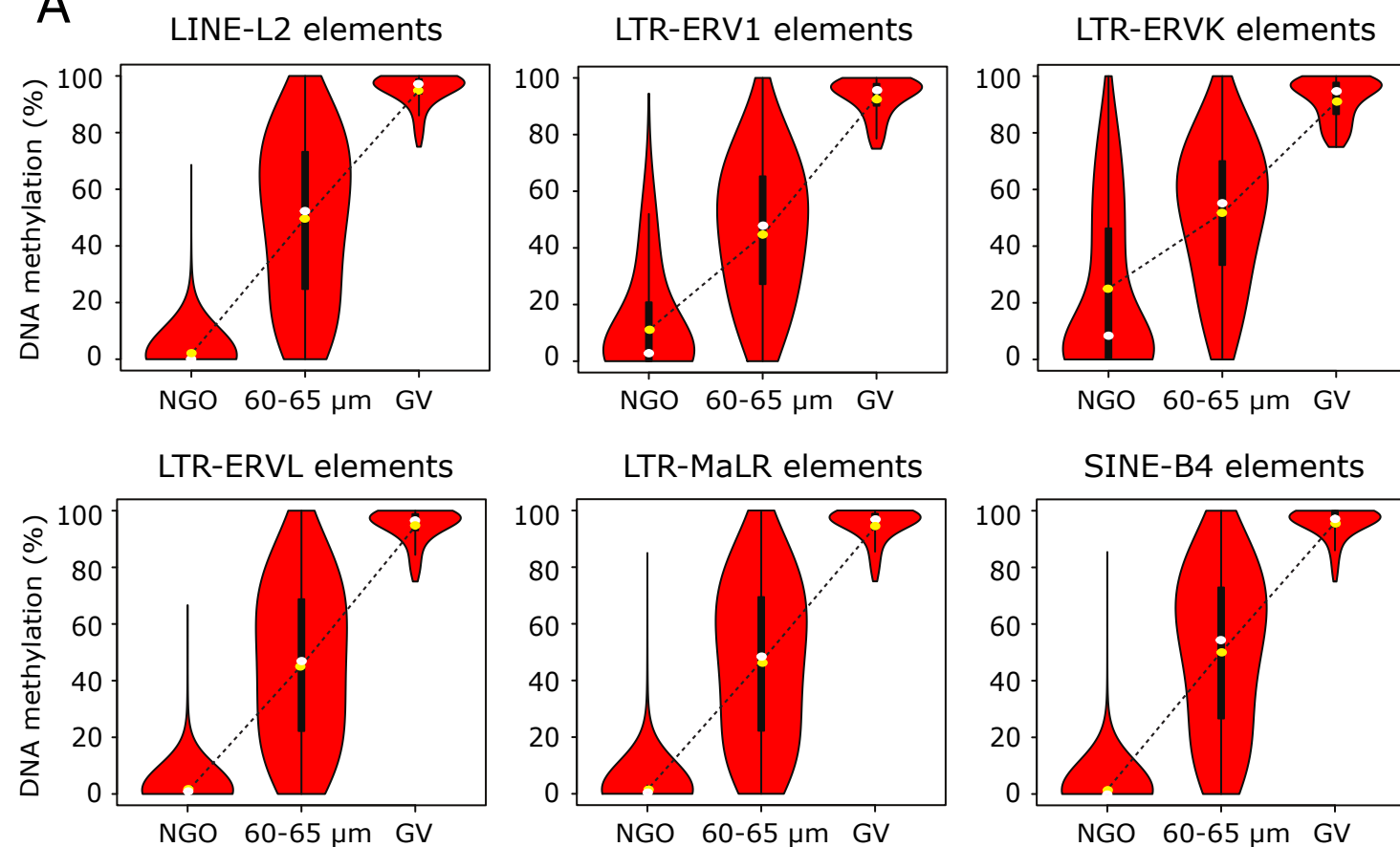


Progression of DNA methylation at transposable elements (TEs) during oocyte growth, compleme
Figure1.

