

Box plot showing the distribution of the number of reads for three genotypes: Homo_AA (red), Het_Aa (blue), and Homo_aa (yellow). The y-axis represents the number of reads, ranging from 0 to 100. The x-axis is labeled '2:214837:G:A'. The Homo_AA group has a median around 45, Het_Aa around 50, and Homo_aa around 55. Individual data points are overlaid on the box plots.

