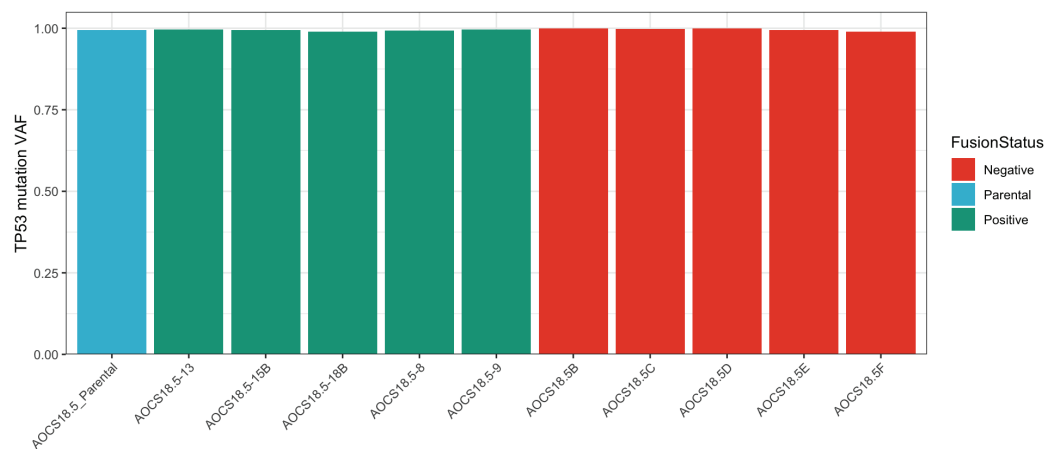
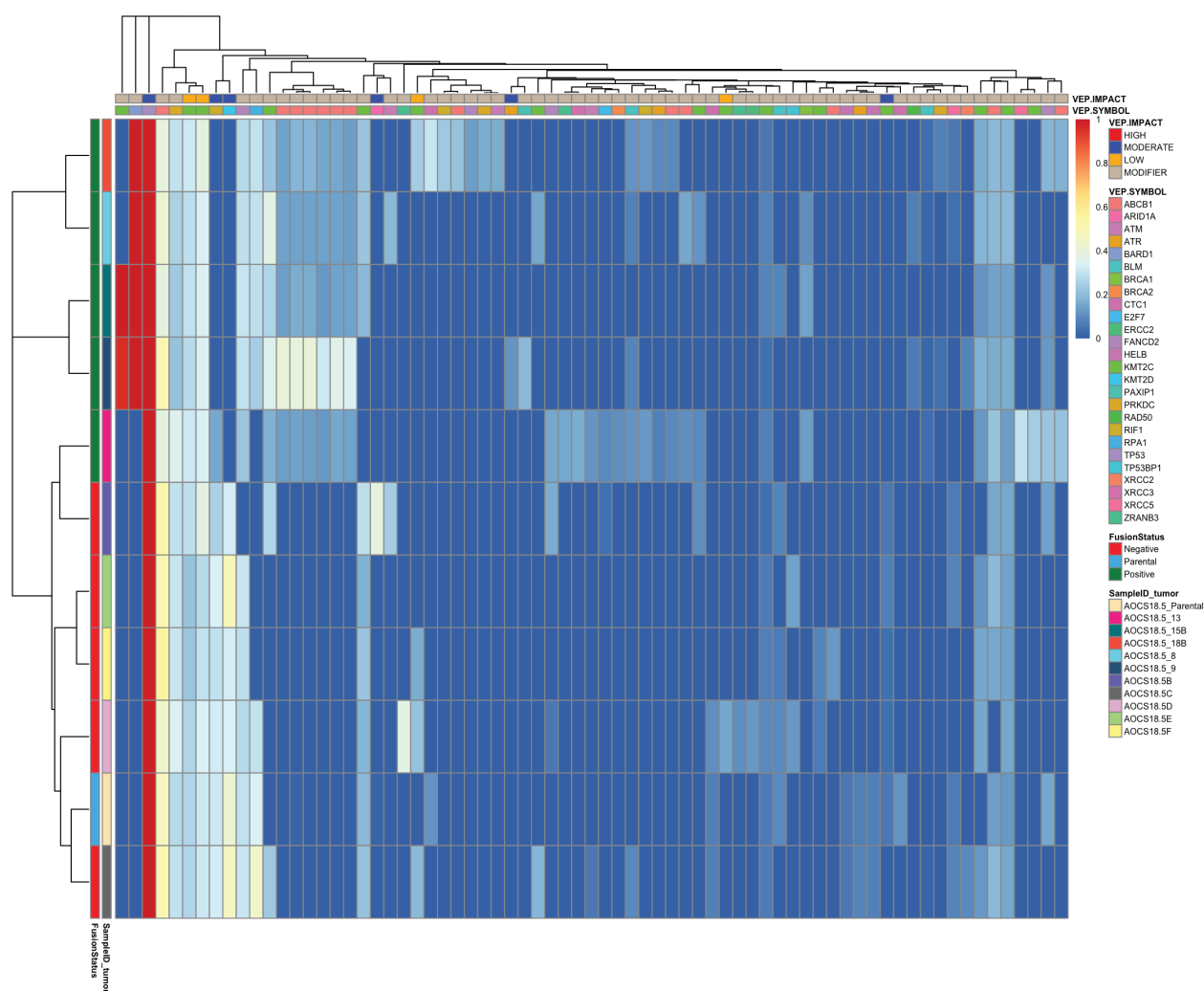


**A**



**B**



**Supplementary Fig. S4.** Mutational analysis of AOCs18.5 lines identifies similarities and differences between fusion positive and negative clones.

(A) A single high variant (ENSP00000269305.4:p.Lys132Met) was identified in TP53 in all AOCs18.5 lines (parental and clones), with variant allele frequencies (VAF) >98%. (B) A heatmap of the VAF of all mutations detected sees the fusion positive clones clustering together and the fusion negative clones clustering with the parental line.