SUPPLEMENTAL FIG. S1. Validation of microarray results on transcriptome of conceptus cells by RT-PCR. Data represent the expression of tubular (TUB) and filamentous (FIL) conceptuses relative to ovoid (OV) conceptuses within gene expression technique.

SUPPLEMENTAL FIG. S2. Networks from causal analyses of genes differentially expressed by conceptus cells from different stages of elongation (OV, TUB, and FIL). Network A combined 1 predicted upstream regulators, 3 target genes differentially expressed between OV and TUB, and 1 predicted downstream effect with a consistency score of 4.0. Network B combined 3 predicted upstream regulators, 3 target genes differentially expressed between TUB and FIL, and 1 predicted downstream effect with a consistency score of 4.0. Network C combined 18 predicted upstream regulators, 24 target genes differentially expressed between OV and FIL, and 5 predicted downstream effects with a consistency score of 10.0. Red denotes genes upregulated and green denotes genes downregulated in the latter group. Orange and blue represent predicted increased and predicted decreased activation, respectively. Solid and dashed lines imply on direct and indirect relationships, respectively. The pointed and blunted arrowheads represent activating and inhibitory relationships, respectively.

SUPPLEMENTAL FIG. S3. Potential upstream regulators IGF1 and insulin, and their target genes that were differentially expressed between OV and FIL conceptuses. Red denotes genes upregulated and green denotes genes downregulated in FIL. Orange and blue represent predicted increased and predicted decreased activation, respectively. Solid and dashed lines imply on direct and indirect relationships, respectively. The pointed and blunted arrowheads represent activating and inhibitory relationships, respectively.

SUPPLEMENTAL FIG. S4. Potential upstream regulators AKT and lysophosphatidic acid, and their target genes that were differentially expressed between OV and FIL conceptuses. Red denotes genes upregulated and green denotes genes downregulated in FIL. Orange and blue represent predicted increased and predicted decreased activation, respectively. Solid and dashed lines imply on direct and indirect relationships, respectively. The pointed and blunted arrowheads represent activating and inhibitory relationships, respectively.


SUPPLEMENTAL FIG. S6. PPARγ response elements (PPRE) DR1 (direct repeat with a 1 bp spacer) and Pal3 (palindromic sequence with a 3 bp spacer) motifs in regulatory regions of genes whose expression is highly correlated with PPARG expression in conceptus cells on day 15 after AI. LASAGNA-Search II web tool was used to identify the presence of these transcription factor binding sites between positions -1000 and 200 from transcription starting site of the target genes. The cutoff $P$ value used was 0.001. Arrow from PPARγ to other gene represents the presence of at least one PPRE in the regulatory region of that specific gene.

SUPPLEMENTAL FIG. S7. Scatterplot and coefficient correlation between log peak intensities of arachidonate and prostaglandin from the metabolomics results.

SUPPLEMENTAL FIG. S8. Relative mRNA expression of genes of interest in endometrium biopsies collected on Day 15 after insemination from lactating cows according to their pregnancy classification: nonpregnant (NPREG) or pregnant with an ovoid (OV), tubular (TUB) or filamentous (FIL) conceptus recovered after uterine flushing. NPREG samples were use as reference for comparison. Different letters
(a, b, c) represent different ($P < 0.05$) least squares means. Error bars represent the 95% confidence limits for group means.
SUPPL. FIG. S1.

Expression relative to OV conceptuses

- TUB-PCR
- FIL-PCR
- TUB-Array
- FIL-Array

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SUPPL. FIG. S2.

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SUPPL. FIG. S3.

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SUPPL. FIG. S5.
SUPPL. FIG. S6.
SUPPL. FIG. S7.

$R^2 = 0.281$

Prostaglandin, Log of Peak Intensity

Arachidonate, Log of Peak Intensity
SUPPL. FIG. S8.

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