* From the plots we can that the homozygous alleles **02** and **04**. However, in an heterozygous state the tradeoff between the allele differ by the combinations.
* Allele **04** tend to be less dominant when coupled with another allele, making the observation we see closer to *1* in state 2 to be incorrect and they should be homozygous.
* Allele **02** when coupled with either allele **06** or **07** there is an equal allelic usage.
* Allele **05** is lowly expressed in all combinations and state, making him a suspect of mis-assignment. When coupled with allele **04** its relative use is closer to *0.1* but the amount of sequences is quite low.
* Allele **06** seems to have high usage when in combinations with other alleles, hence it is less likely that in states 3 and 4 it will appear in such low usage. In those cases we can speculate of a mis-assignment, which could be allele **05**, its closest allele.