

LIST OF SUPPLEMENTAL ITEMS:

SUPPLEMENTAL FIGURES

Figure S1. Dynamic DNA methylation of imprinted DMRs in the context of global de novo methylation, related to Figure 1

Figure S2. Broad low-level intergenic transcription occurs in prospermatogonia, related to Figure 2

Figure S3. Transcription initiates from maternally methylated DMRs in fetal male germ cells, related to Figure 3

Figure S4. Chromatin landscape of control regions, related to Figure 4

Figure S5. DMRs of imprinted genes follow the general epigenetic remodeling pattern in fetal MGC, related to Figure 5

Figure S6. Germ line DMRs lack H3K79me3, H3K9me3, and H3K36me3 marks in female and male fetal germ cells at 15.5 dpc, related to Figure 6

SUPPLEMENTAL TABLES

Table S1. Results of the RNA-seq experiment, related to Figure 1D.

Table S2. Statistics of the genome-wide transcription in MGC, related to Figure 2

Table S3. Summary of transcription patterns at all known MAT DMRs, related to

Table S4. List of CpG island methylation classes and categories, related to Figure 4

SUPPLEMENTAL EXPERIMENTAL PROCEDURES

Purification of germ cells

Genomic DNA extraction from germ cells and sperm

Chromatin Immunoprecipitation

Bioinformatics Analysis

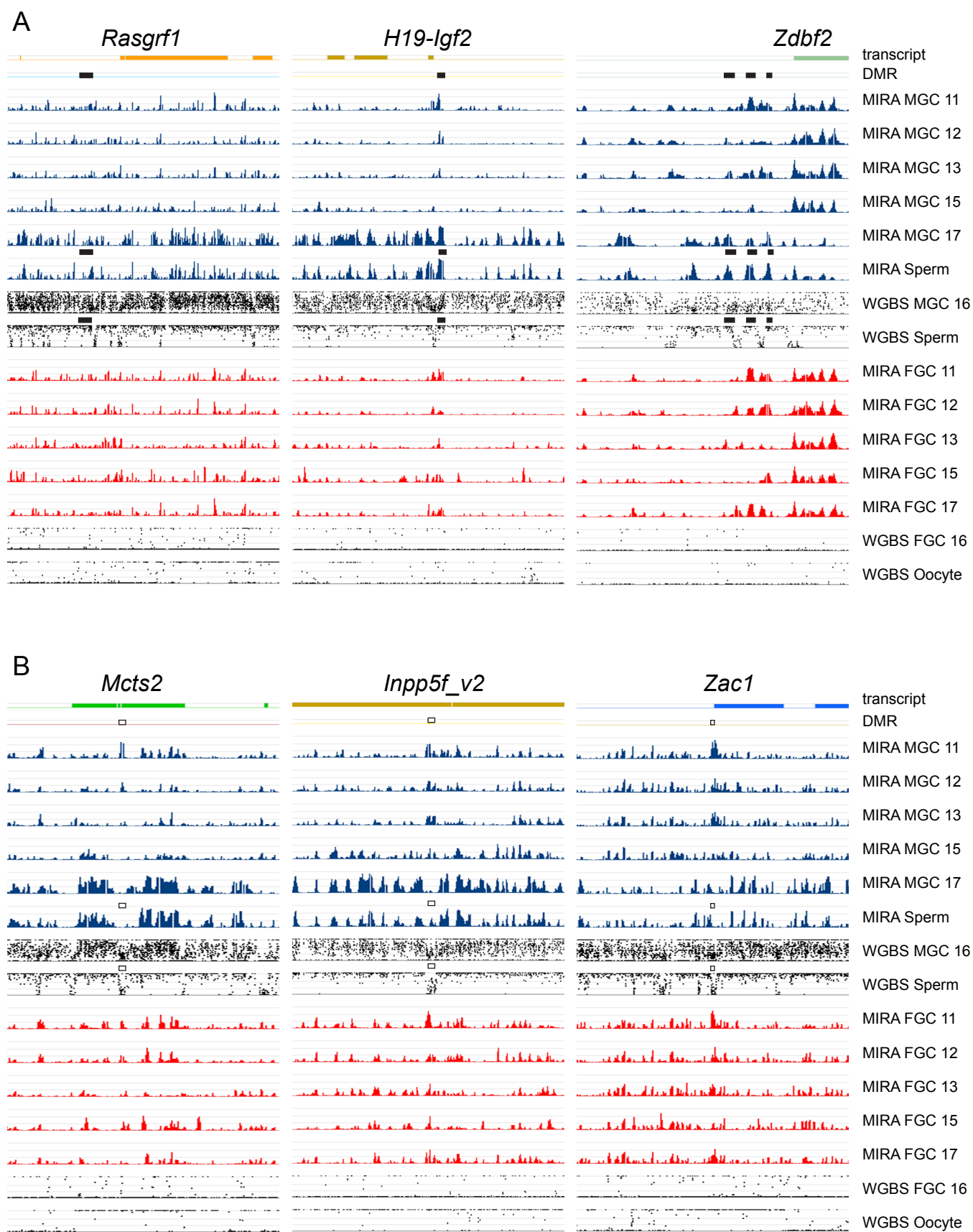
RNA-seq analysis:

