change directionality of concordant gene misexpression as well as pathway enrichment between blastocysts and corresponding adult tissues. Genes and pathways also present in the 'Embryo Common Fingerprint' of *in vitro* manipulation are highlighted in red. Legends are applicable to all heatmaps in the figure.

Figure 6: No common IVF signature between embryos and adult tissues from homogenous conditions

A-C) Misregulation in adult male 40wk cardiac tissue derived from IVF WM 20% oxygen mice. A) Of the 1361 genes significantly misexpressed in IVF heart compared to controls, only 16 showed a fold-change greater than ± 2-fold. B) Ingenuity Pathway Analysis of canonical pathways most significantly enriched ($p<0.001$) in the altered IVF heart genes and C) their associated networks (network score ≥25). D) Venn diagram indicating the low number of genes (top) and number of pathways (bottom) overlapping between the IVF WM 20% oxygen blastocyst (blue) or ICM (green) transcriptomes and corresponding adult heart (grey). E) The genes similarly misexpressed between blastocyst and heart, or ICM and heart, and their directionality of change. Red asterisks indicate genes commonly altered in both blastocyst and ICM, versus heart. F) Overlap of pathways associated with the altered genes between the embryo data and the heart. Legends are applicable to all heatmaps in the figure.

Figure 7: Common upstream regulators may govern the transcriptional changes present in *in vitro* embryos and adult tissues

Ingenuity Pathway Analysis identifies regulators functioning upstream of the altered genes, and predicts whether these regulators are impaired (negative z-score, blue) or activated (positive z-score, red) based on fold-change misexpression. A) Shared upstream regulators of the ART embryo expression profiles. 15 molecules were predicted to function upstream of the transcriptional alterations present in the *in vitro* blastocyst, 10 of which were similarly highlighted in ICM. B, C) Upstream regulators present in the embryo-to-adult condition-specific comparisons. B) 7 regulators commonly target the altered genes in IVF WM 20% blastocysts, ICM and adult heart, and C) 21 regulators collectively mediate the gene expression changes observed in KAA 5% oxygen blastocysts and corresponding adult female fat, liver and muscle.

Supplemental Figure 1: Common impact of the Effect-of-Culture experiments

A) Venn diagram showing the concordance of gene misexpression after culture of naturally-fertilized zygotes to the blastocyst stage in either KAA or WM, with 5% or 20% oxygen. B) Directionality of the 77 concordantly misexpressed genes, and C) their top associated pathways after Ingenuity Pathway Analysis.

Supplemental Figure 2: Common impact of the Effect-of-Fertilization experiments

A) Venn diagram showing the concordance of gene misexpression after fertilization by IVC, IVF or ICSI and culture of resulting zygotes to the blastocyst stage in WM with 20% oxygen. B) Directionality of the 104 concordantly misexpressed genes, and C) their top associated pathways after Ingenuity Pathway Analysis.

Supplemental Figure 3: Summary of all predicted upstream regulators of the ART expression profiles

Combination of the upstream regulators shared between 1) the embryo common fingerprint, 2) the IVF WM-20% O_2 embryo and adult heart, and 3) the KAA-5% O_2 blastocyst and adult tissues.