0.483967	Rbm20	-2743
0.028068	0.474773	Rbm20	401
0.011688	0.501429	Pdcd4	-890
0.007107	0.477025	Adra2a	124882
0.01124	0.452397	1700019N	12377
0.031602	0.533766	Emx2	3145
0.030519	0.487403	Emx2	9580
0.00803	0.44197	Prlhr	-1840
0.018512	0.49124	Fam107b	86087
0.010744	0.471074	AK006958	20894
0.015758	0.465455	Frmd4a	61176
0.024793	0.492727	Optn	-34143
0.013388	0.440661	Usp6nl	-838
0.015804	0.424615	Gata3	2304
0.023333	0.523434	AK020309	-6864
0.012727	0.490744	AK085384	-7639
0.012397	0.458512	C1ql3	-1039
0.016529	0.440661	Rsu1	-5585
0.006281	0.409917	Ptpla	46674
0.019174	0.503802	A930004D	-1215
0.019339	0.359008	Commd3	-85430
0.011515	0.455909	4921504E	465
0.008848	0.568727	Ptgds	0
0.014091	0.477879	Fam69b	-514
0.004545	0.461558	Brd3	15057
0.021591	0.507045	Ier5l	2492
0.012066	0.49124	Cstad	-48719
0.004628	0.488099	AK138941	16102
0.010667	0.523758	AK138941	938
0.023102	0.568021	1700001O	16041
0.012727	0.510083	Asb6	-330
0.006612	0.491901	Ptges	17456
0.013766	0.508571	Fnbp1	8974
0.029242	0.493788	Ncs1	-6470
0.010909	0.543896	Ncs1	-3157
0.012397	0.539669	Ncs1	-929
0.00876	0.527769	Ncs1	13932
0.017521	0.508926	Fibcd1	-1159
0.015195	0.473896	Prrc2b	3558
0.017273	0.513939	Prrc2b	7464
0.013091	0.496364	Lmx1b	60327
0.016529	0.518017	AK142949	-3
0.008	0.541455	Crb2	-7578
0.012562	0.522149	Crb2	18199

0.018701	0.545714	Nr5a1	21254
0.013554	0.520331	Olfml2a	441
0.018843	0.56281	Cacnb4	-19742
0.013007	0.440699	Fmnl2	69622
0.007769	0.480826	Upp2	-48161
0.022303	0.430788	Fign	-379160
0.030795	0.487045	Galnt3	82512
0.012955	0.558182	Phospho2	11828
0.012364	0.445818	Sp5	-16473
0.005795	0.451364	4933404M	10499
0.015041	0.455207	Gorasp2	-474
0.019545	0.415	Dlx1	3659
0.022149	0.462479	Dlx1	-330
0.014242	0.462273	Cdca7	23639
0.014876	0.441983	Cdca7	31017
0.017686	0.416529	Cdca7	143536
0.027692	0.528252	Hoxd12	-320
0.009818	0.489333	Mir10b	-991
0.009752	0.424793	Hoxd3	2517
0.019394	0.39697	AK144266	-3885
0.025289	0.491074	AK144266	0
0.008926	0.426942	AK053216	48630
0.009587	0.462149	Sestd1	-46887
0.017521	0.460165	Zfp385b	654
0.028364	0.503758	Neurod1	1164
0.02595	0.469752	Neurod1	-3457
0.012308	0.473007	Ube2l6	-8680
0.012727	0.495868	Tnks1bp1	-945
0.028831	0.493896	Olfr1057	8978
0.010909	0.46595	AK020549	4512
0.021322	0.519339	Alx4	2559
0.010909	0.535868	Accsl	-38927
0.025041	0.505537	AI314831	1594
0.022657	0.514825	Wt1	-1687
0.036	0.505697	Pax6	-6431
0.023967	0.491736	Pax6os1	-30
0.029032	0.520293	Pax6os1	-1042
0.011169	0.48961	Pax6	2519
0.031901	0.509917	Ryr3	-367
0.016198	0.439504	meis2a	18287
0.024909	0.412364	meis2a	13792
0.014476	0.420629	AK144485	791
0.015065	0.405714	2810405F1	2117
0.010413	0.464298	Mir674	24361
0.010083	0.505289	Bmf	3789
0.009752	0.473884	Mga	-30301
0.011136	0.543977	Mall	-294

0.014545	0.422159	Bcl2l11	82572
0.020331	0.476198	Polr1b	-127
0.019504	0.481653	Rassf2	-1051
0.021136	0.504205	Plk1s1	-19425
0.020291	0.521236	Nkx2-2as	-1473
0.021399	0.518042	AK041531	-539
0.014215	0.448595	Foxa2	-2308
0.012066	0.512893	Tcf15	-1789
0.014026	0.556364	Id1	-6125
0.005124	0.475537	Bcl2l1	9911
0.011748	0.495245	Hck	895
0.009952	0.606316	8430427H:	17750
0.025289	0.558017	Commd7	48590
0.016043	0.514973	Commd7	23211
0.009576	0.488121	Commd7	-285
0.008926	0.473554	Dnmt3b	-1058
0.012066	0.447603	Mapre1	-606
0.011515	0.481697	Snta1	-11515
0.021678	0.500559	E2f1	-443
0.017902	0.49958	Epb4.1l1	1467
0.013493	0.52622	Ghrh	-1881
0.045292	0.520325	Nnat	0
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0.01	0.508312	Dhx35	439943
0.017212	0.457939	Chd6;mKIA	-68839
0.015795	0.504886	Mmp9	-7872
0.019669	0.56843	1700025C:	-43201
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0.012424	0.515455	AK077074	-34507
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0.008595	0.504959	Fam65c	-15661
0.013884	0.506446	Pard6b	-23274
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0.006434	0.437483	Adnp	6222
0.021157	0.52562	Kcng1	-10489
0.017521	0.438182	Sall4	-70949
0.015702	0.515041	Zfp64	50590
0.012576	0.463636	BC042727	-73691
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0.013788	0.532576	BC116387	-106453
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0.012397	0.570744	Pmepa1	23364
0.015636	0.51297	Cdh26	204155
0.014215	0.466281	Adrm1	-1030
0.01026	0.574805	Lama5	6701

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0.010579	0.5	Abhd16b	-9448
0.022424	0.489091	Sox18	1319
0.024156	0.498831	Zfhx4	-7344
0.012841	0.425455	Zfhx4	-3858
0.022488	0.41445	C030034L1	-56389
0.012397	0.460992	Chmp4c	799
0.020992	0.463306	2610100L1	51
0.021914	0.455502	Mir124a-2	0
0.017063	0.454825	Armc1	100567
0.015868	0.419174	Tbl1xr1	6078
0.02	0.465874	Mecom	3546
0.01861	0.448663	Mecom	-2322
0.012562	0.441322	Cldn11	-8613
0.026631	0.415829	Mir1897	2751
0.033673	0.483709	Sox2	11608
0.007841	0.480341	Sox2	16556
0.015207	0.480331	DQ549901	-81460
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0.006818	0.445606	AK029958	323238
0.016485	0.426667	Intu	1299
0.021653	0.47124	Hspa4l;apg	-840
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0.02689	0.456938	ELF2;Elf2	-16651
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0.017416	0.424785	AK040671	-101180
0.017686	0.455702	Nbea	-254481
0.013884	0.409091	Ssr3	-42866
0.026364	0.43197	Lekr1	-214
0.016364	0.435372	AK144610	1171
0.00979	0.460559	Ccnl1	29422
0.020909	0.394805	Shox2	7944
0.015372	0.538347	Kirrel	2892
0.012066	0.530083	Crabp2	-2670
0.015568	0.5475	Nes	1308
0.012597	0.475844	Mef2d	-4385
0.019432	0.482727	Mef2d	-2164
0.009091	0.570413	Mef2d	8386
0.020152	0.536061	Efna4	-763
0.024463	0.54876	Ube2q1	15186
0.017686	0.458512	She	31580
0.013388	0.430579	Ints3	-11974
0.012727	0.486942	Ints3	-14717
0.014685	0.516364	Rorc	-3842
0.01719	0.413884	Pogz	-15428

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0.012364	0.480121	Car14	911
0.015868	0.556859	Sv2a	618
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0.017025	0.476529	Terc	-10730
0.027727	0.48697	Hfe2	-27876
0.016198	0.449917	Txnip	-10609
0.009421	0.467107	Cd160	-402
0.017203	0.482797	Tbx15	-17225
0.028182	0.491061	Tbx15	-3738
0.024026	0.473117	Tbx15	-995
0.013182	0.452727	Tbx15	1812
0.015868	0.499339	Igsf3	28081
0.013566	0.503636	Wnt2b	-1061
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0.017879	0.486515	Fndc7	2133
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0.017424	0.508788	A730020M	54174
0.017025	0.467273	F3	-1701
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0.017521	0.424628	Pitx2	-1444
0.01803	0.404697	Pitx2	-1580
0.014432	0.494091	Pitx2	12121
0.021091	0.426061	Ppp3ca	1221
0.0125	0.43	Gtf2b	-3684
0.013223	0.47124	Hs2st	14137
0.011469	0.398322	Hs2st1	1828
0.016529	0.423141	Sh3glb1	1326
0.020963	0.494011	FJ422280	3523
0.012231	0.424463	Lphn2	-103333
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0.01157	0.47124	Chd7	52977
0.010909	0.482797	Chd7	63424
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0.019545	0.406515	Clvs1	-133692
0.012397	0.478512	Plekhf2	44502
0.019835	0.447438	2310030Nl	30954
0.016364	0.418843	6230409E1	201295