(A) Violin plots showing the distribution of CpG methylation values in ERV1s, ERV2s, ERV3s, ERV4s, ERV5s, ERV6s, ERV7s, ERV8s, ERV9s, ERV10s, ERV11s, ERV12s, ERV13s, ERV14s, ERV15s, ERV16s, ERV17s, ERV18s, ERV19s, ERV20s, ERV21s, ERV22s, ERV23s, ERV24s, ERV25s, ERV26s, ERV27s, ERV28s, ERV29s, ERV30s, ERV31s, ERV32s, ERV33s, ERV34s, ERV35s, ERV36s, ERV37s, ERV38s, ERV39s, ERV40s, ERV41s, ERV42s, ERV43s, ERV44s, ERV45s, ERV46s, ERV47s, ERV48s, ERV49s, ERV50s, ERV51s, ERV52s, ERV53s, ERV54s, ERV55s, ERV56s, ERV57s, ERV58s, ERV59s, ERV60s, ERV61s, ERV62s, ERV63s, ERV64s, ERV65s, ERV66s, ERV67s, ERV68s, ERV69s, ERV70s, ERV71s, ERV72s, ERV73s, ERV74s, ERV75s, ERV76s, ERV77s, ERV78s, ERV79s, ERV80s, ERV81s, ERV82s, ERV83s, ERV84s, ERV85s, ERV86s, ERV87s, ERV88s, ERV89s, ERV90s, ERV91s, ERV92s, ERV93s, ERV94s, ERV95s, ERV96s, ERV97s, ERV98s, ERV99s, ERV100s, ERV101s, ERV102s, ERV103s, ERV104s, ERV105s, ERV106s, ERV107s, ERV108s, ERV109s, ERV110s, ERV111s, ERV112s, ERV113s, ERV114s, ERV115s, 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Figure S1

A



B

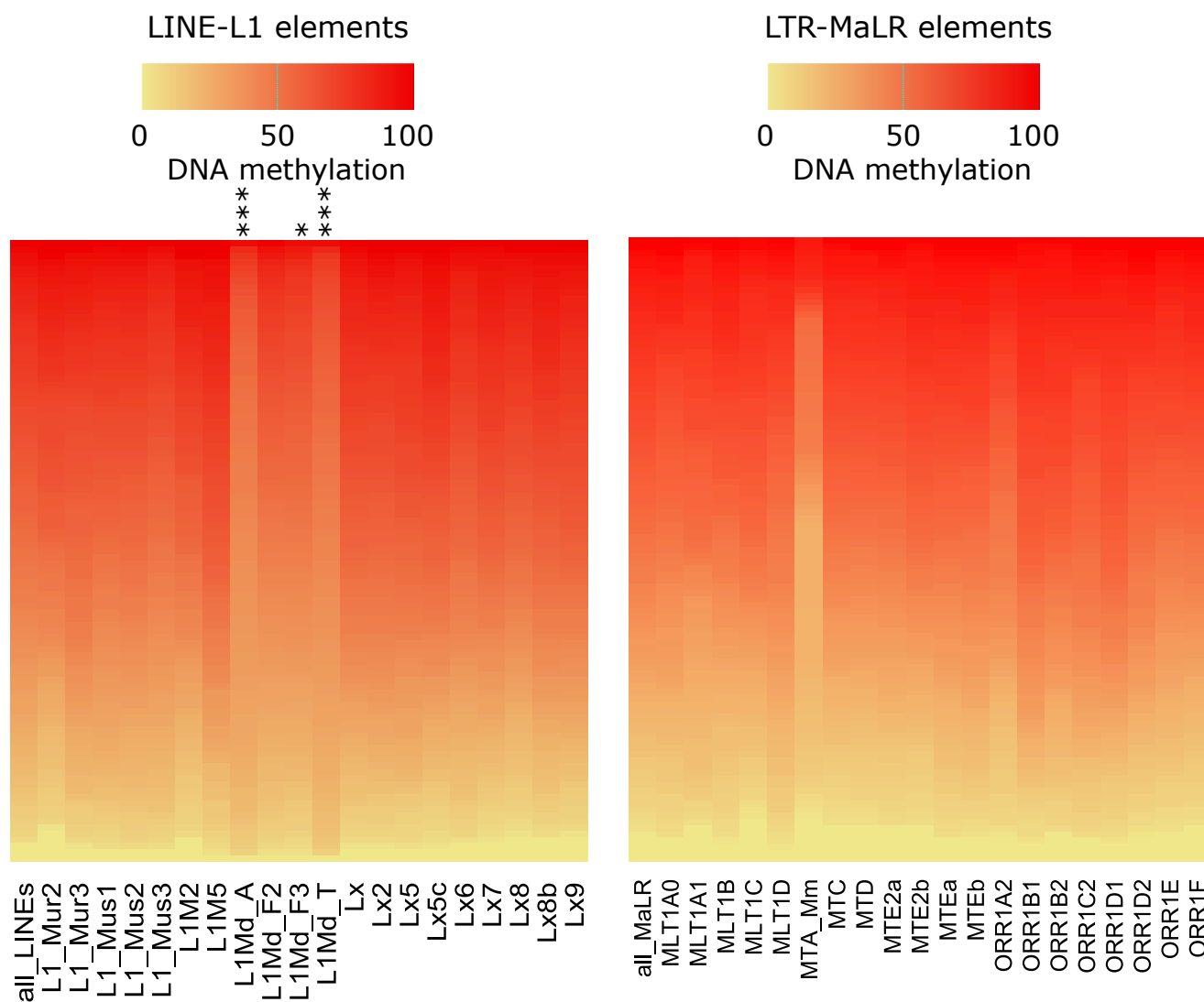
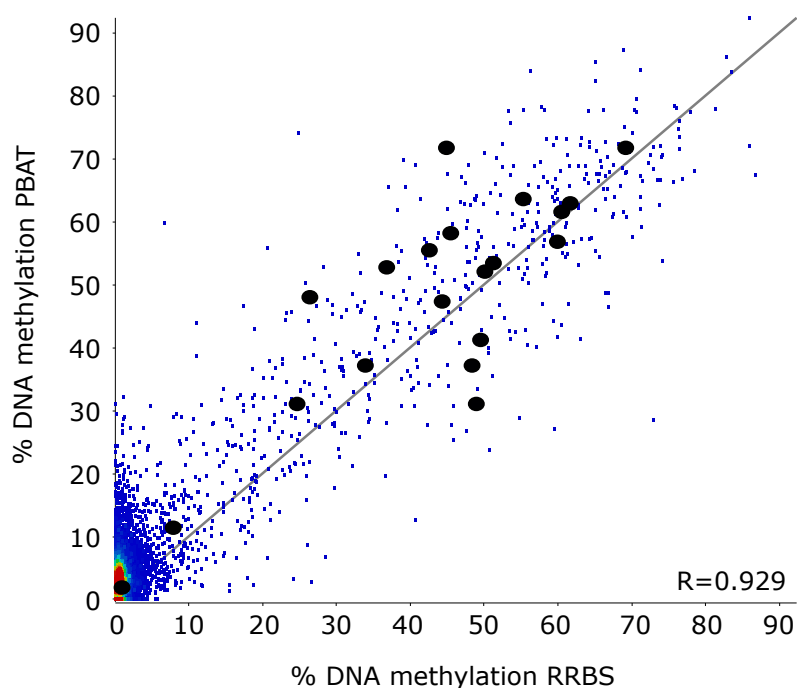
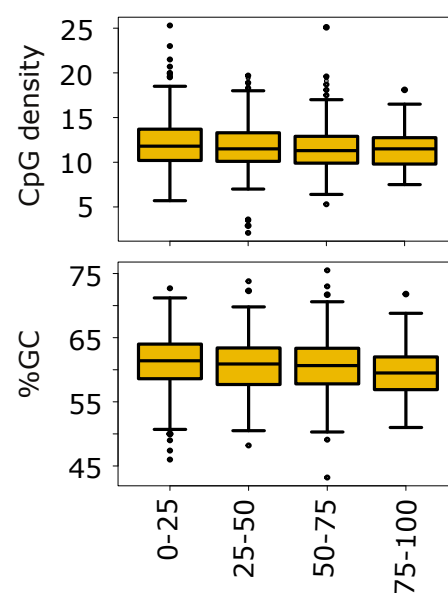


