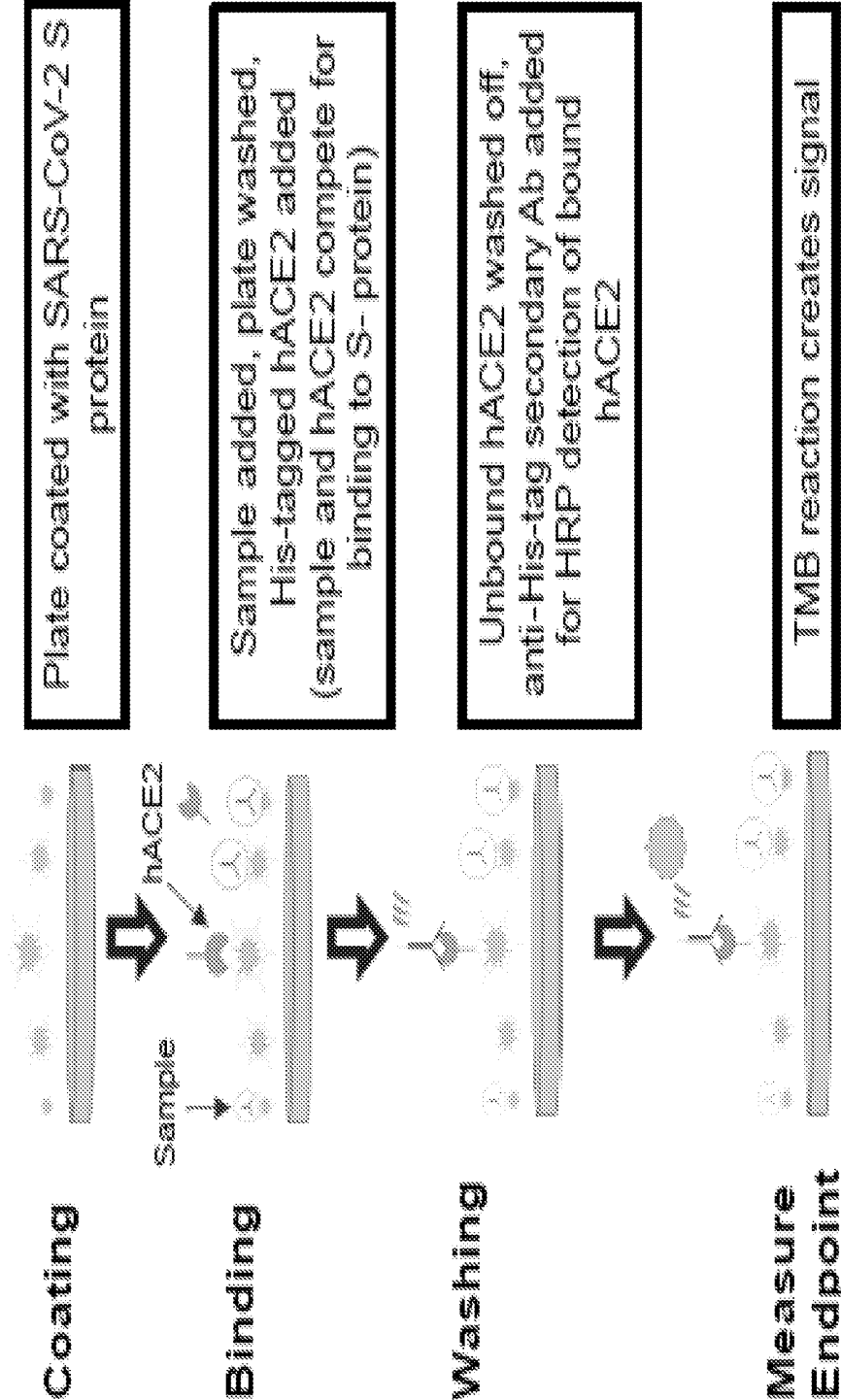


Fig. 1



Positive sample will result in inhibition titer due to suppressed signal.

Fig. 2

$$\begin{aligned} \ln SD1(Inter - Assay) &= \exp\left(\sqrt{\text{var}(\text{Analyst}) + \text{var}(\text{Day})}\right) \\ \ln SD2(Intra - Assay) &= \exp\left(\sqrt{\text{var}(\text{Error})}\right) \\ \%GCV(Inter - Assay) &= 100 \times \left(\sqrt{\exp((\ln SD1^2) - 1)}\right) \\ \%GCV(Intra - Assay) &= 100 \times \left(\sqrt{\exp((\ln SD2^2) - 1)}\right) \end{aligned}$$

Fig. 3

$$\ln SD3 = \exp \left(\sqrt{\text{var}(\text{Analyst}) + \text{var}(\text{Day}) + \text{var}(\text{residual})} \right)$$
$$\text{Total \%GCV}(\text{Intermediate Precision}) = 100 \times \left(\sqrt{\exp((\ln SD3)^2) - 1} \right)$$

Fig. 4

$$\% \text{ reduction} = 100 - \frac{\text{Results with S protein or without S protein incubation}}{\text{Results without S protein incubation}} \times 100]$$

Fig. 5

$$\% \text{ Relative Bias} = 100 \times \frac{\text{Observed overall hACE2 binding inhibition GMT} - \text{Expected hACE2 binding inhibition GMT}}{\text{Expected hACE2 binding inhibition GMT}}$$

Fig. 6

$$\% \text{ recovery} = 100 \times \frac{\text{Test value}}{\text{Reference value}} \quad \% \text{ difference} = \% \text{ recovery} - 100$$

