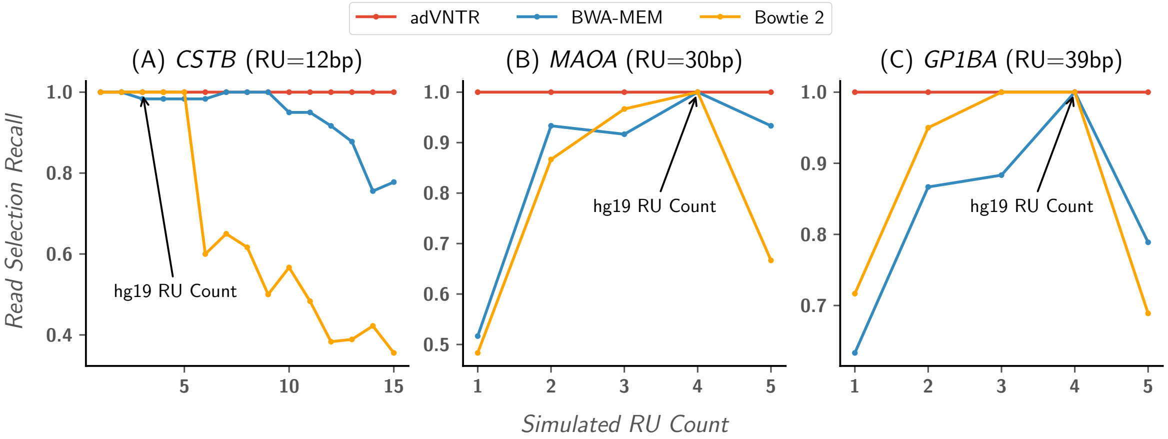

Figure S2: **Sensitivity of Illumina read recruitment at specific VNTR loci.** Comparison of adVNTR read selection with BWA-MEM and Bowtie 2 mapping for Illumina reads (short VNTRs). Each plot shows the sensitivity of mapped/selected reads as a function of the number of repeats for different VNTRs. These plots show examples of alignment tools' behavior when RU count of VNTR deviates from the RU count in the reference genome. (A) Shows the comparison for the VNTR in *CSTB* gene, in which the pathogenic cases have more then 12 repeats and as it is shown alignment tools perform poorly in those cases. (B) Shows the comparison for the VNTR in *MAOA* gene, where the 4 repeats corresponds to both pathogenic case and number of repeats in reference genome. However, other tools perform poorly in normal cases. (C) Shows the comparison for the VNTR in *GP1BA* gene, and again, alignment tools only perform well when RU count is same as RU count in reference genome.