

Supplementary Figures and Tables to Functional signaling and gene regulatory networks
between the oocyte and the surrounding cumulus cells.

Fernando H. Biase*, Katelyn M. Kimble

Department of Animal Sciences, Auburn University, Auburn, AL

*Corresponding author

Address: 559 Devall Dr, Auburn, AL 36849

Email: fbiase@auburn.edu

Phone: 334 844 1680

Fax: 334-844-1519

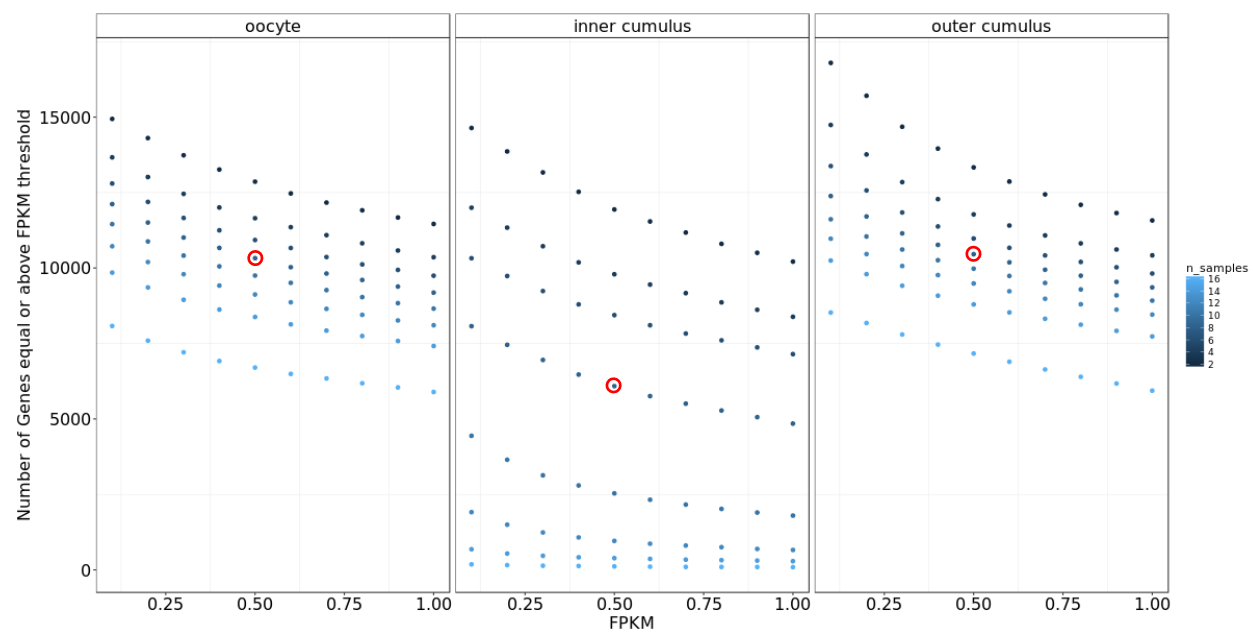


Fig S1. Number of genes detected by RNA-seq according to different thresholds. Red circles mark the number of genes used for analytical procedures.

