

# Transcriptional profile of the heterochromatin

## impact of the transposable elements in *D. melanogaster*

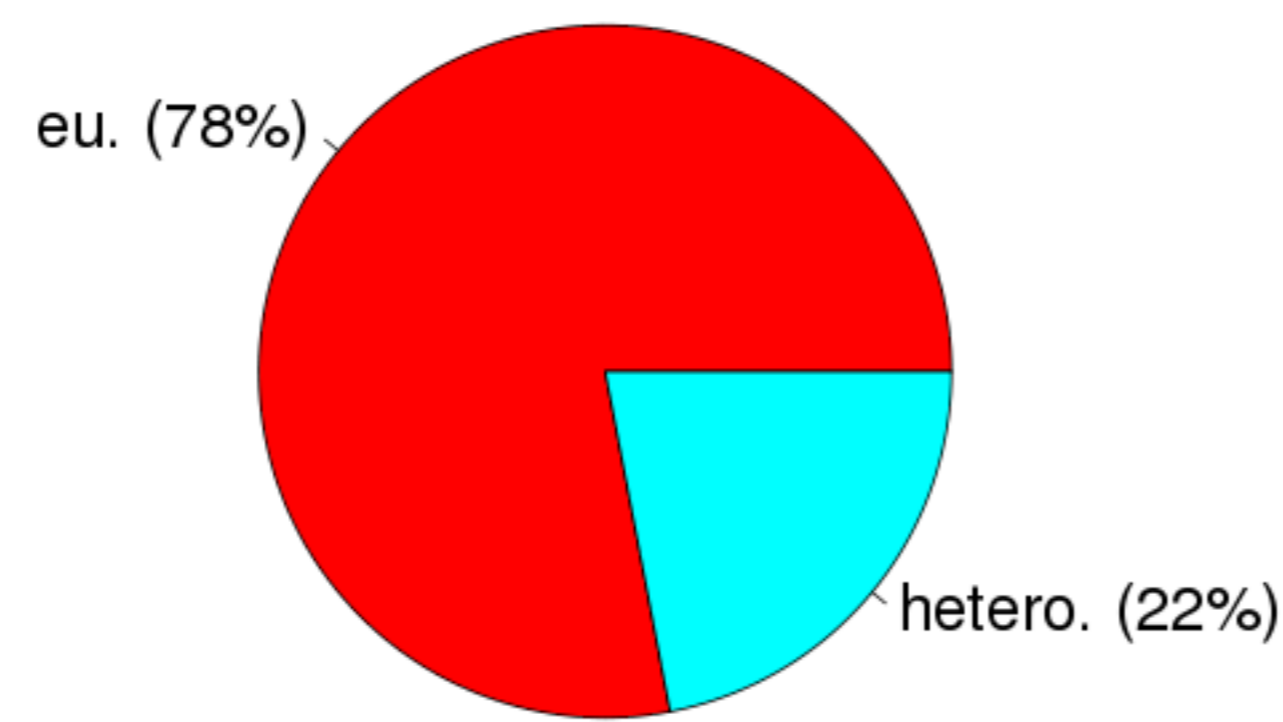