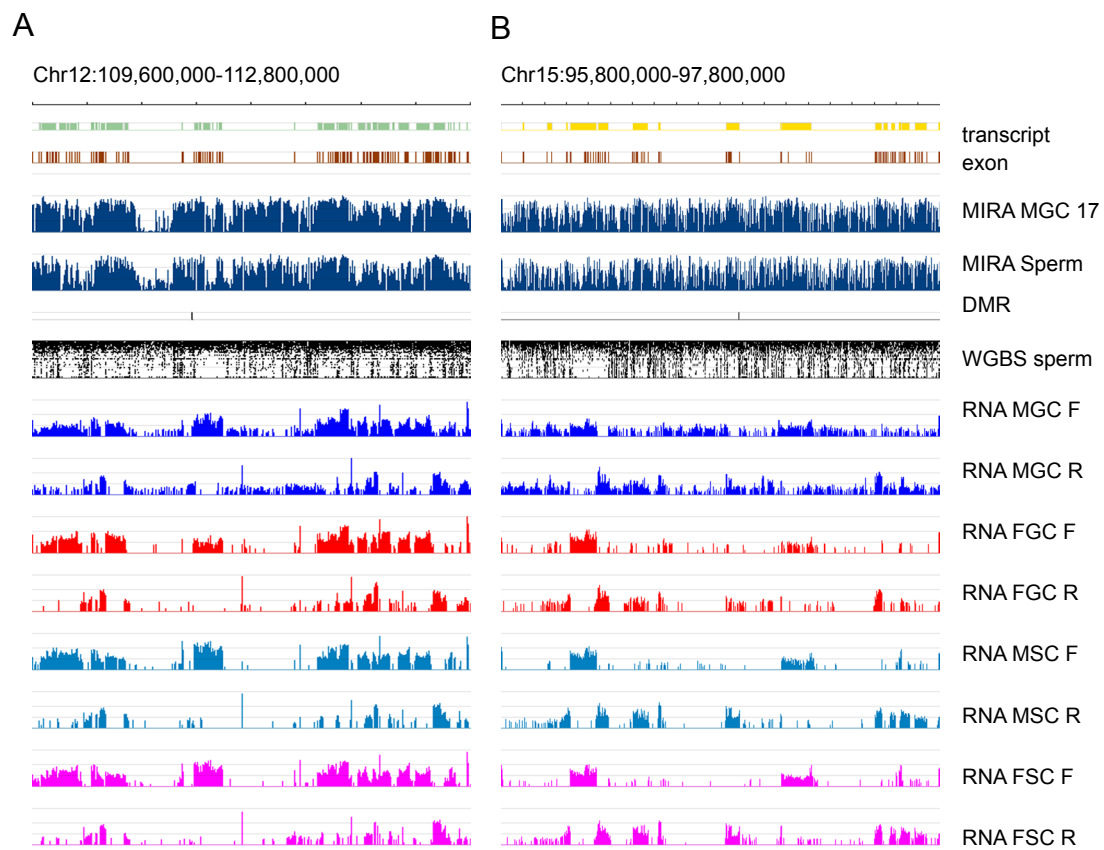
Normalization of microarray results