Fig. 7

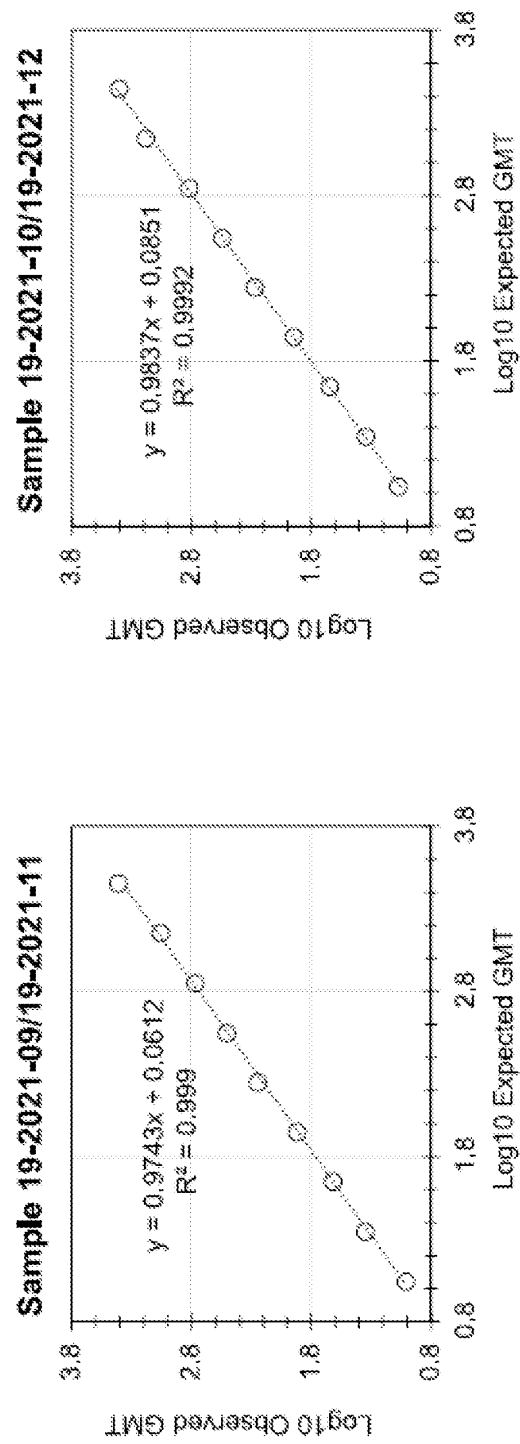


Fig. 8

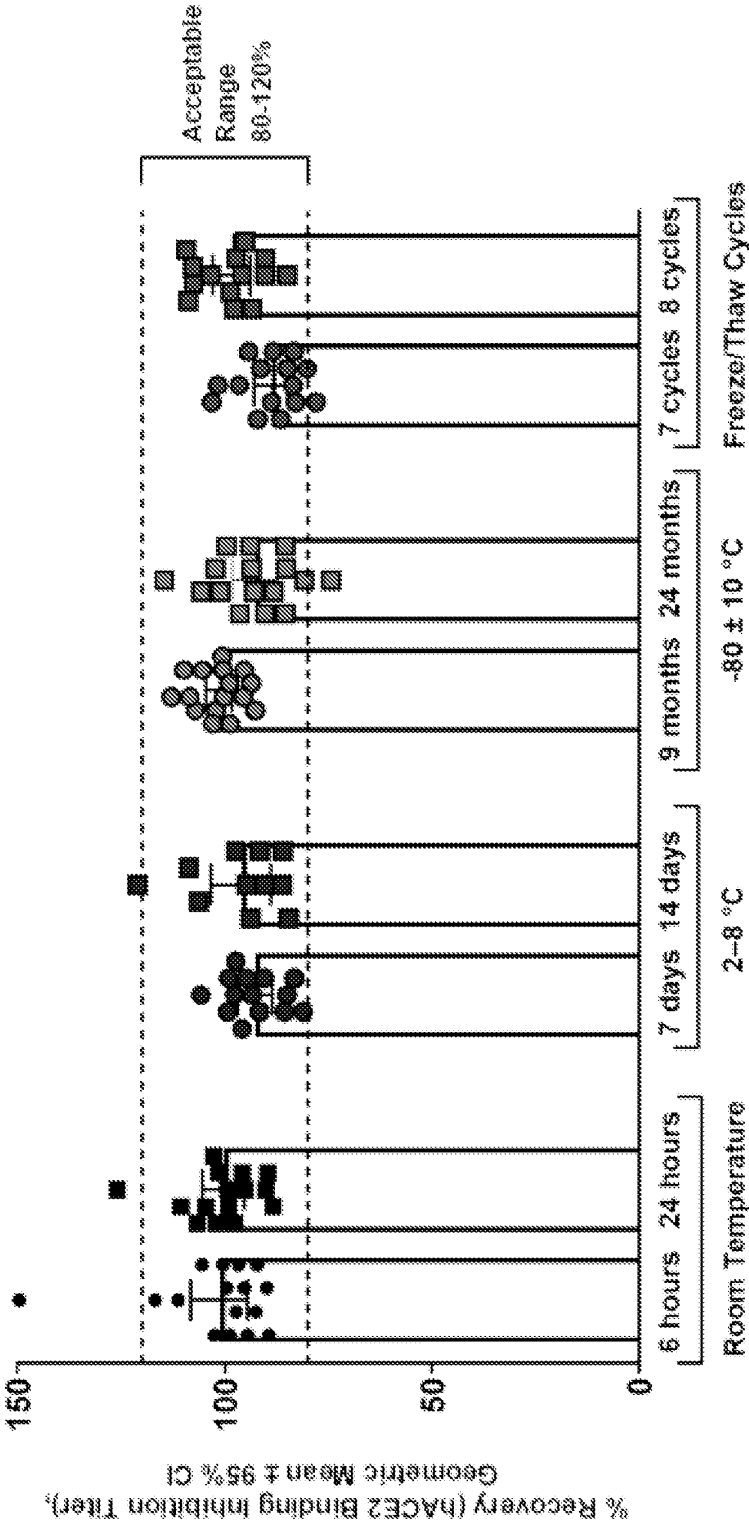
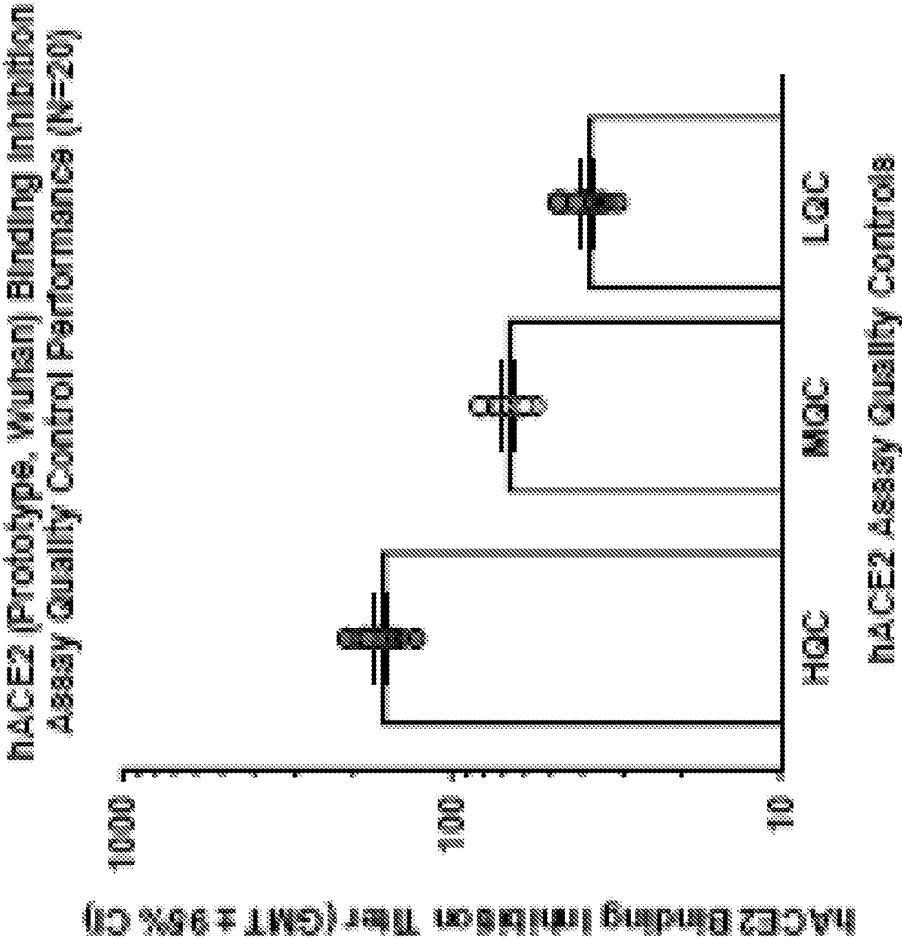