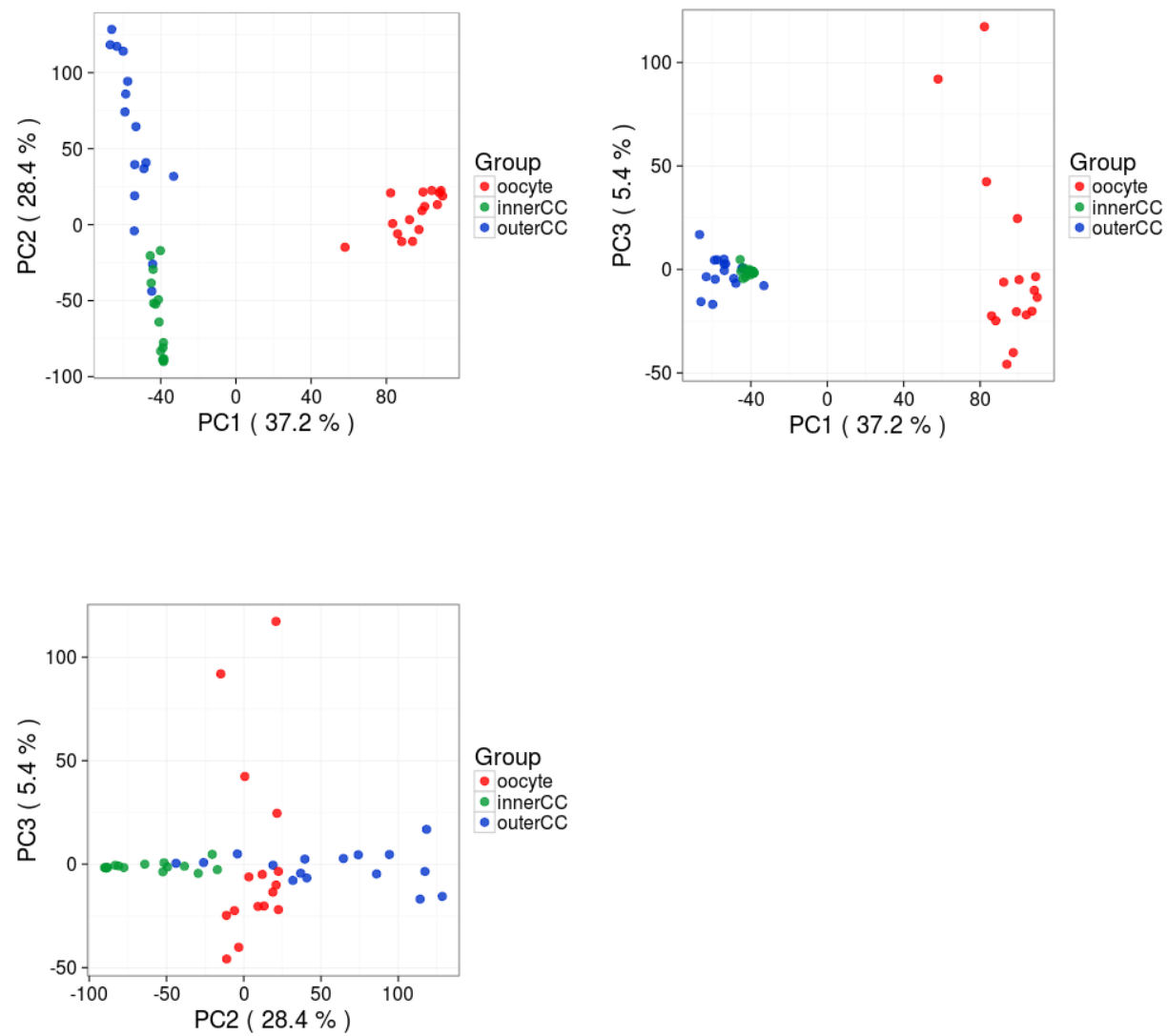


Fig S2. Principal component analysis of the samples collected.