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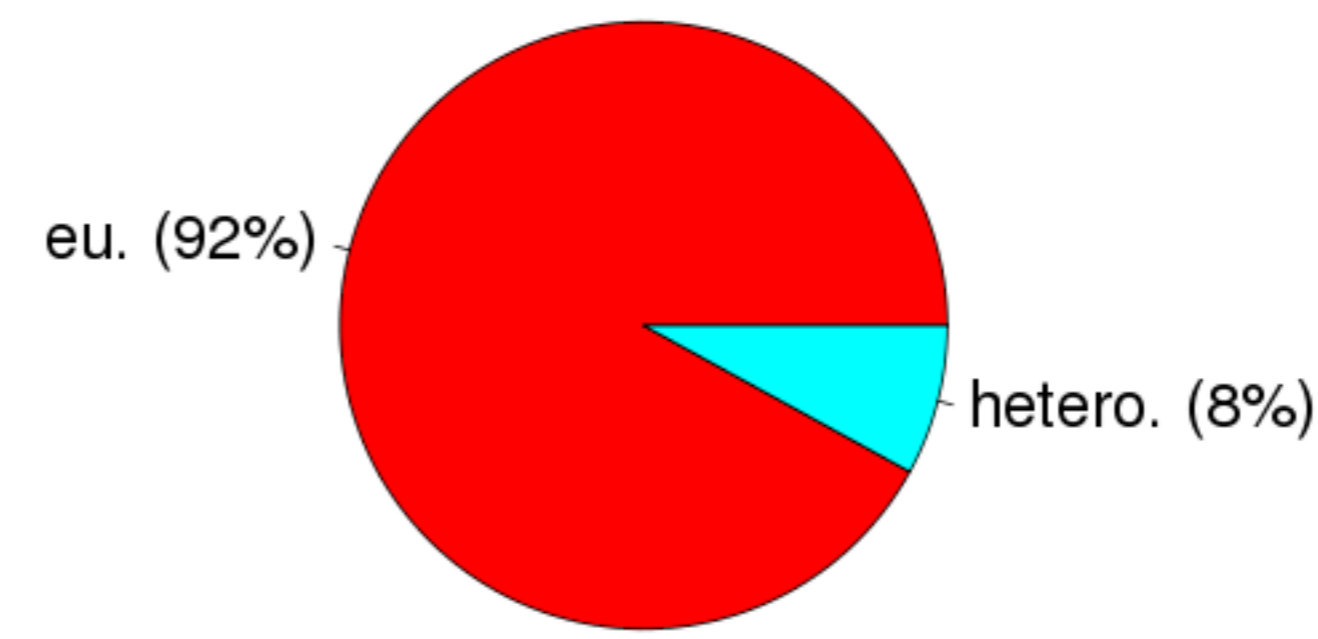
### Transcribed part of the genome