Fig. 9A



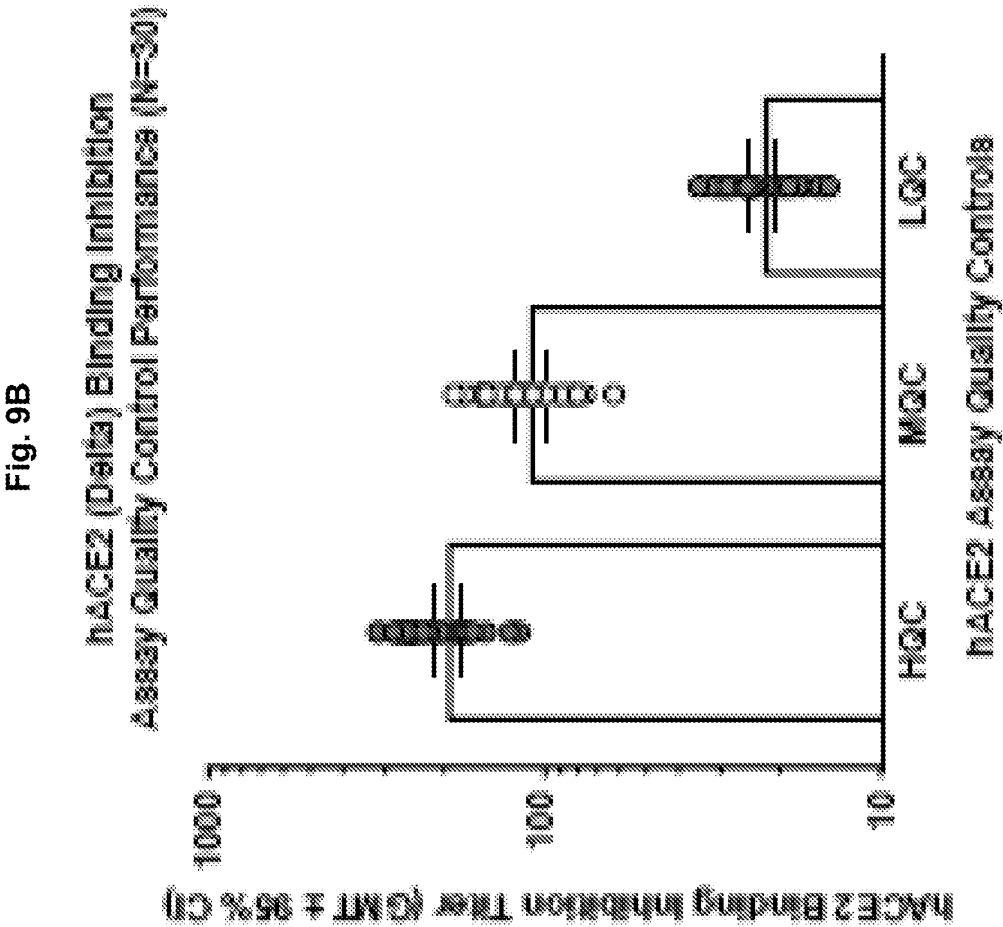
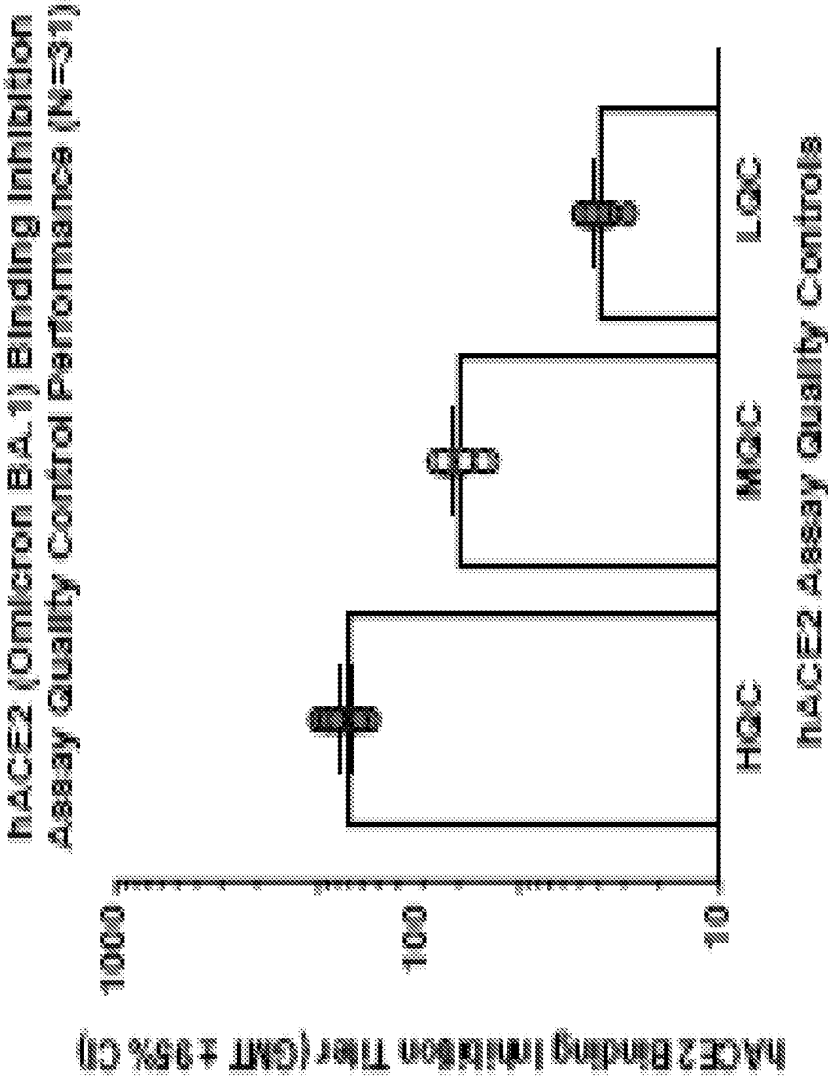


