**General Instructions**

**Matlab codes for simulations:**

**genepaired\_scenario1.m:** gene-paired embryos stochastic model scenario 1

A single-cell level stochastic model incorporating the negative feedback loop established by two different dimers. In this model, transcription of *her1* and *her7* only occur from genes free of repressor dimers. Transcription rates of *her1* and *her7* were kept equal to each other and between the two chromosomes.

**geneunpaired\_scenario1.m:** gene-unpaired embryos stochastic model scenario 1

A single-cell level stochastic model incorporating the negative feedback loop established by two different dimers. In this model, transcription of *her1* and *her7* only occur from genes free of repressor dimers. Transcription rates of *her1* and *her7* were kept equal to each other and between the two chromosomes.

**genepaired\_scenario2.m:** gene-paired embryos stochastic model scenario 2

Additional scenarios in which the transcriptional firing of two clock genes occurred at different rates.

**geneunpaired\_scenario2.m:** gene-unpaired embryos stochastic model scenario 2

Additional scenarios in which the transcriptional firing of two clock genes occurred at different rates.

**genepaired\_scenario3.m:** gene-paired embryos stochastic model scenario 3

Additional scenarios in which the transcriptional firing of two clock genes occurred at different rates.

**geneunpaired\_scenario3.m:** gene-unpaired embryos stochastic model scenario 3

Additional scenarios in which the transcriptional firing of two clock genes occurred at different rates.

**Python codes for image analysis:**

Custom Python codes that split PSM tissue into single cell wide slices. Codes take Supplementary Table 1-7, 9, 10 each sheet separately and subtract background mRNA count for *her1* and *her7*, group cells based on its special location into single cell wide slices. Calculate mean *her* expression in each slice. The “PythonImageProcessingPipeline.docx” explains the code in more detail.