

detection of rearrangements in cancer genome with ChIP-seq data

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structural rearrangements

types:

A B C D E F G

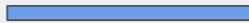


S T U V W X Y



deletion:

A B E F G



inversion:

A B C E D F G



insertion:

A B C T U D E F G



duplication:

A B C D E F E F G



translocation:

A B C D W X Y



S T U V E F G



motivation

rearrangement - cancer causes:

- mutation of tumor suppressor gene
- activation of oncogene
- metastasis and drug resistance¹

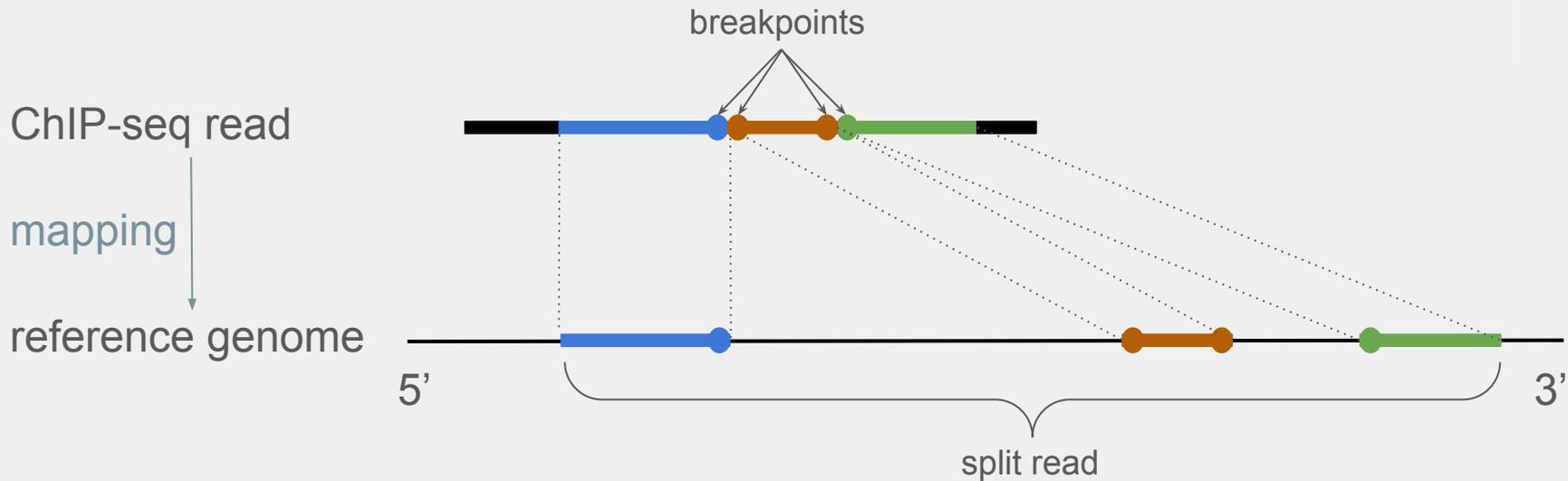
detection of rearrangements:

- DNA-PET (Paired-end tag)
 - need material
 - costs time and money²
- this method
 - only use already determined data
 - freely available data

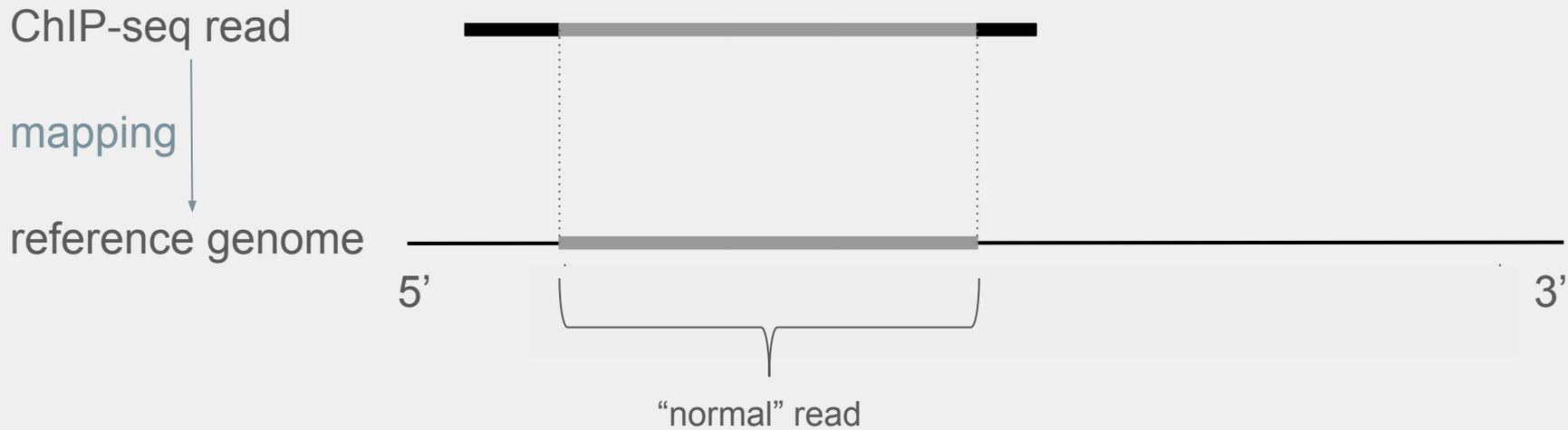
[1] Hasty, P. and Montagna, C. (2014). Chromosomal rearrangements in cancer Detection and potential causal mechanisms