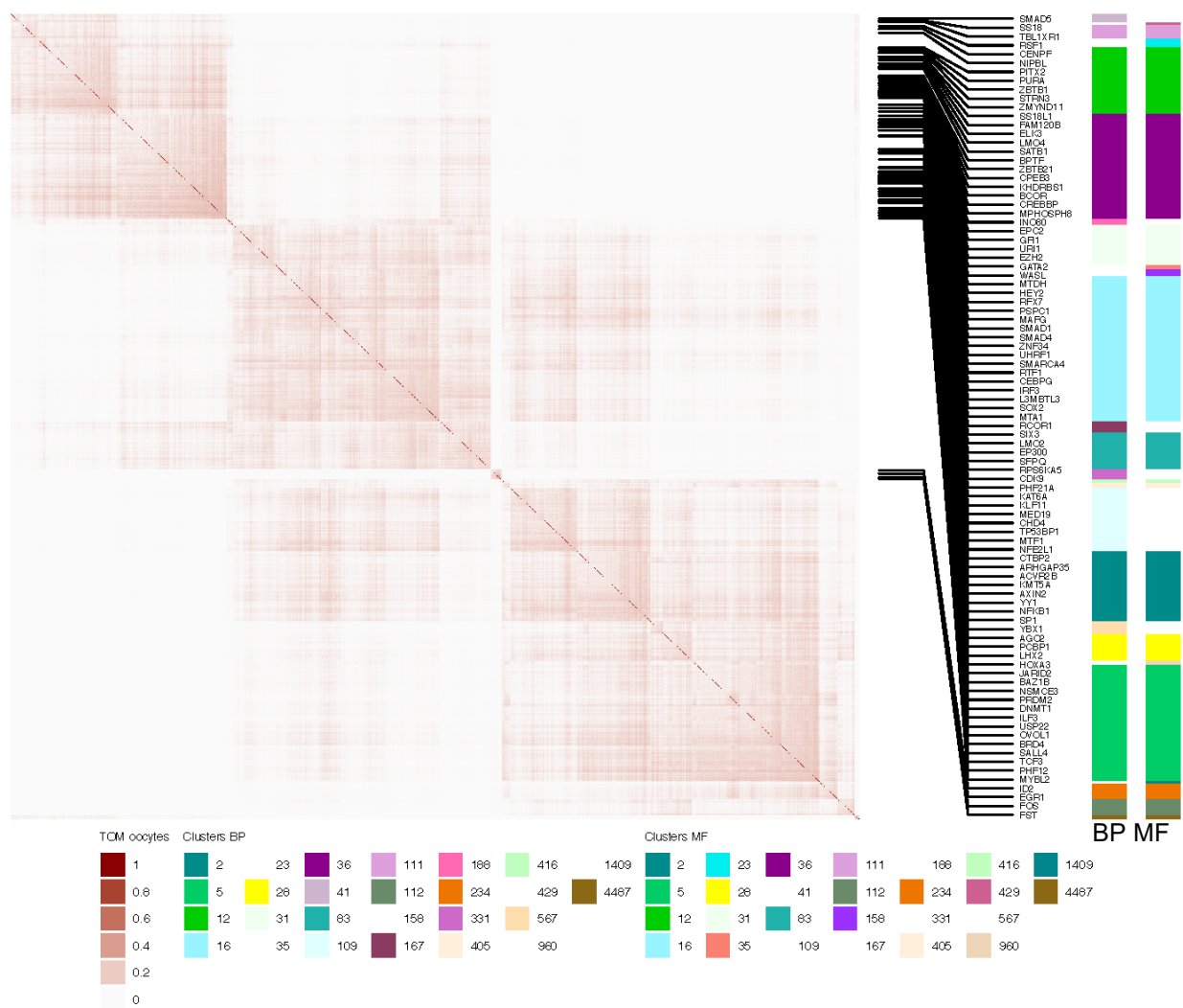


Fig. S3. Topological overlap of transcript levels for 2,222 genes expressed in oocytes. Genes related to regulation of transcription are annotated. The two vertical bars on the right-hand side of the panel annotate clusters with enrichment for gene ontology biological processes (BP) and molecular functions (MF).

