

Map / filter reads (combined *S. cer.* and *S. pombe* genomes) for cut and all cut sample

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graph TD; A[Map / filter reads (combined S. cer. and S. pombe genomes) for cut and all cut sample] --> B[Count cut 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 counts within window near cut sites to correct for resection]; E --> F[Calculate normalization factor between cut and all cut sample using S. pombe sites]; F --> G[Calculate shearing probability for background correction]; G --> H[Estimate accessibility at each cut site using cut counts of cut and all cut sample];
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Count cut fragments at all genomic positions

Determine cut site positions with RE motif

Remove RE sites with close neighbour RE sites

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

Calculate normalization factor between cut and all cut sample using *S. pombe* sites

Calculate shearing probability for background correction

Estimate accessibility at each cut site using cut counts of cut and all cut sample