[2] Yao, F. et al. (2012). Long Span DNA Paired-End-Tag (DNA-PET) Sequencing Strategy for the Interrogation of Genomic Structural Mutations and Fusion-Point-Guided Reconstruction of Amplicons. 3

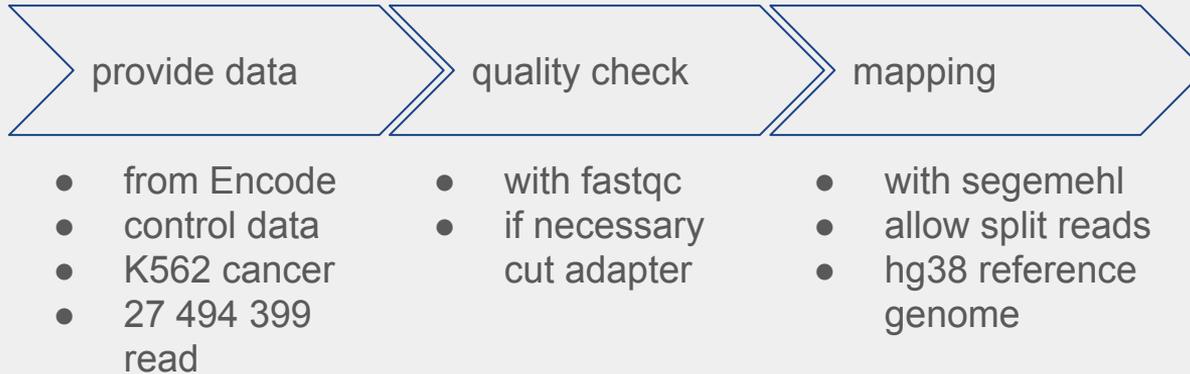
basic idea



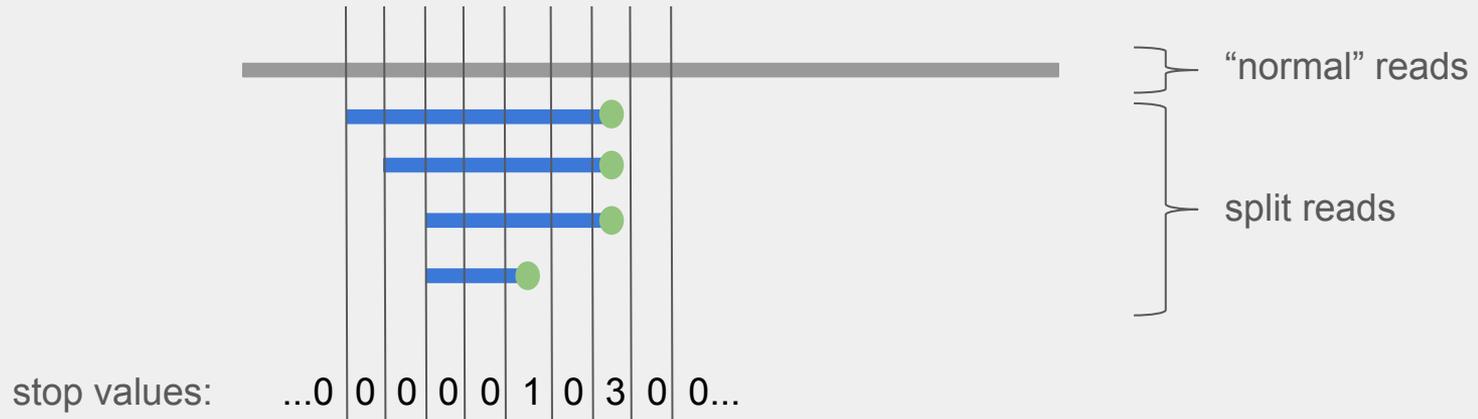
basic idea



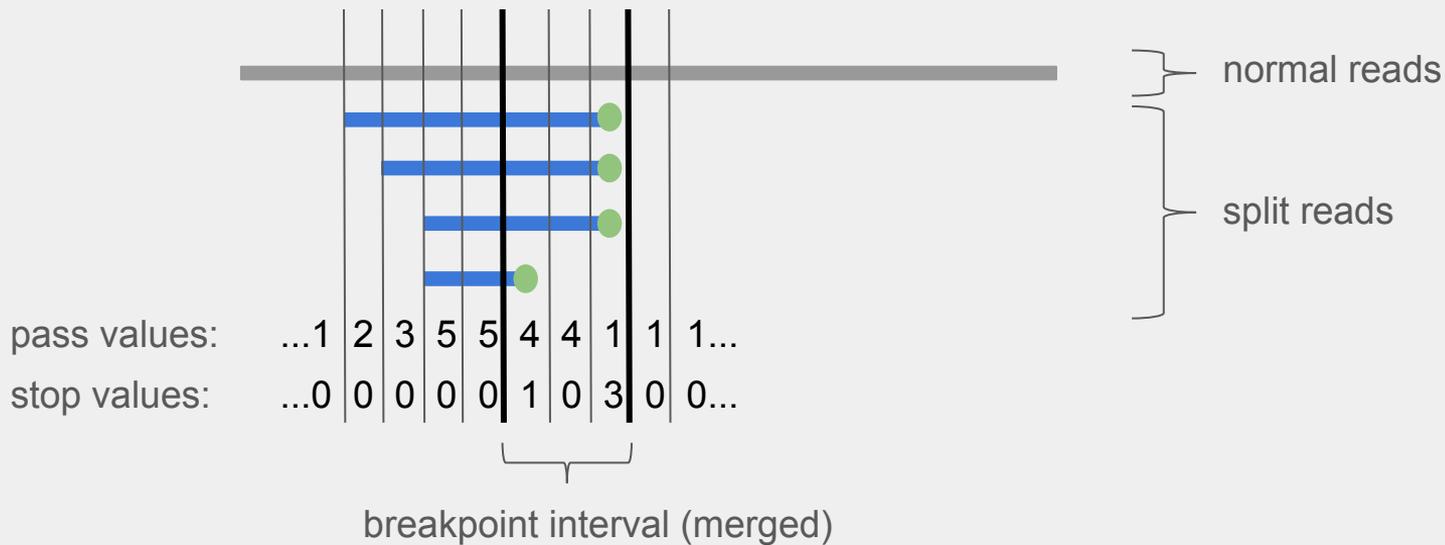
first part of the workflow - preparation