Data:

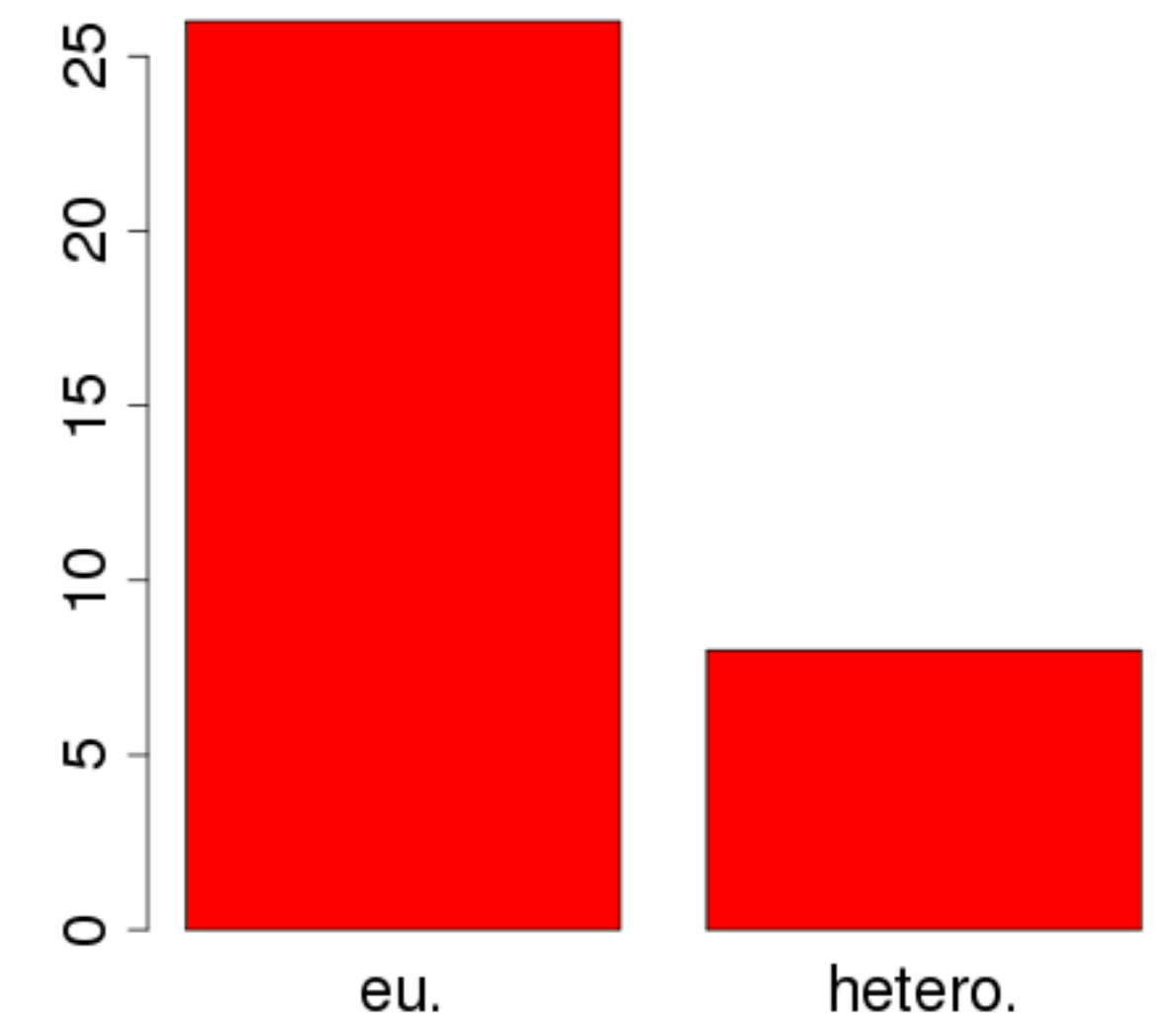
- ESTs from GenBank,
- unique match, 100% identity,
- euchromatin/heterochromatin bounds defined by Bergman *et al.*, 2006.



