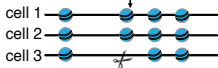


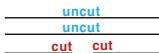
cut - uncut

Chromatin RE digestion
e.g. AluI, BamHI, HindIII

RE cleavage site



DNA purification



DNA shearing to ~150 bp
sequencing library preparation

Illumina® Sequencing

cut - all cut

Chromatin RE digestion
e.g. AluI, BamHI, HindIII

RE cleavage site

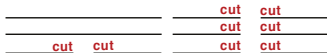


DNA purification

+ RE^{spike-in}-digested *S. pombe* spike-in
split sample

No 2nd digest (X%)

2nd digest (100%)



DNA shearing to ~150 bp
sequencing library preparation

Illumina® Sequencing

Accessibility
calculation:

$$\frac{\text{cut fragments}}{2 \times \text{uncut f.} + \text{cut f.}}$$

$$\frac{\text{cut f. } X\% / \text{S. pombe spike-in}}{\text{cut f. } 100\% / \text{S. pombe spike-in}}$$