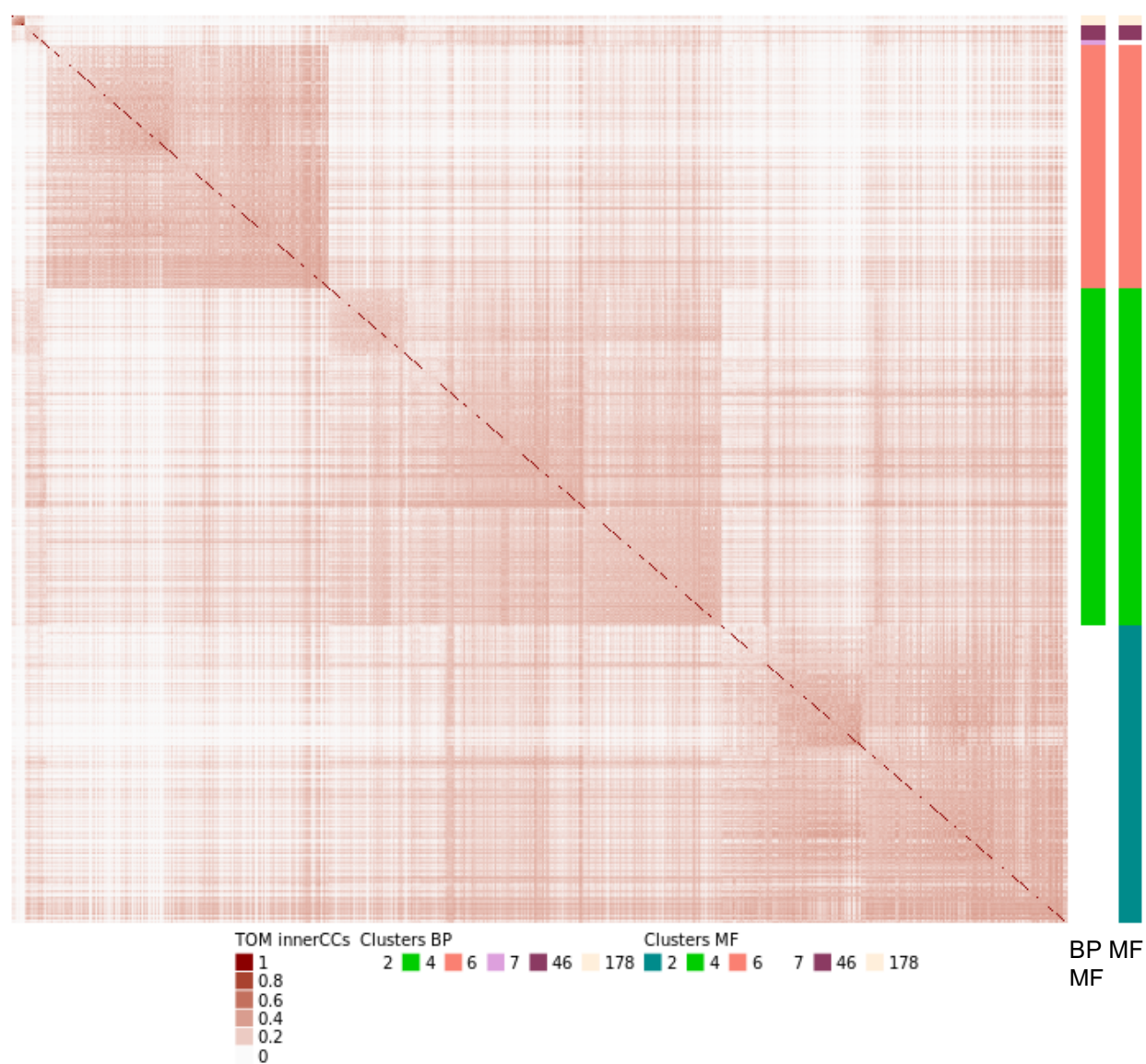


Fig. S4. Topological overlap of transcript levels for 1,222 genes expressed in cumulus cells forming the corona radiata of the cumulus-oocyte complex. The two vertical bars on the right-hand side of the panel annotate clusters with enrichment for gene ontology biological processes (BP) and molecular functions (MF).

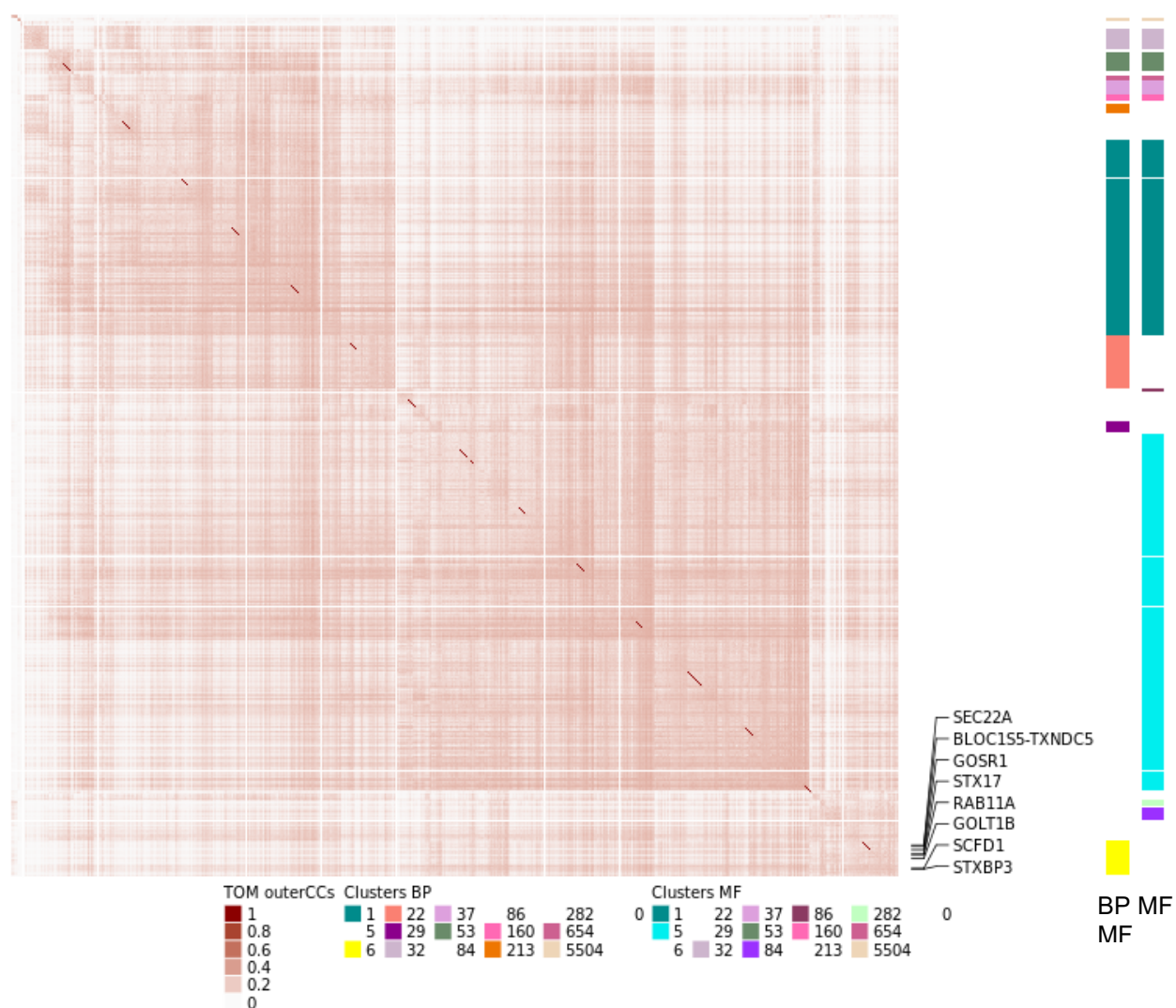


Fig. S5. Topological overlap of transcript levels for 3,990 genes expressed in cumulus cells on the periphery of the cumulus oocyte complex. Genes composing vesicle-mediated transport are annotated on the heatmap. The two vertical bars on the right-hand side of the panel annotate clusters with enrichment for gene ontology biological processes (BP) and molecular functions (MF).

