

Supplementary Figure Legends

Figure S1. *In situ* hybridization of asRNAs.

Expression of 4 asRNAs (3 known and 1 un-annotated) and control genes in the mouse retina by in situ hybridization (ISH).

Positive control – probe designed against mouse *Ppib* gene.

Negative control - probe designed against bacterial *dapB* gene.

White punctate dots represent the signal detected by ISH probes. DAPI staining of the nucleus is shown in blue. ONL, outer nuclear layer; INL, inner nuclear layer; GCL, ganglion cell layer.

Figure S2. GO terms enrichment analysis for genes overlapping with known and un-annotated asRNA.

GO terms associated with genes showing significant correlation score to asRNA, are presented as a bar graph. Y-axis shows individual GO terms and X-axis shows the number of genes associated with the term. Color gradient represent the p-value of the enrichment of each term, red most significant (on the top of Y-axis) to blue least significant (on the bottom of Y-axis).

Figure S3. Additional *in situ* hybridization of lncRNAs.

Expression of additional 12 lncRNAs and control genes in the mouse retina by in situ hybridization (ISH).

White punctate dots represent the signal detected by ISH probes. DAPI staining of the nucleus is shown in blue. ONL, outer nuclear layer; INL, inner nuclear layer; GCL, ganglion cell layer.

Figure S4. GO terms enrichment analysis for individual WGCNA modules.

GO terms associated with genes in each WGCNA module are presented as a dot graph. Y-axis shows individual GO terms and X-axis shows the WGCNA modules. Color gradient represent the FDR (false discovery rate) of the enrichment of each term, red representing low FDR and blue high. Size of each dot represents the number of genes associated with the term. GO terms are grouped by function allowing showing distinct enrichments in each cluster.