Fig. 9C



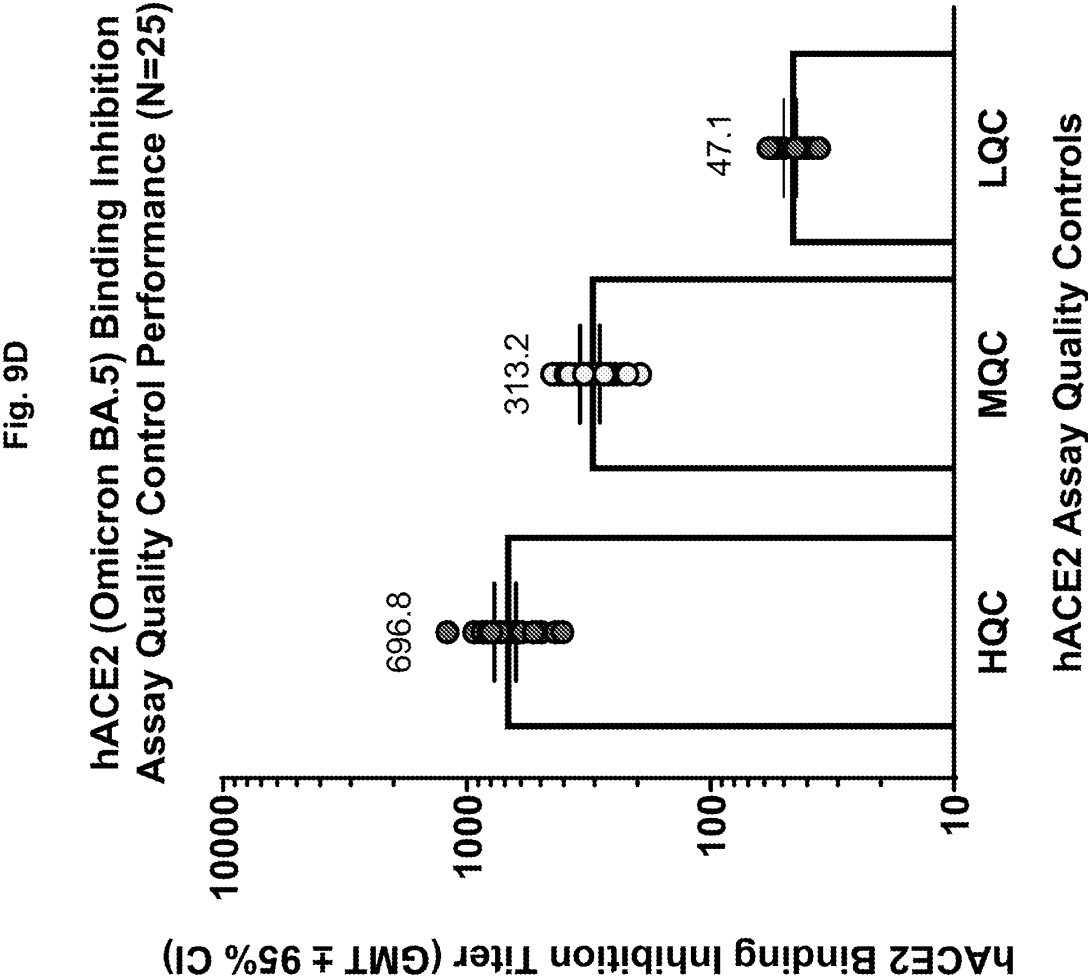


Fig. 10A

**Prototype/Wuhan Strain
IgG vs hACE2 Binding
Inhibition Titers (N=192)**

