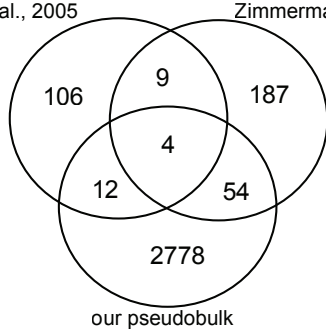


Single-cell transcriptomics reveals that glial cells integrate homeostatic and circadian processes to drive sleep–wake cycles

In the format provided by the
authors and unedited

Cirelli et al., 2005

Zimmerman et al., 2006



Supplementary Figure 1. Bulk transcriptomics is insufficient to capture molecular sleep/wake correlates.

Comparing sleep/wakefulness correlates across all cells combined found in this study with two previous bulk microarray studies (Cirelli et al. 2005, Zimmerman et al. 2006), that similarly profiled differences between sleep and wakefulness conditions, shows that the overlap of significant genes is minimal between all three studies.