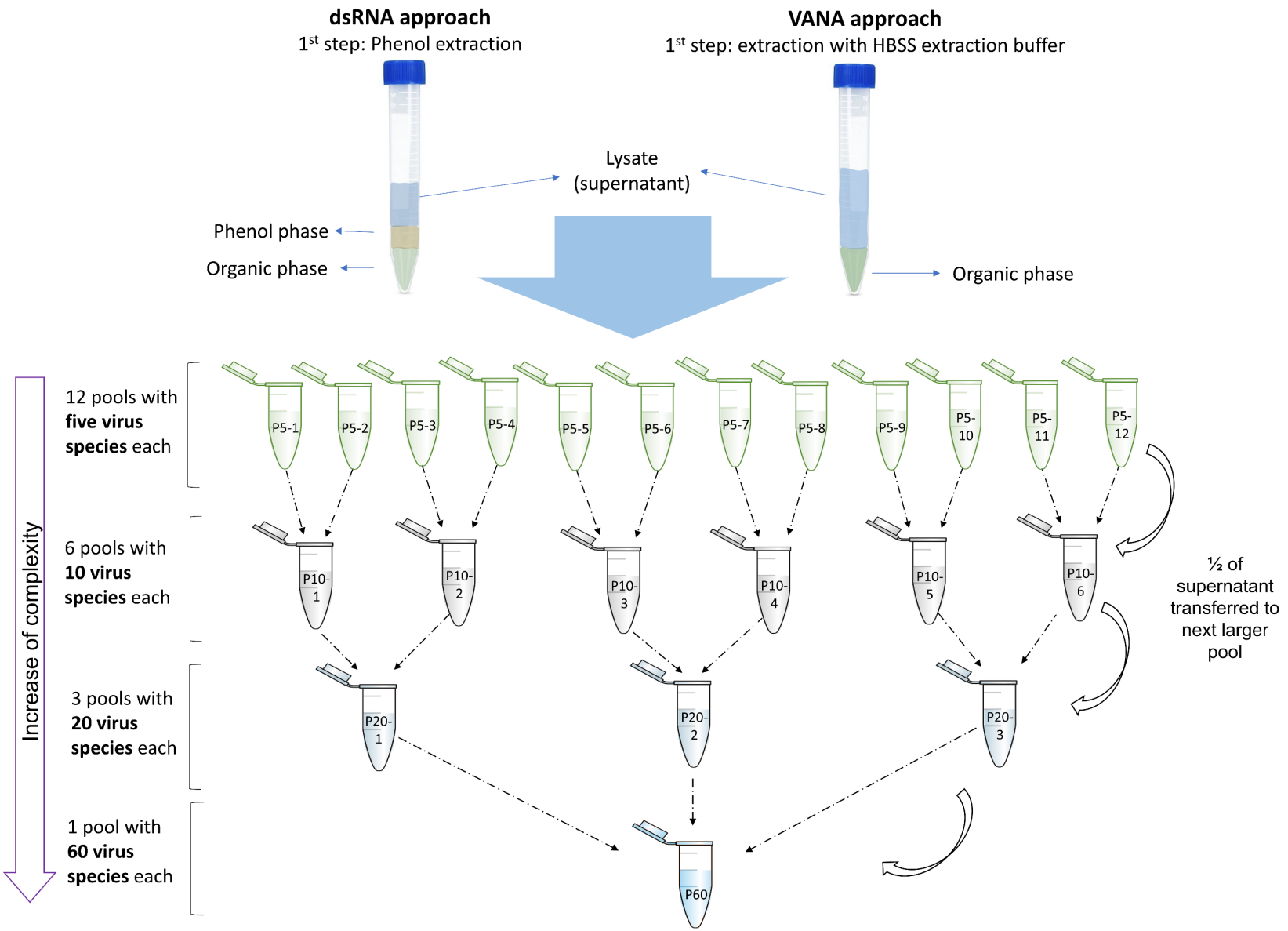
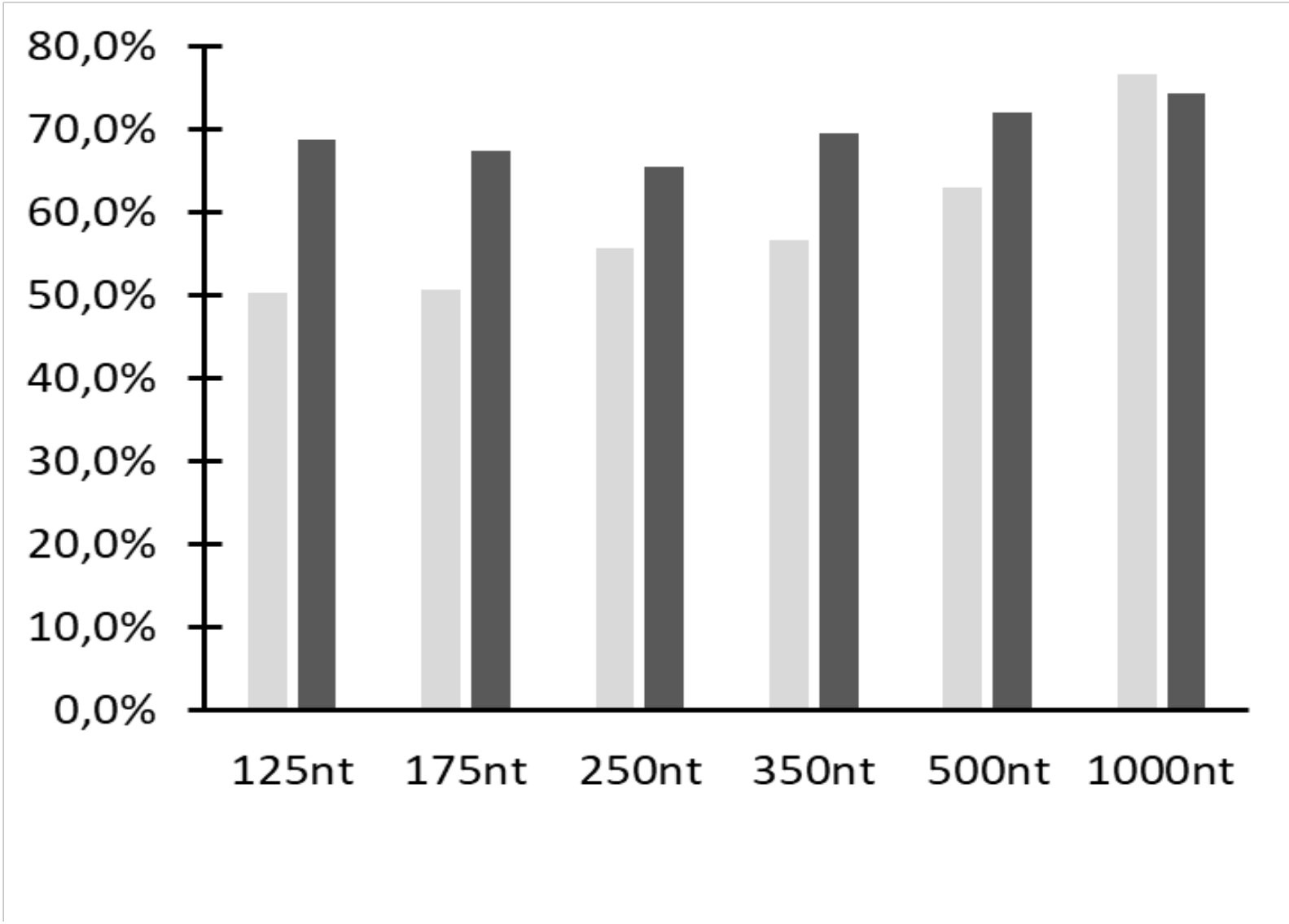
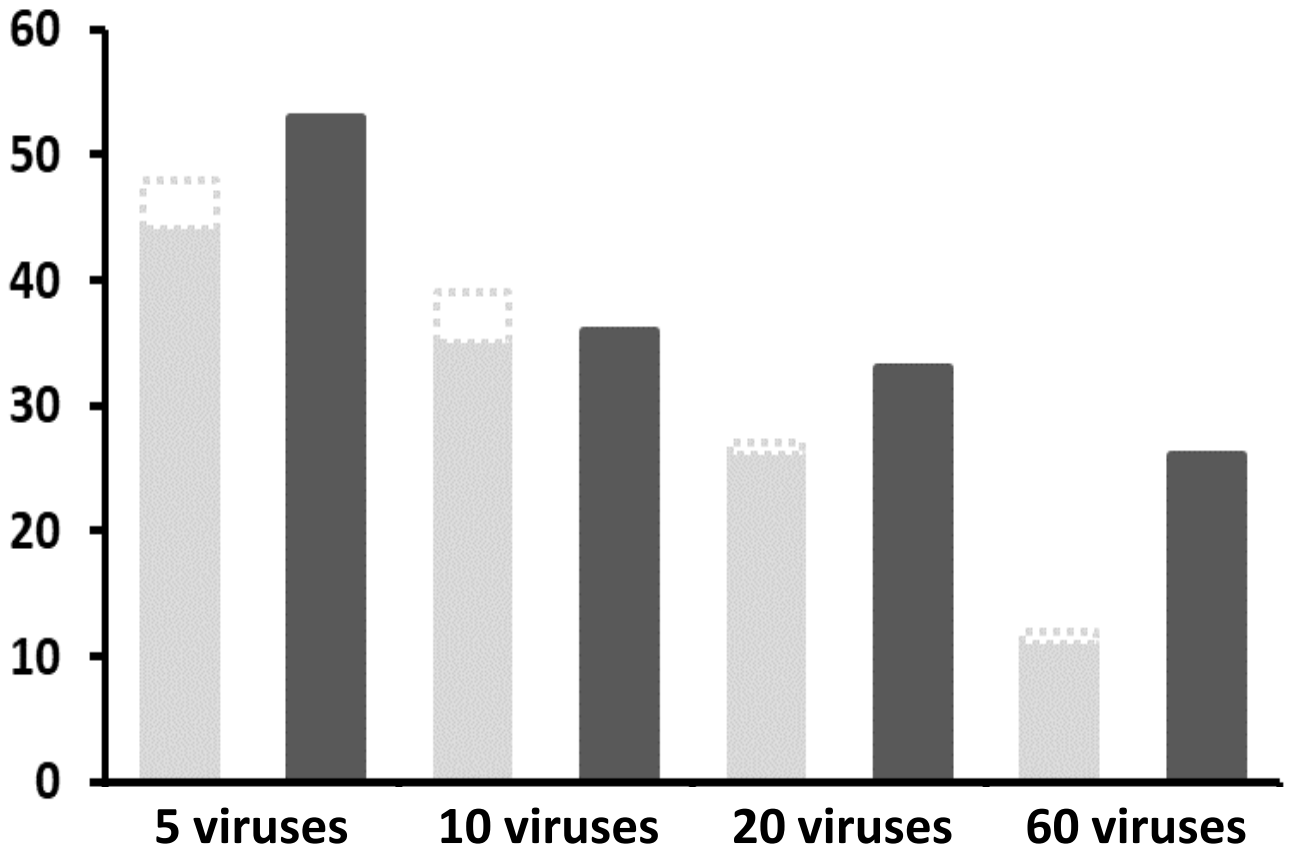
Supplementary Figure S1: Pooling strategy to generate mock virus communities with different degrees of complexity (5, 10, 20, and 60-viruses communities)



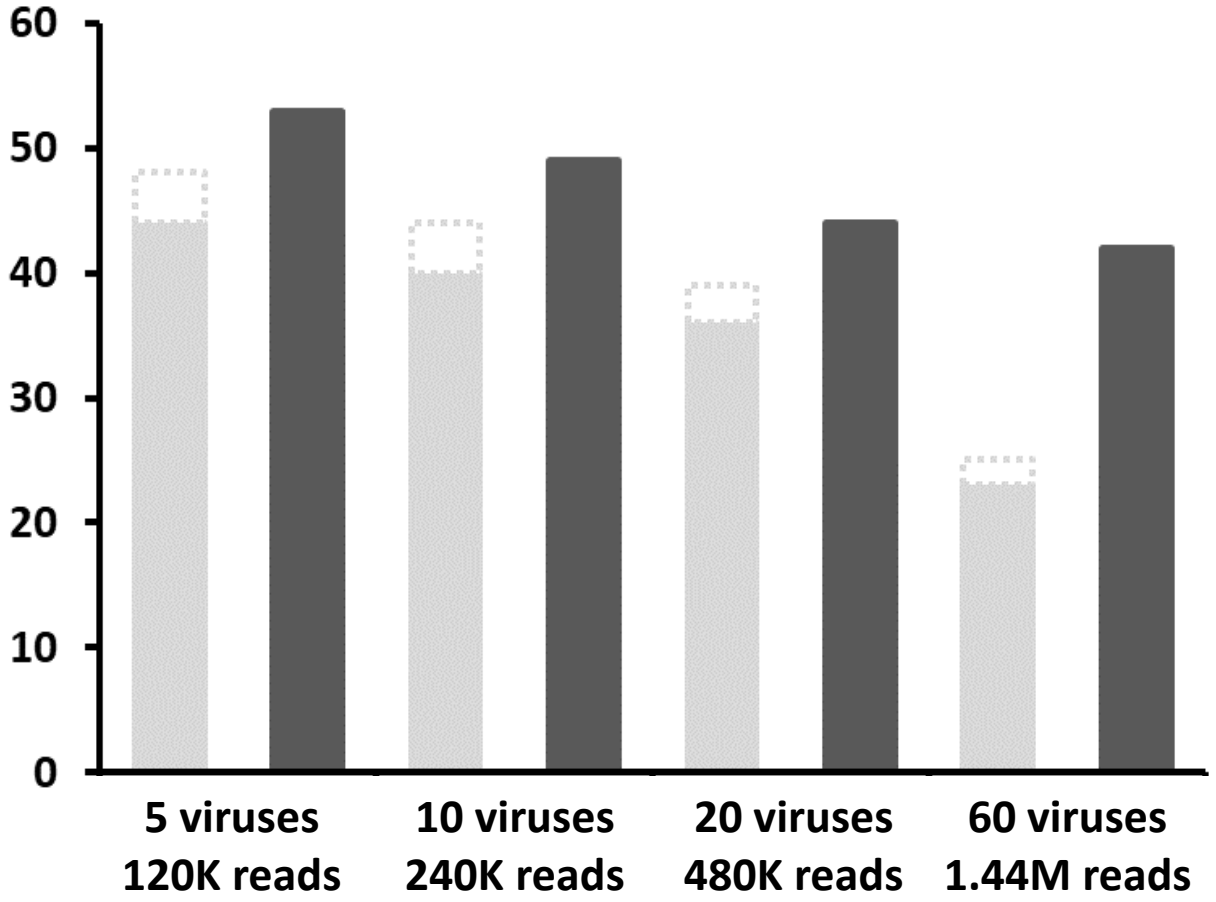
Supplementary Figure S2: Percent coverage of detected viral molecules as a function of minimal contig length for the VANA (light grey) or the dsRNA (dark grey) approaches on the 60 viruses community at a 10 millions reads sequencing depth



Supplementary Figure S3: Number of detected viruses based on *de novo* assembled contigs from the VANA (light grey) or the dsRNA (dark grey) approaches for datasets normalized at a 120K reads sequencing depth and for viral communities with different degrees of complexity. RNA viruses are indicated by solid bars while DNA viruses are indicated by dashed bars.



Supplementary Figure S4: Number of detected viruses for viral communities with different degrees of complexity using *de novo* assembled contigs from the VANA (light grey) or the dsRNA (dark grey) approaches. Datasets were normalized so as to compensate for community complexity (120K reads for 5 viruses communities, 240K for 10 viruses, 480K for 20 viruses and 1.44M for 60 viruses). RNA viruses are indicated by solid bars while DNA viruses are indicated by dashed bars.



Supplementary Figure S5: Average proportion of the length of detected viral molecules of the 60 viruses community represented by contigs obtained for the VANA (light grey) or the dsRNA (dark grey) approaches at different sequencing depth. For each sequencing depth 5 independent random resamplings were performed and error bars represent the standard deviations of the coverage obtained