

# Virus Entry Receptor Binding – VERB kit

## **Application note**

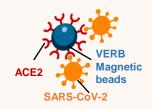
VERB assay as an innovative tool to isolate intact SARS-CoV-2 particles

#### Introduction

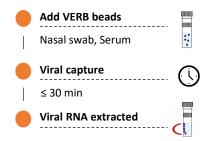
The highly efficient binding of SARS-CoV-2 via its spike protein to its cellular entry receptor ACE2 is the basis for the successful initiation of the viral infection cycle and forms the molecular principle of the VERB (Virus Entry Receptor Binding) approach developed by Covirabio. A capture matrix has been developed which allows the highly efficient isolation of intact SARS-CoV-2 particles as well as the determination of the presence of neutralizing antibodies and spike protein in a biosafety level 2 environment.

The VERB assay is a stand-alone sample preparation method compatible with downstream detection methods such as RT-qPCR and thus can be easily integrated into existing laboratory procedures. The product is for research use only (RUO).

Numerous publications and recent research highlight the potential applications of harnessing interactions between ACE2 and spike proteins for COVID-19 research. The application note focuses on the isolation of intact SARS-CoV-2 viral particles.



#### **Procedure**



- Automatic mode for medium and high throughput
- Manual mode for low sample numbers

### **Key Features**

Characteristics	<ul> <li>Capture and enrich only intact virus from patient samples</li> <li>Free of viral RNA fragments and debris</li> <li>Comparable to the labor-intensive viral plague assay</li> </ul>
Kit components	Magnetic beads functionalized with recombinant human ACE2
Required material	<ul> <li>Magnetic devices (block or automatic device e.g. TANBead Maelstrom, KingFisher Flex)</li> <li>Sample mixer (e.g., benchtop shaker, rotary wheel)</li> </ul>

### Performance

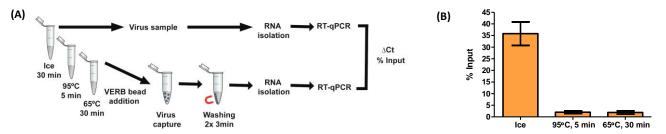


Fig. 1 Intact virus particles with VERB beads. (A) Flow scheme of the assay setup (B) Heat inactivation of a SARS-CoV-2 containing clinical samples abolish the isolation of RNA with VERB beads (< 5% input), when compared to the sample kept on ice (ca. 35% input). Percent capture (% input) is normalized to the total RNA of a sample that was kept on ice and calculated based on the  $\Delta$ Ct value. Mean values and standard deviation of three biological replicates are shown.

