

Table S1. Gene Ontology biological process terms (size > 300) that were significantly upregulated (FDR < 0.25) in the outer part of a longer-term PGE₁-treated human ductus arteriosus (DA) tissue (Case 4) compared to the tunica media of shorter-term PGE₁-treated DA tissues (Cases 2 and 3).

Gene Set Name	Size	NES	FDR <i>q</i> -Value	Rank at MAX
GO_ORGANELLE_FISSION	431	1.46	0.071	7016
GO_NEGATIVE_REGULATION_OF_CELL_CYCLE_PROCESS	315	1.38	0.181	7124
GO_MICROTUBULE_BASED_MOVEMENT	314	1.38	0.132	7727
GO_MICROTUBULE_CYTOSKELETON_ORGANIZATION	516	1.37	0.115	5962
GO_MICROTUBULE_BASED_PROCESS	740	1.34	0.149	5962
GO_REGULATION_OF_CELL_CYCLE_PHASE_TRANSITION	421	1.30	0.249	6256
GO_REGULATION_OF_CELL_CYCLE_PROCESS	705	1.29	0.234	6958
GO_CELL_CYCLE_PHASE_TRANSITION	578	1.29	0.212	5961
GO_CELL_DIVISION	546	1.27	0.239	5612

Abbreviations: NES, normalized enrichment score; FDR, false discovery rate

Table S2. Twenty genes that overlapped and were enriched (> 8-fold) in the outer part of a longer-term PGE₁-treated DA tissue (Case 4) compared to the IT of shorter-term PGE₁-treated DA tissues (Cases 2 and 3).

Gene Name	Description	Fold Change	
		Case 1 vs. Case 2	Case 1 vs. Case 3
<i>CLEC3A</i>	C-type lectin domain family 3 member A	19.5	187.6
<i>ATP6V1G3</i>	ATPase H ⁺ transporting V1 subunit G3	67.6	62.6
<i>SAA4</i>	serum amyloid A4, constitutive	56.5	59.0
<i>BEX1</i>	brain expressed X-linked 1	74.4	10.3
<i>PCP4</i>	Purkinje cell protein 4	71.7	10.2
<i>SPATA17</i>	spermatogenesis associated 17	35.4	32.2
<i>RGS13</i>	regulator of G-protein signaling 13	32.7	30.1
<i>ZNF837</i>	zinc finger protein 837	10.4	29.2
<i>RNF17</i>	ring finger protein 17	26.9	8.4
<i>KIAA1024L</i>	PREDICTED: <i>KIAA1024</i> -like	17.5	17.3
<i>LCMT2</i>	leucine carboxyl methyltransferase 2	15.8	17.7
<i>ATP8A2</i>	ATPase phospholipid transporting 8A2	14.9	13.7
<i>EPPIN</i>	epididymal peptidase inhibitor	14.1	13.1
<i>ARRB1</i>	arrestin beta 1	18.0	8.9
<i>CHRDL2</i>	chordin-like 2	17.7	8.8
<i>CIAPIN1</i>	cytokine induced apoptosis inhibitor 1	10.4	14.0
<i>VTCN1</i>	V-set domain containing T cell activation inhibitor 1	12.6	8.6
<i>FEM1A</i>	fem-1 homolog A	10.3	10.8
<i>DSCC1</i>	DNA replication and sister chromatid cohesion 1	8.8	9.7
<i>VIT</i>	vitrin	9.5	8.4

