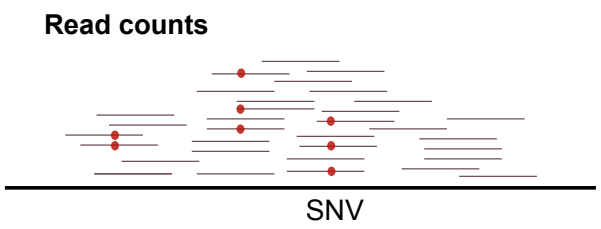
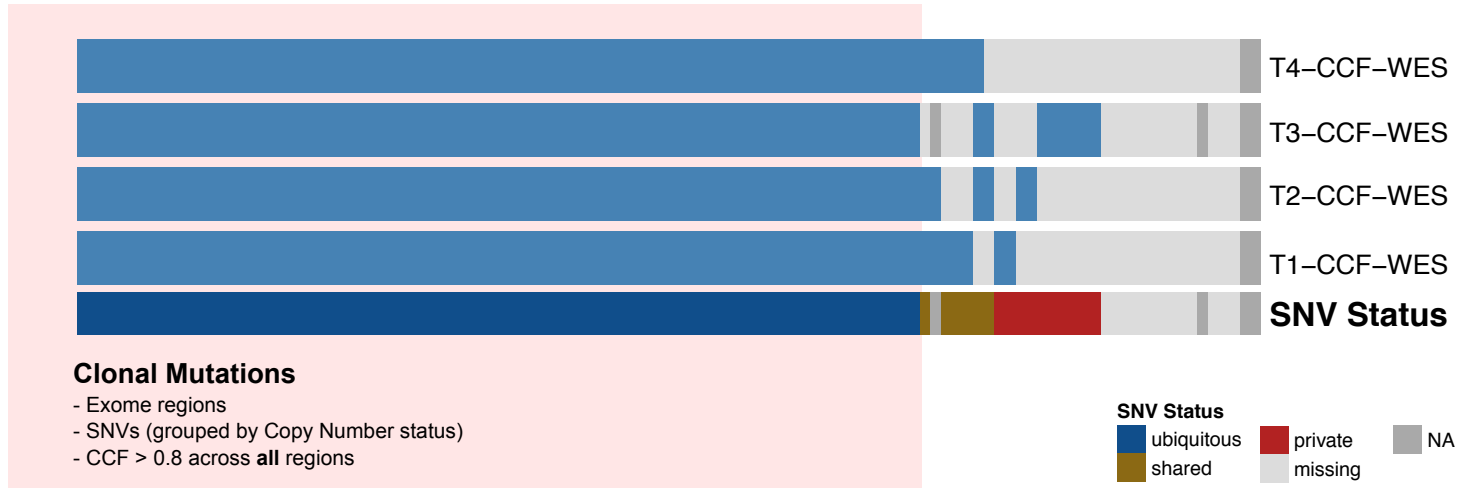
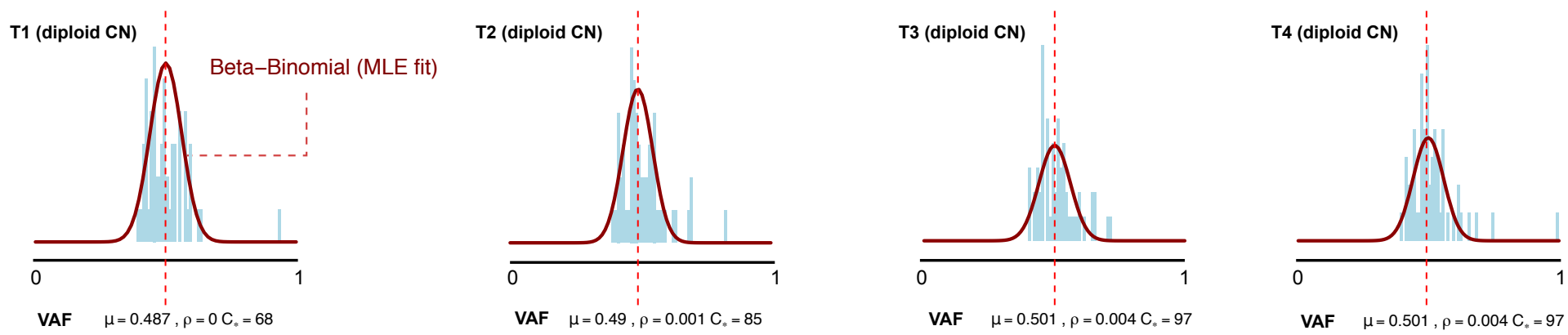
A **PATIENT 52**

Cancer Cell Fractions (CCF) from Whole Exome Sequencing of 4 primary tumour regions



