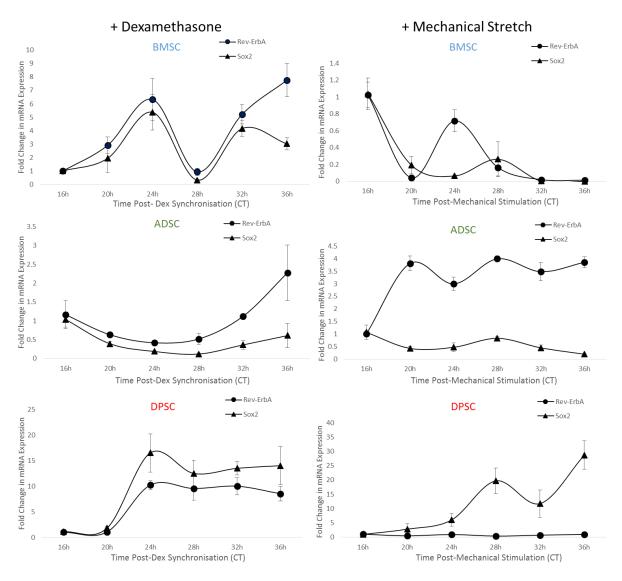


Supplementary Fig 1. Comparison of temporal clock gene expression between unsynchronised and dexamethasone-synchronised BMSCs. Quantitative RT-PCR analyses overlays of temporal clock gene expression in dexamethasone synchronised and unsynchronised (negative control) samples (NC). Data is expressed as the mean of Δ Ct ±SEM calculated from the Ct value of each gene relative to the 16 h time point and normalised against the housekeeping gene *GAPDH*. Bars represent means ±SEM of 2-3 independent experiments.



Supplementary Fig 2. Comparison of the cyclical expression of *Rev-ErbA* and *Sox2* following synchronisation by dexamethasone or rhythmic mechanical stretch. Quantitative RT-PCR analyses overlays of *Rev-ErbA* and *Sox2* temporal gene expressions over 1 circadian cycle (16 h to 36 h) following synchronisation with dexamethasone or mechanically. Data is expressed as the mean of Δ Ct ±SEM calculated from the Ct value of each gene relative to the 16 h time point and normalised against the housekeeping gene *GAPDH*. Bars represent means ±SEM of 3 independent experiments.