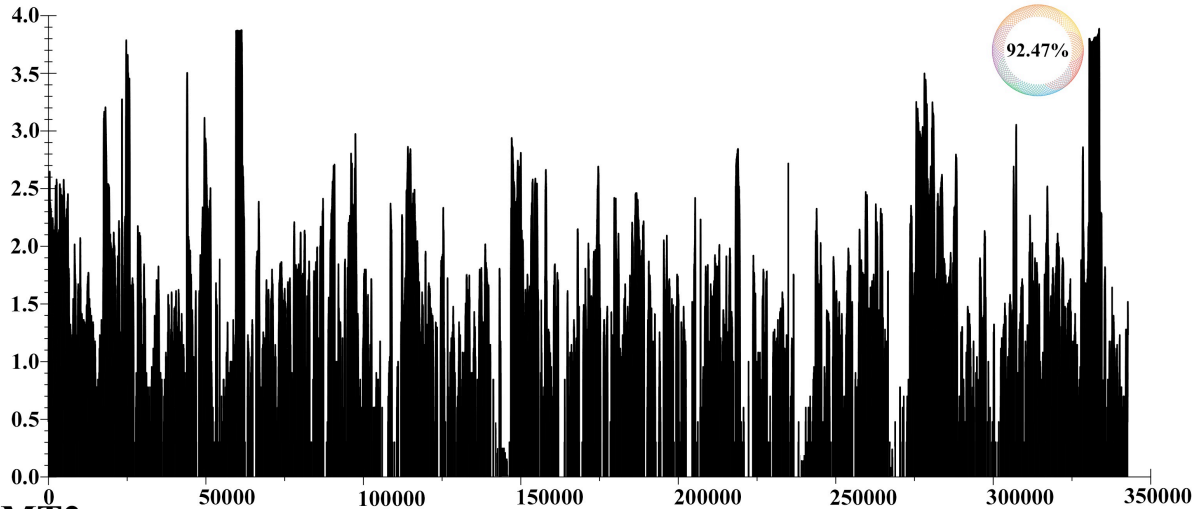
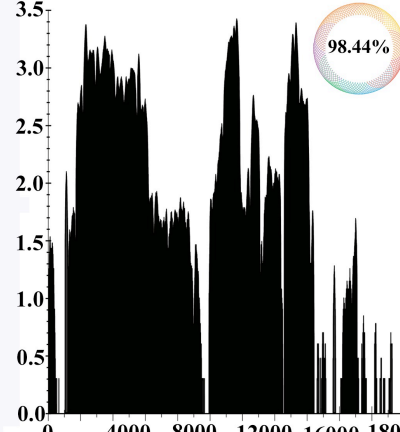


