Figure S5 - Insert size distribution is smallest in the RVI-seq bait capture method

The insert size distribution for a Twist synthetic SARS-CoV-2 sample (100k copies) is shown, from which the largest proportion of reads below 100bp length were removed by Kneaddata filtering from the inHouse method (**a**), compared to the Ampheus method (**b**) and the Illumina method (**c**).