Genome distribution



% in eu/heterochromatin



% covered by the ESTs

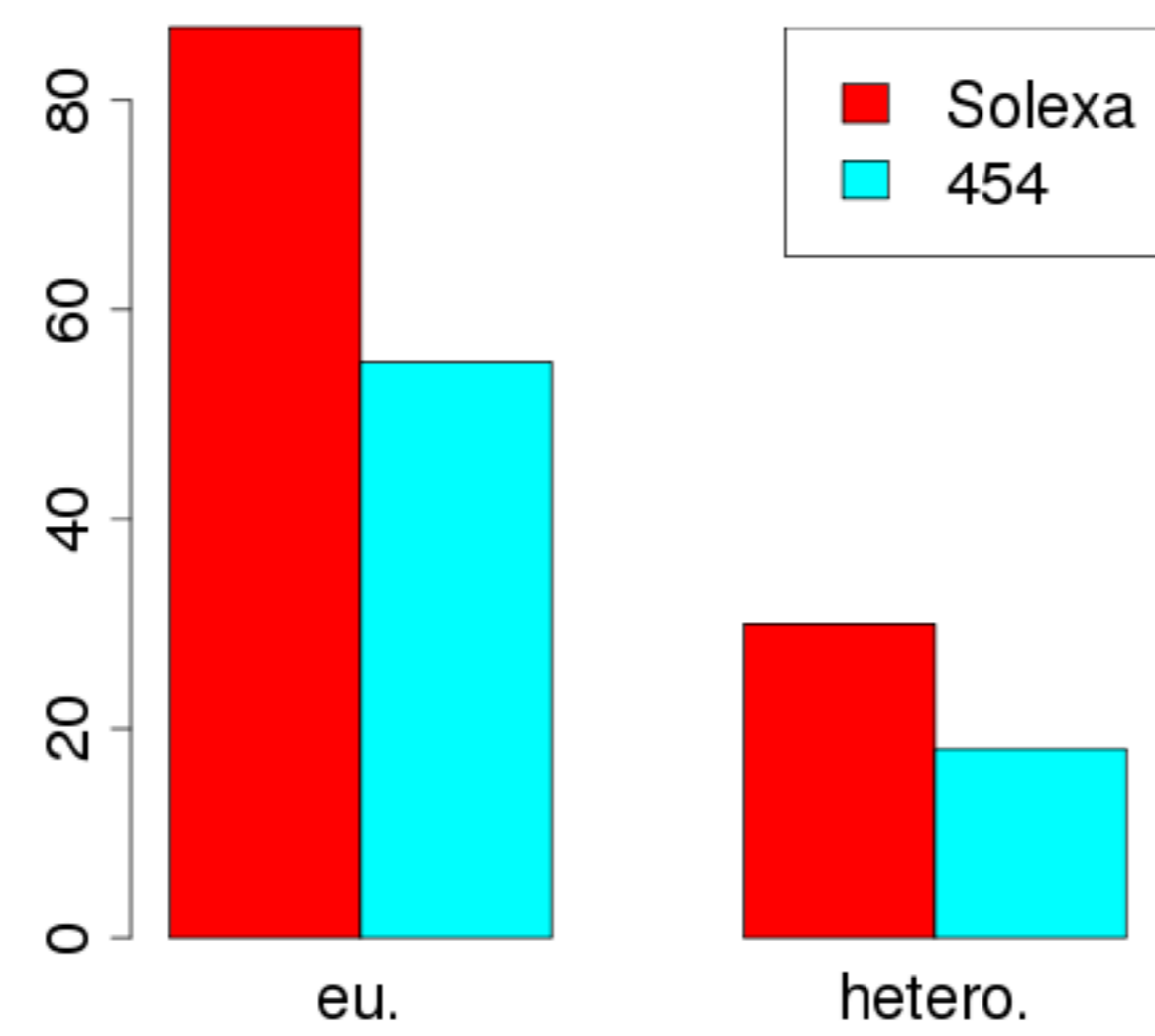
⇒ Euchromatin is more transcribed than heterochromatin.

△ However, a notable part of heterochromatin is transcribed.