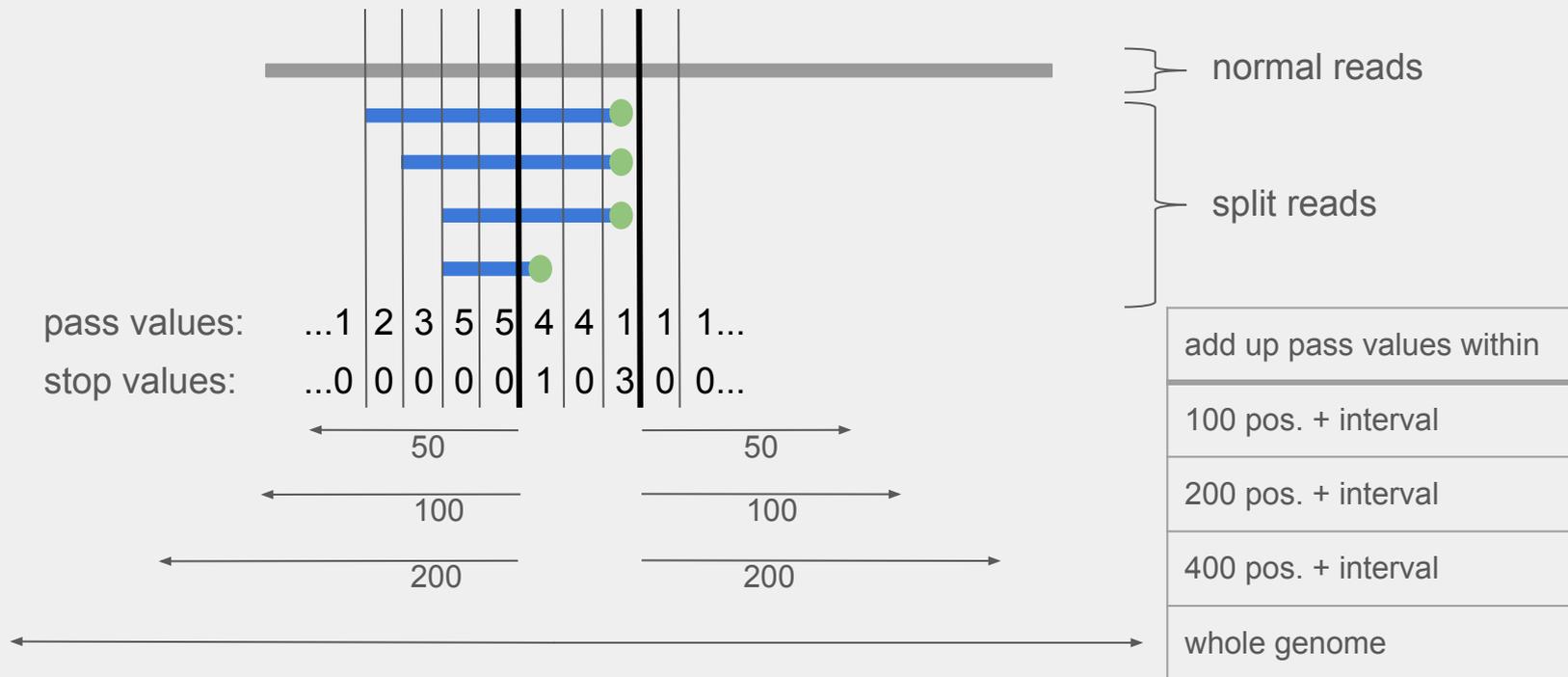
extraction of breakpoints



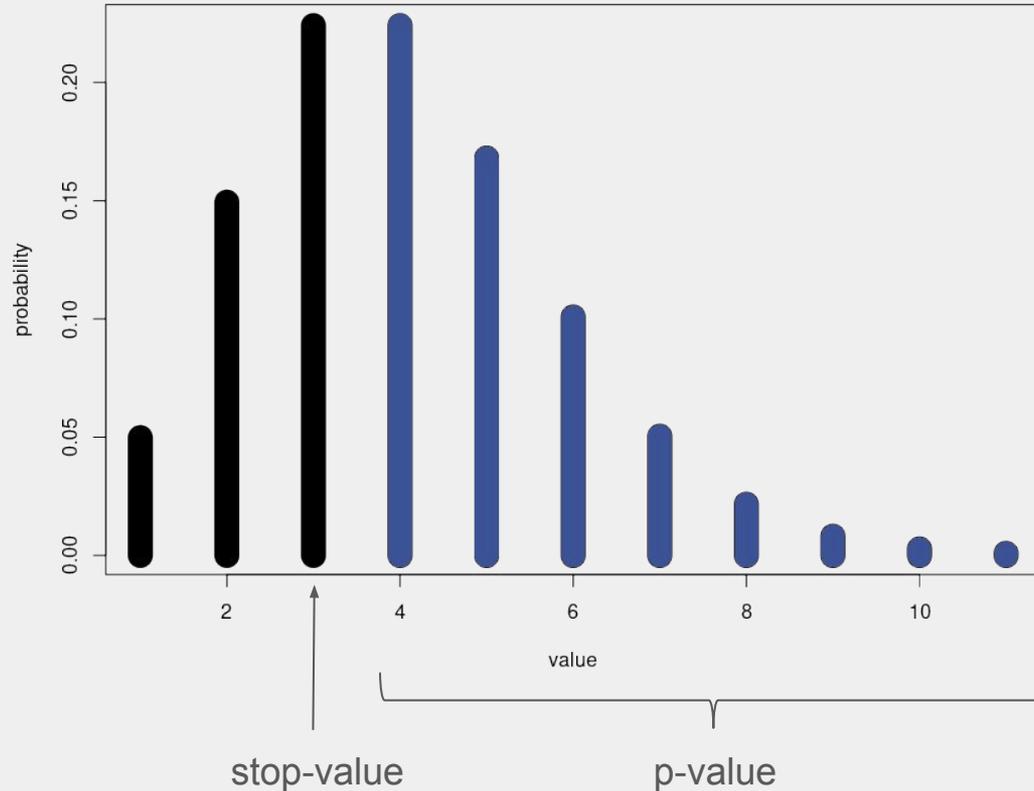
extraction of breakpoints



extraction of breakpoints



calculation of the p-values



following tasks



thank you for your attention