Figure S2

A



B



Additional file 3: Figure S2

(A) Scatterplot of CGI methylation in 60-65 μ m oocyte RRBS and PBAT datasets. X and Y axis show DNA methylation values in RRBS and PBAT datasets, respectively. R value of 0.929 suggests high level of correlation between these two datasets. Black dots highlight individual gDMRs.

(B) Box whisker plots of CpG density and %GC of CGIs binned by % methylation in 60-65 μ m oocytes (PBAT dataset). The numbers of CGIs in each DNA methylation category (from lowest to highest) are: 470, 329, 384 and 63.

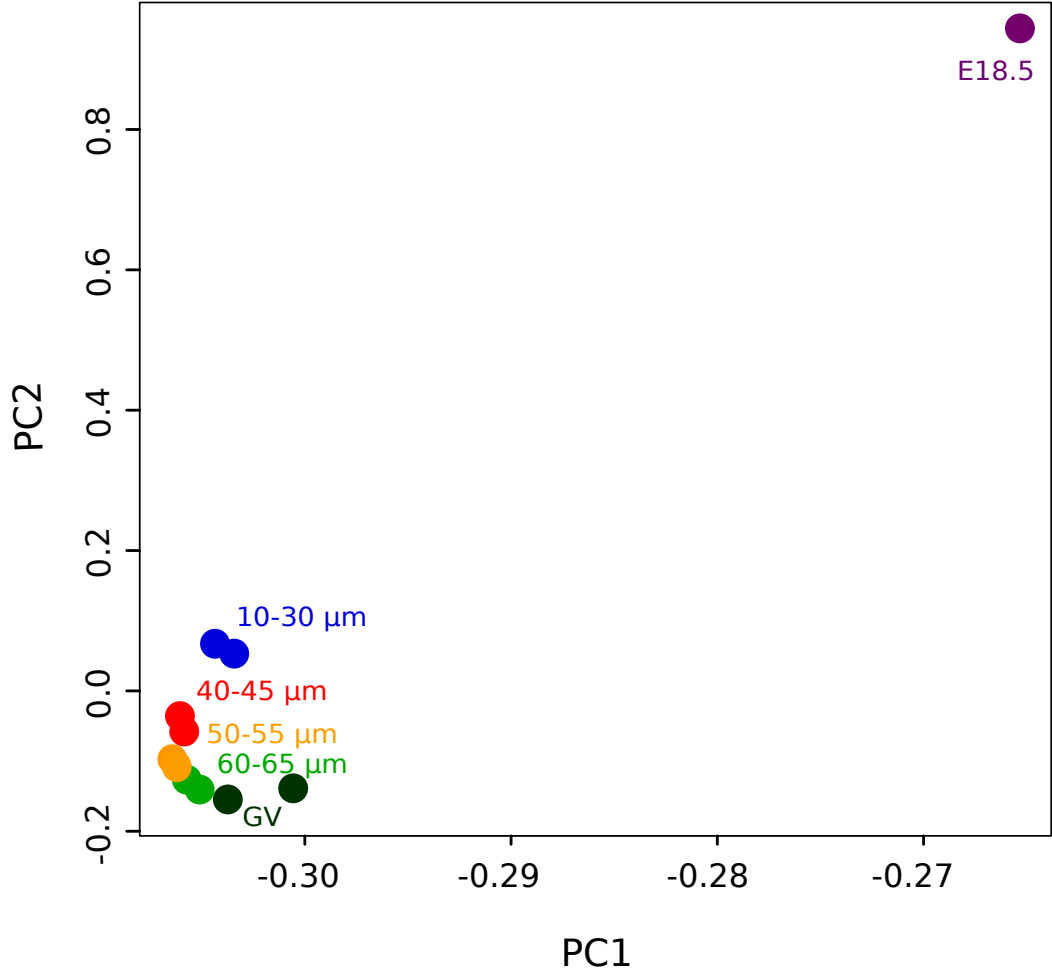
Additional file 3: Figure S3

PCA plots for oocyte mRNA-seq libraries.

Top graph represents PCA plot for all RNA-seq datasets from E18.5 to GV oocytes, in which PC1 explains 96.0% of the variance and PC2 a further 2.6%. Bottom graph represents PCA plot with the E18.5 dataset excluded from the analysis, in which PC1 explains 98.4% and PC2 a further 0.9% of the variance.

Figure S3

all RNA-seq datasets (including E18.5 oocytes)



growing oocytes RNA-seq datasets (excluding E18.5 oocytes)

