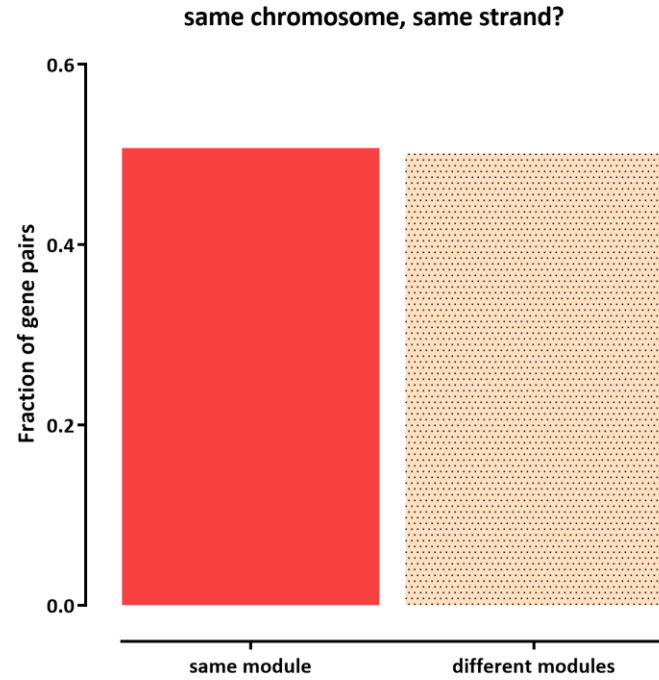
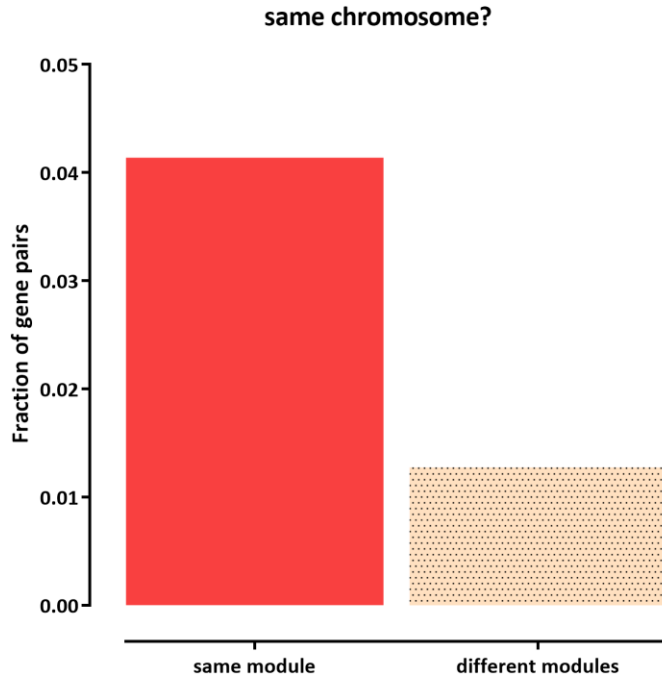