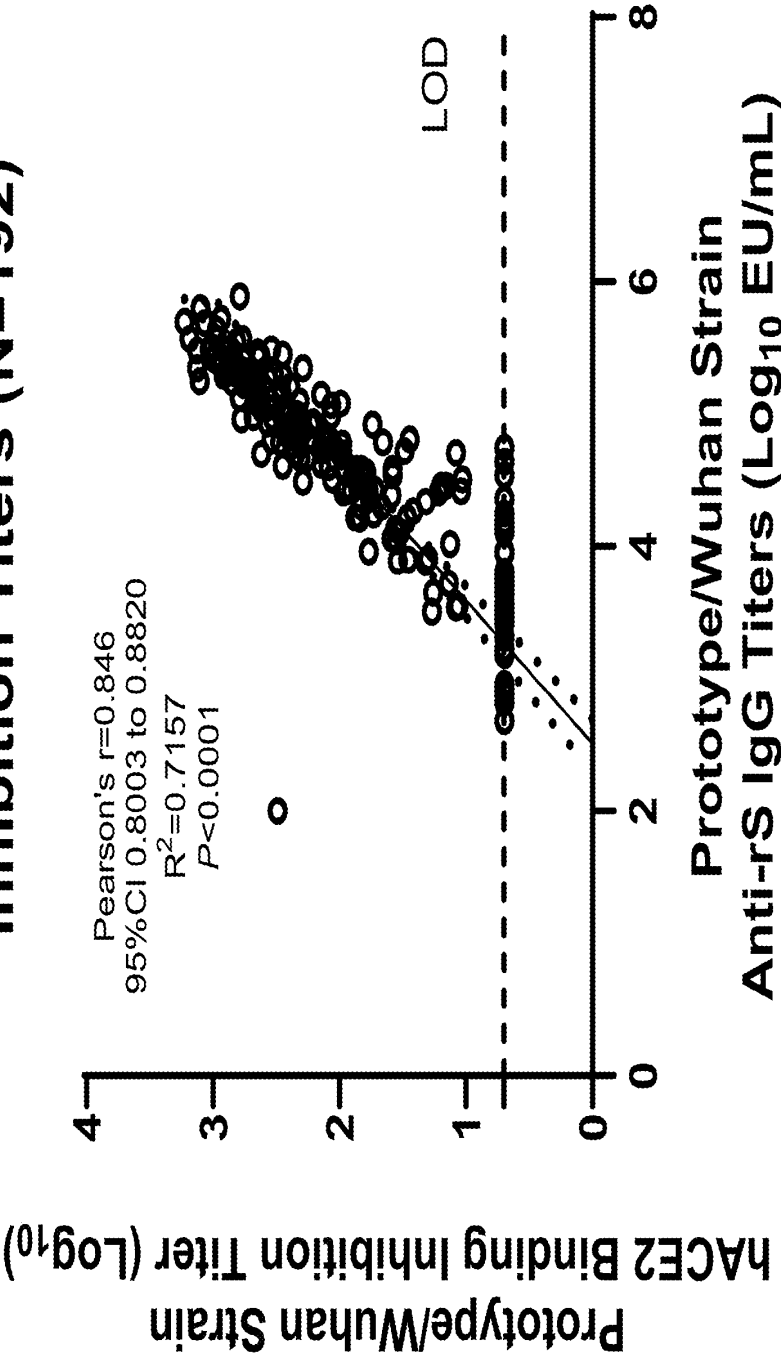


Fig. 10B

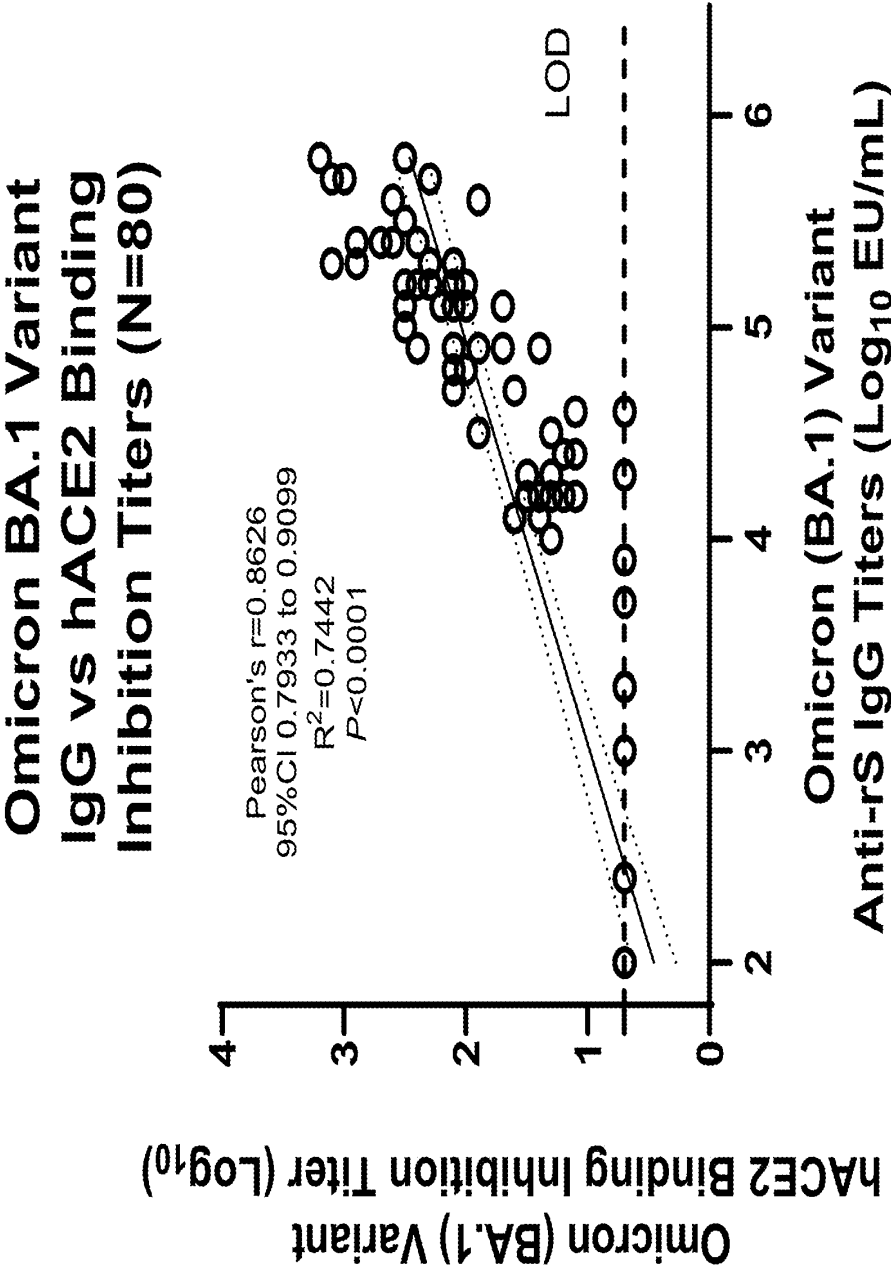


Fig. 10C

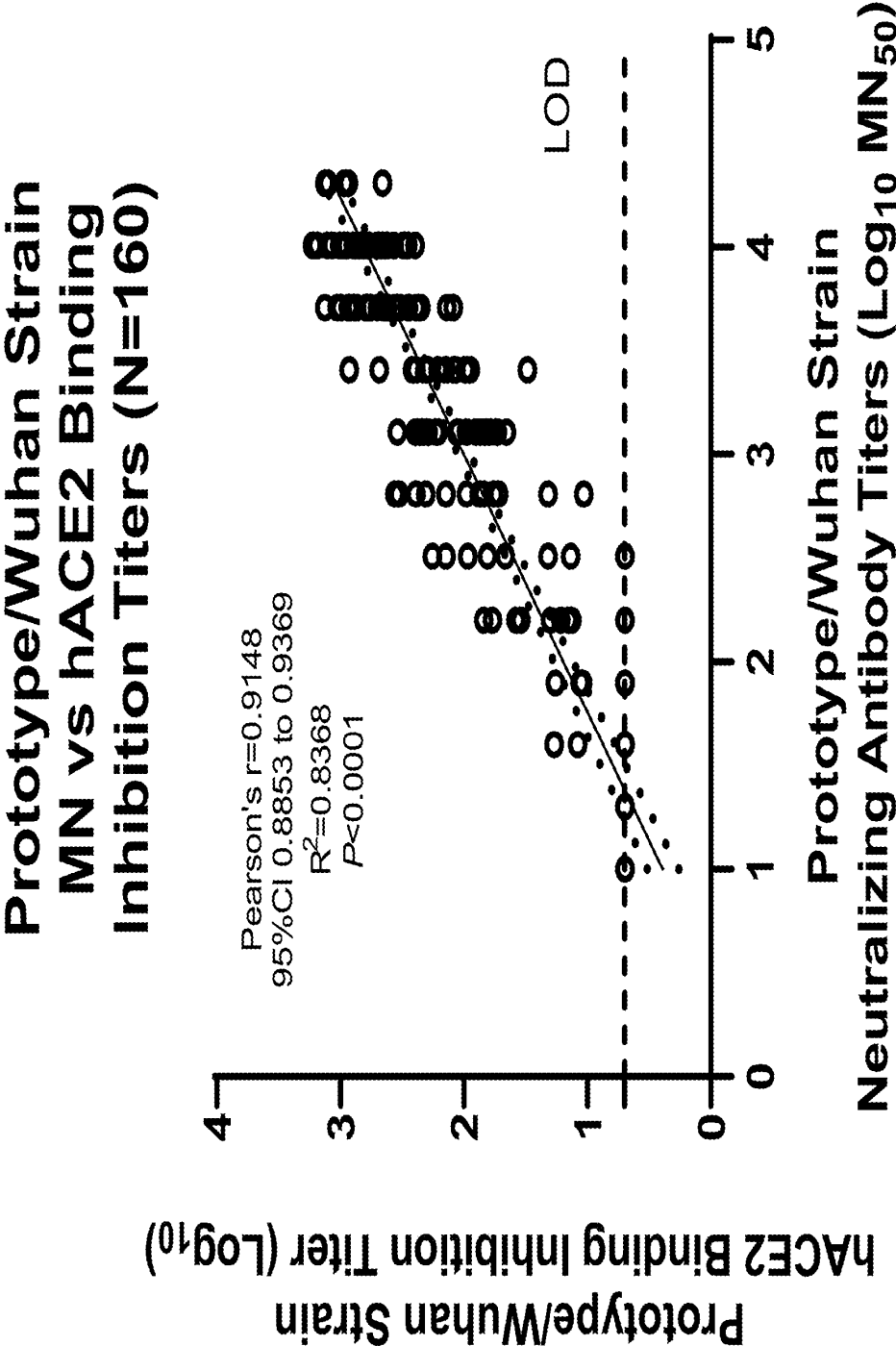


Fig. 10D

**Omicron BA.1 Variant
MN vs hACE2 Binding