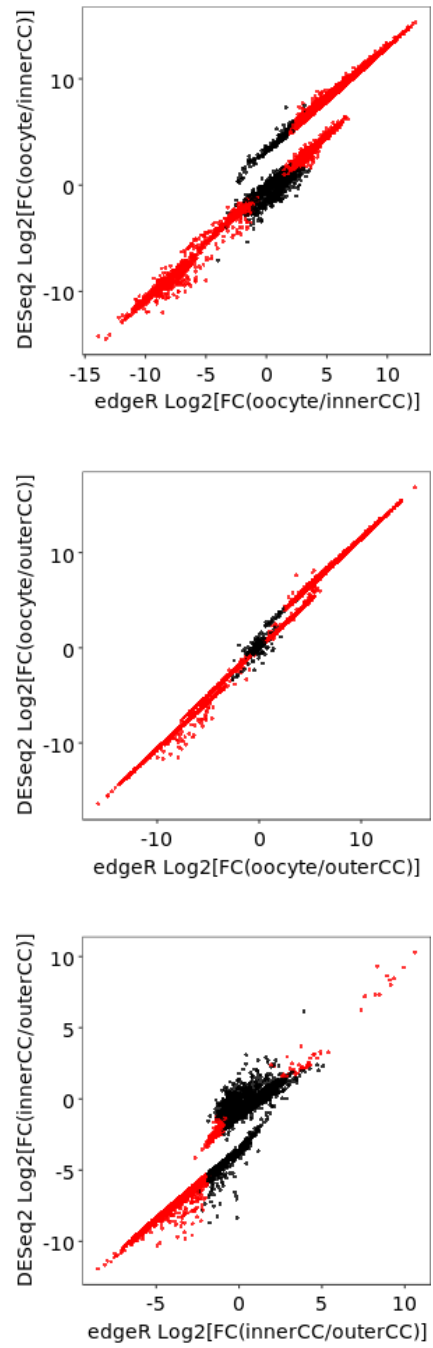


Fig. S6. Comparative results obtained from two algorithms used for pairwise contrast of gene expression levels among oocyte, innerCC and outerCC samples. Red dots represent differentially expressed genes between two groups (FDR<0.01).