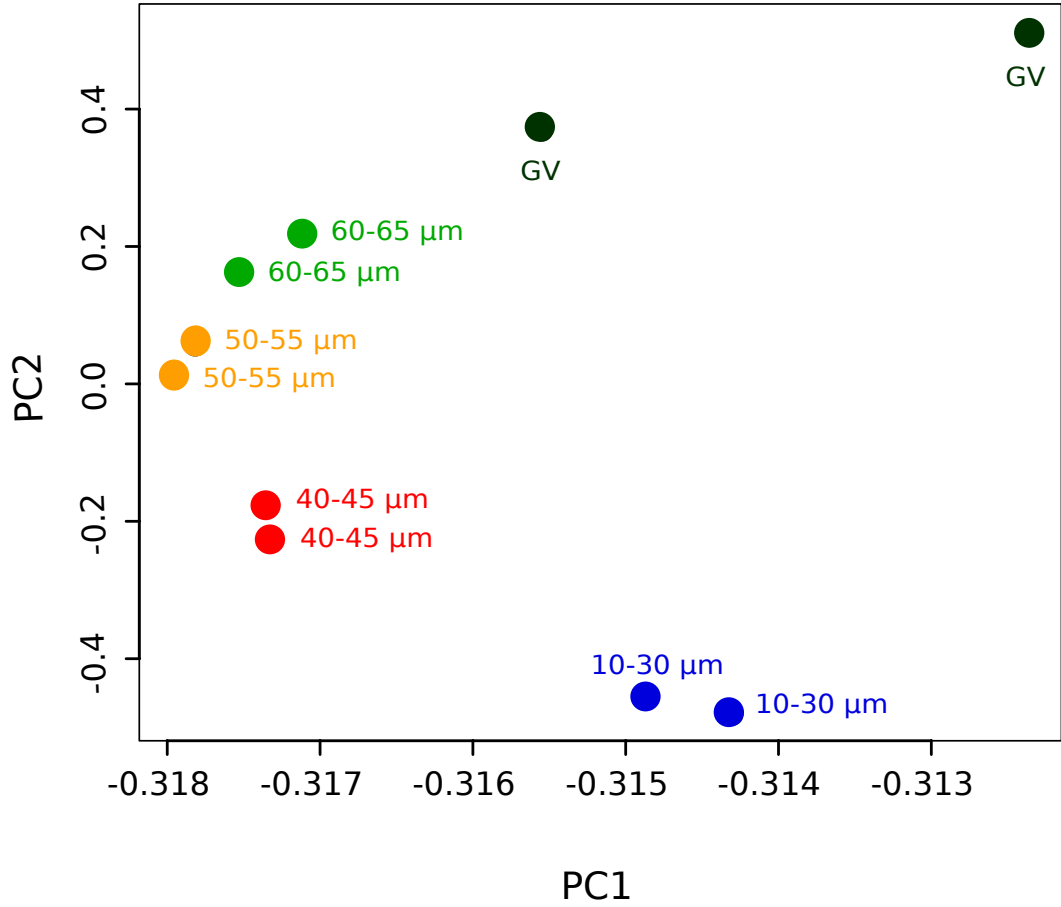
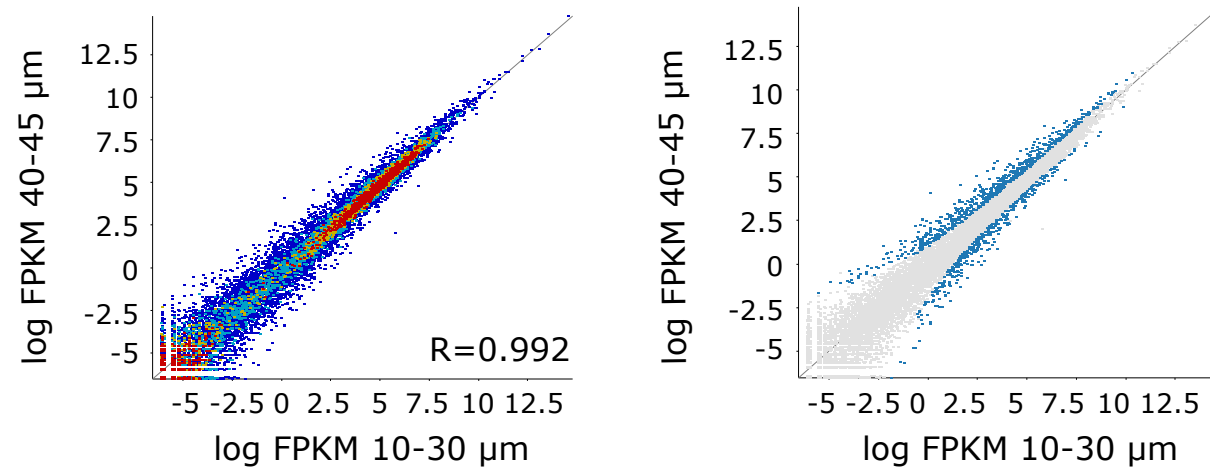
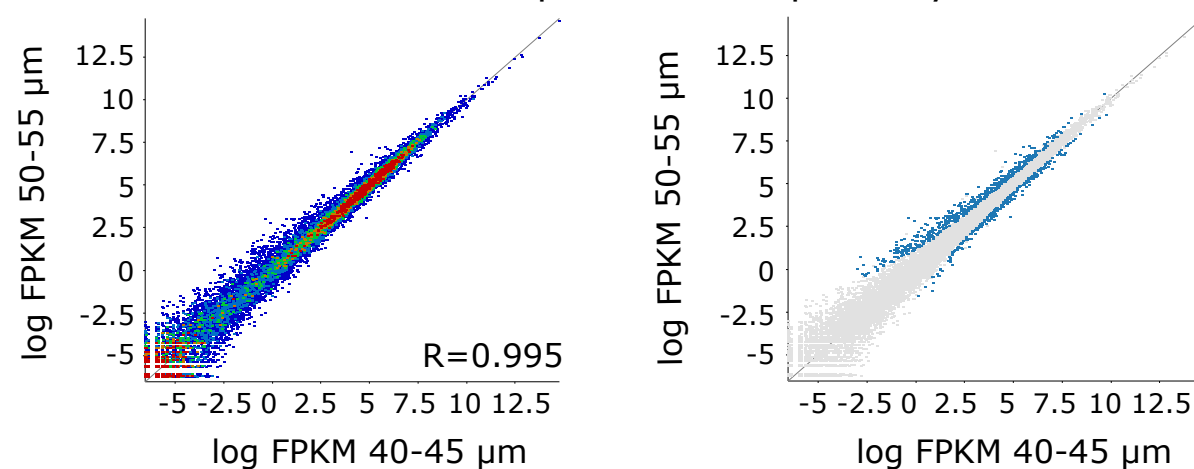