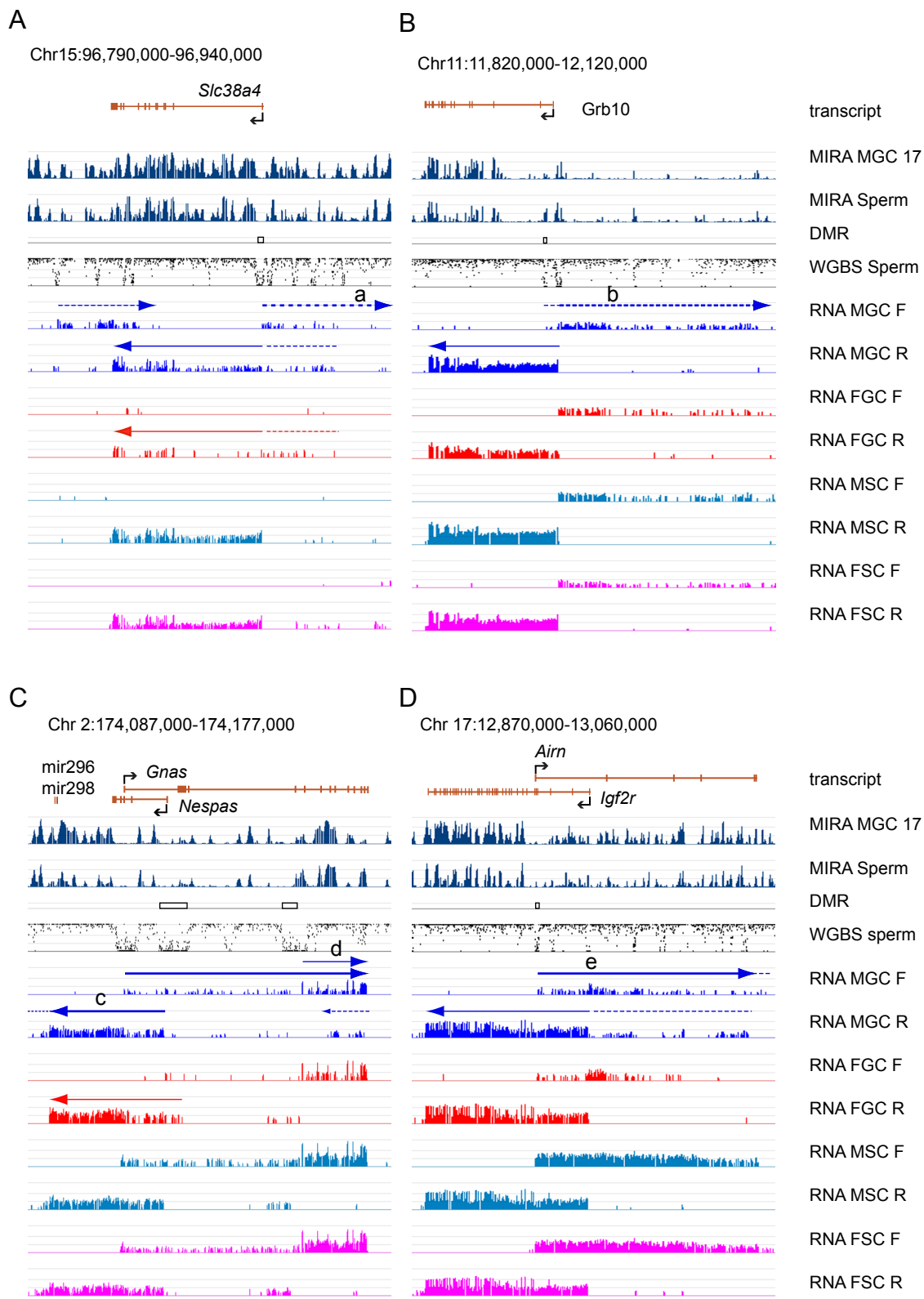
Peak finding

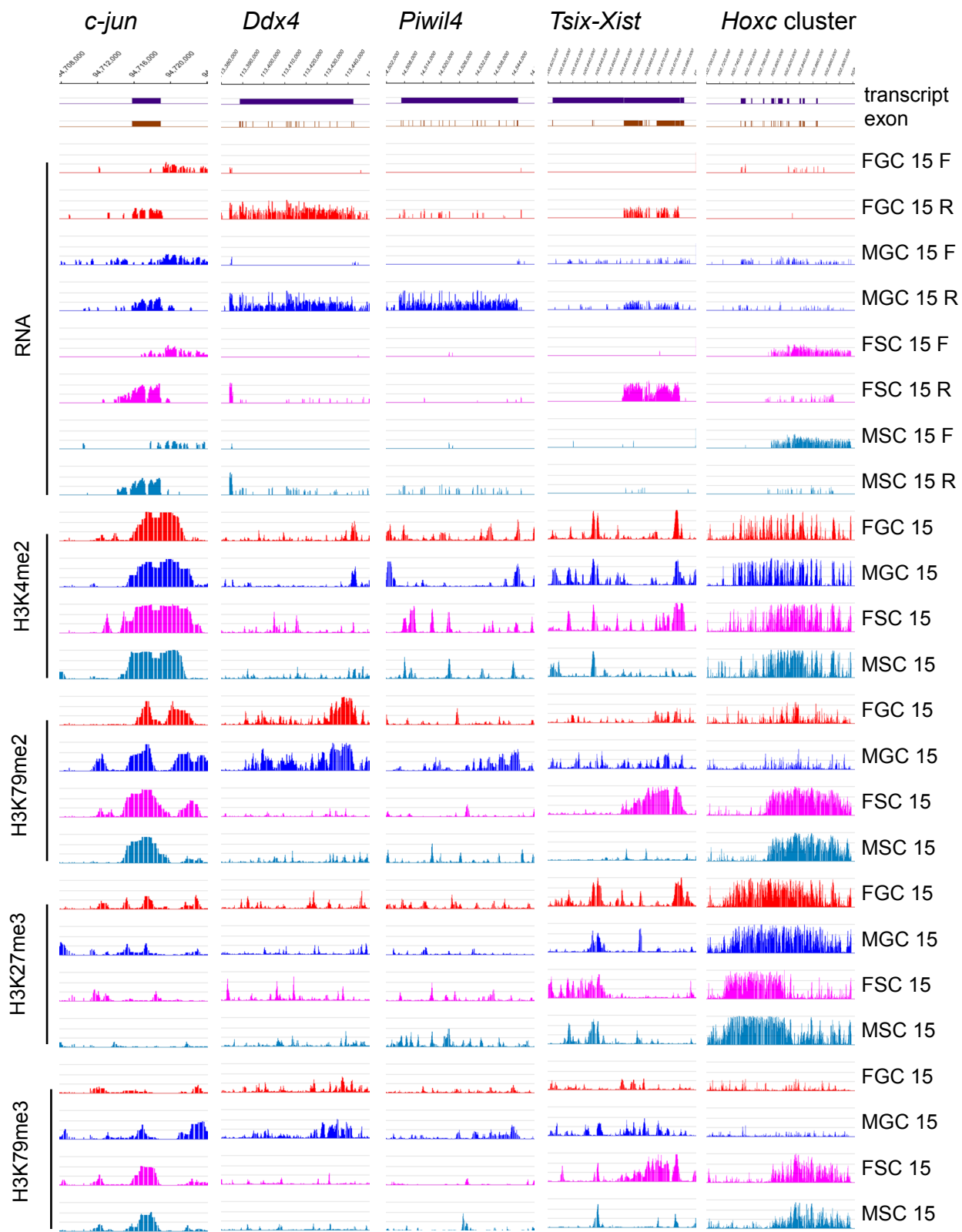