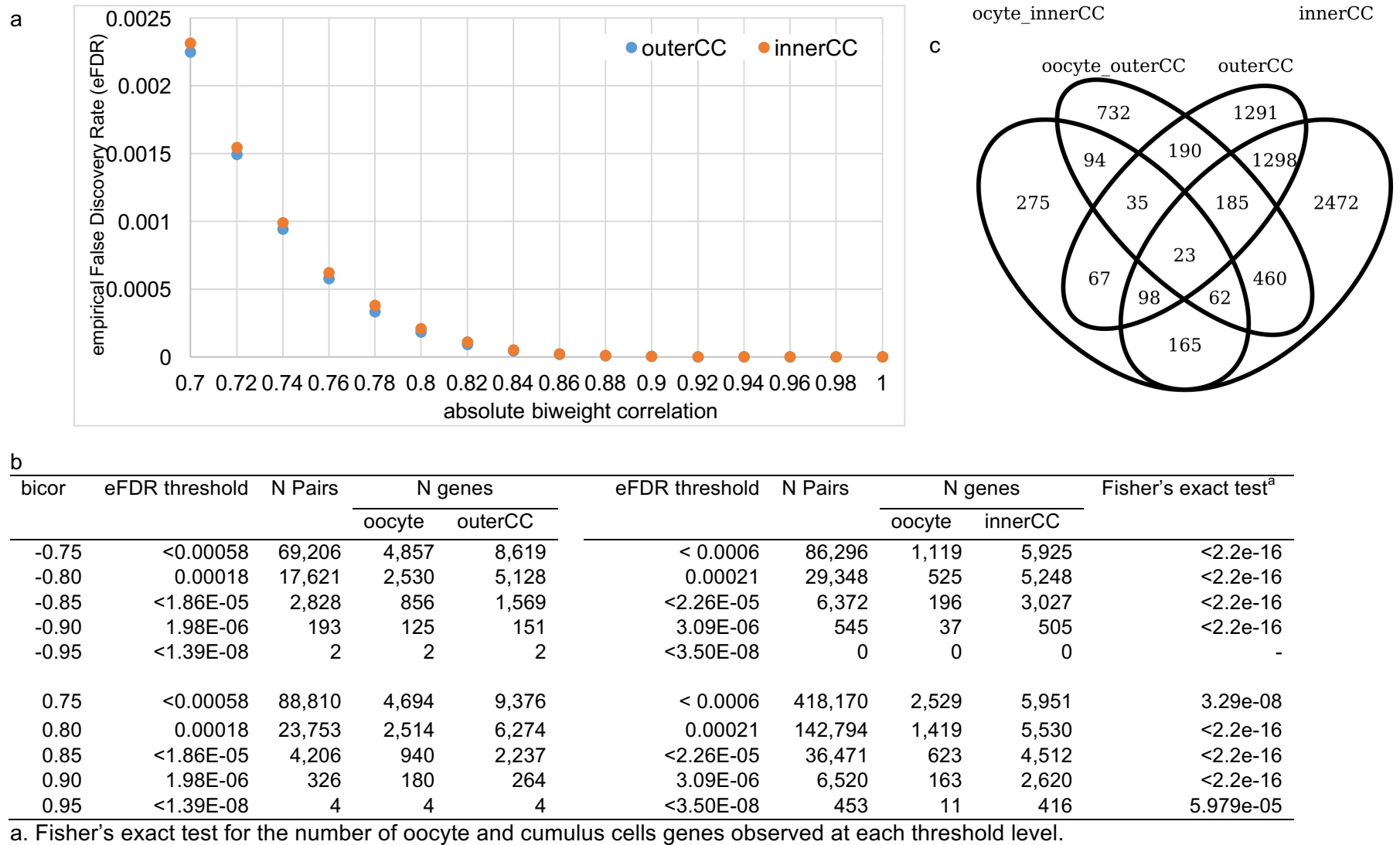


Fig. S7. Descriptive properties of the co-expression between oocytes and cumulus cells. (a) Estimates of eFDR from the correlations obtained from scrambled oocyte data and outerCCs and innerCCs data. (b) Distribution of genes and pairs of genes according to different thresholds. (c) Overlapping of genes forming significant correlation links at $|\text{bicor}| > 0.85$ and $\text{eFDR} < 1.86\text{E-}05$.

