

## Description of Additional Supplementary Files:

**Supplementary Data 1:** Output from meta2d, using scRNAseq pseudobulk data calculated from dermal fibroblasts as the input. There are 1946 significantly rhythmic genes (JTK\_p-value < 0.05) in dermal fibroblasts.

**Supplementary Data 2:** Output from meta2d, using scRNAseq pseudobulk data calculated from dermal immune cells as the input. There are 432 significantly rhythmic genes (JTK\_p-value < 0.05) in dermal immune cells.

**Supplementary Data 3:** Gene Ontology terms from clusterProfiler applied to different quarter-day rhythmic genes lists from dermal fibroblasts (Methods). Quarter-day information is stored in the quarter-day column (morning, day, evening, night). Terms with p-value < 0.05 were considered significant in the manuscript.

**Supplementary Data 4:** Gene Ontology terms from clusterProfiler applied to different quarter-day rhythmic genes lists from dermal immune cells (Methods). Quarter-day information is stored in the quarter-day column (morning, day, evening, night). Terms with p-value < 0.05 were considered significant in the manuscript.

**Supplementary Data 5:** Within-sample normalized training data: tauFisher was trained on mouse skin microarray data (GSE38622) and tested on mouse skin bulk RNAseq data (GSE83855). Columns, gene pairs; rows, time points.

**Supplementary Data 6:** Within-sample normalized test data: tauFisher was trained on mouse skin microarray data (GSE38622) and tested on mouse skin bulk RNAseq data (GSE83855). Columns, gene pairs; rows, samples.