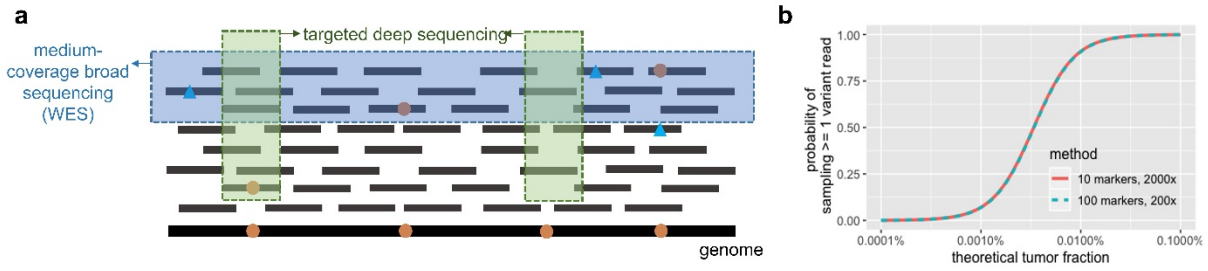

Figure S1. The difference in tumor signal detection between targeted deep sequencing data and medium-coverage broad sequencing data. (a) Illustration of observed sequencing reads as a sample from the pool of cfDNA. The blue box indicates the observed reads from medium-coverage broad sequencing, while the green box indicates the observed reads from targeted deep sequencing. **(b)** The theoretical detection probability of tracking 10 markers at 2000x and 100 markers at 200x. The probability of sampling >= 1 variant read is determined by a binomial distribution over all markers given a fixed tumor fraction, which is the probability of a read from tumor cells.