## *Silene vulgaris*

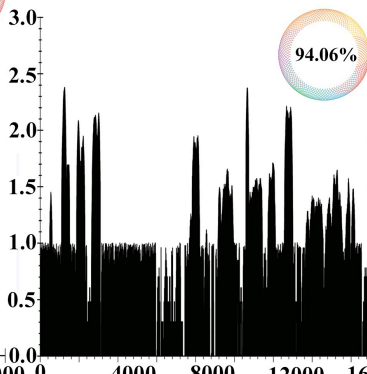
### MT1



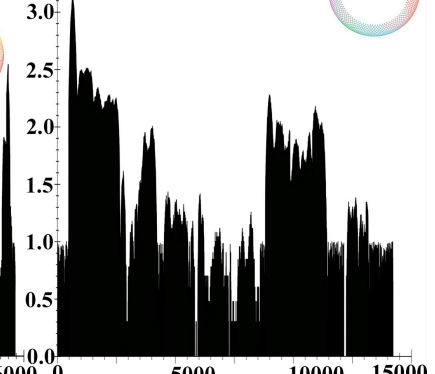
### MT2



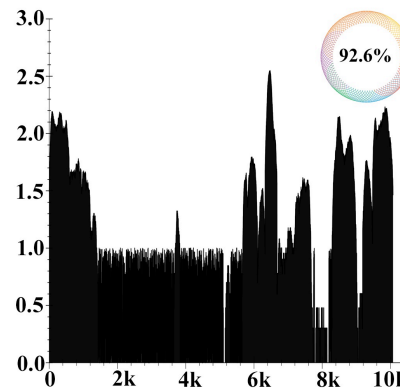
### MT3



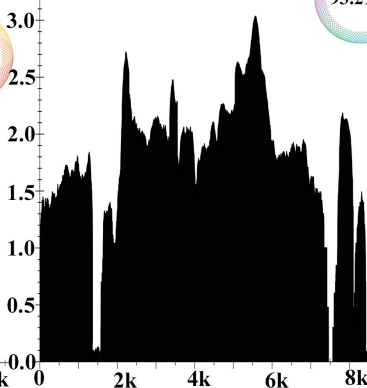
### MT4



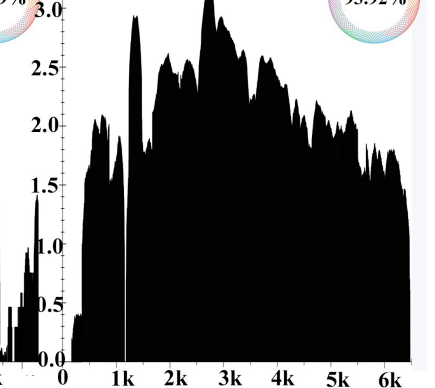
### MT5



### MT6



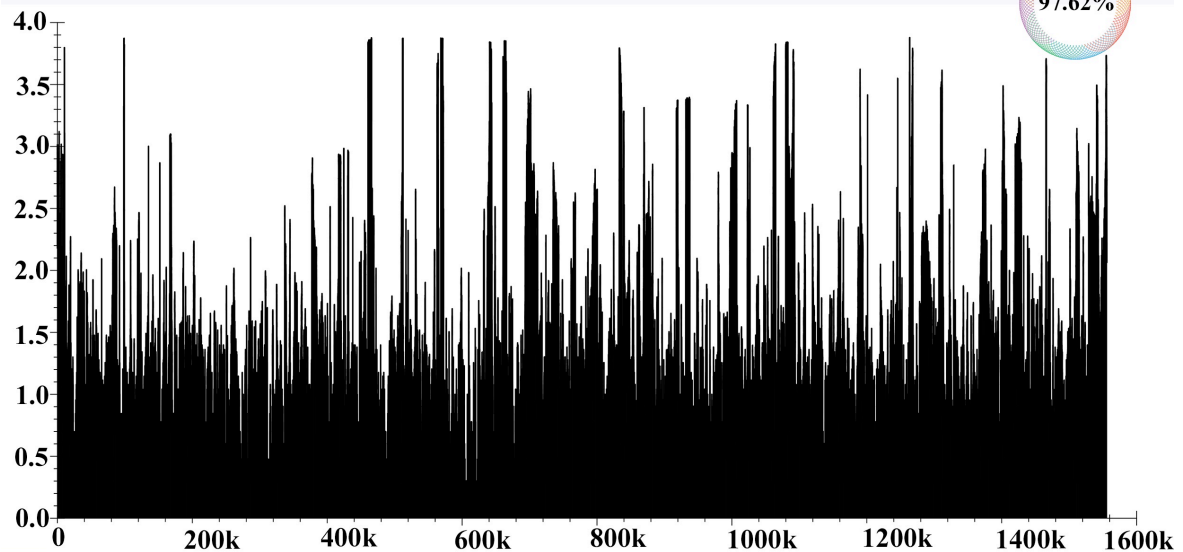
### MT7



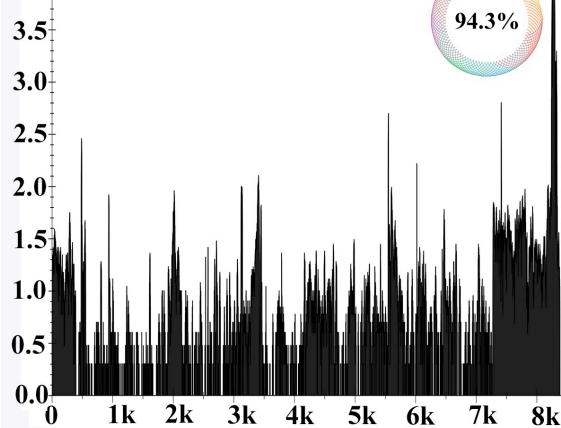
Mapping of SRA transcriptomic reads from *Silene vulgaris* to the seven mitochondrial chromosomes of the plant. The SRA datasets mapped were: SRR2106277; SRR2106278; SRR2106279; SRR342041; ERR142350; ERR1425350; ERR2356579; SRR1536113; SRR1536178; SRR245489 and SRR096785. In all cases read mapping to the individual chromosomes provided > 92% coverage, indicating that all the chromosomes and transcribed in their entirety.

