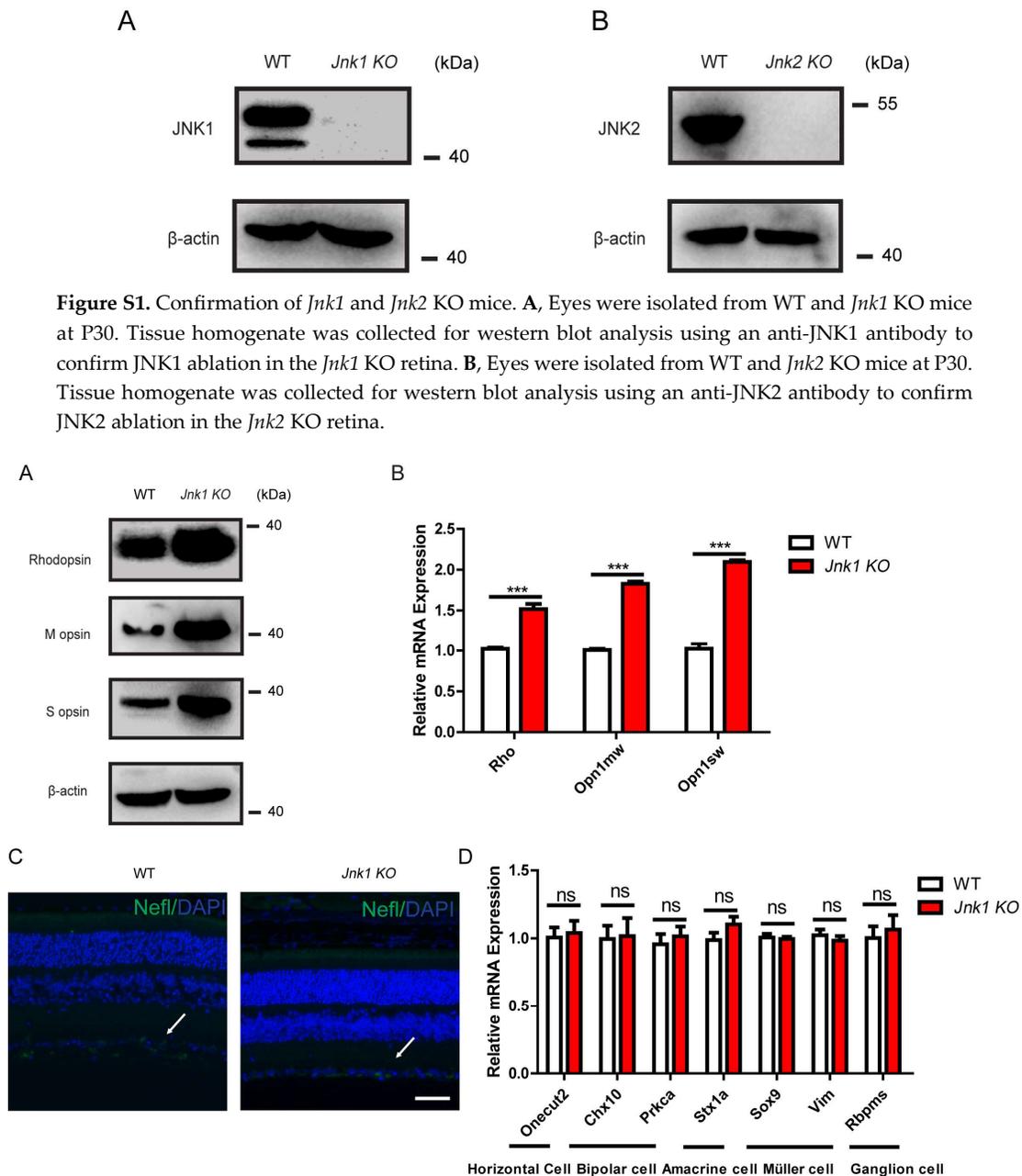
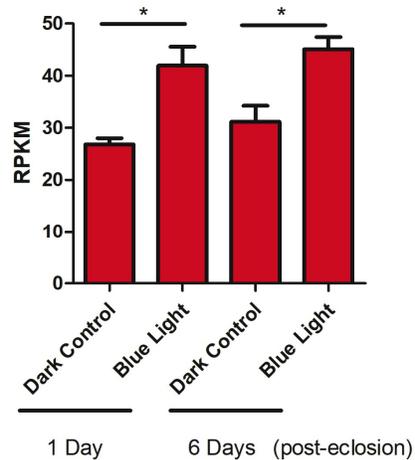
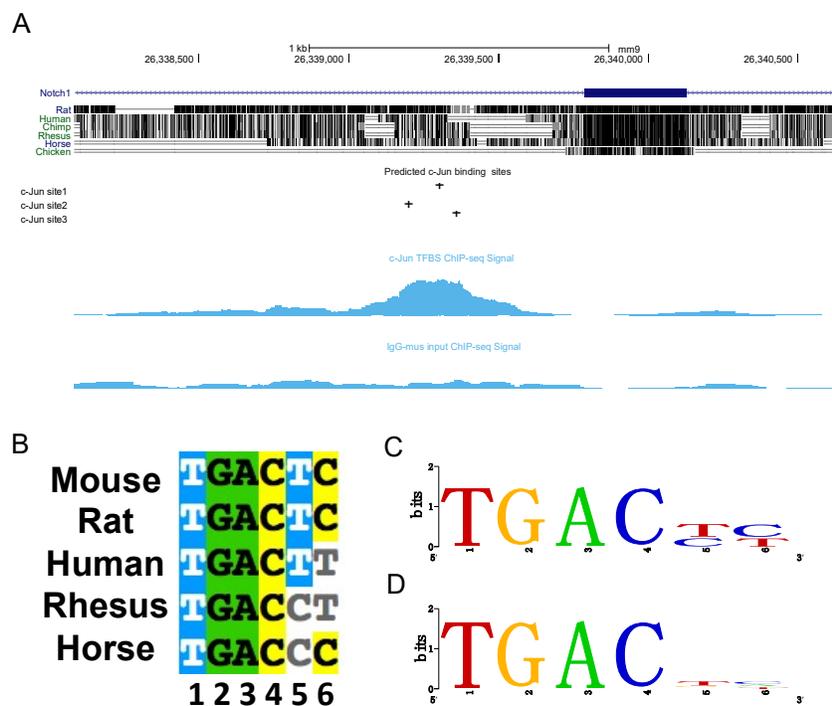