Figure S4

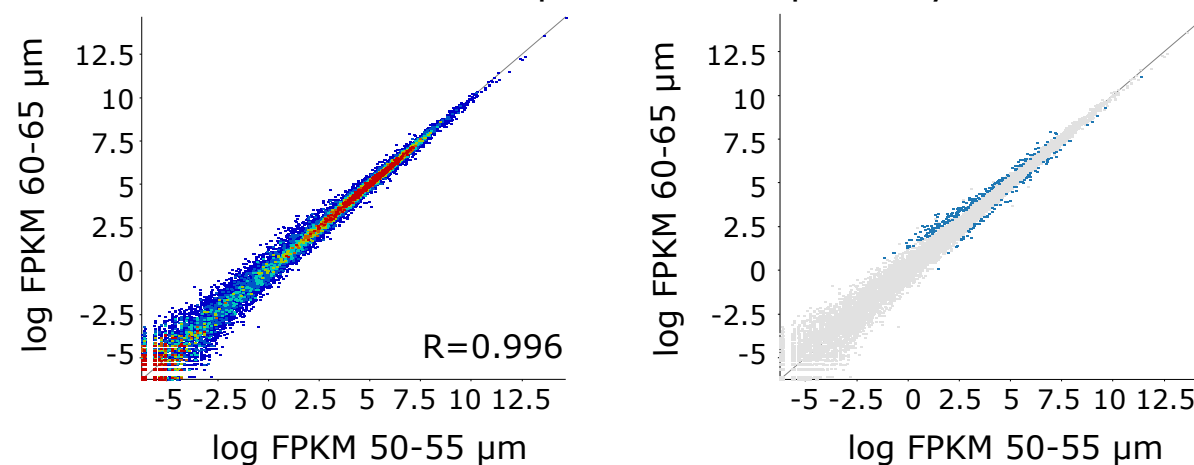
10-30 μm vs 40-45 μm oocytes



40-45 μm vs 50-55 μm oocytes



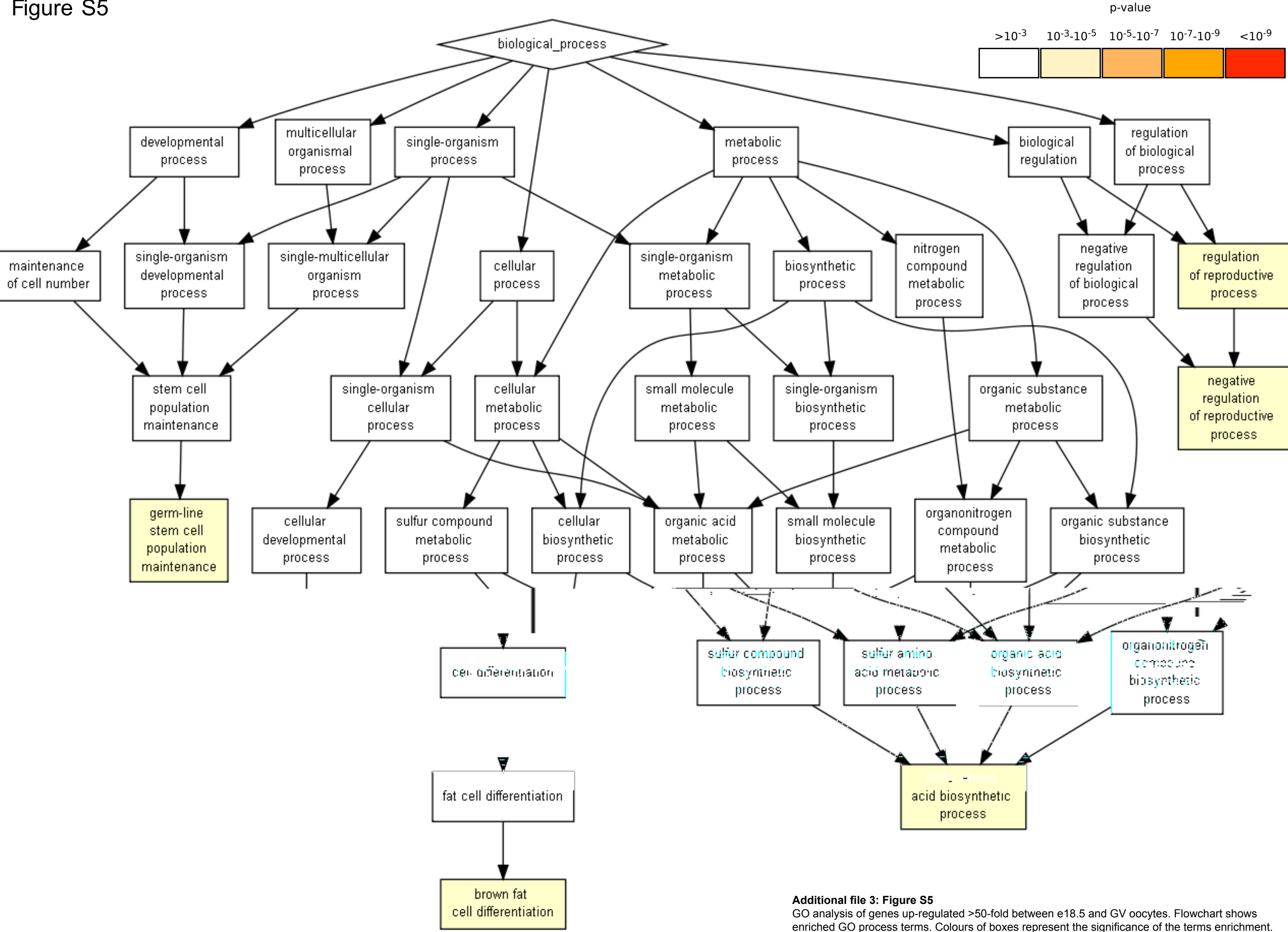
50-55 μm vs 60-65 μm oocytes



Additional file 3: Figure S4

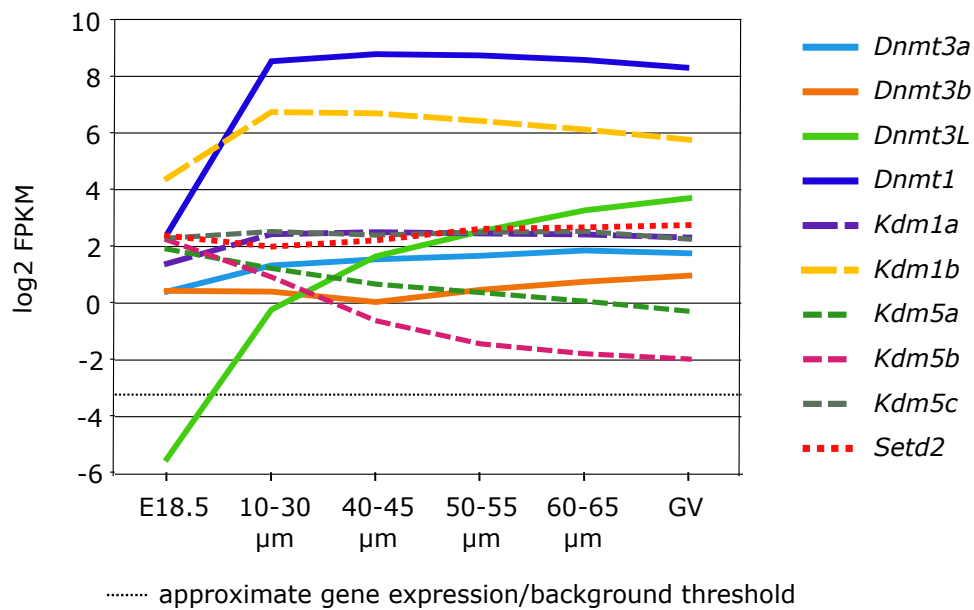
Scatterplots for pair-wise comparison of RNA-seq datasets from consecutive size populations of growing oocytes. Replicate RNA-seq datasets for each size population were combined for this analysis. The left-hand panels show colour-coding density plots for all 25,965 annotated genes, and right-hand panels highlight differentially expressed genes identified by DESeq2, at a p value ≤ 0.01 . The number of genes identified as differentially expressed in each paired comparison is: 1062 genes between 10-30 μm and 40-45 μm ; 717 between 40-45 μm and 50-55 μm ; and 278 between 50-55 μm and 60-65 μm .

Figure S5



Additional file 3: Figure S5
GO analysis of genes up-regulated >50-fold between e18.5 and GV oocytes. Flowchart shows enriched GO process terms. Colours of boxes represent the significance of the terms enrichment.