## *Cucumis sativus*

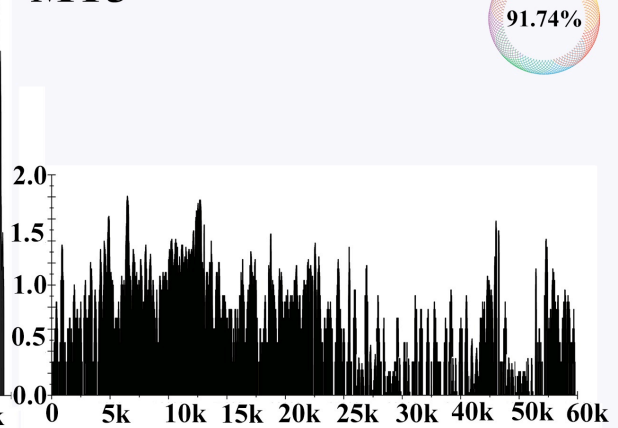
### MT1



### MT2



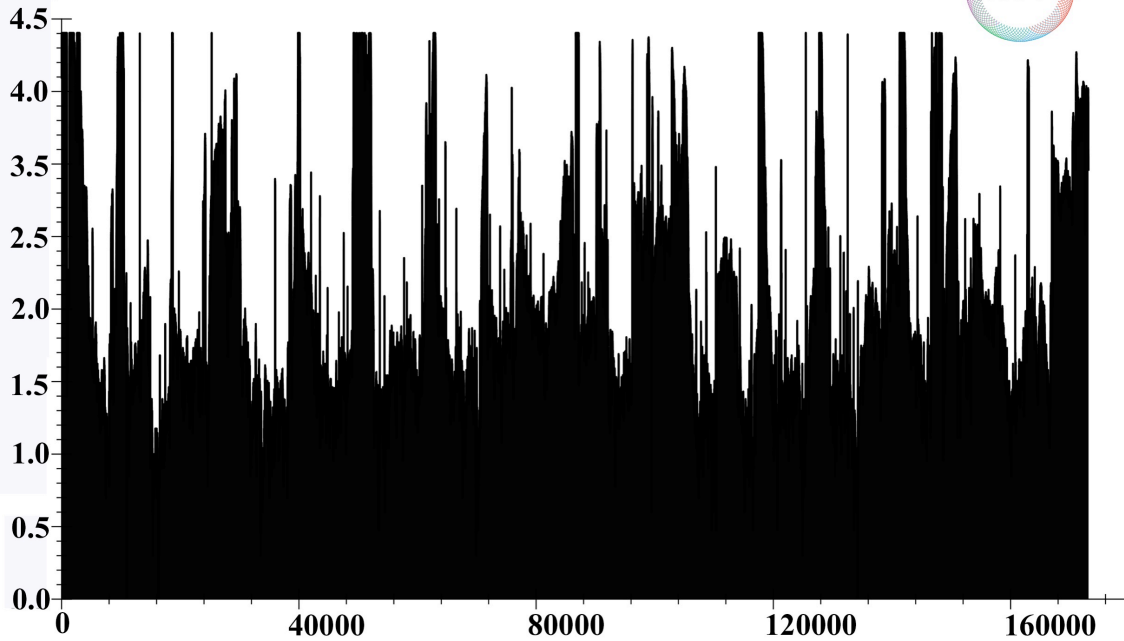
### MT3



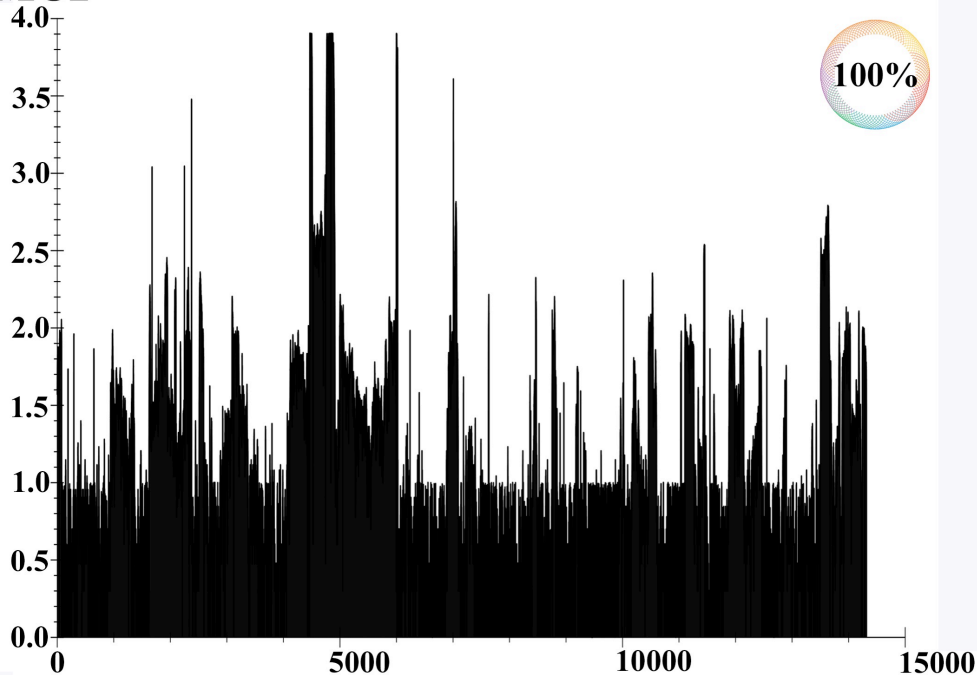
Mapping of SRA transcriptomic reads from *Cucumis sativus* to the three mitochondrial chromosomes of the plant. The SRA datasets mapped were: SRR6418022; SRR6650087; SRR6837824; SRR6957092; SRR7609886; SRR7609893; ERR662024; ERR662030; SRR2157748; SRR351499; SRR494480; SRR518995; SRR518990; SRR1548540, SRR1104924, SRR1104921, SRR1104922 and SRR1104901. In this instance there was >91.74% coverage of each mitochondrial chromosome from RNA-seq data, again indicating that each chromosome is transcribed in its entirety.

# Allium cepa Mitochondrial Genome

## MC1



## MC2



Mapping of SRA transcriptomic reads from *Allium cepa* to the two mitochondrial chromosomes of the male sterile plant. The SRA datasets mapped were: SRR1056445; SRR1958737; SRR2814816; SRR4418767; SRR073446; SRR4418768; SRR4418769; DRR068967; DRR068968; DRR068969; DRR068994; DRR068995 and DRR068996. In this case the two maxicircles of the mitogenome had 100% transcript coverage, demonstrating that they are both transcribed in their entirety.