Heat maps

Composite Profile

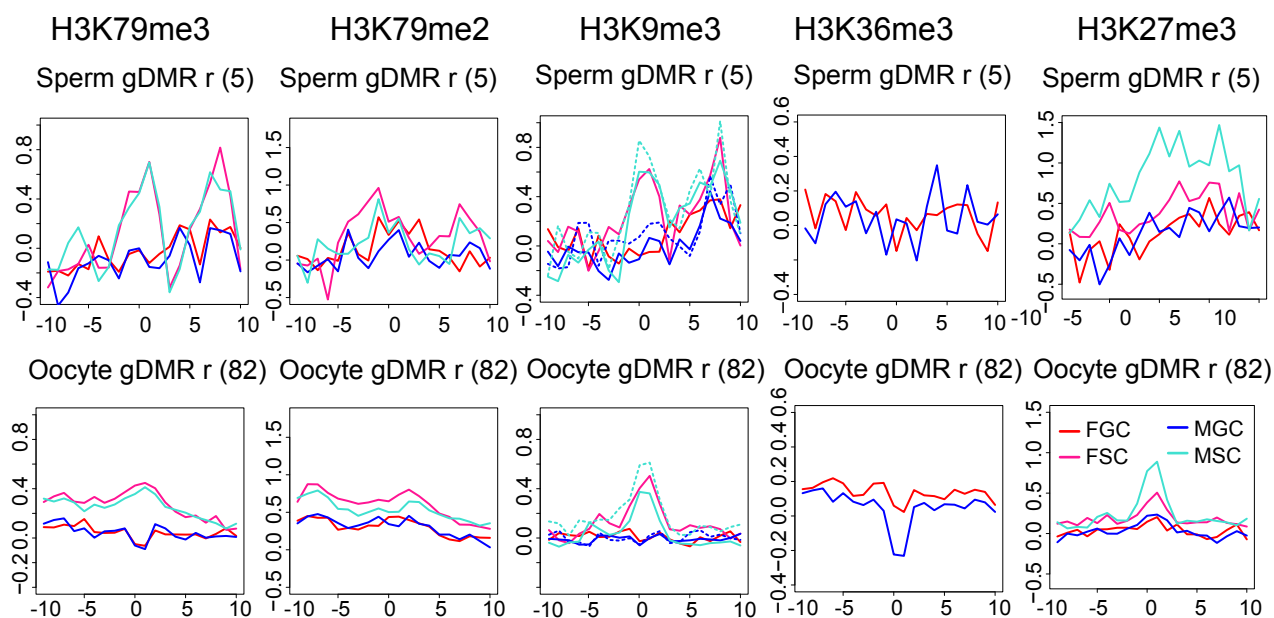




