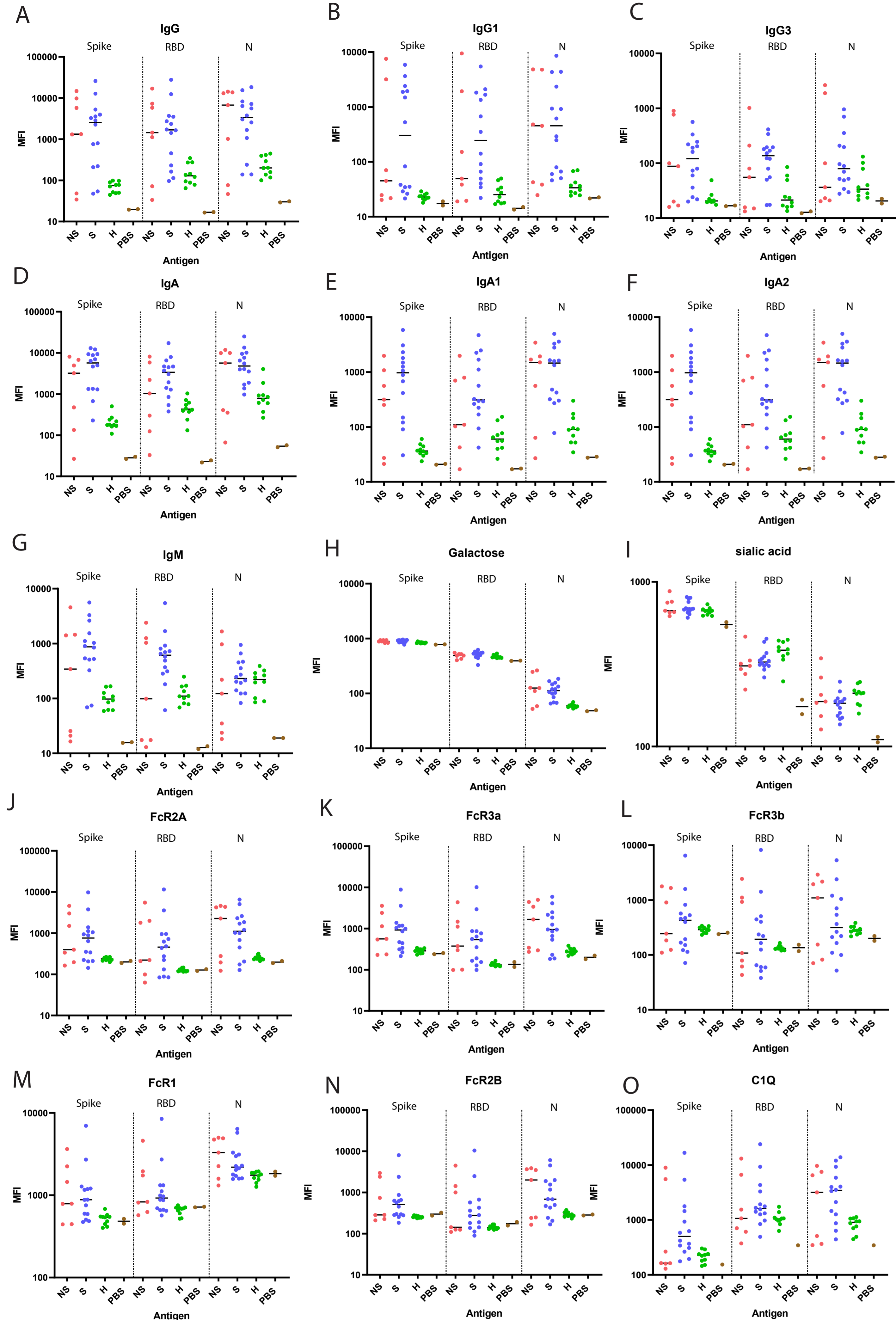


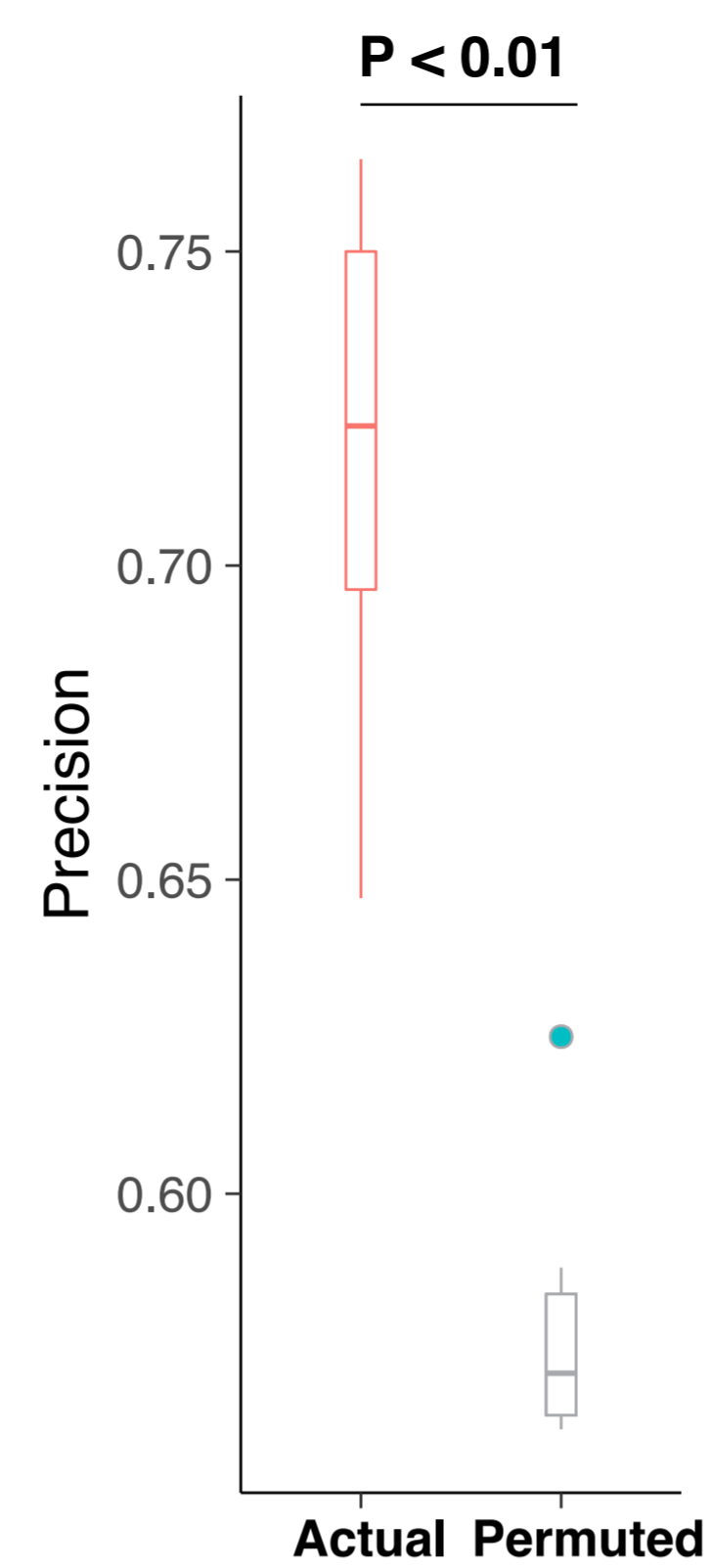
Supplemental information

**Antibodies targeting conserved