KO – S-cone like photoreceptors

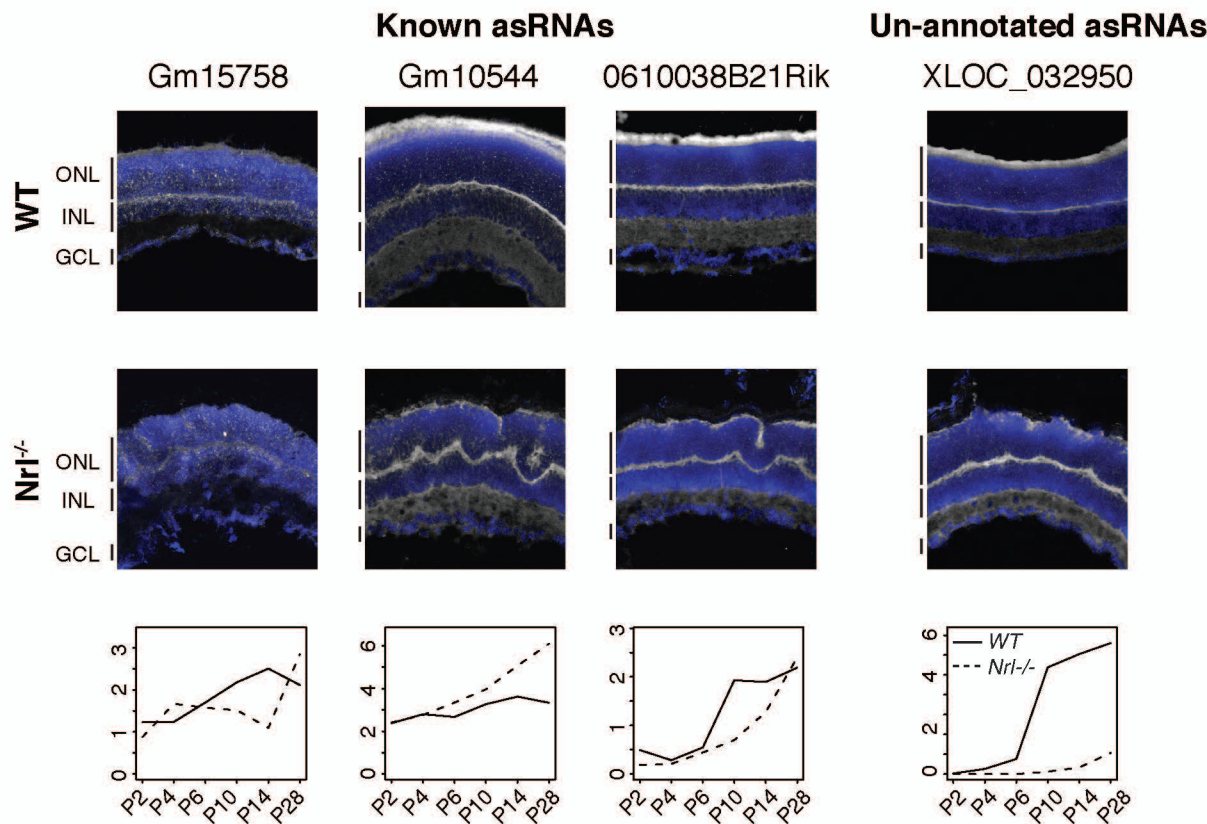
WT – Rod photoreceptors

Figure S5. qRT-PCR validation of un-annotated lncRNAs.

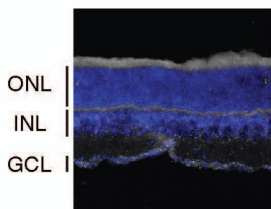
A. Summary delta CT values of 10 lncRNAs normalized to endogenous control gene *Htrp*.

