Title page:

Non-coding RNAome of RPE cells under oxidative stress suggests unknown regulative aspects of Retinitis pigmentosa etiopathogenesis

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Supporting information captions

Supplementary Table 1. RNA-Seq Statistics. In this table information on input data transcriptome analysis is reported.

Supplementary Table 2. ncRNAs expression variations throughout all analyzed time points. All selected ncRNAs showed particular fold–change trends, between treated and untreated samples, during evaluated time points (0h, 1h, 2h, 4h, 6h). All results were statistically validated by Bonferroni–corrected EDGE test, and p–values are all about 0 (values not shown). Global ncRNA parameters: Reference gene name=The gene_name attribute of the reference GTF record for this transcript, if present; otherwise gene_id is used. Reference transcript id=The transcript_id attribute of the reference GTF record for this transcript. Class code=The type of relationship between the Cufflinks transcripts and the reference transcript. Cufflinks gene id=The Cufflinks internal gene id. Cufflinks transcript id=The Cufflinks internal transcript id. Fraction of major isoform (FMI)=The expression of this transcript expressed as a fraction of the major isoform for the gene; Ranges from 1 to 100. Length=The length of the transcript. Major isoform ID=The Cufflinks ID of the gene's major isoform. Reference match length=The length of reference transcript. CircRNAs specific parameters: IsoformName=Name of isoform. Chrom=Chromosome. Start=Start of circular RNA. End=End of circular RNA. Name=Circular RNA/Junction reads. Strand=+ or - for strand. ExonSizes=Exon sizes. ExonOffsets=Exon offsets. CircType=Type of circular RNA. GeneName=Name of gene. Index=Index of exon or intron.

Supplementary Table 3. qRT–PCR data for ncRNA expression validation. In this table fold–changes values for 20 most dysregulated ncRNAs involved in the highest number of biochemical pathways are reported. qRT–PCR results (columns with gray background) confirm RNA–Seq expression data (columns with white background). T = Treated sample. U = Untreated sample.

Supplementary Table 4. CircInteractome results of RNA-binding protein sites and miRNAs matching to circular RNAs. Table shows RBPs binding in different regions of analyzed circRNAs or in their flanking regions, along with TargetScan predictions of miRNAs "sponged" by given circRNAs.

Supplementary Table 5. Read mapping settings for exploited aligners. In this table specific parameters for CLC Genomics Workbench, TopHat2 and STAR aligners are reported.