Supplementary figures for “BitPhylogeny: A probabilistic framework for reconstructing intra-tumor phylogenies”

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Figure S1: Correlation profiles of three molecular clocks studied in Sottoriva et al. [1]. Percentage of significant correlation (Kendall’s τ) between CpG sites among all samples. Most sites are uncorrelated.
Figure S2: **Tree comparison based on datasets with 1% noise.** Trees shown in the same row are constructed from the same underlying true tree: (A-E) represent trees of monoclonal, polyclonal-(low, medium and high) and mutator phenotype. The corresponding true trees are in Figure 3 of the main text. The trees shown in the same column are constructed with the same method: BitPhylogeny (left), hierarchical clustering (middle) and k-centroids (right). For BitPhylogeny trees, the length of each edge is proportional to the branch length between the two clones. For each clone, the in-edge width is proportional to the number of associated reads.
Figure S3: Estimated genotype profiles of eight key genes. Probability of mutation of 12 SNVs located in eight genes across all cells. The error bars summarize 50,000 MCMC samples and are colour-coded according to clone membership.
References