B. Amplification plots showing the efficiency of the reaction, and similarity between triplicates.

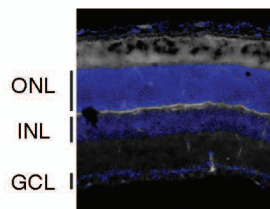
Supplementary Figure S1



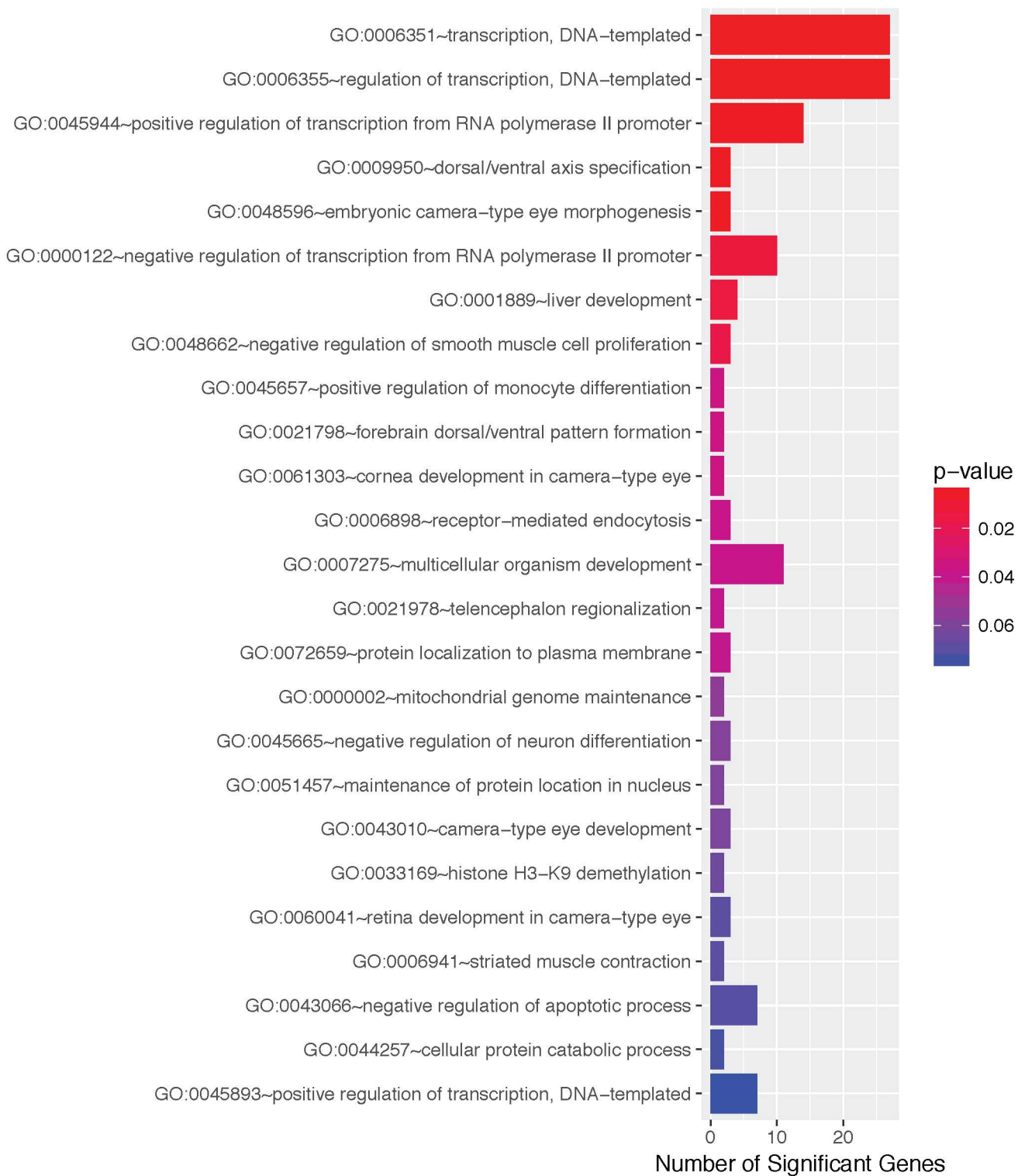
Positive control (Ppib)



