



**Supporting Figure 4. Low levels of *tim* and *per* transcripts are detected via brain RNA seq from *Clk*<sup>out</sup> flies.** Brain RNA-seq libraries were made from both wild-type (w118) and *Clk* deletion (*Clk*<sup>out</sup>) flies. The resulting data is shown using the Integrated genome viewer (IGV). *Clk* transcripts are high at ZT2 and low at ZT14 in w118 flies, and not detectable in *Clk*<sup>out</sup> flies (top). *Tim* and *Per* transcripts are low at ZT2 and high at ZT14 in w118 brains (as expected). Interestingly, both *tim* and *per* transcripts are still detectable at low levels (similar to that observed at ZT2 in w118 flies) in *Clk*<sup>out</sup>.