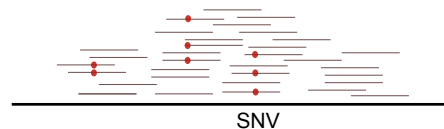


WES (training)

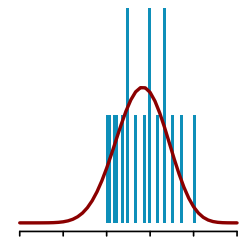
Clonal SNVs

across all primary CCF > 0.8 and CN = c



Expected read counts

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

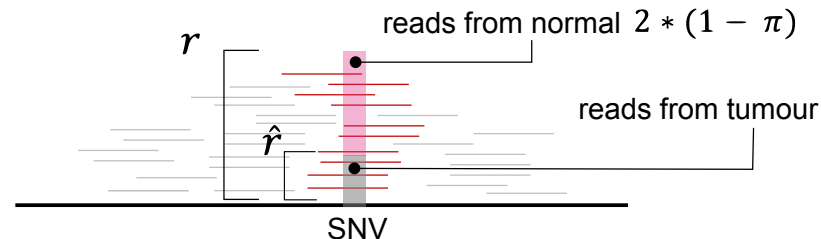
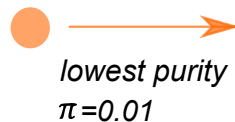


• Beta-Binomial (MLE fit)

Targeted panels (test)

Deep-resolution clonal SNVs (~3000x)

NV = 0 in M; tested with read coverage
from tumour (NR).



$$H_0: \text{BetaBin}(v = 0 | \hat{r}; \alpha, \beta)$$