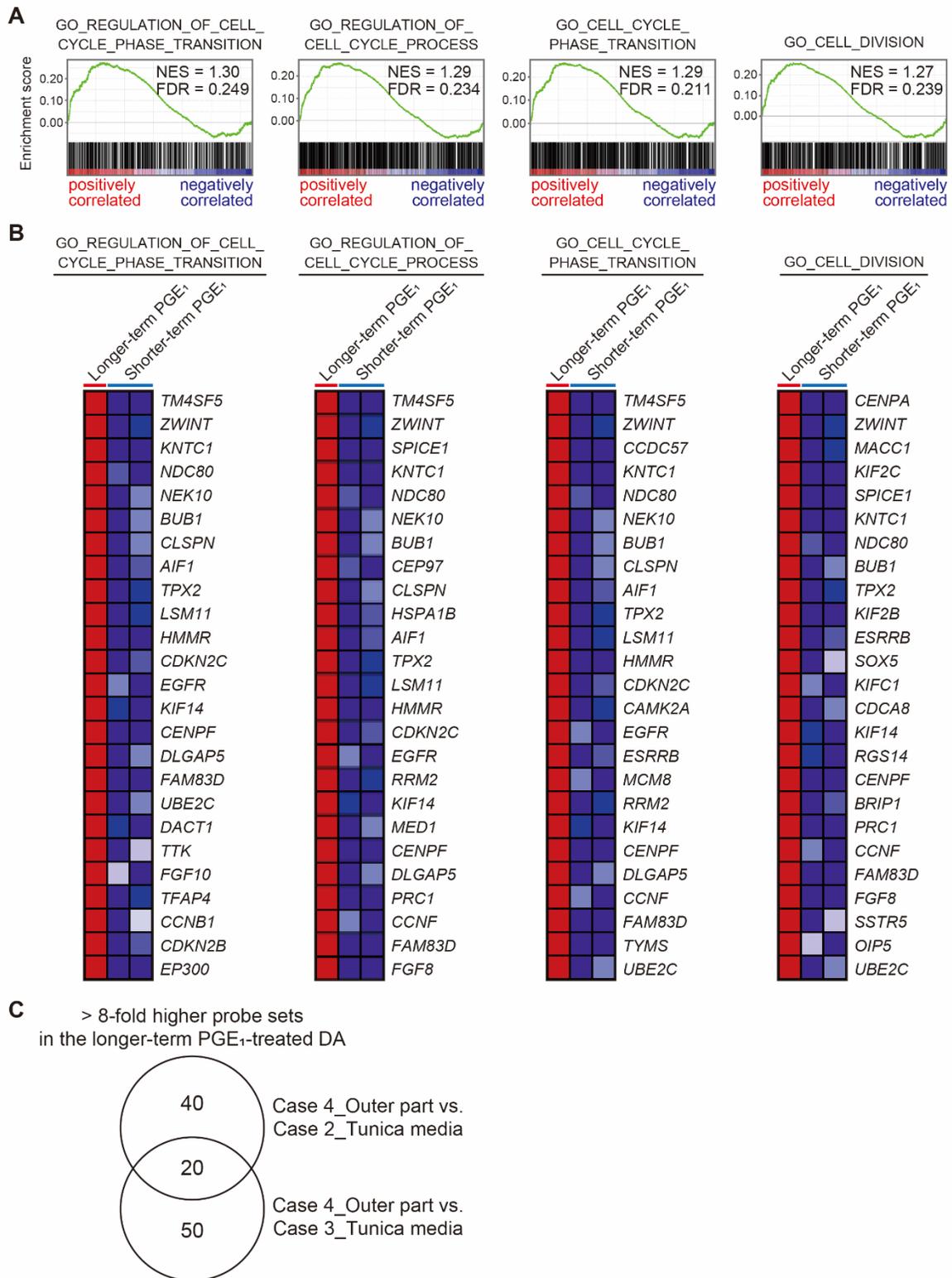


Figure S1. Differential gene expression between the longer-term PGE₁-treated human ductus arteriosus (DA)

tissue (Case 4) and the shorter-term PGE₁-treated DA tissues (Cases 2 and 3). **(A)** Gene-set enrichment analyses (GSEAs) revealed positive correlations between the outer part of the long-term PGE₁-treated DA tissue and cell-cycle related genes. **(B)** The top 25 genes that comprise the leading edge of the enrichment score in **(A)** are shown as a heatmap. **(C)** A Venn diagram shows the numbers of probe sets that were highly expressed (> 8-fold) in the outer part of longer-term PGE₁-treated DA tissue (Case 4) compared to the tunica media of shorter-term PGE₁-treated DA tissues (Cases 2 and 3). NES, normalized enrichment score; FDR, false discovery rate. .