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0.014876	0.497025	Gm829	52705
0.013576	0.508242	E230008N:	-19920
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0.022208	0.467013	Klf4	16454
0.011901	0.461983	Ctnnal1	-826
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0.022645	0.46281	Gng10	1182
0.01405	0.498017	OTTMUSGI	43703
0.015702	0.439339	Zfp37	-480
0.009752	0.50843	Rgs3	-11988
0.026014	0.52014	Frmd3	393
0.012397	0.430579	Nfib	-37454
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0.012576	0.39197	Cdkn2a	2134
0.012397	0.465289	Cyp2j9	-92
0.021322	0.492397	AK047309	2725
0.01405	0.507603	AK166708	10619
0.006446	0.43686	Foxd3	-93034
0.03103	0.504	Foxd3	5356
0.009091	0.472893	Echdc2	-1552
0.016643	0.498601	Fam159a	24901
0.014215	0.52843	Pdzk1ip1	7838
0.034685	0.492308	Dmbx1	1485
0.029545	0.533485	Dmbx1	-360
0.02595	0.48595	AK078255	53
0.015041	0.573388	Rnf220	-33955
0.011196	0.482392	Rnf220	-36984
0.015207	0.549917	Ptprf	1699
0.010413	0.493719	Mpl	-12824
0.025114	0.454659	Olfcr1339	9130
0.011515	0.517576	Slc2a1	-32985
0.013884	0.492727	Slc2a1	-3353
0.01303	0.488636	Hivep3	19163
0.009421	0.456694	Hpcal4	-6657
0.010606	0.495758	AK018866	5891
0.02	0.454788	Pou3f1	-41099
0.014215	0.500661	Sf3a3	-4815

0.012468	0.474156	Ftl2	32920
0.019394	0.532424	2610028Ec	193671
0.014545	0.472397	Tmem54	-19198
0.010152	0.486818	C77080	-1915
0.01405	0.500826	C77080	-2041
0.024298	0.554711	Khdrbs1	-29787
0.0175	0.498977	Fgr	-13706
0.013939	0.533939	Fgr	1140
0.014848	0.557424	Ahdc1	3512
0.011405	0.532066	Ahdc1	8781
0.013719	0.491074	Slc9a1	7028
0.019504	0.441983	Fam46b	-12282
0.008112	0.540699	Fam46b	2424
0.019174	0.526777	Aim1l	-10039
0.02	0.528442	Grrp1	643
0.016529	0.580826	Grrp1	-2040
0.013554	0.46843	Clic4	30296
0.019205	0.57875	Grhl3	2325
0.019669	0.501653	Il28ra	-18826
0.01438	0.480331	Il28ra	-12479
0.004959	0.442645	Tceb3	4927
0.024141	0.481414	Rpl11	-30140
0.013247	0.465455	Luzp1	-4748
0.008052	0.426364	Kdm1a	2113
0.012727	0.472121	Alpl	-5439
0.011074	0.466116	Camk2n1	2752
0.010629	0.551468	Vwa5b1	-11273
0.020826	0.520661	Vwa5b1	-41537
0.017851	0.464132	Ubxn10	23379
0.013554	0.586777	Pax7	69604
0.020165	0.581653	Padi4	-99
0.016529	0.500331	Epha2	-12128
0.010248	0.553554	Fam131c	5740
0.011736	0.408595	Spen	-3025
0.017025	0.464132	Pdpn	-1163
0.015868	0.475702	Fbxo6	1556
0.016136	0.432841	Gm572	2448
0.020839	0.573287	Gm572	68213
0.012424	0.509394	Casz1	61510
0.015868	0.541157	Casz1	-60060
0.021399	0.525455	Pik3cd	1647
0.016694	0.431901	Gpr157	-872
0.012562	0.539339	Gpr157	6771
0.031169	0.534935	Car6	24372
0.011189	0.453846	Rere	-36062
0.010606	0.442879	Rere	-32670
0.010758	0.528788	Tas1r1	173

0.016212	0.567273	Gpr153	-1815
0.015868	0.53405	Hes3	-1425
0.009587	0.511901	AK131834	84396
0.020992	0.556364	Arhgef16	381
0.025758	0.417424	Crot	-361
0.017212	0.404364	Psmc2	437
0.010758	0.526818	Nos3	-494
0.013554	0.509091	Wdr86	-1311
0.016136	0.533523	Xrcc2	36822
0.014909	0.480848	En2	-5192
0.02014	0.52042	En2	-2678
0.021322	0.476198	Mnx1	6445
0.024364	0.463273	Mnx1	5145
0.009587	0.460496	Mnx1	2403
0.016364	0.52314	Mnx1	-6277
0.00843	0.46281	AK153014	56314
0.009752	0.488595	Fam59b	4637
0.011212	0.501364	mKIAA180	-4837
0.011074	0.492397	Plb1	-9496
0.009917	0.458347	Ywhah	-890
0.010083	0.419339	Ywhah	24284
0.016198	0.497025	Rnf4	-8458
0.007769	0.473388	Stk32b	-922
0.016364	0.507107	Msx1	-6090
0.014406	0.508392	Msx1	-6669
0.00993	0.476084	Msx1	-8339
0.019221	0.402208	Zfp518b	-89345
0.017902	0.437343	Nkx3-2	7608
0.015041	0.489917	Cc2d2a	0
0.017622	0.491049	Rbpj	-85857
0.016364	0.435273	Rbpj	10046
0.019192	0.507778	AK164362	31837
0.014545	0.482614	Tbc1d1	-647
0.009394	0.474394	Klh15	-47474
0.014091	0.503182	Apbb2	35339
0.027769	0.515537	Phox2b	3425
0.033884	0.484628	Phox2b	1549
0.03438	0.463058	Phox2b	71
0.036364	0.487194	Phox2b	-1330
0.013058	0.472397	Gabra4	1687
0.013058	0.426446	Slain2	-17494
0.015372	0.521322	Hopx	-22612
0.012879	0.460606	art3	-5683
0.012028	0.492867	Sept11	-23789
0.03197	0.512576	Prkg2	-405
0.01124	0.466446	Rasgef1b	-34755
0.015702	0.479669	Wdfy3	26070

0.015702	0.429917	Arhgap24	30035
0.024132	0.478017	AK043904	-53
0.030736	0.514719	Barhl2	-8891
0.02625	0.455227	Barhl2	-10451
0.013007	0.46993	Zfp644	-12992
0.024959	0.479504	AK042124	94
0.019339	0.542314	AK138421	6266
0.046845	0.462674	Mn1	-1575
0.018843	0.530248	Sgsm1	-7130
0.014424	0.509939	1700069L1	1009
0.02314	0.455702	Rnf10	-2608
0.008264	0.467273	Hspb8	21704
0.013566	0.455105	Hspb8	13985
0.01405	0.478843	Srrm4	-1372
0.017025	0.519339	Rnft2	30461
0.015207	0.481157	Med13l	6989
0.013455	0.515394	Tbx3	-10084
0.023636	0.513554	Tbx3	-2649
0.019659	0.44875	Tbx3	3686
0.025175	0.545315	Dtx1	1010
0.018678	0.535372	Dtx1	-184
0.013884	0.5	Dtx1	-1154
0.012834	0.480107	Orai1	-751
0.020826	0.492397	Morn3	6842
0.019515	0.486061	Morn3	-2799
0.017851	0.49405	Zfp664	50640
0.012562	0.523471	Scarb1	68252
0.017025	0.446281	Ubc	-12236
0.01803	0.521818	Tmem132c	-674
0.008977	0.472386	Glt1d1	-526
0.00876	0.50595	Gusb	925
0.013939	0.420455	Auts2	2549
0.009421	0.433554	AK076755	-87390
0.019008	0.440992	Gtf2i	-8041
0.010248	0.507438	Clip2	12429
0.01197	0.470606	AK188353	-4012
0.011023	0.453864	Fzd9	3744
0.013719	0.527107	Hspb1	-4595
0.012727	0.496234	14-3-3 gamma	-10824
0.020455	0.479091	Ephb4	-2012
0.013273	0.567636	Lfng	-1618
0.012397	0.486612	Sdk1	-1657
0.015041	0.445289	0610040B:	9967
0.018512	0.475868	Nptx2	-88922
0.01438	0.465455	Nptx2	-2093
0.024848	0.450758	Nptx2	1586
0.013719	0.451405	Tmem130	3109