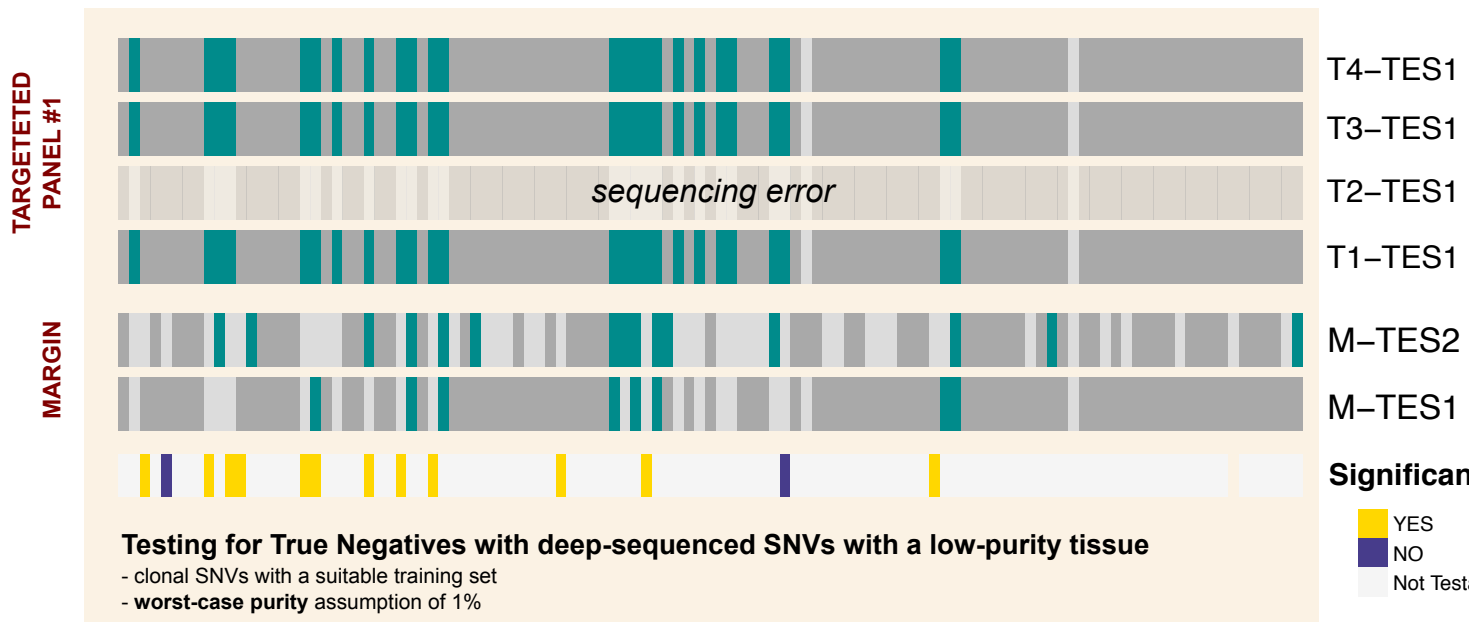


B **Training model.** *Expected read counts harbouring a variant allele, for a clonal SNV (adjusted for Copy Number)*



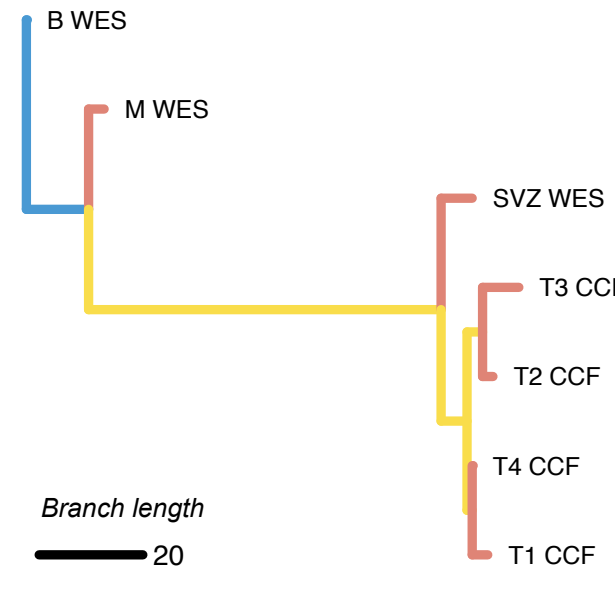
*Number of reads (NV)s with mutant alllele from a primary region with CN = **c**.*

C **Test data.** *Deep Sequencing reveals clonal SNVs in the primary tumour that are missing in the margin samples.*



Testing for True Negatives with deep-sequenced SNVs with a low-purity tissue
- clonal SNVs with a suitable training set
- **worst-case purity** assumption of 1%

D **Phylogenetic analysis.** *The tree supports margin samples being ancestral to primary tumour regions.*

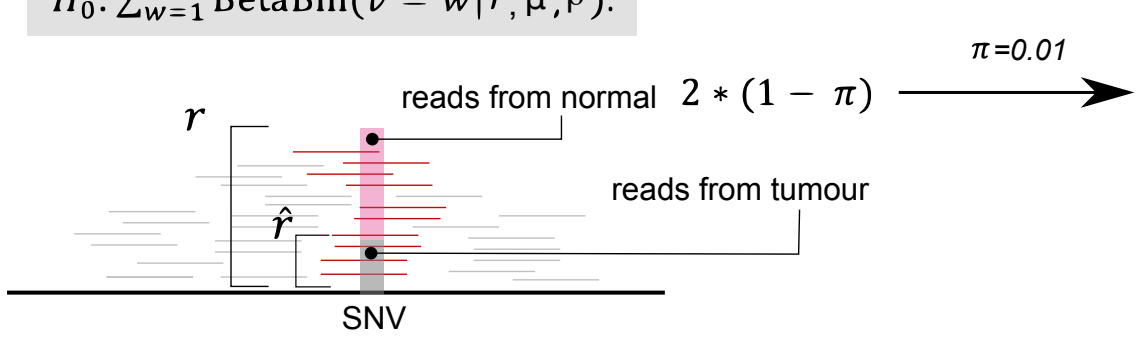


E

Deep-resolution clonal SNVs (~*3000x*)

NV < k in M; tested with read coverage from tumour (NR).

$$H_0: \sum_{w=1}^{k} \text{BetaBin}(v = w | \hat{r}; \mu, \rho).$$



Test power for μ = 0.5 and ρ =5 x 10^{-2} *at significance level* α = 0.05