non-canonical
antigens and endemic coronaviruses associate
with favorable outcomes in severe COVID-19**

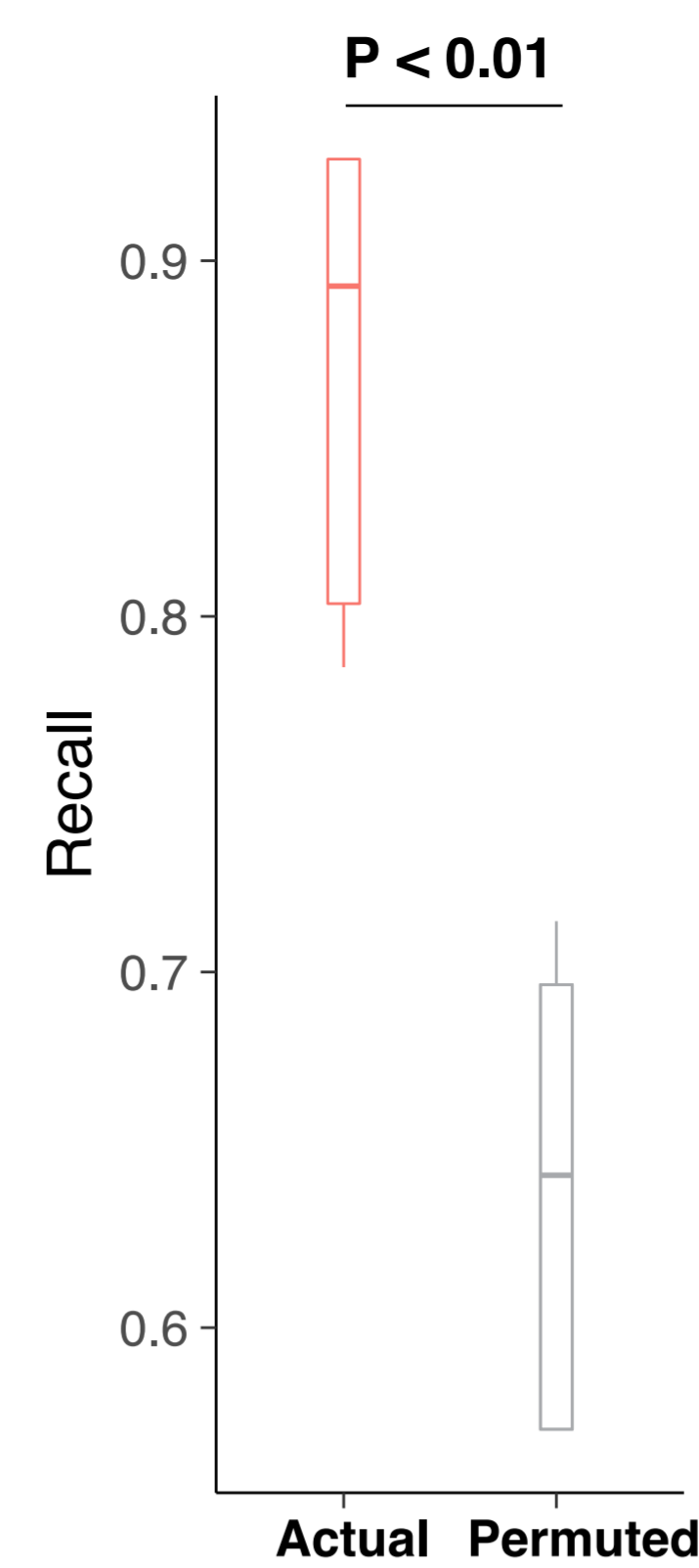