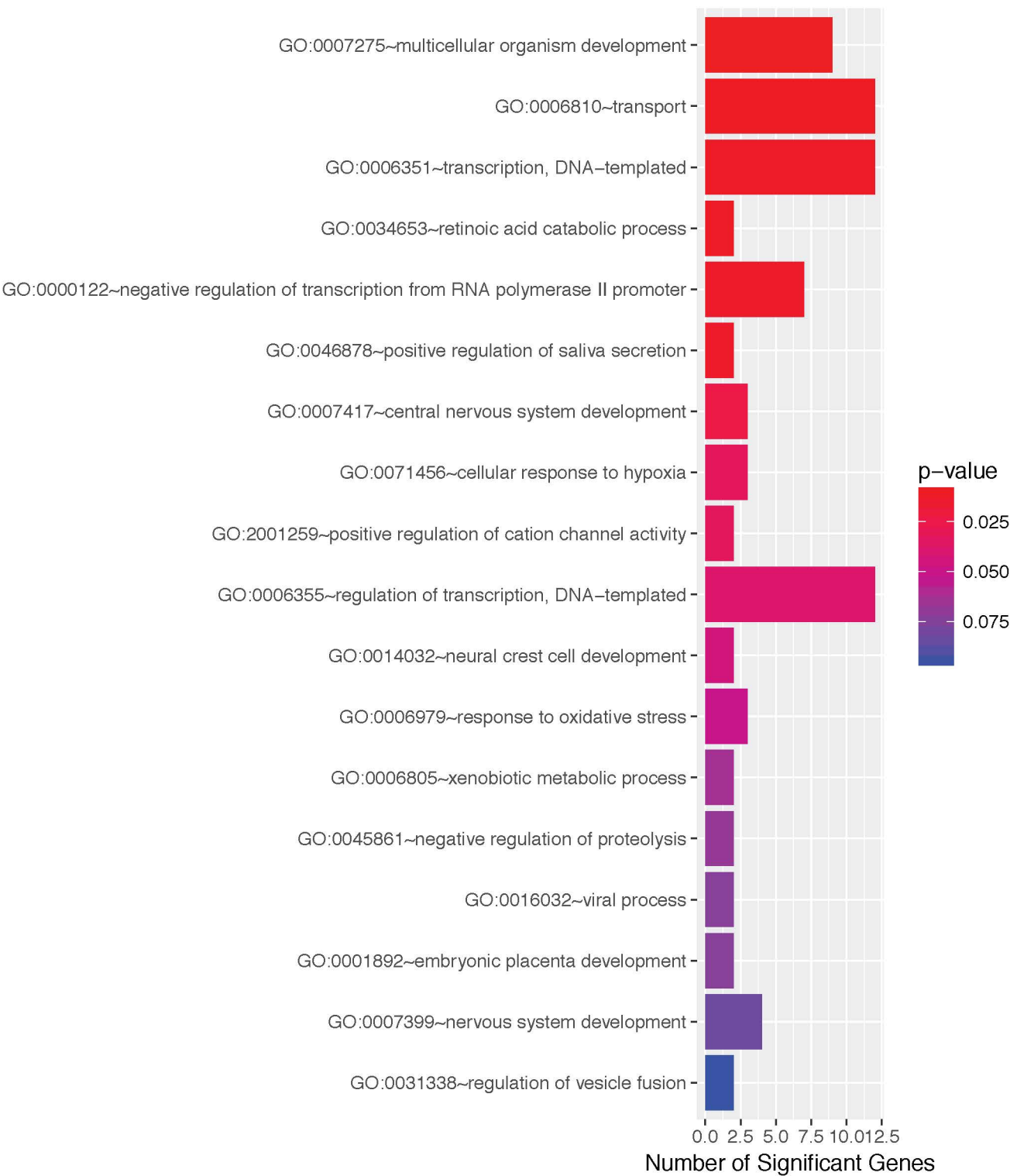
Negative control (dapB)