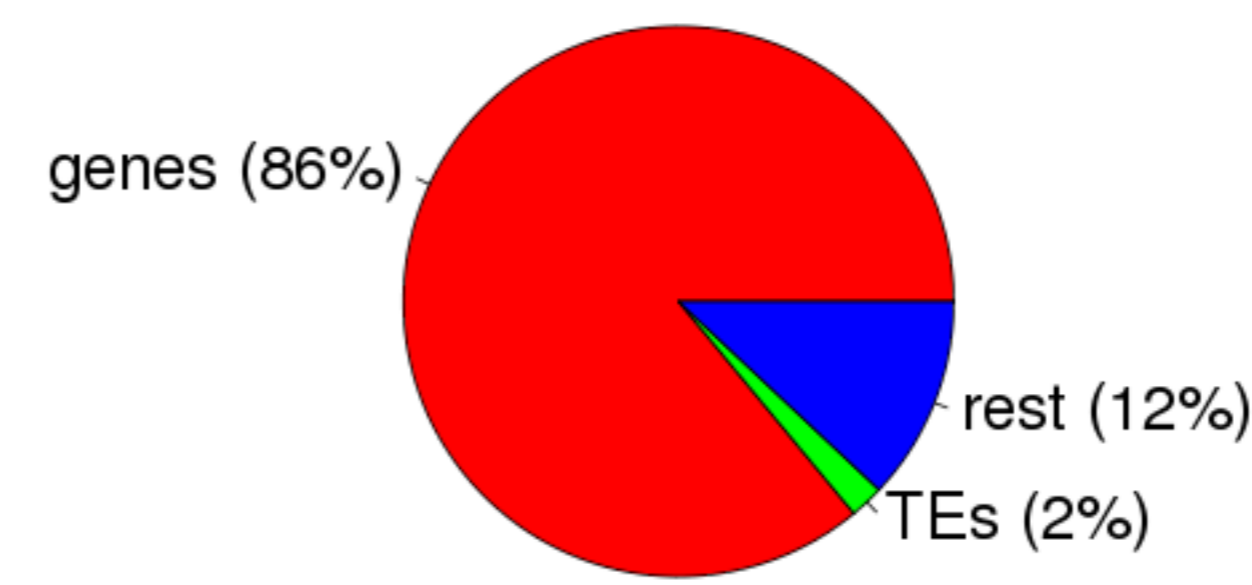
### Expressed regions

Data:

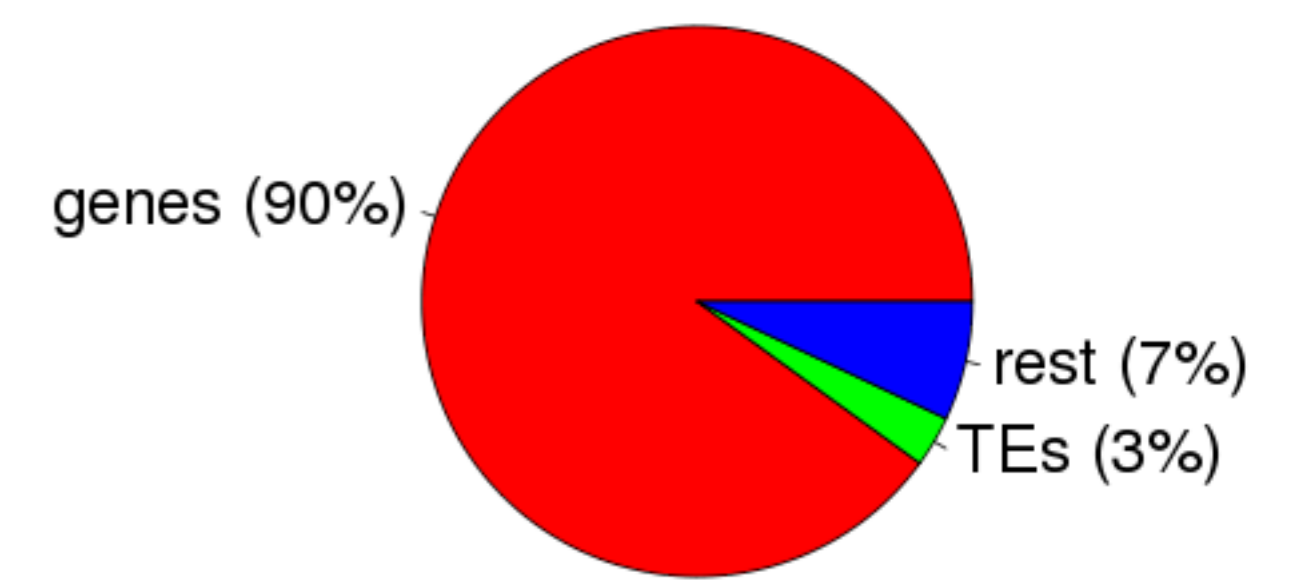
- 5,095,341 reads Solexa (5' capped),
- 274,091 reads 454 (5' capped, normalized),
- unique match, 100% identity,
- clustered.



Number of clusters per Mb.



