Figure 1.

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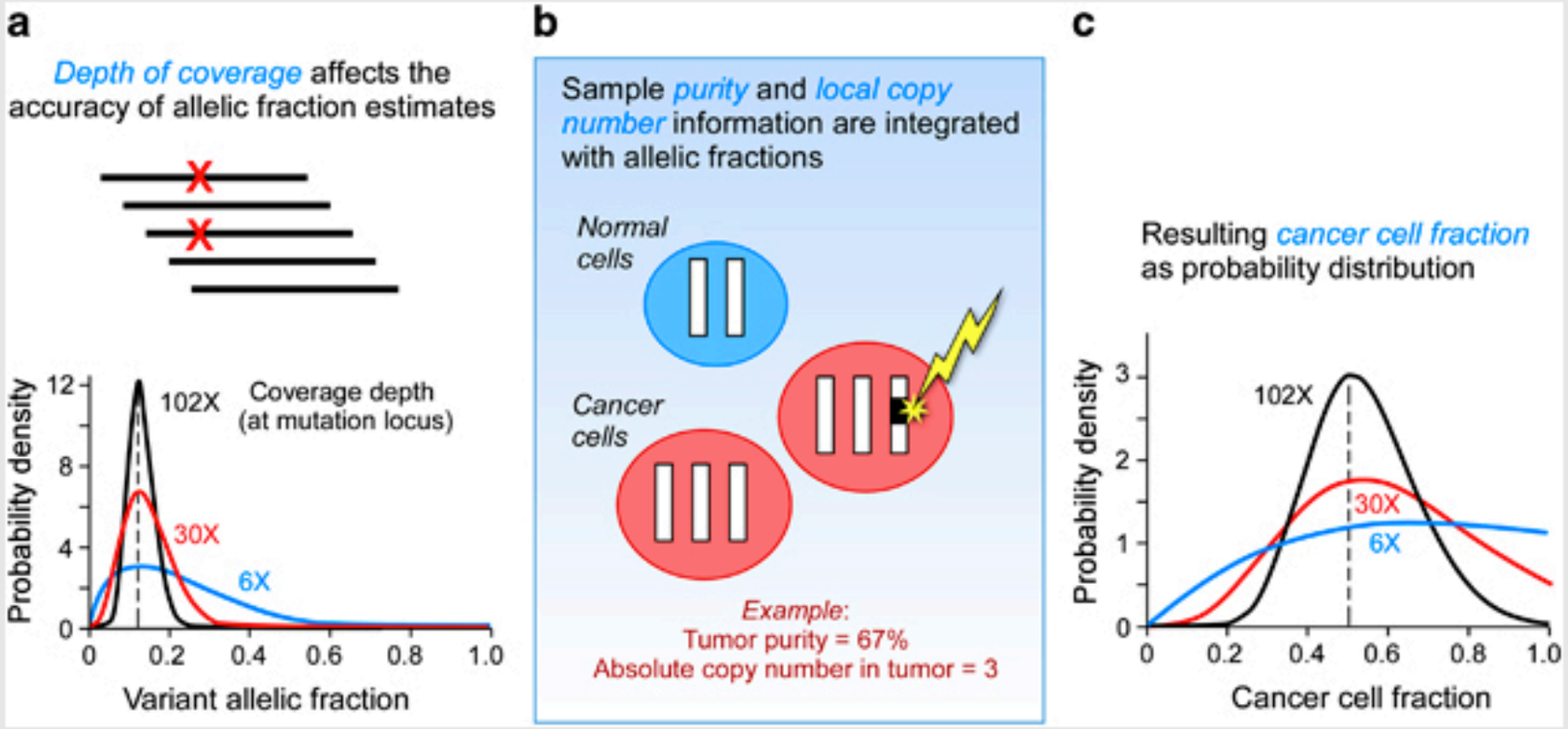

Inferring the size of a subpopulation affected by somatic mutations from genomic data. MPS provides an estimate of VAF, which is calculated by counting the number of reads with the variant alleles and dividing it by the total number of reading from the specific location. The certainty of the estimate is a function of the depth of coverage, using the Beta distribution (**a**). Subsequently, the VAF estimates are integrated with the purity and local copy number information (**b**) to yield cancer cell fractions (**c**). In the example provided, a somatic mutation with a VAF of 0.125, a local copy number of 3 and a purity of 67% yields cancer cell fraction estimates of 0.5.