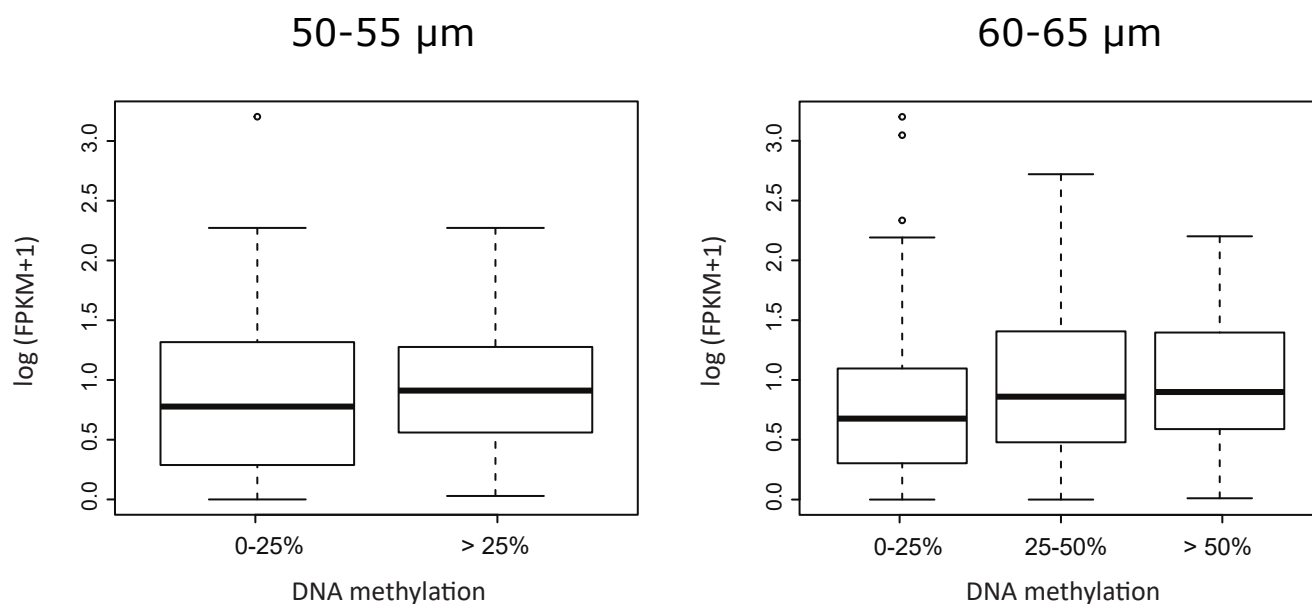
Figure S6



Additional file 3: Figure S6

Graph showing expression levels over oocyte growth of transcripts for Dnmts, Kdm1s and Kdm5s, and SetD2. Dashed line represents an approximate FPKM threshold when genes are considered to be expressed (based on quantification of threshold values for individual datasets).

Figure S7

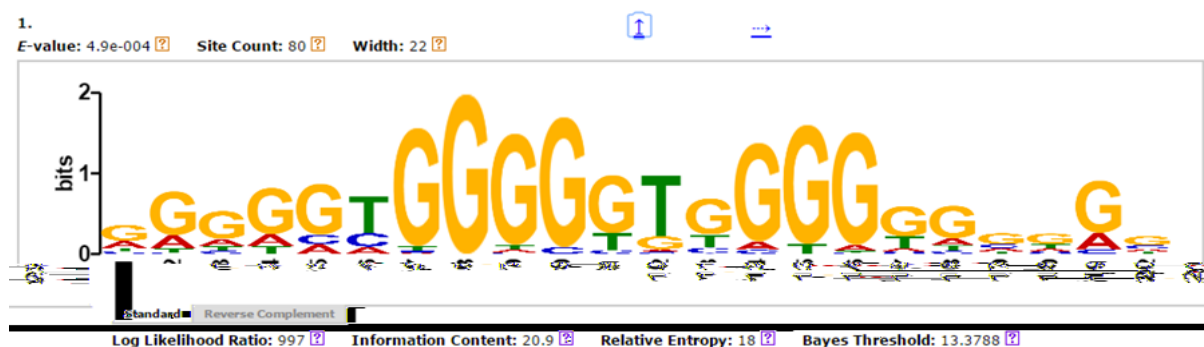


Additional file 3: Figure S7

Methylation level of intragenic CGIs in RRBS datasets in relation to expression level of the corresponding gene. Only CGIs that are methylated in GV oocytes are considered for the analysis. Methylation levels in 50-55 µm and 60-65 µm oocytes are compared with RNA-seq dataset from 50-55 µm and 60-65 µm, respectively. The numbers of CGIs analysed each methylation category (from lowest to highest) are: 335 and 97 for 50-55 µm oocytes and 180, 122 and 130 for 60-65 µm oocytes.

Figure S8

0-25% methylated vs 50-75% methylated CGIs



Motif occurrence in 0-25% methylated CGIs: 336/470 (71%)
Motif occurrence in 50-75% methylated CGIs: 237/384 (62%)

0-25% methylated vs 75-100% methylated CGIs



Motif occurrence in 0-25% methylated CGIs: 343/470 (73%)
Motif occurrence in 75-100% methylated CGIs: 30/63 (48%)

Additional file 3: Figure S8

MEME output of search for motifs enriched in late methylated CGIs ($\leq 25\%$ DNA methylation in 60-65 μm oocytes) compared to CGIs with 50-75% and $\geq 75\%$ methylation in 60-65 μm oocytes.