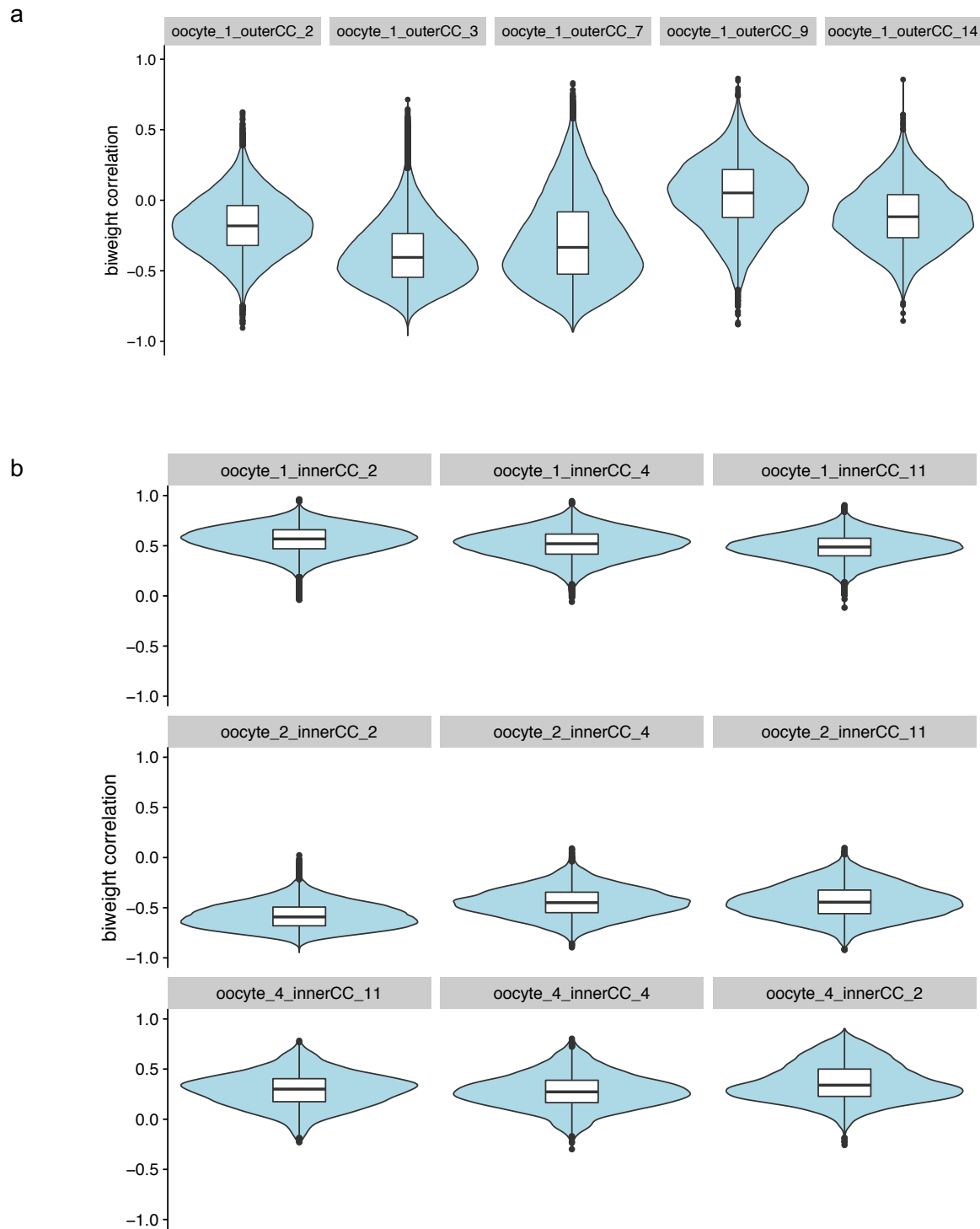


Fig. S8. Average pair-wise gene correlation between transcript levels in oocytes and outerCCs (a) or innerCCs (b). Each violin plot represents a block of co-expressing genes delimited by their clusters (see Fig. 4a, a), and are named according to the cluster in oocyte and cluster in cumulus cells (i.e.: oocyte_4_innerCC_2, means cluster 4 formed by oocytes genes and cluster 2 formed by innerCC genes).