Known Antisense RNA

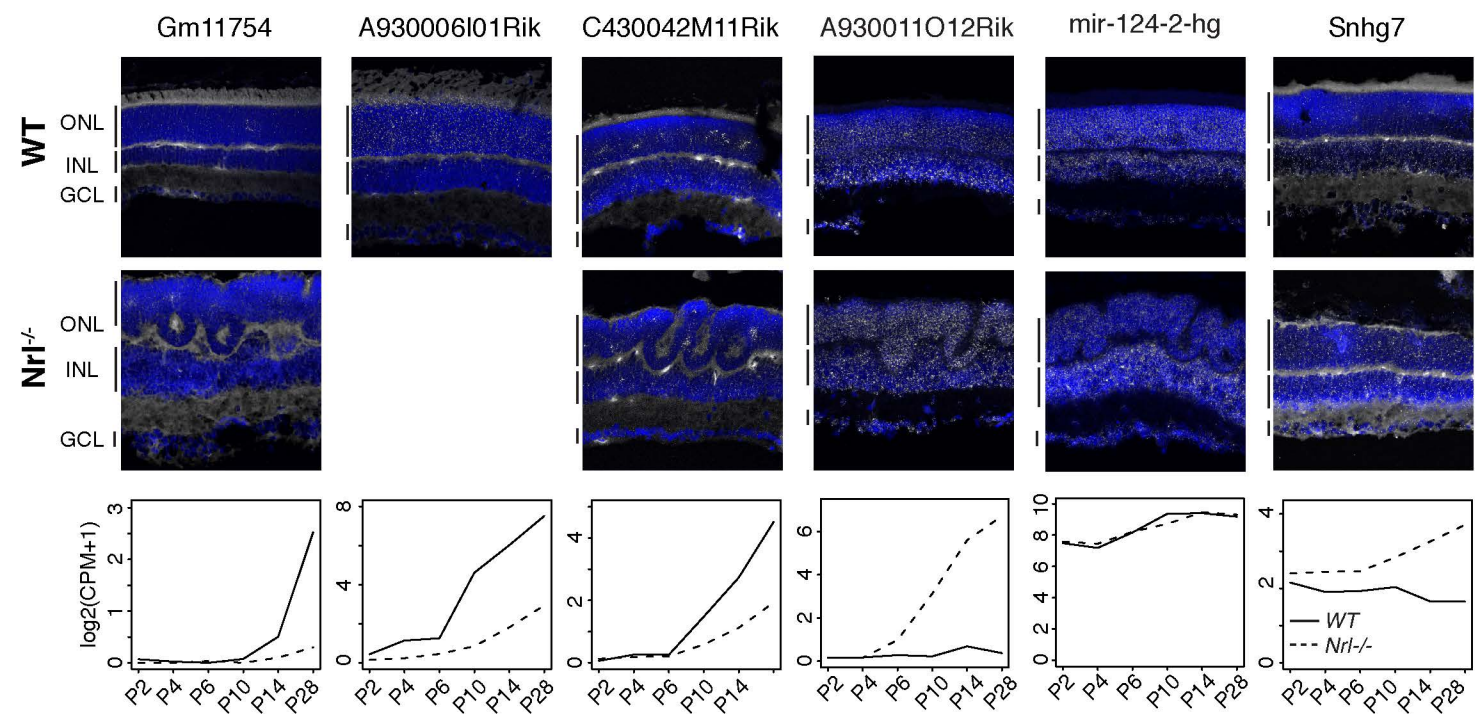


Un-annotated Antisense RNA



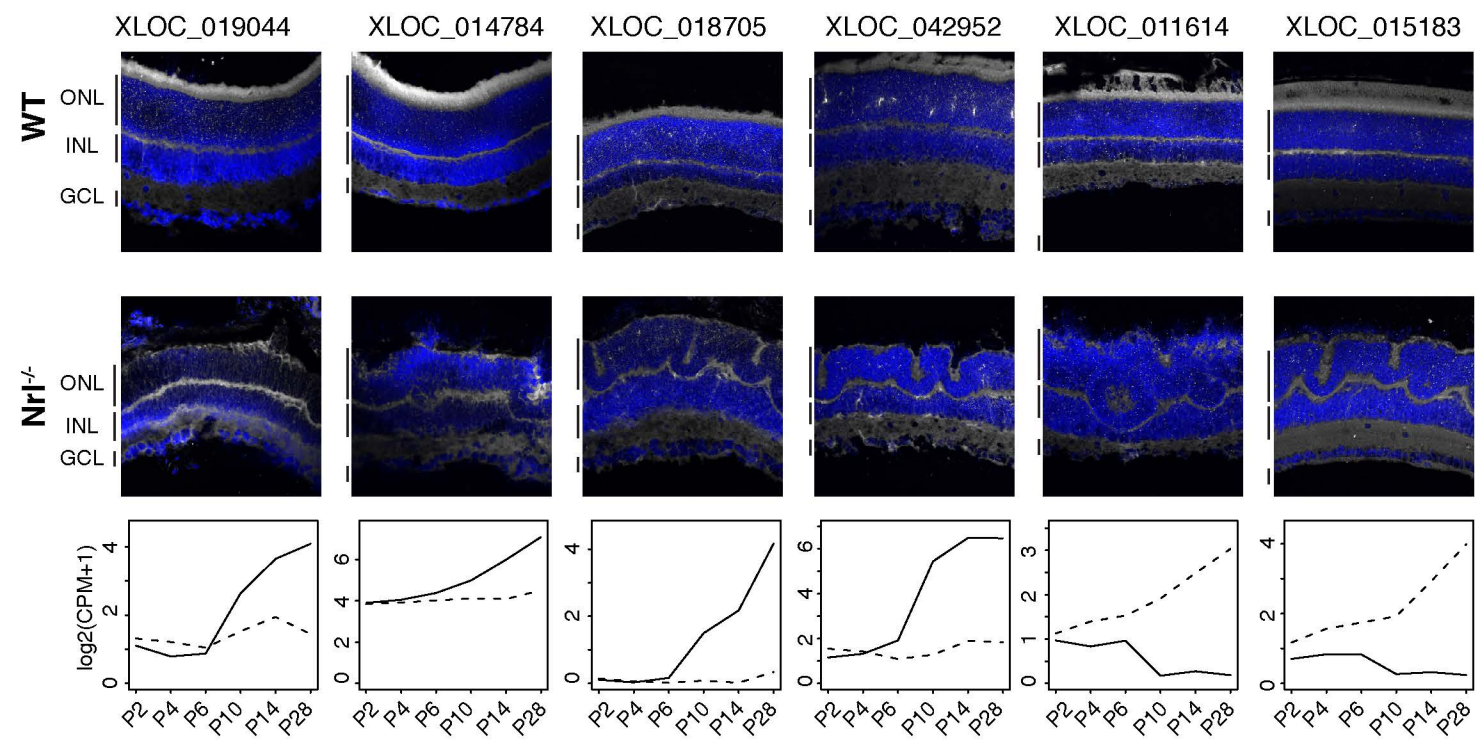
A

Known lncRNAs

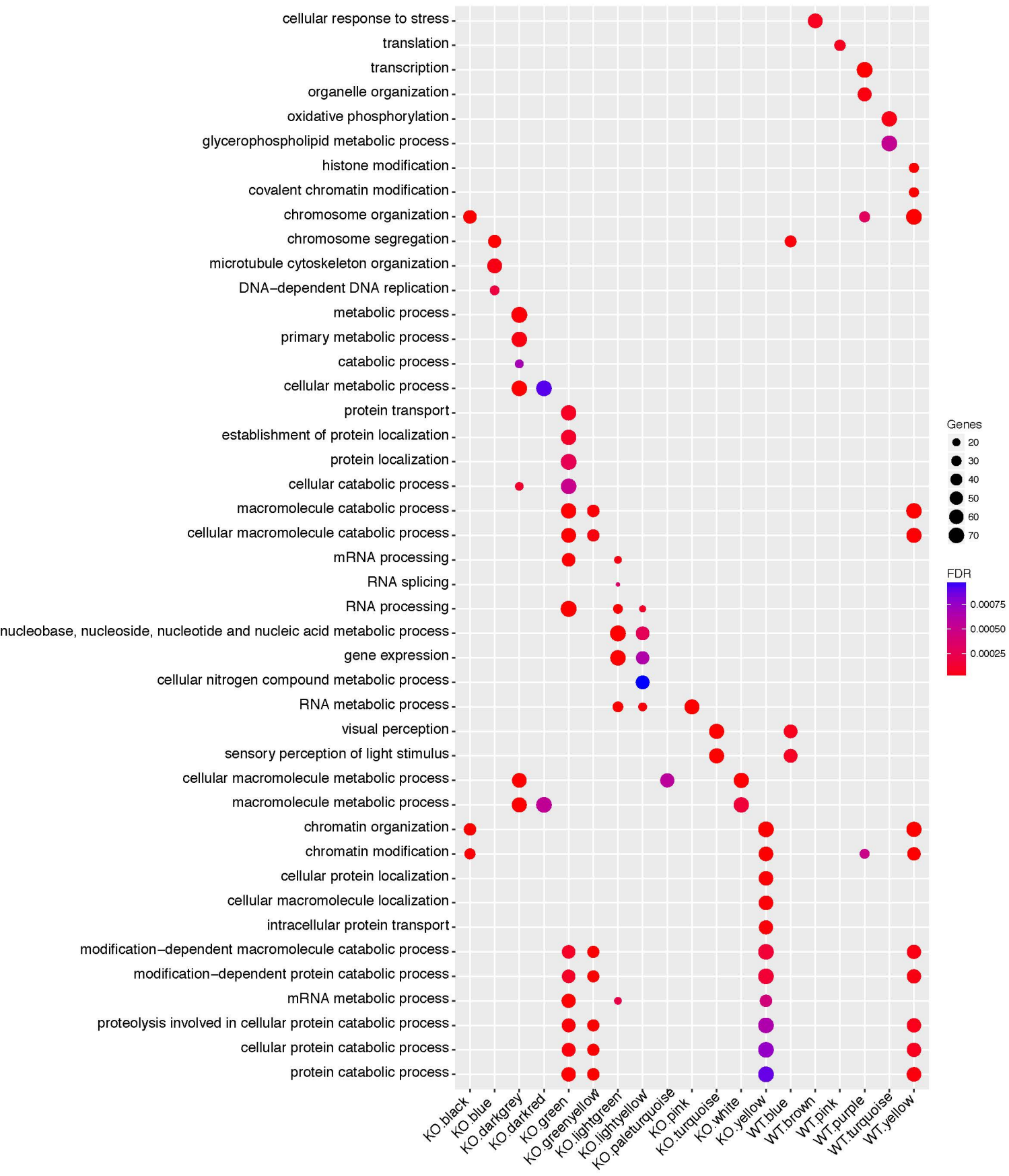


B

Un-annotated lncRNAs



Supplementary Figure S4



Supplementary Figure S5

A

	GeneID	Chr	Start	Stop	dCT_WT_Retina
1	XLOC_006814	10	118803718	118805307	6.82
2	XLOC_067593	7	115039130	115050292	5.05
3	XLOC_052301	4	106039767	106044251	6.83
4	XLOC_042952	2	166352928	166379814	5.76
5	XLOC_037508	19	8132429	8141474	9.38
6	XLOC_025762	15	7442199	7456852	4.57
7	XLOC_019082	13	107996336	108006376	8.31
8	XLOC_015161	12	58923019	58944382	6.74
9	XLOC_014784	12	102440700	102468126	4.84
10	XLOC_018705	13	35940592	35951984	8.94

B

Amplification Plot