0.016198	0.432231	Arpc1a;Sid	-13462
0.010909	0.45719	Lnx2	5550
0.025929	0.498182	Gsx1	3287
0.021157	0.509421	Gsx1	36950
0.013333	0.50803	Gsx1	38008
0.012168	0.51021	Cdx2	-1342
0.034141	0.519125	Cdx2	-5184
0.034242	0.492273	Casd1	569
0.027879	0.472727	Casd1	52023
0.012231	0.48314	Ppp1r9a	-6006
0.014876	0.491405	Pon3	-63
0.015868	0.473388	Dlx6os1	6563
0.025114	0.45625	Acn9	-165
0.017273	0.434286	Ndufa4	113794
0.017355	0.472727	Gm6578	-153359
0.025175	0.388392	Foxp2	-3232
0.024545	0.471515	Foxp2	-2034
0.027438	0.472231	Zfp800	58324
0.011364	0.457121	Lrrc4	60782
0.030769	0.471608	Prrt4	-541
0.010303	0.573939	FlnC	1492
0.016364	0.453706	AK006282;	-344
0.011212	0.465606	Ube2h	34871
0.016033	0.492397	AK008857;	-311
0.020992	0.454215	Jhdm1d	-63218
0.015207	0.460992	AnMKRN1	2158
0.015207	0.451074	Zyx	-955
0.016818	0.442576	Epha1	-5695
0.018512	0.482149	Zfp467	5702
0.019394	0.490303	Dfna5	25460
0.014965	0.482657	Skap2	204145
0.012562	0.430579	Hoxa1	5473
0.02281	0.41157	AK142386	-2998
0.024432	0.502955	2700086A(	4438
0.009256	0.474876	Hoxa4	2092
0.029282	0.490239	Hoxa7	0
0.02595	0.415207	Hoxa10	1050
0.014545	0.480227	Evx1	-620
0.011405	0.490744	Jazf1	66266
0.014711	0.489587	Jazf1	-50735
0.015537	0.426777	Znrf2	-786
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0.00803	0.490303	AK029473;	-7932
0.013377	0.466494	AK029473;	-6947
0.018333	0.432727	Serbp1	-38246
0.010744	0.401984	Serbp1	-1415
0.011705	0.516591	Tlx2	3168

0.018512	0.560661	Tlx2	-1375
0.011736	0.475041	Vax2os2	5638
0.018788	0.523333	Vax2os2	-1713
0.019886	0.448068	1700019G	6237
0.010083	0.460826	Tgfa	-994
0.01405	0.520331	Tgfa	15566
0.016033	0.535207	AK009724	-8750
0.010083	0.511405	Asprv1	-41851
0.008099	0.497686	Tpra1	29482
0.013455	0.520364	Klf15	-11616
0.010579	0.504132	Trh	-461
0.01405	0.447934	AK007436	-1184
0.020121	0.466545	Lrig1	-72786
0.018843	0.418182	Frmd4b	1233
0.018182	0.466212	Frmd4b	1478
0.02843	0.492893	Mitf	-65761
0.020496	0.499174	Gpr27	-728
0.004793	0.538182	Rybp	101460
0.009848	0.496061	Rybp	74751
0.020331	0.561322	Rybp	73236
0.006942	0.479669	Rybp	-91531
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0.016198	0.513223	AK006738	0
0.010053	0.469412	AK002866	0
0.012727	0.517025	Il17rc	-2491
0.014242	0.495303	Tatdn2	-7282
0.037576	0.594697	Atg7	-77176
0.020455	0.534848	VglI4	-13603
0.015758	0.519394	Cacna1c	-80849
0.016033	0.581157	Lrtm2	0
0.012397	0.473223	Adipor2	-547
0.014545	0.455702	Ninj2	19561
0.015207	0.560496	Ninj2	92500
0.013719	0.554545	Nanog	-1084
0.016033	0.422975	Slc2a3	-2705
0.013058	0.470909	Foxj2	-34601
0.019008	0.489256	Foxj2	-33660
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0.018636	0.510909	Plekhg6	375
0.01686	0.53124	Vwf	-24412
0.015702	0.546446	Ntf3	2334
0.015537	0.538182	Ccnd2	-100103
0.037143	0.43013	Magohb	-44
0.021558	0.455974	Csda	-295
0.005785	0.426116	Lrp6	21654
0.004755	0.421119	Lrp6	6854

0.011736	0.43124	Gpr19	-3122
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0.011074	0.452066	Pde3a	-146364
0.010248	0.391901	Kcnj8	2851
0.012857	0.473507	AK008222	40335
0.013576	0.461576	4833442J1	-16104
0.012727	0.460909	Nlrp12	-14149
0.013636	0.476515	Cacng8	-25125
0.018202	0.488031	Cacng6	28921
0.00951	0.530629	Zfp628	-16089
0.008264	0.454545	A430110N	6583
0.017686	0.503141	Zbtb45	-723
0.013388	0.525455	Snord23	4644
0.010303	0.476364	Bbc3	-8055
0.013014	0.531866	Ptgir	-4024
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0.013223	0.500992	Nova2	22631
0.02876	0.502149	AK034341	-321
0.009752	0.535537	Gipr	-2009
0.028182	0.534545	Mark4	-6711
0.012893	0.494545	Pvrl2	-3792
0.013884	0.500661	Bcl3	-2642
0.005289	0.47686	Zfp575	-4624
0.01438	0.53124	Fcgbp	-11703
0.013554	0.489917	Supt5h	-3160
0.013576	0.499152	Kcnk6	0
0.021932	0.510568	Ppp1r14a	467
0.014215	0.435372	Dpf1	4551
0.021515	0.52803	Fxyd3	6862
0.026294	0.412168	Kctd15	58169
0.014545	0.476667	Chst8	-36475
0.017521	0.491736	Cebpa	-1809
0.032231	0.456859	Lrp3	-18334
0.012066	0.463802	Tshz3	-171580
0.028517	0.476555	Tshz3	-6028
0.026014	0.433986	AK019701	-44269
0.024091	0.491818	Zfp619	27145
0.023802	0.510579	Shank1	-190
0.014286	0.531818	Slc17a7	536
0.029587	0.537025	mKIAA065	114
0.02625	0.544205	Tulp2	649
0.012066	0.518347	Plekha4	1747
0.011074	0.558678	Hsd17b14	-766
0.019432	0.486591	Sult2b1	1969
0.009752	0.54843	Abcc6	16764
0.017121	0.567879	Ldha	-10469
0.027159	0.524091	Nav2	355

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0.015041	0.464628	Dbx1	-25764
0.012121	0.458788	Dbx1	-50776
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0.016694	0.444628	AK149394	-1519
0.020325	0.494156	AK049871	3900
0.020826	0.470909	AK049871	3180
0.028312	0.510167	AK049871	-8894
0.02303	0.468333	Nr2f2	502
0.02014	0.51958	Nr2f2	-933
0.011736	0.486281	Fanci	-1569
0.008252	0.519021	Rhcg	10517
0.015303	0.476212	Plin1	761
0.00843	0.469752	Zfp710	-2199
0.013223	0.513058	Crtc3	-10602
0.012397	0.469422	E230029C	1005
0.018017	0.48562	Dlg2	-54518
0.010061	0.449576	Mir326	21866
0.00703	0.447273	Rnf169	3995
0.016529	0.409421	P2ry2	19273
0.012893	0.49405	Art1	218
0.021322	0.504793	Dkk3	-159
0.019242	0.437424	AK009335	-15146
0.012893	0.461818	AK009335	-16693
0.01157	0.452893	Tead1	51515
0.022517	0.521259	Arntl	-19226
0.01405	0.465785	Rras2	29914
0.024463	0.444793	Sox6	0
0.010744	0.494876	Prkcb	115978
0.010424	0.47297	AK043947	23282
0.015868	0.45719	Zfp747	11433
0.014876	0.46314	Nsmce4a	-4549
0.01157	0.462314	Plekha1	-5869
0.011364	0.498788	AB033524	-45602
0.011364	0.453788	Gpr26	-67039
0.011405	0.527273	Fam53b	-4560
0.00876	0.44281	Dhx32	7740
0.025124	0.522645	Dock1	-358
0.012562	0.477521	Mgmt	-398
0.010303	0.465	Ifitm1	-138
0.007769	0.496033	Ifitm6	-8390
0.009939	0.415758	Ifitm6	-9155
0.016364	0.487922	B4galnt4	2073
0.011074	0.527603	Mrpl23	513
0.021488	0.522975	Cdkn1c	-4718

0.009917	0.534545	Mrgprg	0
0.009256	0.496364	Fgf4	-4821
0.012867	0.46	Ccl25	63664
0.025909	0.440341	Zfp958	-294
0.013554	0.493058	AK082314	-5802
0.021983	0.460331	Arglu1	-294914
0.018788	0.499091	Arglu1	-301756
0.015207	0.470083	Arglu1	-304969
0.018017	0.402479	Baff;Tnfsf1	979
0.019669	0.503306	3930402G;	-18354
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0.007603	0.549421	Ankrd10	-10055
0.022576	0.437121	Sox1	-1095
0.018678	0.427934	Sox1	2793
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0.019351	0.521688	AK017331	-61665
0.010744	0.41405	4930444A	-384
0.012614	0.505114	AK040272	0
0.010083	0.453388	Adrb3	-2941
0.009091	0.440979	Gm3985	158136
0.010413	0.432231	Wrn	1053
0.038462	0.527413	Tex15	-328
0.013884	0.527273	Rbpms	-62169
0.02028	0.444755	Mtus1	-710
0.022937	0.469091	Mtnr1a	40806
0.027273	0.457851	Ankrd37	-494
0.017686	0.406281	AK144632	51481
0.025541	0.421558	Wwc2	-18094
0.01961	0.437143	AK032387	-78765
0.025124	0.433719	AK032387	-37755
0.014545	0.495207	Hand2	18927
0.009256	0.546116	Sh3rf1	-81568
0.018017	0.425455	Cpe	-311
0.026446	0.470744	Tmem192	-25072
0.015868	0.563802	Mef2b	-1689
0.009421	0.522479	Slc25a42	14469
0.026281	0.593719	Tmem59l	133
0.013884	0.557686	Il12rb1	1955
0.021488	0.552893	Plvap	-935
0.027273	0.588099	Insl3	-1818
0.017902	0.407273	Ttc29	-98837
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0.013091	0.42497	Ttc29	-60319
0.01049	0.368531	Ttc29	-59508
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0.016485	0.455394	Cd97	-42210

