* From the allele relative fraction plots we can see that the dominants alleles are **01** and **04**, they appear in all states.
* Alleles **01** and **03** are closer to each other, hence in state 3 for the threshold of 0.5\% we suspect that the sequences are mis-assigned and should be allele **01**. Otherwise we should have seen the allele in one of the other stated as well.
* Further the relations between **01** and **04** tends to heterozygosity with equal usage, thus the appearance of the lowly expressed allele in state 2 are likely erroneous.