Inhibition Titers (N=33)**

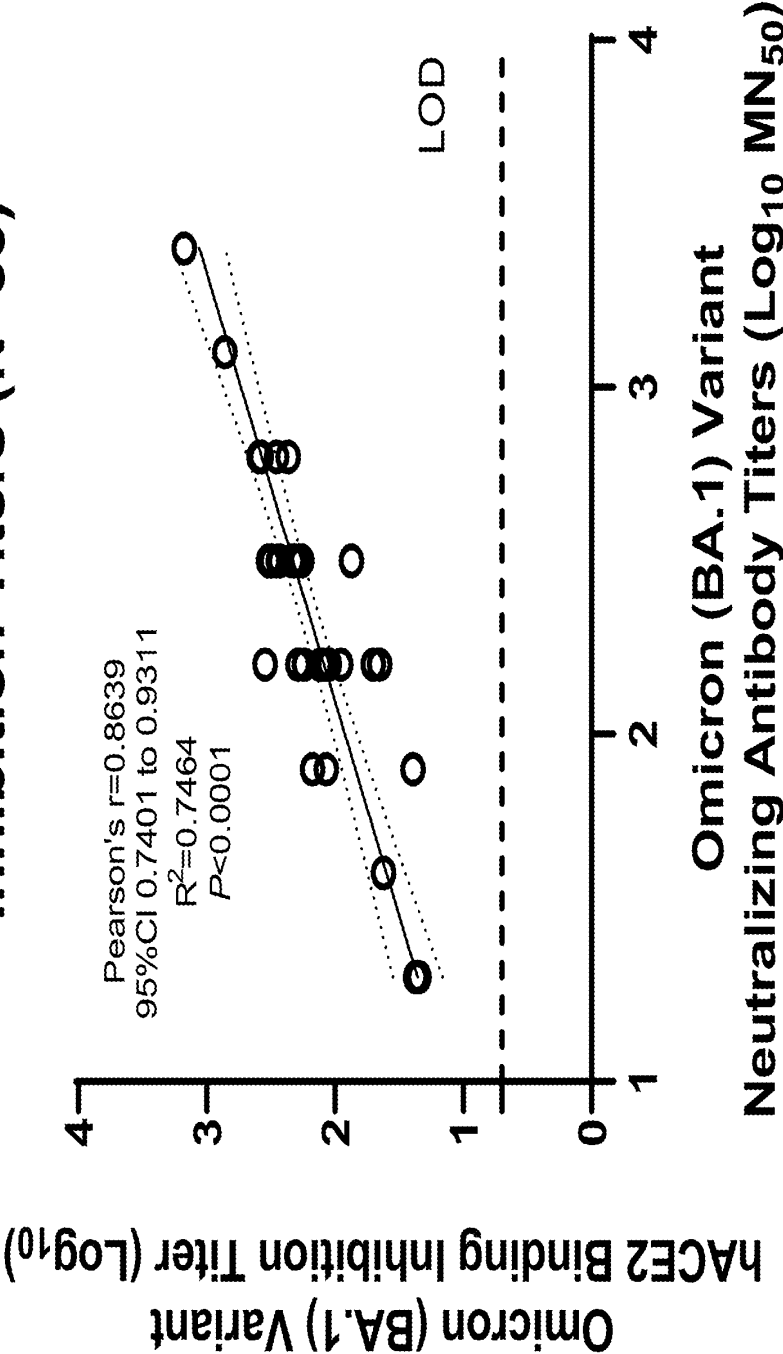


Fig. 10E

**Prototype/Wuhan Strain
IgG vs hACE2 Binding