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0.012893	0.51719	Lyl1	699
0.00876	0.530248	AK168184	17433
0.020848	0.553818	AK168184	20359
0.018545	0.549212	Nfix	1315
0.016623	0.566883	Junb	-2989
0.009697	0.534091	Zfp423	-17430
0.01375	0.540341	Snx20	26431
0.031901	0.526612	Sall1	93476
0.023939	0.496667	Sall1	92458
0.013554	0.410248	Sall1	-520963
0.010303	0.488788	Chd9	23204
0.011667	0.479545	Chd9;mKIA	-34562
0.022303	0.460727	Fto	16621
0.008926	0.478347	Fto	181457
0.027955	0.512159	BC100534	1234
0.015879	0.491758	BC100534	64685
0.030909	0.525455	Irx5	6220
0.009421	0.449587	Mt3	1962
0.015702	0.450579	Ndrg4	-6386
0.018545	0.504364	Cdh5	-9250
0.014545	0.460661	AK007545	4060
0.025455	0.498347	Zfhx3	-22604
0.020992	0.426612	Zfhx3	-17001
0.024848	0.481667	Dhx38	29742
0.011394	0.459758	Znrf1	5234
0.00876	0.481322	Chst5	7138
0.010909	0.46028	Gan	1090
0.013388	0.458347	Lrrc50	580
0.03007	0.576364	AK039624	-78669
0.012727	0.587071	Gse1	9019
0.013719	0.562975	Gse1	-3491
0.01297	0.516121	Irf8	52897
0.017762	0.538322	Foxl1	-4388
0.016121	0.510424	Zcchc14	-22879
0.015041	0.557851	Jph3	30139
0.018182	0.553766	Banp	108578
0.015152	0.585909	Zfpm1	-11603
0.013058	0.537521	Zfpm1	38352
0.011901	0.550909	Acta1	9774
0.012606	0.524848	AK041328	-8984
0.013223	0.441653	Tmem123	-1107
0.012562	0.475041	Fam76b	53432
0.025124	0.493388	Zfp558	-205
0.01124	0.518347	A230050P:	-6000
0.028099	0.506777	Icam4	886
0.011136	0.508977	Pde4a	-232

0.012727	0.492066	Elavl3	4052
0.027818	0.491	Tbx20	-3846
0.020992	0.467603	Tbx20	-7233
0.012338	0.492208	Opcml	165915
0.018333	0.497576	Barx2	17846
0.02314	0.471901	Tmem218	-373
0.014545	0.514091	Esam	1295
0.012468	0.498052	9030425E1	9272
0.014876	0.409917	Mir125b-1	341
0.021653	0.462149	Sorl1	839
0.012231	0.555702	Mcam	1211
0.009231	0.501958	Scn4b	-1339
0.016503	0.556364	AK014786	-1079
0.008099	0.47686	4931429L1	-99284
0.014091	0.489697	4931429L1	-118948
0.020227	0.467614	2900052Nl	-169227
0.019669	0.527438	Nnmt	-44786
0.011039	0.443896	Dixdc1	-5360
0.023802	0.457025	Idh3a	-297
0.010083	0.426777	Wdr61	-1351
0.012867	0.48042	BC082591	-70381
0.013377	0.504286	Odf3l1	17960
0.010083	0.476529	Cspg4	13922
0.009256	0.496364	1700017B(	-37066
0.02	0.477172	Mpi	-161
0.013388	0.495702	Islr2	1009
0.009917	0.561157	Loxl1	6910
0.012424	0.426818	Senp8	16668
0.02843	0.515702	Larp6	-208
0.012066	0.482479	Itga11	-56065
0.015041	0.495537	Fem1b	21668
0.019394	0.491818	Skor1	7180
0.012231	0.460165	AK039256	308
0.011736	0.507273	AK214683	-98172
0.014866	0.485348	Klph;Lctl	-32777
0.010579	0.517355	Klph;Lctl	-29492
0.014876	0.535702	DDM36;Igc	1857
0.009371	0.465734	Parp16	-22505
0.010579	0.48595	Mtfmt	-616
0.015372	0.476694	9530091C(	190964
0.035829	0.479786	Foxb1	-1167
0.017203	0.483776	Foxb1	-4507
0.021157	0.481488	Myo1e	-1108
0.01124	0.423802	Aldh1a2	14213
0.013223	0.449091	DQ072388	-656
0.016364	0.384793	Mns1	-3306
0.010649	0.437532	Prtg	2910

0.011736	0.454876	Rab27a	5165
0.014266	0.494126	Onecut1	-364
0.021818	0.409421	Onecut1	-6366
0.017121	0.513182	Onecut1	-4964
0.017521	0.469091	Myo5c	937
0.014848	0.501667	Myo5c	5639
0.014711	0.475537	Sh3bgrl2	68088
0.035804	0.517483	Zic1	11806
0.027273	0.491515	Zic1	10529
0.016694	0.50281	BC043934	-17315
0.011074	0.478017	Rasa2	2328
0.010579	0.45405	AK089981	0
0.017521	0.447934	Spsb4	-5663
0.009333	0.436242	Pik3cb	-5379
0.018843	0.42	Sox14	1000
0.020165	0.539339	Amotl2	-6929
0.008264	0.479174	Amotl2	-656
0.022545	0.534727	Ppm1m	-258
0.010744	0.537521	Tlr9	4072
0.009917	0.467438	Nicn1	-10409
0.012066	0.446446	Cspg5	-10
0.008264	0.549917	Tmie	5241
0.016023	0.451364	Susd5	28209
0.00876	0.48595	Trim71	18714
0.01021	0.461818	Rbms3	84063
0.016818	0.455152	Eomes	-85948
0.026942	0.425455	Eomes	-8777
0.008264	0.479008	Eomes	-5918
0.010083	0.482975	Golga4	-9422
0.01125	0.4675	Xirp1	13009
0.013388	0.539008	Rpl14	118167
0.021653	0.535537	4930524L2	-343
0.018843	0.473223	Magix	0
0.017355	0.518678	Glod5	1920
0.01303	0.479394	Mporc-b;P	-11892
0.014545	0.492562	Gm4906	139311
0.017025	0.461488	Gm4906	361676
0.014364	0.485727	Bcor	327308
0.02823	0.549665	Bcor	81789
0.032576	0.550303	Bcor	79121
0.026545	0.494	Bcor	-1937
0.019339	0.540165	AK075658	59903
0.021091	0.472242	Gm6938	0
0.020535	0.519572	Zcchc12	370
0.021818	0.484298	C1galt1c1	-4308
0.012727	0.436694	Xiap	-2420
0.018182	0.469256	Dcaf12l2	-122

0.0225	0.477273	AK021262	-473
0.01958	0.49972	Zic3	-110859
0.039773	0.516932	Zic3	-109887
0.034876	0.457686	Zic3	-15409
0.043316	0.493155	Sox3	1910
0.030909	0.511909	Slitrk4	-134
0.025455	0.435584	Prkx	-14779
0.027107	0.469422	Tmem47	-181880
0.015789	0.469474	Arx	13438
0.028264	0.573554	Efnb1	1336
0.028112	0.488252	Cited1	-561
0.045303	0.480606	Pou3f4	1015
0.017727	0.494659	Tsc22d3	31607
0.042208	0.442208	Ddx3x;Ddx	0

Table S4: Biased-Enhancers-pro DNMT3A/DNMT3B

pro DNMT3A				
chrom	start	end	n_cpgs	losest_genene_distance
chr8	62985050	62985250	3	Aadat 129
chr5	64203950	64204150	3	0610040J0 216
chr13	1E+08	1E+08	5	AK135852 227
chr7	1.34E+08	1.34E+08	4	Zfp771 410
chr10	21139710	21139910	3	AK006189 427
chr18	81130150	81130350	5	Atp9b;MM 446
chr7	1.25E+08	1.25E+08	4	XT-I -505
chr7	16508230	16508430	3	Sepw1 -510
chr10	5914700	5914900	4	Rmnd1 511
chr19	10294130	10294330	3	Gm98 -512
chr18	44820600	44820800	3	A930012L1 -518
chr11	98901850	98902050	3	Igfbp4 -523
chr17	26389130	26389330	3	Luc7l -524
chr12	33986650	33986850	3	Atxn7l1 -529
chr7	13550450	13550650	3	Zfp324 -562
chr11	51781760	51781960	4	Cdkn2aipnI 627
chr4	1.16E+08	1.16E+08	3	Mmachc 629
chr6	1.2E+08	1.2E+08	3	B4galnt3 656
chr7	29478820	29479020	3	Fbxo27 657
chr7	28291950	28292150	3	Prx -669
chr9	23026650	23026850	3	Bmpcr -669
chr7	1.28E+08	1.28E+08	3	Vwa3a 679
chr18	36357530	36357730	3	Nrg2 -716
chr18	36357550	36357750	3	Nrg2 -736
chr7	87470080	87470280	3	Rccd1 -740
chr13	55793500	55793700	3	B230219D: -784
chr6	71220690	71220890	3	Krcc1 -791
chr15	1E+08	1E+08	5	Nramp2 842
chr7	16870850	16871050	7	Ccdc9 -842
chr8	34494930	34495130	3	Wrn 844
chr11	55018710	55018910	3	Slc36a1 868
chr2	32175060	32175260	4	Dnm1;mkl 883
chrX	5978150	5978350	3	Shroom4 887
chr7	36104350	36104550	3	Gpatc1;Gp -891
chr3	32408350	32408550	4	Zfp639 -921
chr3	1.3E+08	1.3E+08	4	Ccdc109b -926
chr15	99287050	99287250	3	Nckap5l 928
chr15	76503050	76503250	3	Ppp1r16a 940
chr7	52240550	52240750	3	Prmt1 951
chr6	88676820	88677020	3	AK029023 -966
chr11	1.06E+08	1.06E+08	3	Limd2 -977
chr3	1.42E+08	1.42E+08	3	Gtf2b 979
chr4	1.26E+08	1.26E+08	4	Eif2c1 1014
chr5	1.14E+08	1.14E+08	4	2900026A( -1037
chr9	56481950	56482150	3	Lingo1 1058
chr15	55140390	55140590	3	Col14a1 1085