## Supplementary figures





**Figure S3.** The expression changes of *Jra* after 3 h blue light exposure in fly photoreceptor. *Jra*, the orthologous gene of *c-Jun* of mouse, was significantly induced after 3 h blue light exposure in both 1 day and 6 days post-eclosion flies. The RNA-seq data were downloaded from GEO [32]. The gene expression quantification and differential expression were estimated using feature Counts and edgeR, respectively. Graph shows the mean  $\pm$  SEM, and the data shown are representative of three replicates. \*  $p < 0.05$  (Negative binominal test, FDR  $< 5\%$ ).



**Figure S4.** The predicted *c-Jun* binding sites in the *c-Jun* ChIP-seq peak region. (A), The five tracks show *Notch1* gene structure, overall region sequence conservation of 7 vertebrate species, predicted *c-Jun* binding site, *c-Jun* ChIP-seq signal and IgG ChIP-seq signal. The *c-Jun* binding site was predicted using TRANSFAC based on the vertebrate non-redundant PWM (Position Weight Matrix) of *c-Jun*. (B), The multiple sequence alignment of *c-Jun* binding site 1 across five mammalian species (Mouse, Rat, Human, Rhesus and Horse). (C), The consensus sequence of *c-Jun* binding site 1 across five mammalian species represented using sequence logo. The consensus magnitude is measured using Shannon information content in bits. Low bit value represents all nucleotides occur with similar probability at specific position. (D), The consensus sequence of canonical *c-Jun* binding site based on PWM annotated by TRANSFAC (*c-Jun*, T00131).