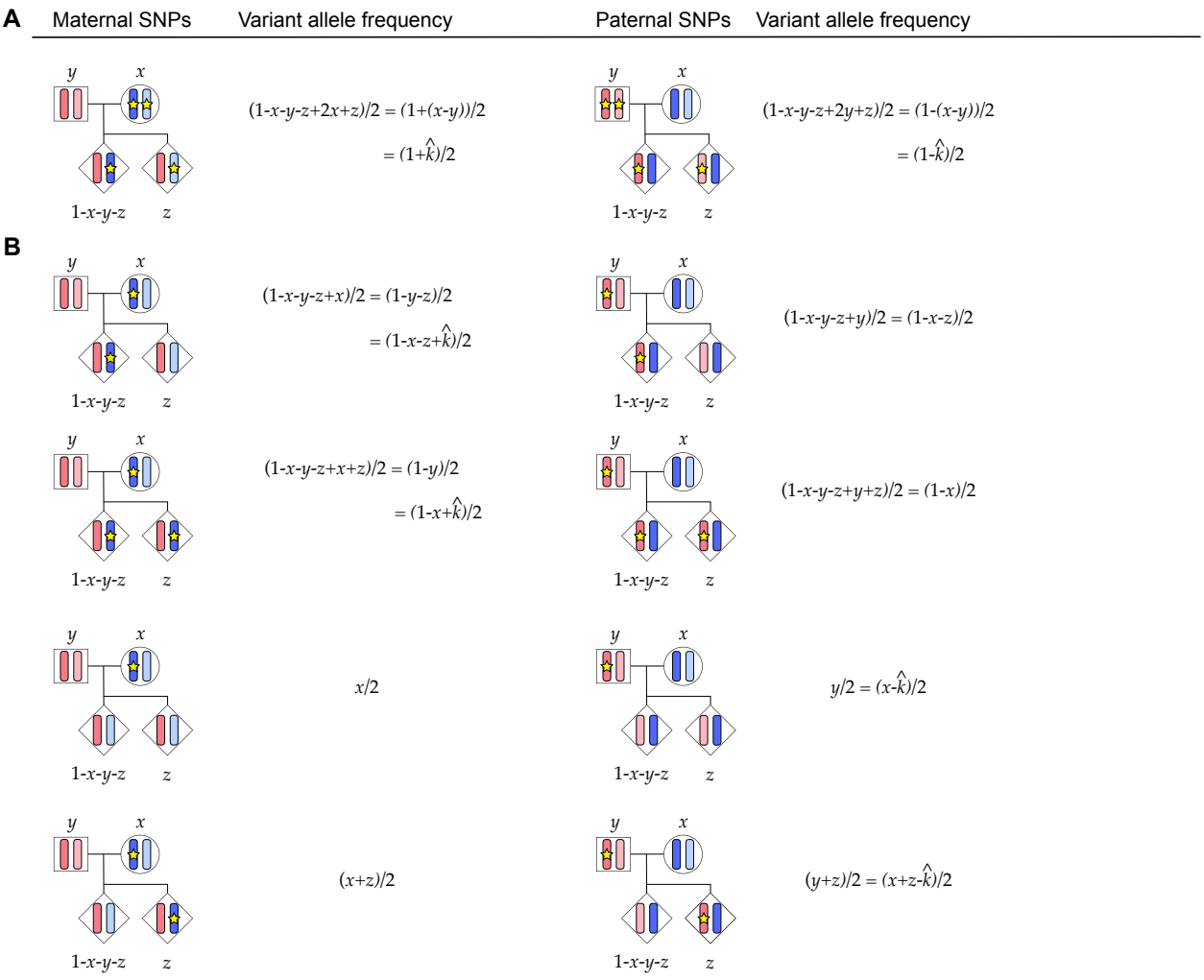

Supplemental Figure S3. Maximum likelihood estimation framework for offspring DNA contamination by multiple family members. (A) SNP loci where one parent is a *homo-alt* and the other parent is a *homo-ref* parent (GroupA SNPs) can be used to calculate the difference between the two parents. Contamination by the parent with *homo-alt* genotype is multiplied by 2 since the variant allele is present in both homologous chromosomes. Variant allele frequencies of mother, father, sibling, and target offspring are set as x, y, z, and $1\text{-}x\text{-}y\text{-}z$, respectively. Using these SNP loci, we calculate $\hat{k}$, the difference between the contribution of the mother's DNA and the father's DNA $(x\text{-}y)$. (B) SNP loci where one parent is *het* and the other parent is *homo-ref* (GroupB SNPs) can be used for estimating the remaining variables x and z by substituting $y = x\text{-}\hat{k}$ for all variant allele frequencies.