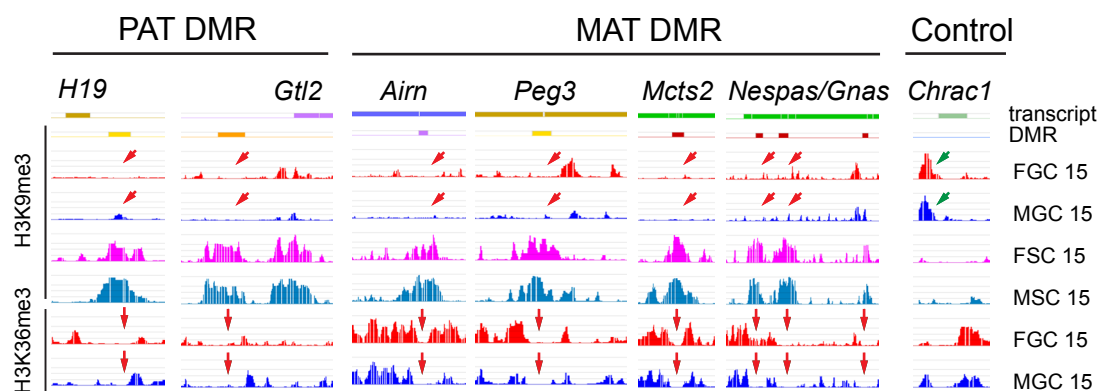




A



B



C

