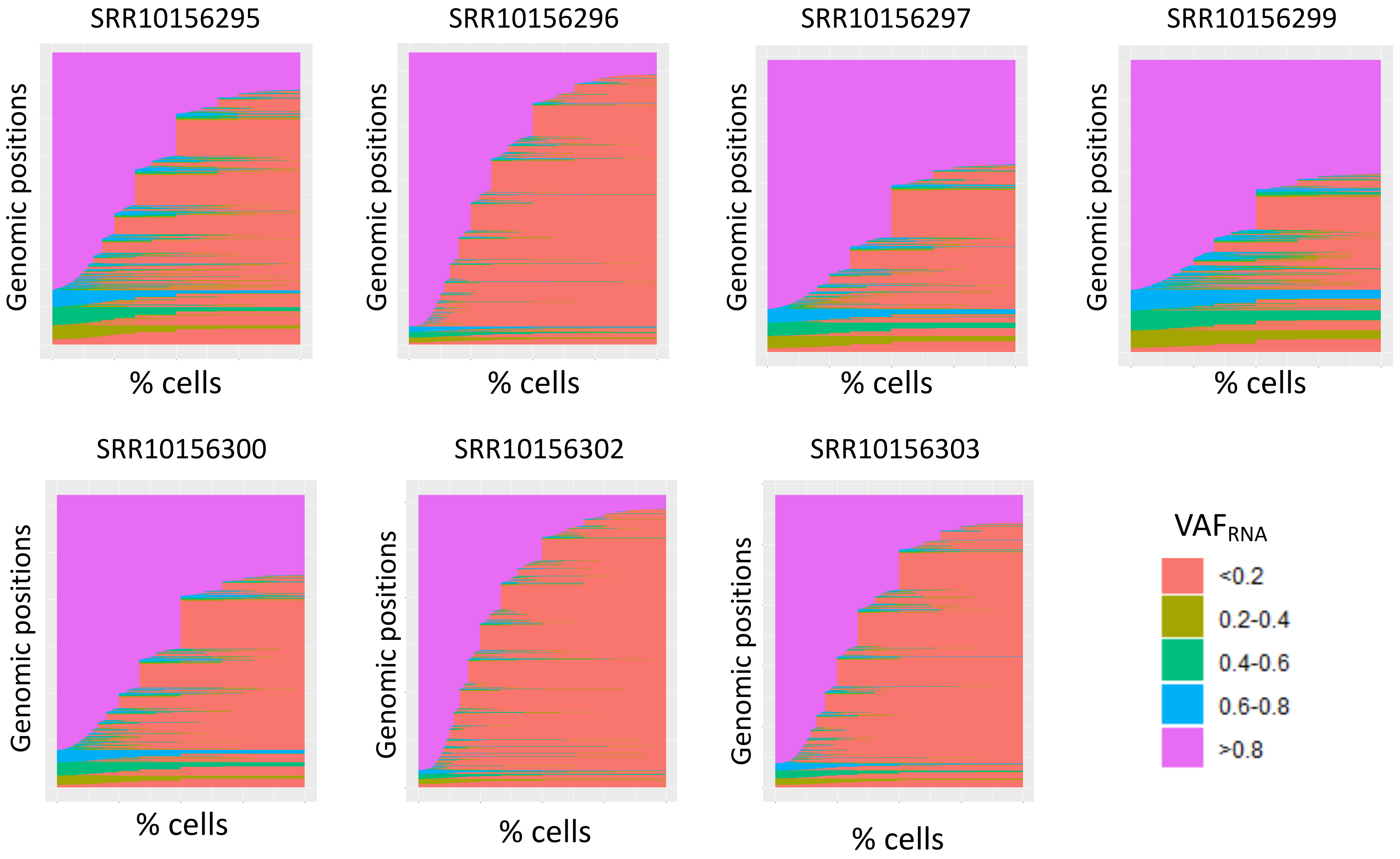

Supplementary Figure 3. $scVAF_{RNA}$ estimated at genomic positions covered by a minimum of 5 sequencing reads (minR=5) at the sites with bi-allelic calls (GATK) in the 7 neuroblastoma samples; the positions are sorted by VAFRNA (y-axis). For the majority of positions, VAF_{RNA} showed predominantly mono-allelic expression, with a substantial proportion of the $scVAF_{RNA}$ estimations in the intervals 0-0.2 (orange) and 0.8-1.0 (purple). The percentage of cells with the corresponding VAFRNA is displayed on the x-axis.