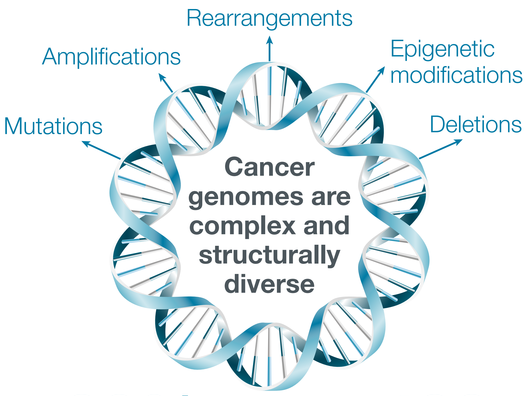
Oxford Nanopore Technologies

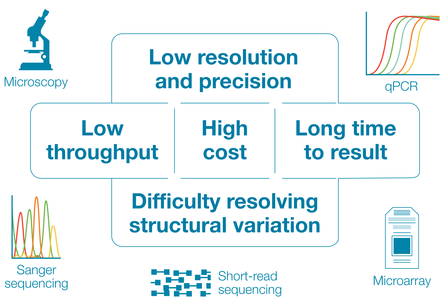
Cancer research



90%
of CML patients have the *BCR-ABL1* fusion[1]

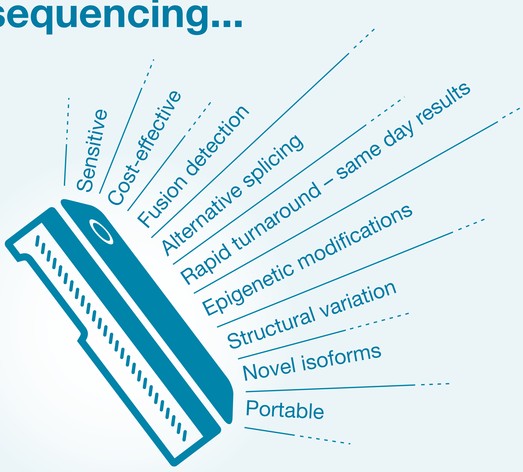
>400
human genes somatically mutated and implicated in cancer[2]

Methods typically used to investigate cancer genomes can be limited



Detect a greater range of genomic variation, in a single run, with

long-read nanopore sequencing...



Nanopore sequencing also provides...

> ***Nanopore sequencing allows same-day detection of structural variants, point mutations, and methylation profiling using a single device with negligible capital cost.***
>
> Euskirchen *et al.*[3]

Scalability
From portable MinION™ to high-yield, high-throughput PromethION™

Real-time analysis
Immediate access to results and sequence until sufficient data are generated

Read length equal to fragment length
Obtain full-length transcripts, perform accurate transcript and genome assembly, and analyse phasing

Easy, rapid prep
Streamlined library prep in just 10 minutes (gDNA) from as little as 1 ng input (PCR-cDNA)

MinION | GridION^{XS} | PromethION

Download the white paper at
nanoporetech.com

1. X. An *et al.* 2010 Leukemia Research. DOI: 10.1016/j.leukres.2010.04.016
2. P.J. Stephens *et al.* 2009. Nature. DOI: https://doi.org/10.1038/nature08545
3. P. Euskirchen *et al.* 2017. Acta Neuropathol. DOI: 10.1007/s00401-017-1743-5

IG_1022(EN)_V1_05March2019