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SUPPLEMENTARY MATERIAL

corresponding to:

Comparative molecular portraits of human unfertilized oocytes and primordial germ cells at 10 weeks of gestation

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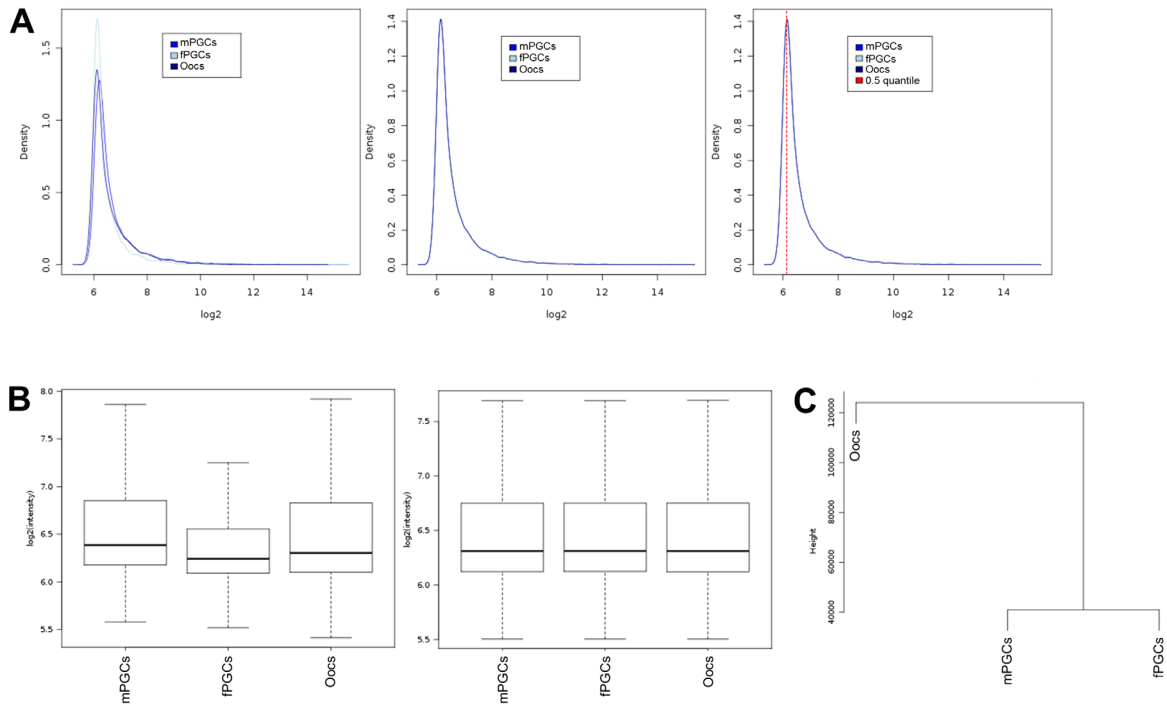

Supplementary Figure 1. Quality control of the transcriptome data derived from the microarray experiments. (A) *Distribution of the overall fPGCs, oocytes and mPGCs gene expression signal intensities plotted prior to (left) and after (middle) quantile normalization. We defined all genes with an expression value above the 0.5 quantile of the overall normalized signal intensity distribution (right, red line) as expressed.* **(B)** *Box plots of the overall fPGCs, oocytes and mPGCs gene expression values prior to (left) and after (right) normalization. (C) Dendrogram illustrating hierarchical clustering of the fPGCs, mPGCs and oocytes samples upon microarray-based transcriptome profiling (Euclidean distance and complete linkage hierarchical clustering).*

SUPPLEMENTARY TABLE 1 (EXCEL FILE)

RESULTS OF THE VENN DIAGRAM-BASED ANALYSIS OF FEMALE PGCs, MALE PGCs AND OOCYTES-DERIVED TRANSCRIPTOMES

These gene lists correspond to the numbers depicted in Fig. 1A, which represent specific or overlapping genes with elevated expression levels in fPGCs (red), mPGCs (blue) and oocytes (green). "Novel" genes which have not been functionally annotated to date, including, e.g. "LOC389936", "C12orf12", "FAM10A6", "FLJ31568", "KIAA0895L", "MGC35361" are marked by value "1" in the novel genes column at the right hand side of each gene symbol.

SUPPLEMENTARY TABLE 2 (EXCEL FILE)

RESULTS OF THE DAVID ANALYSIS OF FEMALE PGCS- AND OOCYTES-SPECIFIC GENES

All genes exclusively expressed in either fPGCs (873) or oocytes (1141) or overlapping between fPGCs and oocytes (967) were assessed for functional enrichment of biological pathway-associated GOs (BP), cellular component-associated GOs (CC), molecular function-associated GOs (MF) and KEGG pathways using the DAVID database. The complete database output for each set of genes is given in separate spreadsheets; significantly enriched terms ($p < 0.01$) are highlighted in orange.

SUPPLEMENTARY TABLE 3 (EXCEL FILE)

RESULTS OF THE IPA CANONICAL PATHWAY ANALYSIS OF FEMALE PGC AND OOCYTES TRANSCRIPTOMES

The total number of genes expressed in fPGCs (9210) and oocytes (9207) were assessed for enrichment of canonical signaling pathways using IPA. The complete database output for each set of genes is given in separate spreadsheets; significantly enriched terms are highlighted ($p < 0.0001$ in orange, $p < 0.001$ in yellow).

SUPPLEMENTARY TABLE 4 (EXCEL FILE)

RESULTS OF THE IPA BIOLOGICAL FUNCTIONS ANALYSIS OF FEMALE PGCS AND OOCYTES TRANSCRIPTOMES

The total number of genes expressed in fPGCs (9210) and oocytes (9207) were assessed for functional enrichment of diseases and disorders, molecular and cellular functions as well as physiological system development and function using IPA. The complete database output for each set of genes is given in separate spreadsheets.

SUPPLEMENTARY TABLE 5 (EXCEL FILE)

RESULTS OF THE NUCLEOTIDE BLAST SEARCH TO IDENTIFY POTENTIAL ORTHOLOGOUS GENES IN HUMAN AND MOUSE

For details of the analysis please refer to the Material and Methods section. The resulting 1632 pairs of potential human and mouse orthologous genes that met our BLAST search expectation value threshold of 1E-10 are given. Novel orthologous genes either human or mouse are highlighted in blue. Highlighted in red are the 118 mouse orthologs of the human olfactory receptor (OR)-encoding genes.