Elements captured by clustered Solexa



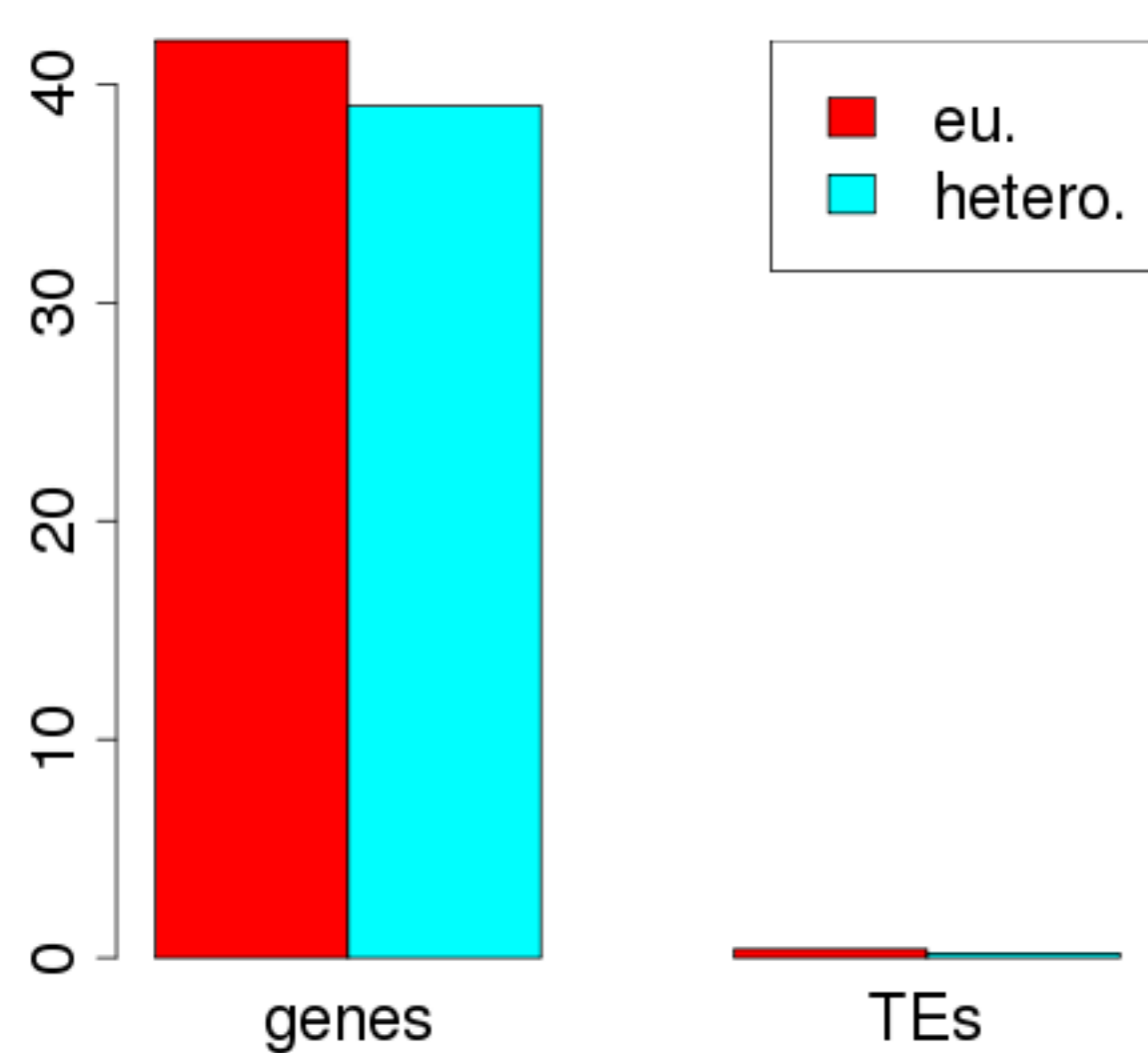
Elements captured by clustered 454

⇒ The most transcribed elements are genes in euchromatin.