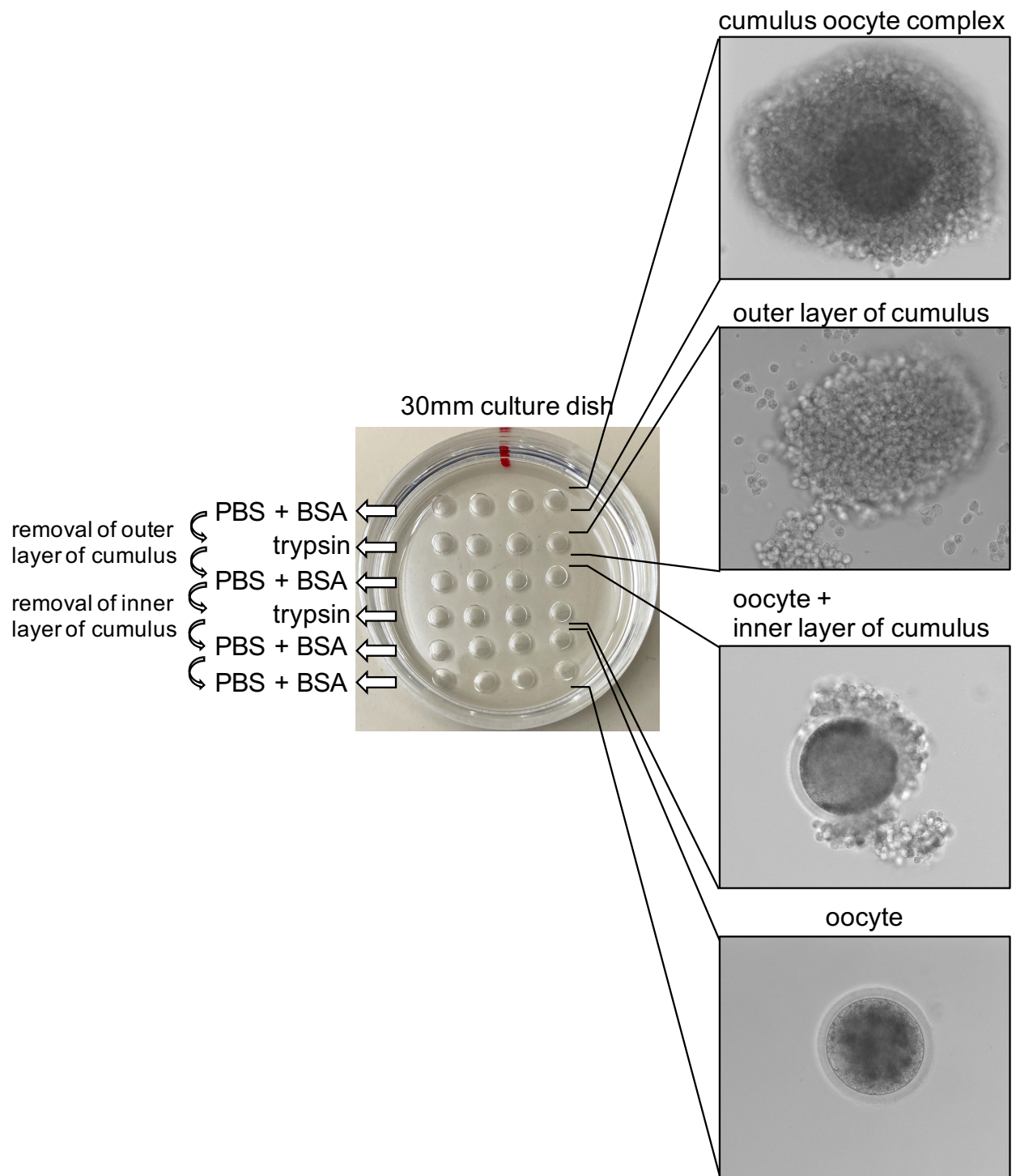


Fig. S9. Schematics of the sample collection. Please, see Methods section for detailed description of the sample collection.

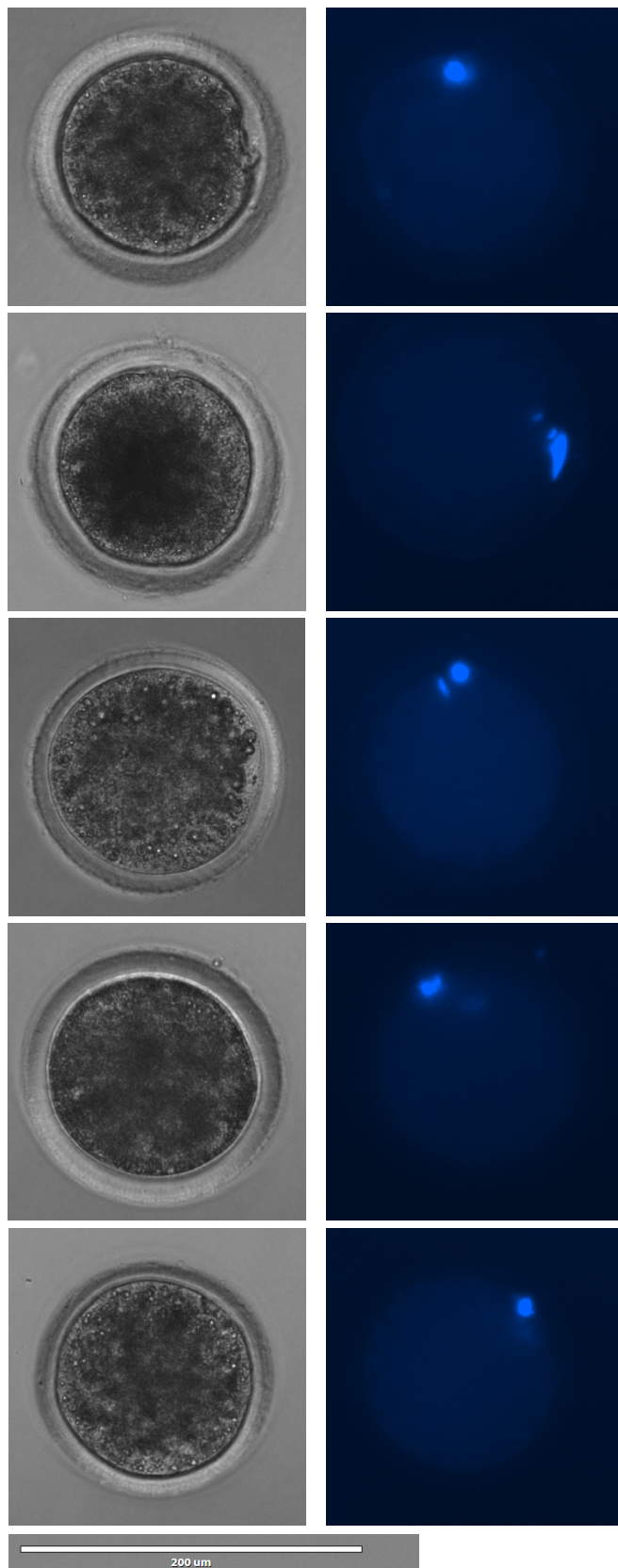


Fig. S10. Representative oocytes free of cumulus cells collected for RNA-sequencing. Left panel: Bright field, Right panel DAPI, the scale bar (200 μ m) is used for all pictures.