chr8	46149450	46149650	3	AY512931	1121
chr6	1.08E+08	1.08E+08	3	Itpr1	-1129
chr5	1.13E+08	1.13E+08	3	Tfip11	-1138
chr6	1.08E+08	1.08E+08	3	Itpr1	-1139
chr6	1.21E+08	1.21E+08	3	Pex26	1145
chr8	1.13E+08	1.13E+08	3	Mtss1l	-1185
chr2	91475180	91475380	3	F2	1190
chr11	78351150	78351350	3	Ift20	1212
chr1	1.74E+08	1.74E+08	3	Atp1a2	1224
chr9	1.15E+08	1.15E+08	4	Cnot10	1267
chr18	38159850	38160050	3	Arap3	-1288
chr12	85956850	85957050	3	Abcd4	1312
chr19	47585950	47586150	4	AK158434	-1321
chr18	38159910	38160110	3	Arap3	-1348
chr7	86292390	86292590	3	Mfge8	1355
chr7	1.47E+08	1.47E+08	3	AK040659;	1445
chr2	1.57E+08	1.57E+08	3	Manbal	1450
chr10	93496840	93497040	3	Vezt	1452
chr4	83172950	83173150	3	AK029637	1478
chr15	84865800	84866000	3	Fam118a	-1491
chr17	26087810	26088010	3	Nhlrc4	1499
chr8	1.2E+08	1.2E+08	3	Gan	1515
chr6	1.2E+08	1.2E+08	3	Cecr5	1516
chr2	1.32E+08	1.32E+08	3	Slc23a2	-1526
chr11	1.02E+08	1.02E+08	3	Meox1	1537
chr14	61401650	61401850	3	Mipep	-1552
chr15	1.03E+08	1.03E+08	3	Hoxc4	-1557
chr8	97297650	97297850	6	Cx3cl1	1570
chr15	57964770	57964970	3	Atad2	1666
chr12	85116410	85116610	3	Papln	-1685
chr8	1.1E+08	1.1E+08	3	Wwp2	1704
chr11	68906850	68907050	6	Per1	-1705
chr14	1.06E+08	1.06E+08	3	Rbm26	-1706
chr11	1.07E+08	1.07E+08	3	Helz	-1743
chr7	52717020	52717220	3	Ftl1	-1764
chr17	47746410	47746610	3	Bysl	1830
chr8	28283080	28283280	3	Rab11fip1	1837
chr17	31793650	31793850	3	U2af1	1848
chr10	80751960	80752160	3	Tjp3	1851
chr1	77509550	77509750	3	Epha4	1912
chr3	87555940	87556140	3	Megf12	1991
chr2	32585320	32585520	3	Sh2d3c	2094
chr8	1.08E+08	1.08E+08	3	Thap11	2097
chr19	8790500	8790700	4	Slc3a2	-2113
chr3	95121300	95121500	3	Lass2	2126
chr4	1.23E+08	1.23E+08	3	Mfsd2a	2150
chr8	28287350	28287550	3	Rab11fip1	-2232
chr7	1.07E+08	1.07E+08	3	Snord15b	2256
chr3	89764850	89765050	3	Atp8b2	2379
chr7	19753880	19754080	3	Gipr	-2404

chr15	79842420	79842620	5 Pdgfb	2617
chr4	45492850	45493050	4 Shb	2623
chr1	1.37E+08	1.37E+08	10 Ppp1r12b	2656
chr17	45906810	45907010	3 AK080425	2666
chr8	1.08E+08	1.08E+08	3 4931428FC	2704
chr17	45906850	45907050	3 AK080425	2706
chr4	45492760	45492960	3 Shb	2713
chr8	1.14E+08	1.14E+08	4 Chst5	-2781
chr4	1.54E+08	1.54E+08	4 5930403L1	2834
chr2	32504960	32505160	3 Eng	2845
chr17	12959470	12959670	3 Igf2r	2901
chr2	1.81E+08	1.81E+08	4 Tcea2	-3014
chr7	19605650	19605850	3 Foxa3	3037
chr11	96201810	96202010	4 Hoxb3	-3072
chrX	1.66E+08	1.66E+08	3 Fxy	3075
chr9	1.2E+08	1.2E+08	3 Xirp1	3105
chr3	28676210	28676410	3 AK007174	3211
chr2	91782900	91783100	3 Dgkz	3442
chr4	88786790	88786990	3 Mtap	3516
chr17	46862300	46862500	3 Gnmt	3613
chr7	87256410	87256610	3 Idh2	3625
chr6	1.46E+08	1.46E+08	5 Rassf8	3650
chr8	72418450	72418650	3 Yjefn3	-3666
chr12	1.06E+08	1.06E+08	3 Dicer1	3716
chr9	13230650	13230850	3 Phxr4	-3730
chr17	24131050	24131250	3 Prss22	3816
chr19	47393090	47393290	3 Sh3pxd2a	-3849
chr11	70787600	70787800	3 Rpain	3885
chr16	8734340	8734540	5 Usp7	3894
chr1	1.37E+08	1.37E+08	4 Nav1	3901
chr10	70415190	70415390	3 Bicc1	-3953
chr3	32394950	32395150	3 Kcnmb3	-4059
chr6	88177730	88177930	4 1700031F1	-4097
chr3	89639390	89639590	4 She	4098
chr19	57344080	57344280	3 AK019620	-4169
chr3	95100150	95100350	3 Fam63a	4242
chr9	67118670	67118870	4 Tln2	4358
chr5	1.11E+08	1.11E+08	3 Galnt9	-4413
chr11	1.18E+08	1.18E+08	3 Dnahc17	-4437
chr7	1.49E+08	1.49E+08	3 Ap2a2;mKI	4441
chr19	6271900	6272100	4 AK149321	4477
chr15	78677590	78677790	3 Cdc42ep1	4513
chr6	1.27E+08	1.27E+08	3 Fgf6	4620
chr14	54868630	54868830	3 Dad1	4773
chr1	1.72E+08	1.72E+08	3 Nos1ap	5087
chr3	1.08E+08	1.08E+08	4 Sort1	5400
chr10	41471950	41472150	3 BC048559	5423
chr13	95070420	95070620	3 AK089519	-5459
chr4	1.52E+08	1.52E+08	4 Acot7	5477
chr11	1.16E+08	1.16E+08	3 AK038665	-5491

chr3	1.52E+08	1.52E+08	3 Zzz3	5492
chr17	15518320	15518520	3 Dll1	-5533
chr5	93332600	93332800	3 Shroom3	5576
chr8	47570680	47570880	3 Acsl1	-5607
chr16	44193400	44193600	3 Gm608	-5610
chr5	1.09E+08	1.09E+08	3 Pigg	5627
chr17	29478960	29479160	3 Mtch1	5688
chr5	1.48E+08	1.48E+08	3 Lnx2	5697
chr8	1.22E+08	1.22E+08	3 Hsbp1	5772
chr5	1.48E+08	1.48E+08	3 Lnx2	5797
chr17	84403750	84403950	3 AK020236	5858
chr9	58058390	58058590	3 Islr2	-6264
chr7	1.48E+08	1.48E+08	3 BC024386	6318
chr11	1.15E+08	1.15E+08	3 Nt5c	6367
chr2	1.1E+08	1.1E+08	3 Lgr4	6426
chr8	28231050	28231250	3 Tem5	6498
chr16	91790940	91791140	3 Itsn	6632
chr2	1.36E+08	1.36E+08	3 Plcb4	-6906
chr7	1.34E+08	1.34E+08	3 Sept1	-6911
chr7	29559420	29559620	5 AK040398	6912
chr11	1.17E+08	1.17E+08	3 Snord1a	7159
chr12	70982520	70982720	3 Map4k5	-7199
chr5	1.14E+08	1.14E+08	3 Coro1c	7244
chr3	85782580	85782780	3 SH3d19	7251
chr15	99474570	99474770	3 Racgap1	7281
chr9	1.19E+08	1.19E+08	3 Scn5a	-7407
chr7	37475520	37475720	3 Tshz3	-7416
chr3	1.07E+08	1.07E+08	3 Ubl4b	-7439
chr6	91749730	91749930	3 Grip2	7456
chr12	1.14E+08	1.14E+08	3 Tmem179	-7569
chr3	1.09E+08	1.09E+08	3 4930443G:	7583
chr17	45830910	45831110	4 Mrpl14	7589
chr7	1.36E+08	1.36E+08	4 Bag3	7993
chr15	82160950	82161150	4 Naga	8105
chr4	1.4E+08	1.4E+08	3 Klhdc7a	-8129
chr3	1.22E+08	1.22E+08	3 Arhgap29	8132
chr13	69664300	69664500	3 Papd7	8241
chr12	88028150	88028350	4 Vash1	8500
chr5	75462850	75463050	4 Gsx2	-8575
chr6	54268160	54268360	3 Prr15	-8645
chr4	43271170	43271370	3 Atp8b5	-8660
chr12	73870880	73871080	3 Ppm1a	8682
chr9	67416250	67416450	3 Tln2	-8740
chr11	1.15E+08	1.15E+08	4 Gpr142	8812
chr13	51838970	51839170	4 Sema4d	-8884
chr9	65230240	65230440	3 Kbtbd13	9018
chr19	10472850	10473050	3 Syt7	9270
chr7	1.18E+08	1.18E+08	3 Ampd3	9362
chr14	1.22E+08	1.22E+08	4 Dock9	9368
chr15	73263140	73263340	3 FAK	-9430