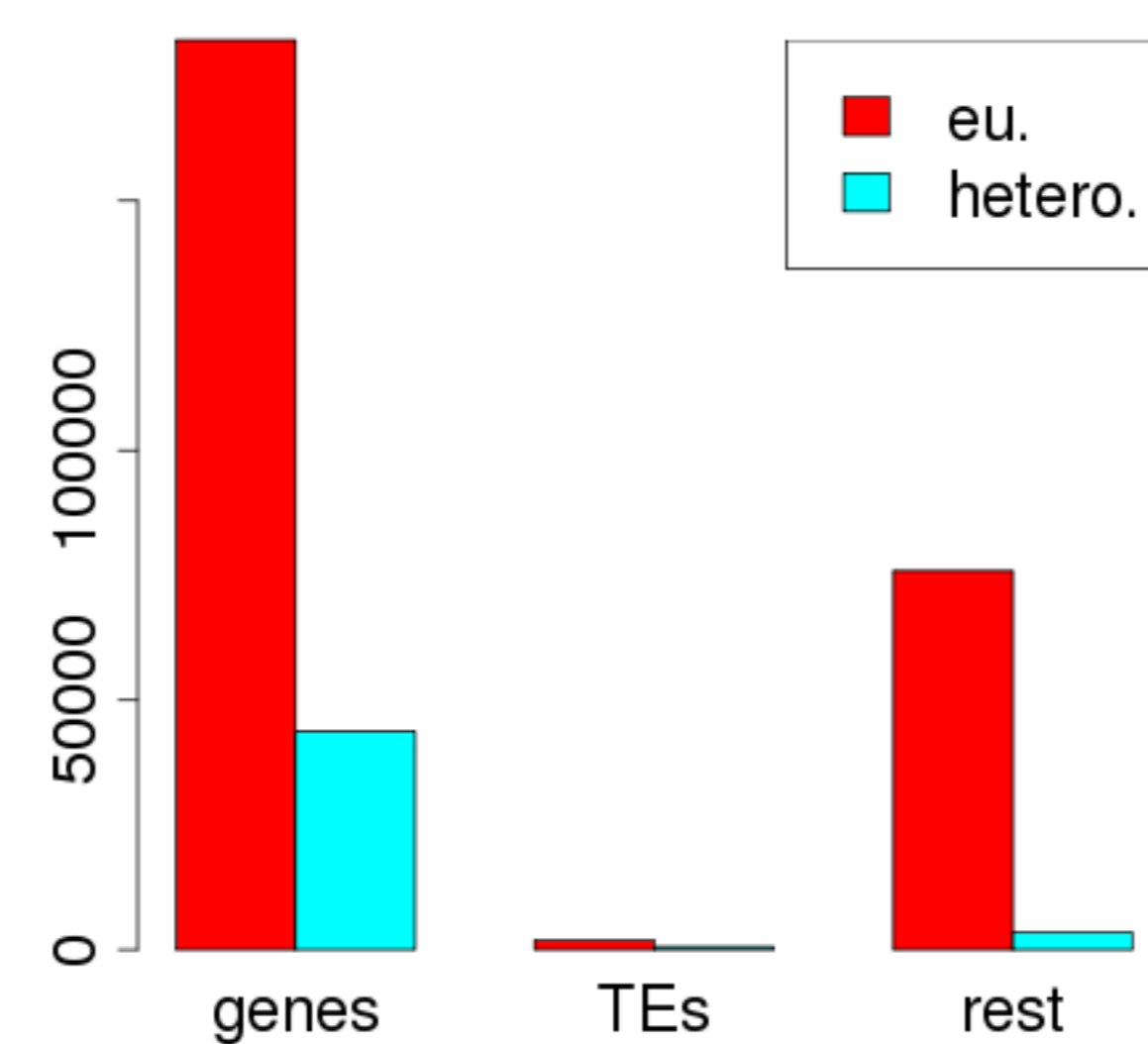
△ Heterochromatin is also transcribed.

△ TEs are transcribed too.