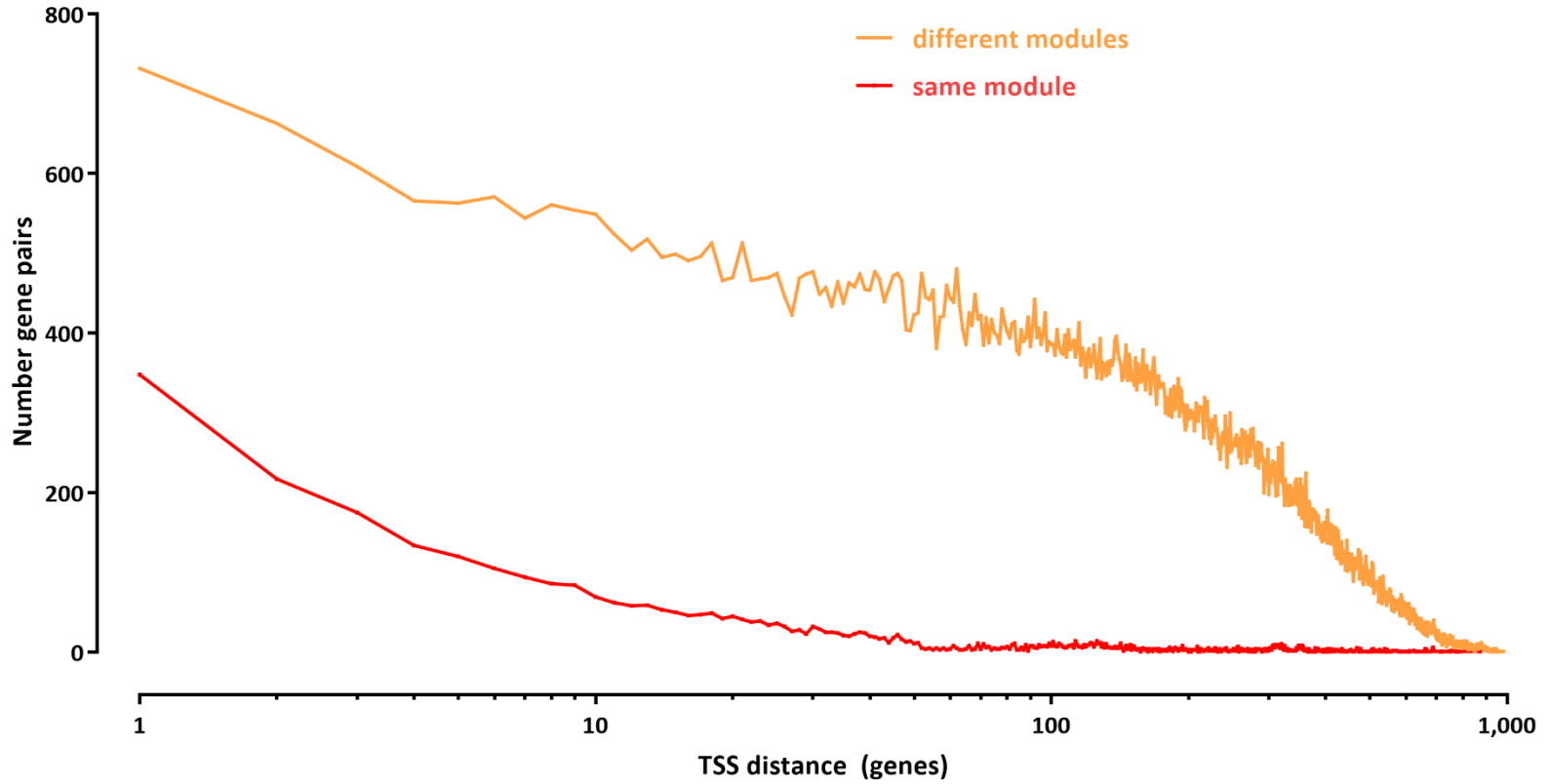
## Summary of what was done

- Mapped transcripts to new assembly with GMAP
- Note that 2,852 transcripts did not map uniquely to the assembly
- Looked for how often genes within the same coexpression module and in different module were:
  - on the same chromosome
  - on the same chromosome and on the same strand
  - within a given distance (in units of genes) from each other

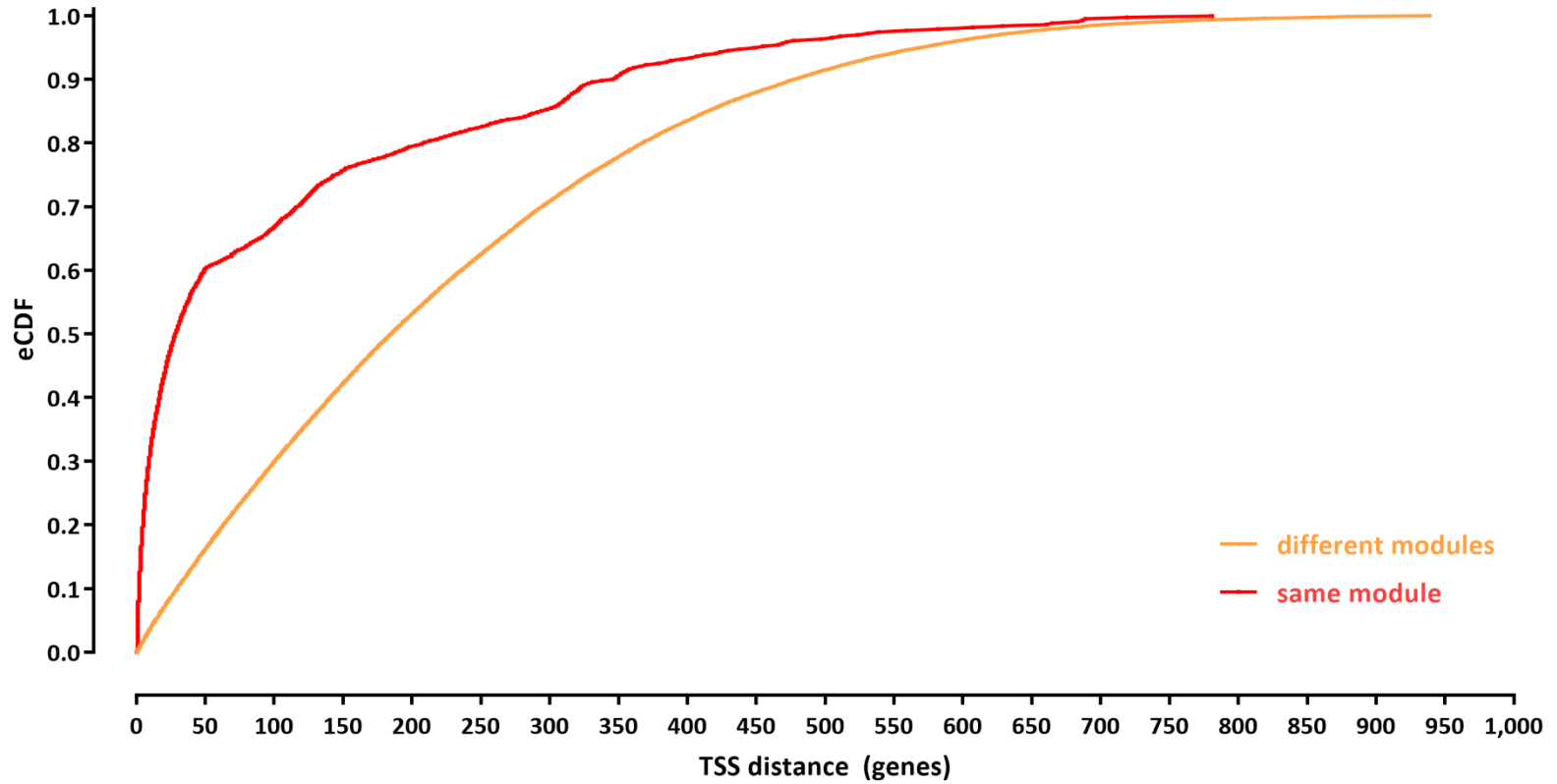


- While there are more genes on the same chromosome within a module, the majority of genes in a given module are not on the same chromosome
- Note that it is possible that we are confounded by partial transcripts, i.e. the same gene but assembled in more than one piece in the transcriptome assembly

### TSS distance (raw)



### TSS distance (cdf)



### TSS distance (cdf)