chr11	77605000	77605200	3	Myo18a	-9603
chr4	11422760	11422960	3	1110037FC	9655
chr19	53205070	53205270	3	Add3	-9664
chr17	15851610	15851810	3	Chd1	9679
chr17	29205950	29206150	3	LOC100499	9755
chr2	1.73E+08	1.73E+08	3	BC116387	-9780
chr1	91837550	91837750	4	Gbx2	-9799
chr7	87938150	87938350	4	Iqgap1	9866
chr13	1.08E+08	1.08E+08	3	Kif2a	-9898
chr2	1.25E+08	1.25E+08	3	AK148297	9945
chr5	1.11E+08	1.11E+08	3	Mir701	10077
chr8	1.09E+08	1.09E+08	4	Slc7a6os	10282
chr5	1.26E+08	1.26E+08	3	Ncor2	10399
chr6	98943010	98943210	3	Foxp1	10463
chr4	1.48E+08	1.48E+08	3	Ubiad1	10629
chr7	1.29E+08	1.29E+08	3	AK199184	10781
chr17	28155340	28155540	3	Anks1	10810
chr11	11778950	11779150	3	AK006690	10824
chr8	1.12E+08	1.12E+08	3	Gm1943	-10892
chr10	60857250	60857450	3	X99384	-10979
chr2	36046450	36046650	3	AK142949	-11181
chr2	1.67E+08	1.67E+08	6	AK077074	-11280
chr2	60379770	60379970	3	Pla2r1	11347
chr16	32656200	32656400	3	Tnk2	11471
chr19	10983390	10983590	3	Zp1	11500
chr11	75621270	75621470	4	Doc2b	-11711
chr6	1.45E+08	1.45E+08	3	Kras;Nras	-11739
chr2	1.54E+08	1.54E+08	3	Snta1	-12008
chr7	86926190	86926390	3	Mesp1	12085
chr2	1.31E+08	1.31E+08	3	Gfra4	12103
chr17	28381950	28382150	3	Ppard	12251
chr4	40102610	40102810	3	Aco1	12312
chr9	83454280	83454480	4	Sh3bgrl2	12335
chr4	40102660	40102860	3	Aco1	12362
chr6	54779520	54779720	3	Znrf2	12610
chr2	1.04E+08	1.04E+08	3	A930018P2	-12625
chr11	62862310	62862510	3	Tekt3	-12650
chr17	26193270	26193470	3	Rab11fip3	12651
chr15	12682400	12682600	3	Pdzd2	-12721
chr17	46982050	46982250	4	BC032203	-12787
chr1	93231460	93231660	3	Espnl	12808
chr12	1.01E+08	1.01E+08	3	Foxn3	-12969
chr2	1.32E+08	1.32E+08	3	svct2	-13017
chr6	54780110	54780310	3	Znrf2	13200
chr6	54780180	54780380	3	Znrf2	13270
chr10	1.2E+08	1.2E+08	3	Mir763	-13284
chr11	55220090	55220290	3	Sparc	13291
chr9	31109150	31109350	4	Prdm10	-13341
chr9	31109120	31109320	3	Prdm10	-13371
chr14	27412440	27412640	4	Fam116a	13404

chr8	48424050	48424250	3	Stox2	13451
chr18	60947810	60948010	3	Rps14	13560
chr5	1.01E+08	1.01E+08	3	AK133807	-13614
chr4	44110830	44111030	3	Gne	-13781
chr7	1.06E+08	1.06E+08	3	A630091E0	13869
chr2	1.73E+08	1.73E+08	3	Zbp1	-14447
chr8	11512030	11512230	3	Carkd	14462
chr4	1.33E+08	1.33E+08	3	Wasf2	-14497
chr19	55905560	55905760	3	Ppn1	-14621
chr5	1.24E+08	1.24E+08	3	Hip1r	14623
chr10	8007160	8007360	3	Ust	14679
chr5	1.41E+08	1.41E+08	3	Grifin	-14929
chr13	25346730	25346930	3	Nrsn1	14934
chr1	36630210	36630410	3	Sema4c;ml	-14984
chr5	1.44E+08	1.44E+08	3	Fbxl18	15026
chr10	18142550	18142750	3	Nhs1	15069
chr8	83419470	83419670	3	Gab1	-15092
chr19	60235730	60235930	3	E330013PC	15152
chr4	1.39E+08	1.39E+08	3	Iffo2	15287
chr5	68222780	68222980	3	AK035785	-15324
chr1	1.22E+08	1.22E+08	3	Tmem37	-15463
chr11	1.01E+08	1.01E+08	3	Ghdc	-15599
chr5	1.26E+08	1.26E+08	3	Ncor2	15933
chr14	80154280	80154480	3	Mir759	16042
chr11	54792530	54792730	3	Tnip1	-16088
chr17	27288400	27288600	3	Ip6k3	16108
chr2	30640750	30640950	3	1700001O	16276
chr6	17715960	17716160	4	Fam4a2;St	16744
chr18	60806740	60806940	3	Synpo	-17001
chr8	1.25E+08	1.25E+08	3	Cbfa2t3	17224
chr1	75339380	75339580	3	Des	-17338
chr18	50195100	50195300	3	Tnfaip8	-17635
chr2	1.73E+08	1.73E+08	3	Rbm38	17667
chr12	82109700	82109900	3	Smoc1	-17894
chr17	28011580	28011780	3	Uhrf1bp1	18128
chr4	41624030	41624230	3	Cntfr	18246
chr17	32011110	32011310	3	Sik1	-18373
chr4	1.41E+08	1.41E+08	3	Epha2	-18694
chr8	94567060	94567260	3	AK049522	18719
chr4	1.34E+08	1.34E+08	3	Ldlrap1	-18881
chrX	1.03E+08	1.03E+08	4	Atp7a	18935
chr6	94214650	94214850	3	Magi1	19047
chr17	36365940	36366140	3	AK138323	-19625
chr19	57251890	57252090	3	Ablim1	19891
chr15	76934750	76934950	3	AK007154	19922
chr15	76934770	76934970	3	AK007154	19942
chr7	1.43E+08	1.43E+08	3	AK031861	-20034
chr4	1.36E+08	1.36E+08	3	Ephb2	20359
chrX	1.66E+08	1.66E+08	4	Mid1	-20445
chr3	35807850	35808050	3	Dcun1d1	20945

chr18	57064030	57064230	3	March3	20971
chr1	1.36E+08	1.36E+08	4	Optc	21039
chr4	1.55E+08	1.55E+08	3	Ski	21213
chr8	1.27E+08	1.27E+08	4	2310022Bc	21218
chr10	42243440	42243640	4	Snx3	21580
chr12	1.1E+08	1.1E+08	3	Wdr25	21648
chr14	64584630	64584830	3	4930578I0	21786
chr11	3001910	3002110	3	Pisd-ps1	-21913
chr16	92104210	92104410	3	AK087806	-22122
chr15	97513690	97513890	3	Rpap3	22362
chr5	1.41E+08	1.41E+08	3	Gna12	22554
chr6	88698440	88698640	4	AK029023	-22586
chr2	1.73E+08	1.73E+08	3	BC116387	-22780
chr15	27419460	27419660	3	Ank	23028
chr13	12409690	12409890	3	Actn2	23108
chr2	1.61E+08	1.61E+08	3	Chd6;mKIA	23161
chr7	29723750	29723950	4	Actn4	23348
chr4	1.29E+08	1.29E+08	3	AK019743	23696
chr13	48782120	48782320	3	Barx1	23715
chr2	1.57E+08	1.57E+08	4	Ndr3;Ndrg:	23826
chr3	1.22E+08	1.22E+08	3	ABCR	-23982
chr2	1.64E+08	1.64E+08	3	Stk4	24233
chr7	1.23E+08	1.23E+08	3	Sox6	24952
chr5	1.02E+08	1.02E+08	4	Wdfy3	25581
chr15	66774450	66774650	3	AK085274	-26234
chr16	31174810	31175010	4	Acap2	26313
chr19	46602550	46602750	3	Trim8	26412
chr16	21243470	21243670	3	Ephb3	26580
chr1	1.54E+08	1.54E+08	3	Fam129a	26693
chr12	86912950	86913150	6	Jdp2	-26904
chr4	45448640	45448840	3	9130208Ec	-27002
chr2	1.24E+08	1.24E+08	3	Sema6d	27118
chr2	1.46E+08	1.46E+08	3	mKIAA127:	-27209
chr13	51857370	51857570	3	Sema4d	-27284
chr6	1.46E+08	1.46E+08	3	Sspn	-27706
chr14	32221150	32221350	3	Sh3bp5	27868
chr2	1.8E+08	1.8E+08	3	Ntsr1	28129
chr9	32415050	32415250	3	Ets1	-28555
chr9	43581750	43581950	4	Pvrl1	29091
chr2	1.66E+08	1.66E+08	3	Sulf2	29654
chr17	5070490	5070690	3	Arid1b	29910
chr5	1.43E+08	1.43E+08	3	C330006Kc	-29914
chr10	40761250	40761450	3	Gpr6	29939
chr7	87750760	87750960	5	AK155169	-29945
chr2	1.44E+08	1.44E+08	3	Snord17	30107
chr5	1.18E+08	1.18E+08	3	Nos1	30612
chr2	31574780	31574980	3	Abl1	30704
chr6	1.28E+08	1.28E+08	3	AK214641	30821
chr6	50695000	50695200	3	AK043004	-30913
chr2	1.18E+08	1.18E+08	3	Srp14	-31008

