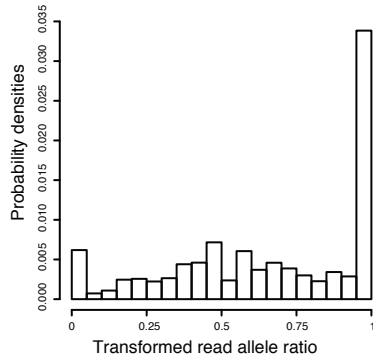


Sample HMM paramter estimator

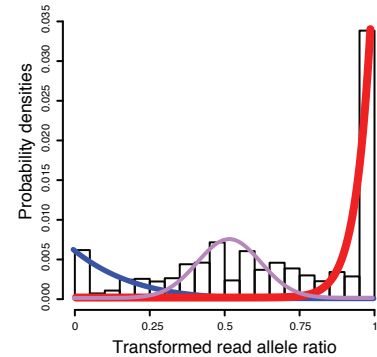
Estimate read  
allele ratio distribution



Fit  $\beta$ -mixture model



HMM Transition- + Emission-probabilities



**Figure S6** Schematic workflow of the parameter estimator for the HMM. For each sample the read allele ratio is estimated from the result of a sliding window approach. The resulting frequencies are then transformed to interval of 0 and 1 as the beta function is only defined at that region. Afterwards the beta-mixture model fit is applied. The probabilities for the sample-specific HMM are estimated from the resulting three curves and the output from the Basecaller.