Inhibition Titers (N=157)**

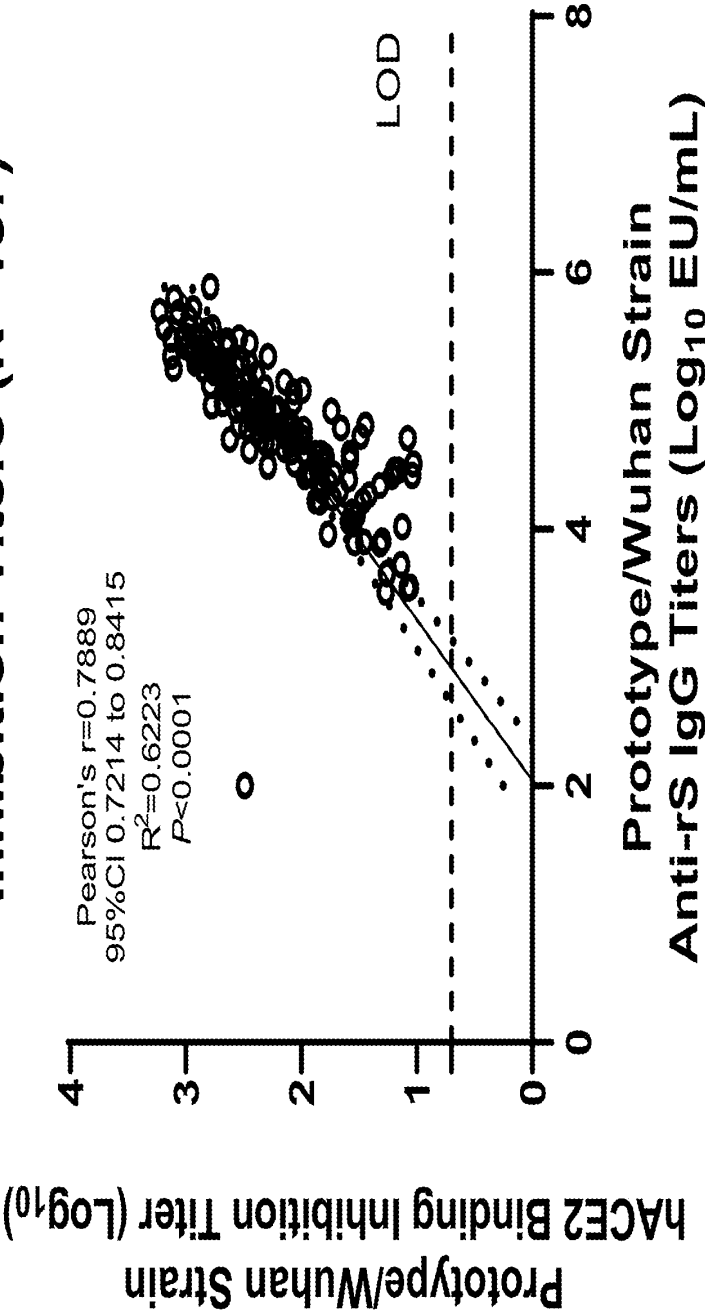


Fig. 10F

**Omicron BA.1 Variant
IgG vs hACE2 Binding
Inhibition Titers (N=56)**