chr19	46607500	46607700	6 Trim8	31362
chr11	90217070	90217270	3 Hlf	32250
chr14	20763920	20764120	3 Gng2	32350
chr11	1.2E+08	1.2E+08	3 AK040159	32538
chr4	1.2E+08	1.2E+08	3 Kcnq4	32710
chr1	1.29E+08	1.29E+08	3 Mgat5	32737
chr11	74370680	74370880	3 Rap1gap2	32779
chr2	1.72E+08	1.72E+08	3 Tcfap2c	-33042
chr9	30783990	30784190	5 Adamts8	33842
chr10	69593940	69594140	3 Ccdc6	34071
chr4	1.17E+08	1.17E+08	3 Rnf220	-34238
chr18	6275890	6276090	3 Kif5b	-34368
chr10	76687220	76687420	3 Gm10941	34547
chr18	56663550	56663750	5 Gramd3	34629
chr6	22340750	22340950	6 Fam3c	-34669
chr12	76974750	76974950	3 Syne2	-35212
chr16	37812400	37812600	3 Fstl1	35259
chr2	1.57E+08	1.57E+08	3 Blcap	-35393
chr17	46212270	46212470	3 Mrps18a	-35482
chr12	82918000	82918200	3 Map3k9	-35843
chr19	46524270	46524470	3 AK204799	36713
chr10	53758450	53758650	3 Man1a	36864
chr6	32972950	32973150	3 Chchd3	37001
chr10	93535830	93536030	3 Fgd6	37084
chr5	1.48E+08	1.48E+08	3 Gsx1	37198
chr6	99150300	99150500	3 Foxp1	-37277
chr11	1.18E+08	1.18E+08	3 Rbfox3	-38012
chr7	97215950	97216150	3 E230029CC	38281
chr9	78367940	78368140	3 Eef1a1	-38409
chr8	1.2E+08	1.2E+08	3 4933407CC	-38919
chr16	91970830	91971030	3 Atp5o	-38955
chr6	15710150	15710350	3 Mdfic	38977
chr3	21936350	21936550	3 Tbl1xr1	-39023
chr11	88538950	88539150	3 LOC100504	40430
chr11	76098060	76098260	3 Rnmtl1	40822
chr3	69566890	69567090	3 Nmd3	40913
chr19	44964250	44964450	3 Fam178a	-41158
chr2	45014150	45014350	3 mKIAA056!	-41235
chr2	1.57E+08	1.57E+08	3 Blcap	-41333
chr2	1.68E+08	1.68E+08	3 Ptpn1	-41616
chr5	1.21E+08	1.21E+08	3 AK076949	41707
chr16	30641850	30642050	3 Fam43a	42041
chr1	1.92E+08	1.92E+08	3 BC030469	-42056
chr17	10691350	10691550	3 AK038428	42268
chr12	77768990	77769190	3 Spnb1	42343
chr1	1.65E+08	1.65E+08	3 Prrx1	-42409
chr1	1.65E+08	1.65E+08	3 Prrx1	-42449
chr14	75248920	75249120	3 Lrch1	-43055
chr1	1.66E+08	1.66E+08	4 Atp1b1	43085
chr12	1.09E+08	1.09E+08	3 Ccdc85c	43246

chr1	1.84E+08	1.84E+08	3	Enah	43760
chr13	60234850	60235050	4	Gas1	43845
chr3	37667290	37667490	3	EG381438;	-44008
chr14	22489490	22489690	4	Dupd1	44107
chr11	94028250	94028450	3	BC096410	44119
chr11	1.19E+08	1.19E+08	4	Tbc1d16	44142
chr4	1.08E+08	1.08E+08	3	Zfyve9	44630
chr19	38553530	38553730	3	PLC-epsilor	-44956
chr11	76167420	76167620	4	Nxn	45022
chr11	1.13E+08	1.13E+08	3	AK029086	-45987
chr5	1.41E+08	1.41E+08	3	Amz1	46360
chr16	50381540	50381740	3	Bbx	48240
chr7	73302930	73303130	3	Chsy1	48529
chr13	52976050	52976250	3	Auh	48795
chr15	12183830	12184030	3	Mtmr12;m	48981
chr10	74574700	74574900	4	Bcr	51059
chr11	20294450	20294650	3	Gm12034	-51749
chr12	55544670	55544870	3	Gm7550	-52365
chr7	53551760	53551960	3	AK006355	52463
chr1	1.66E+08	1.66E+08	3	Atp1b1	52655
chr10	1.11E+08	1.11E+08	3	Phlda1	54138
chr8	48492100	48492300	4	Stox2	-54398
chr2	45027590	45027790	3	mKIAA056!	-54675
chr7	1.03E+08	1.03E+08	3	Odz4	-55886
chr8	35097250	35097450	3	Rbpms	-56937
chr5	36157520	36157720	3	ABLIM2;Ab	56991
chr11	1.17E+08	1.17E+08	6	Sept9	57663
chr14	22377880	22378080	3	Myst4	57773
chr17	84339680	84339880	3	AK020236	-58011
chr17	84339630	84339830	3	AK020236	-58061
chr3	33802630	33802830	3	Ccdc39	-59398
chr12	25576160	25576360	3	LPCAT4;Ml	59696
chr9	96850950	96851150	3	Acpl2	-61109
chr14	61523410	61523610	3	AK215081	-61224
chr11	32604440	32604640	3	Fbxw11;ml	61565
chr2	1.28E+08	1.28E+08	3	Gm14005	63106
chr2	20571510	20571710	3	Etl4	-63227
chr2	1.31E+08	1.31E+08	3	Gfra4	63443
chr14	23468250	23468450	3	1700112Ec	64622
chr11	89983220	89983420	3	BC106170;	-65576
chr15	88212160	88212360	3	AK019614	-66098
chr18	24046550	24046750	3	Zfp397	-66438
chr4	1.48E+08	1.48E+08	3	Gm572	68374
chr4	1.48E+08	1.48E+08	3	Gm572	68404
chr13	48539110	48539310	3	Zfp169	69468
chr16	49768950	49769150	4	Ift57	69543
chr5	1.08E+08	1.08E+08	3	Tgfbr3	70323
chr5	1.08E+08	1.08E+08	3	Tgfbr3	70413
chr15	80320250	80320450	4	Enthd1	70449
chr2	1.69E+08	1.69E+08	3	Sall4	-71049

chr6	1.4E+08	1.4E+08	3 Plekha5	-72479
chr6	1.4E+08	1.4E+08	3 Plekha5	-72619
chr4	20041850	20042050	3 Ggh	72651
chr14	30461650	30461850	3 Cacna2d3	73199
chr10	53239440	53239640	3 Mcm9	73326
chr10	86882680	86882880	5 Ascl1	73524
chr7	1.4E+08	1.4E+08	3 Lhpp	76304
chr11	88401050	88401250	3 AK002838	-79314
chr17	31912070	31912270	3 Sik1	80466
chr17	75496730	75496930	3 Ltbp1	-81291
chr4	1.5E+08	1.5E+08	3 AK033051	-81291
chr16	43156280	43156480	3 Zbtb20	81447
chr17	83532060	83532260	3 Pkdcc	-82362
chr2	28220130	28220330	3 Gm347	-83130
chr19	32092570	32092770	4 Asah2	84859
chr8	1.24E+08	1.24E+08	4 1700018B0	88523
chr2	17743550	17743750	4 Nebl	-90855
chr6	1.15E+08	1.15E+08	4 AK202580	90889
chr18	65302570	65302770	4 Nedd4l	91876
chr10	1.22E+08	1.22E+08	4 Ppm1h	91932
chr2	1.44E+08	1.44E+08	3 Snord17	92187
chr7	71181190	71181390	4 Klf13	-97389
chr10	90733000	90733200	4 Tmpo	-98673
chr14	1.19E+08	1.19E+08	3 Gm9376	100100
chr18	38925870	38926070	3 Fgf1	100330
chr4	95346730	95346930	4 Fggy	100618
chr8	1.25E+08	1.25E+08	4 Banp	103779
chr8	91359470	91359670	3 Cyld	106112
chr5	1.42E+08	1.42E+08	3 Card11	-109140
chr13	1.01E+08	1.01E+08	4 Cartpt	109587
chr1	1.4E+08	1.4E+08	3 Nek7	119372
chr2	68853460	68853660	3 Nostrin	-120196
chr15	59357370	59357570	3 Trib1	-122638
chr17	5293590	5293790	3 Ldhal6b	124976
chr8	95007050	95007250	3 Irx5	125355
chr5	1.08E+08	1.08E+08	3 Tgfbr3	126863
chr4	1.14E+08	1.14E+08	3 Gm12830	-128454
chr2	1.68E+08	1.68E+08	4 Nfatc2	129017
chr16	73821870	73822070	3 mKIAA156	134833
chr8	1.24E+08	1.24E+08	5 1700018B0	138743
chr4	1.14E+08	1.14E+08	3 Gm12824	144521
chr9	28062940	28063140	3 Opcml	-147593
chr8	1.28E+08	1.28E+08	3 Sipa1l2	151402
chr18	25029150	25029350	3 FHOS2;Fhc	161204
chr9	46559780	46559980	4 2900052N0	-161705
chr17	86276480	86276680	3 Srbd1	163023
chr15	3699850	3700050	3 Ghr	-166620
chr10	82631460	82631660	3 Slc41a2	168901
chr8	27916790	27916990	3 Zfp703	-170817
chr13	60098060	60098260	3 Zcchc6	-173552

