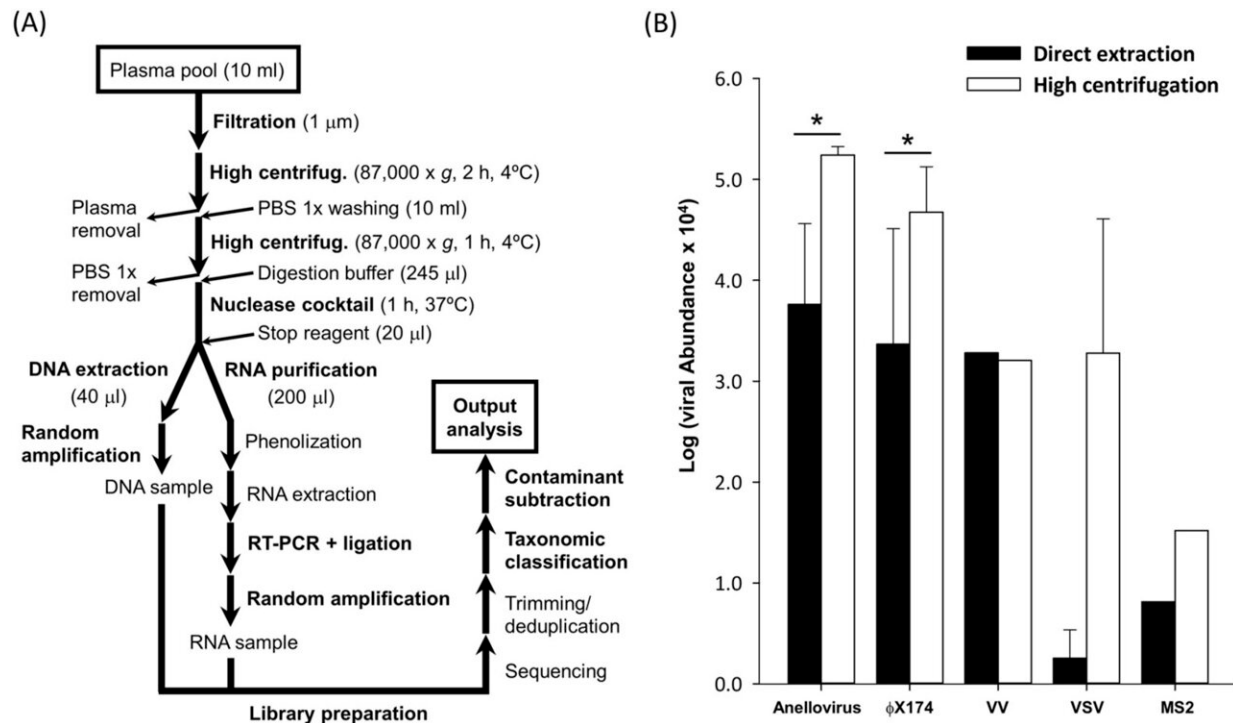


New protocol to improve the detection of viruses in blood samples from healthy people

August 9 2021



Experimental and bioinformatics workflow (A) and comparison between viral abundance estimated with direct extraction from plasma and the protocol involving initial high centrifugation (B). Main steps at panel (A) are marked in bold (See details in Methods section). For panel (B), comparison of normalized data was achieved by transforming total reads for each specific taxonomic group into abundance, which was obtained with Centrifuge using an Estimation-Maximization algorithm³¹ (See details in Methods section). For clarity, abundance × 10⁴ was represented in log scale. Error bars indicate standard error of the mean (SEM, n = 2 replicates). Asterisk indicates the statistical significance of a t-test analyzing the efficiency of the purification protocols (*P

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