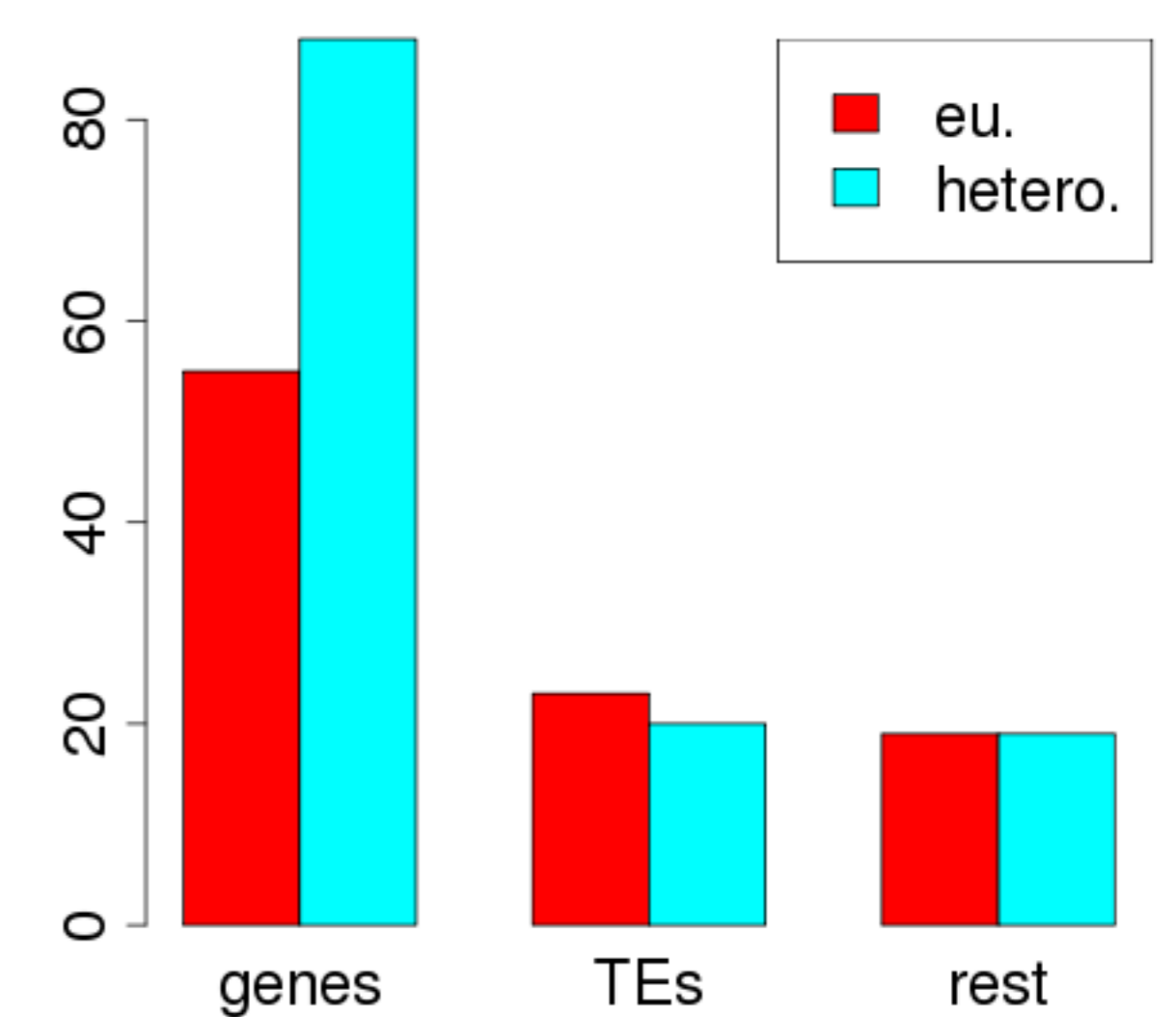
### Level of expression



Proportion of elements captured



Max. number of reads per element



Med. number of reads per element

⇒ The most highly expressed elements are genes in euchromatin.

△ The average expression of genes in heterochromatin is comparable with the expression in euchromatin.

△ Some TEs are also expressed.