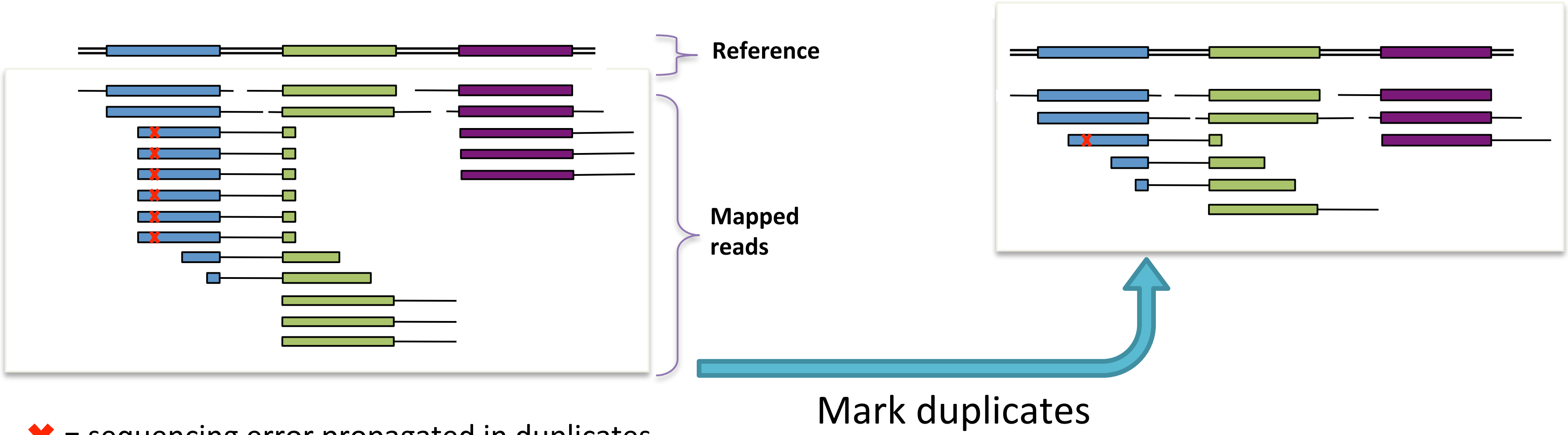
Why mark duplicates?

- Duplicates are sets of reads pairs that have the same unclipped alignment start and unclipped alignment end
- They’re suspected to be **non-independent measurements** of a sequence
  - Sampled from the exact same template of DNA
  - Violates assumptions of variant calling
- What’s more, errors in sample/library prep will get propagated to *all* the duplicates
  - Just pick the “best” copy – mitigates the effects of errors



✖ = sequencing error propagated in duplicates