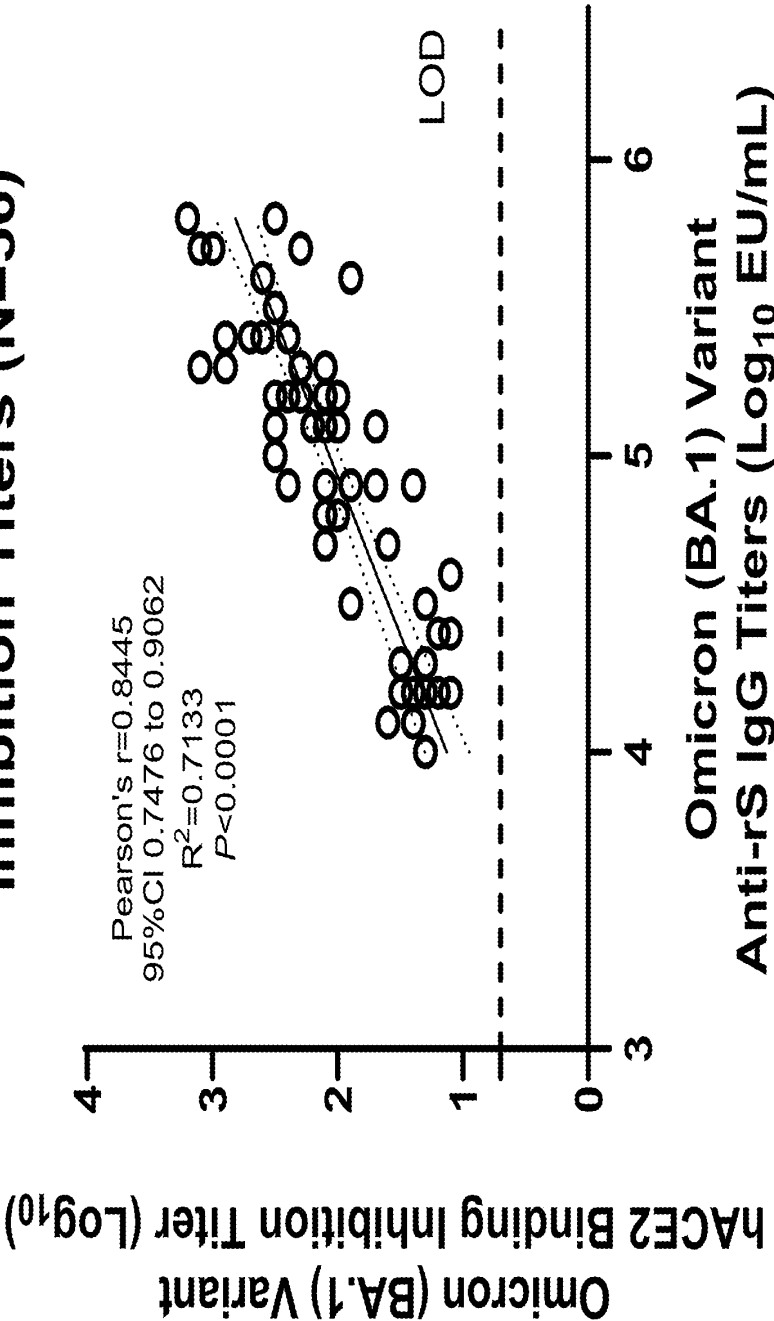


Fig. 10G

**Omicron BA.5 Variant
IgG vs hACE2 Binding
Inhibition Titers (N=17)**

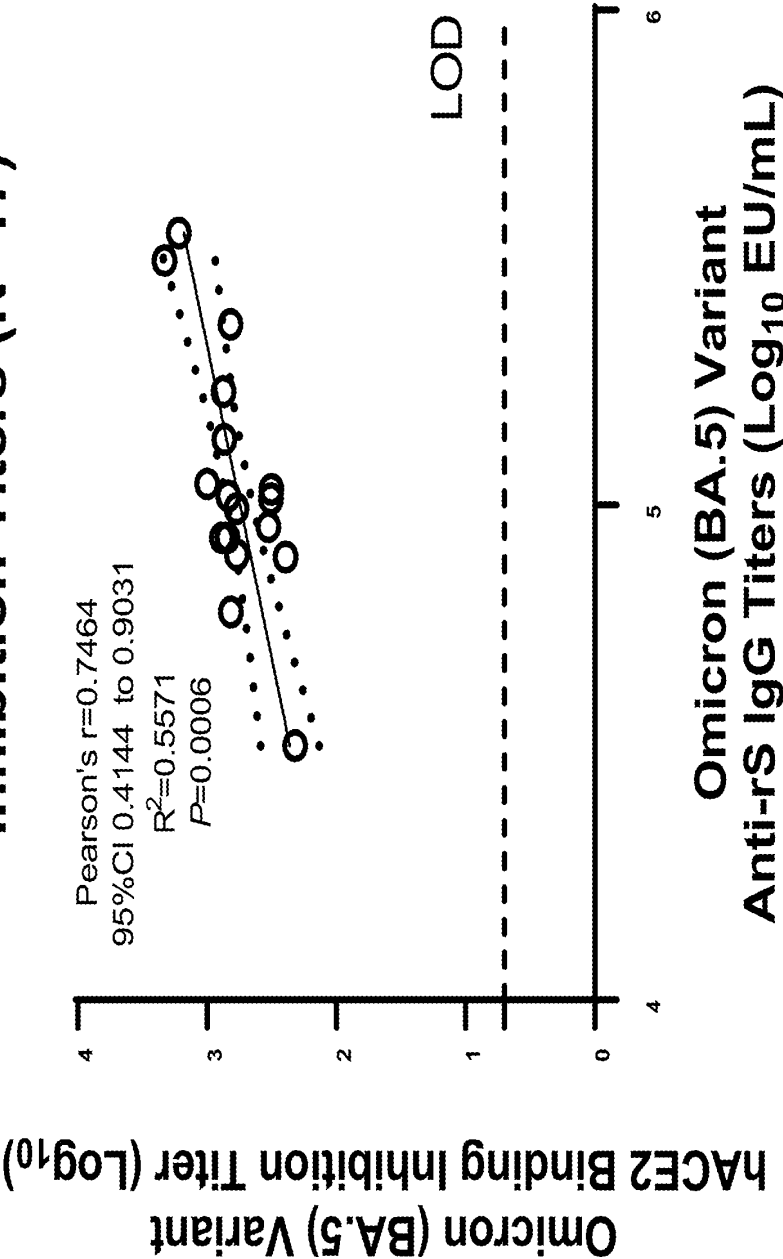


Fig. 10H

