

Map / filter reads (*S. cer.* genome)

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graph TD; A[Map / filter reads (S. cer. genome)] --> B[Count cut and uncut fragments at all genomic positions]; B --> C[Determine cut site positions with RE motif]; C --> D[Remove RE sites with close neighbour RE sites]; D --> E[Collect cut and uncut counts within window near cut sites to correct for resection]; E --> F[Calculate shearing probability for background correction]; F --> G[Recalibrate uncut correction factors or use provided factors]; G --> H[Estimate accessibility at each cut site using cut and uncut counts];
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Count cut and uncut fragments at all genomic positions

Determine cut site positions with RE motif

Remove RE sites with close neighbour RE sites

Collect cut and uncut counts within window near cut sites to correct for resection

Calculate shearing probability for background correction

Recalibrate uncut correction factors or use provided factors

Estimate accessibility at each cut site using cut and uncut counts