Comparative Assembly

Align reads to known genome:

known reference genome

consistent differences =
deviation from reference

rare differences =
sequencing errors
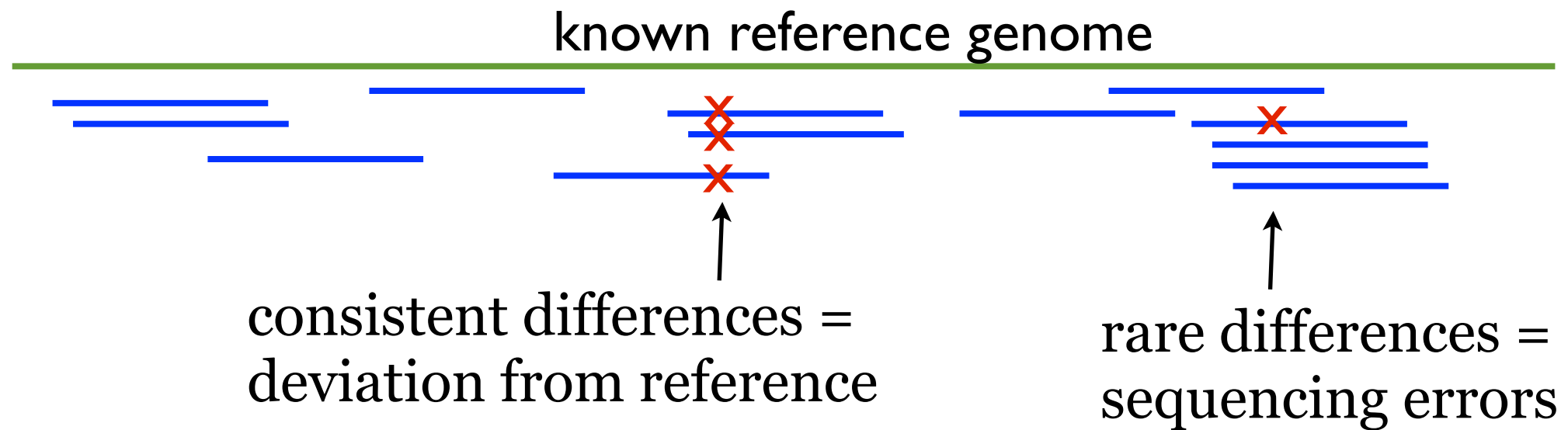
Can use much lower coverage
(e.g. 4X coverage instead of 20-30X for *de novo* assembly).

Aligning a large # of short sequences to one large sequence is an
important special case of sequence alignment.