

Manuscript title:

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

Author list:

Luigi Donato, Concetta Scimone, Carmela Rinaldi, Rosalia D'Angelo, Antonina Sidoti

CLC Genomics Workbench	TopHat 2	STAR
Quality trim limit=0.01 Ambiguity trim maximum value=2 Map to annotated reference: minimum length fraction and minimum similarity fraction=0.8 Maximum number of hits/read=2 Type of organism=eukaryote Paired settings=default	Max realign edit distance=1000 Max edit distance=2 Library Type FR=Unstranded Final read mismatches=2 Use bowtie -n mode=No Anchor length (at least 3)=4 Maximum number of mismatches that can appear in the anchor region of spliced alignment=0 The minimum intron length=40 The maximum intron length=2000 Allow indel search=Yes Max insertion length=3 Max deletion length=3 Maximum number of alignments to be allowed=20 Minimum intron length that may be found during split-segment (default) search=40 Maximum intron length that may be found during split-segment (default) search=2000 Number of mismatches allowed in each segment alignment for reads mapped independently=2 Minimum length of read segments=25 Output unmapped reads=True Do you want to supply your own junction data=No Use coverage-based search for junctions=Yes Minimum intron length that may be found during coverage search=40 Maximum intron length that may be found during coverage search=2000 Use Microexon Search=Yes Do Fusion Search=Yes Set Bowtie2 settings=No Specify read group=No Job Resource Parameters=No	OutFilterMismatchNoverLmax=0.05 OutFilterMatchNmin=16 OutFilterScoreMinOverLread=0 OutFilterMatchNminOverLread=0 AlignIntronMax=1 ChimSegmentMin=10