chr11	31069850	31070050	4	Chac2	-183485
chr19	55626700	55626900	3	Tcf7l2	-189399
chr10	1.11E+08	1.11E+08	3	Phlda1	193808
chr8	94045220	94045420	3	Fto	207796
chr16	93042750	93042950	3	Runx1	-216439
chr6	1E+08	1E+08	3	Rybp	232801
chr12	12658930	12659130	3	Mycn	288291
chr12	75926690	75926890	3	Kcnh5	351428
chr2	43970510	43970710	3	AK135703	-356621
chr11	25753120	25753320	3	5730522EC	357255
chr10	1.05E+08	1.05E+08	3	Tmtc2	384324
chr12	26219230	26219430	4	Id2	-438273
chr15	62545890	62546090	3	H2afy2	-494884

#### Pro DNMT3B

chrom	start	end	n_cpgs	losest_gene_distance
chr2	93031450	93031650	3	C230071H:-242
chr2	1.56E+08	1.56E+08	3	0610011L1:438
chr11	1.15E+08	1.15E+08	3	Nt5c:-572
chr17	27239050	27239250	3	AK131746:-665
chr3	94207450	94207650	3	AK008482:-680
chr6	34266590	34266790	3	Akr1b3:698
chr11	23398670	23398870	3	Ahsa2:-724
chr18	81172520	81172720	3	Sall3:-750
chr1	72329910	72330110	3	Pecr:777
chr3	88904880	88905080	3	Fdps:786
chr1	93392040	93392240	3	Traf3ip1:795
chr14	26276250	26276450	3	AK086741:829
chr15	98817230	98817430	3	AK016307:834
chr15	61937650	61937850	3	Pvt1:-852
chr6	54988940	54989140	3	Gars:945
chr7	50700470	50700670	3	Etfb:957
chr15	76710710	76710910	3	Zfp7:958
chr15	82978600	82978800	3	Poldip3:965
chr11	69830700	69830900	3	Dlg4:-1206
chr4	1.32E+08	1.32E+08	3	Epb4.1:-1312
chr18	42436390	42436590	4	Rbm27:1383
chr6	86961220	86961420	3	Nfu1:1390
chr6	29999450	29999650	4	Nrf1:1462
chr4	1.35E+08	1.35E+08	3	Clic4:1484
chr15	75810870	75811070	3	2410075B1:1644
chr15	31458930	31459130	3	March6:1661
chr9	20971850	20972050	3	Pde4a:1692
chr5	24346200	24346400	3	Rheb:1778
chr11	1.02E+08	1.02E+08	3	Fzd2:2103
chr3	1.08E+08	1.08E+08	3	Atxn7l2:2121
chr17	45872920	45873120	3	1600014C2:-2127
chr11	1.1E+08	1.1E+08	3	Map2k6:2324
chr17	35189760	35189960	4	Clic1:2572
chr11	45668170	45668370	4	Clint1:2704
chr2	1.16E+08	1.16E+08	4	2810405F1:2761

chr10	1.05E+08	1.05E+08	3 Tmtc2	-3345
chr8	93483100	93483300	3 Chd9	3766
chr16	22807450	22807650	3 Crygs	3832
chr17	27997540	27997740	4 Uhrf1bp1	4088
chr4	1.41E+08	1.41E+08	3 Fhad1	4160
chr2	1.58E+08	1.58E+08	3 Vstm2l	4361
chr5	1.11E+08	1.11E+08	3 Galnt9	-4773
chr4	44080260	44080460	3 Gne	5084
chr10	20262380	20262580	4 Pde7b	5553
chr10	20262320	20262520	4 Pde7b	5613
chr4	1.4E+08	1.4E+08	3 AK043690	5852
chr11	96799240	96799440	3 Pnpo	5892
chr7	1.4E+08	1.4E+08	3 AK086971	6207
chr12	3813410	3813610	3 Dnmt3a	6250
chr5	1.17E+08	1.17E+08	3 1500001A1	6875
chr11	90102850	90103050	3 Mmd	-7068
chr8	24161410	24161610	3 Ank1	-7136
chr5	1.4E+08	1.4E+08	3 Adap1	7497
chr9	65121800	65122000	3 Cilp	8180
chrX	96657630	96657830	3 Pja1	8243
chr2	35103250	35103450	4 Gsn	-8480
chr4	81097250	81097450	3 Mpdz	-8541
chr9	1.22E+08	1.22E+08	3 Snrk	8706
chr6	35248670	35248870	3 Slc13a4	9255
chr11	58742380	58742580	3 Rnf187	9827
chr15	51686830	51687030	3 Eif3h	9976
chr6	53161380	53161580	3 AK043311	-10215
chr13	48380800	48381000	3 AK039480	-11547
chr11	1E+08	1E+08	3 Nt5c3l	11783
chr11	1E+08	1E+08	3 Nt5c3l	11843
chr6	38920830	38921030	3 Tbxas1	-12278
chr9	54599840	54600040	3 Crabp1	-12574
chr13	51676490	51676690	3 Shc3	-14037
chr6	1.26E+08	1.26E+08	3 Vwf	14749
chr2	58402250	58402450	3 Acvr1	16788
chr12	1.09E+08	1.09E+08	3 Ccdc85c	20176
chr16	85528530	85528730	3 Cyyr1	22223
chr11	1.19E+08	1.19E+08	3 Rptor	-25808
chr1	1.83E+08	1.83E+08	3 Ccdc121	26471
chr6	8681740	8681940	3 Ica1	26517
chr16	28883750	28883950	3 AB349192	27986
chr11	1.17E+08	1.17E+08	3 Mgat5b	29493
chr6	71182540	71182740	3 Smyd1	29534
chr12	82157470	82157670	3 Smoc1	29675
chr18	84225630	84225830	3 Tshz1	29951
chr17	7064330	7064530	3 AK037830	-31991
chr14	33771630	33771830	3 Lrrc18	-32737
chr13	60556100	60556300	3 AK040640	33787
chr2	1.41E+08	1.41E+08	3 Flrt3	-34238
chr5	35657120	35657320	3 Adra2c	35905

chr8	10971070	10971270	3	AK162519	-36579
chr5	53567450	53567650	3	Sel1l3	37040
chr16	44685010	44685210	3	BC027231	-39201
chr4	1.48E+08	1.48E+08	3	Casz1	39369
chr17	80337910	80338110	3	Atl2	-42447
chr17	31860800	31861000	3	Cryaa	45910
chr2	52367690	52367890	3	Cacnb4	46196
chr6	49090860	49091060	3	AK045244	-46209
chr17	87730750	87730950	4	Ttc7	48524
chr16	89890940	89891140	3	Tiam1	-52820
chr18	64759890	64760090	3	Atp8b1	60563
chr3	1.54E+08	1.54E+08	3	Slc44a5	-62287
chr6	28845800	28846000	3	Lrrc4	-64053
chr1	11319900	11320100	3	Prex2	65856
chr1	1.07E+08	1.07E+08	3	Rnf152	-69473
chr8	1.11E+08	1.11E+08	3	Zfhx3	76006
chr13	12122820	12123020	3	Ryr2	76191
chr15	64061310	64061510	3	Asap1	82526
chr3	1.43E+08	1.43E+08	3	AK035466	85591
chr17	67151720	67151920	5	AK006039	87924
chr9	63780350	63780550	4	Smad6	89315
chr13	48517960	48518160	3	Zfp169	90618
chr13	28744290	28744490	3	AK012007	-90842
chr10	1.19E+08	1.19E+08	3	AK135691	-92315
chr8	35685050	35685250	3	AK076739	98678
chr16	29689310	29689510	3	Opa1	109890
chr11	81275110	81275310	3	1700071KC	111730
chr18	47415740	47415940	4	Sema6a	112581
chr6	6413990	6414190	3	Shfm1	114467
chr16	43394280	43394480	3	AK082948	-115792
chr1	61151950	61152150	3	Icos	117192
chr4	1.05E+08	1.05E+08	3	Ppap2b	120998
chr9	98065150	98065350	4	Nmnat3	-122523
chr13	1.15E+08	1.15E+08	3	Arl15	134554
chr13	60077510	60077710	3	Zcchc6	-153002
chr10	98212370	98212570	3	Atp2b1	-165215
chr10	98212300	98212500	3	Atp2b1	-165285
chr5	1.31E+08	1.31E+08	3	Caln1	175028
chr6	51026600	51026800	3	Mir148a	193108
chr2	8917750	8917950	3	AK006852	-193191
chr4	14014680	14014880	3	AK144882	203575
chr13	1.13E+08	1.13E+08	3	AK134426	206196