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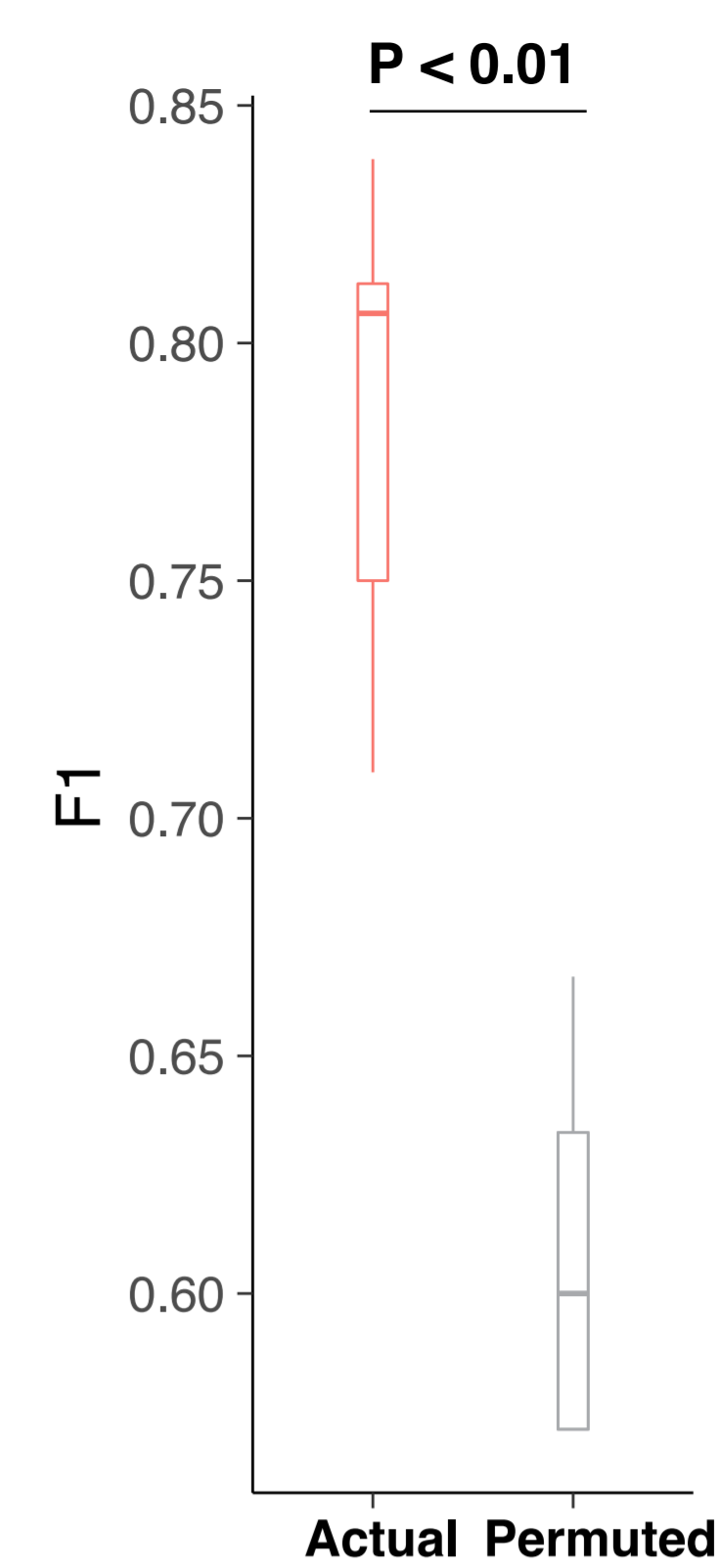
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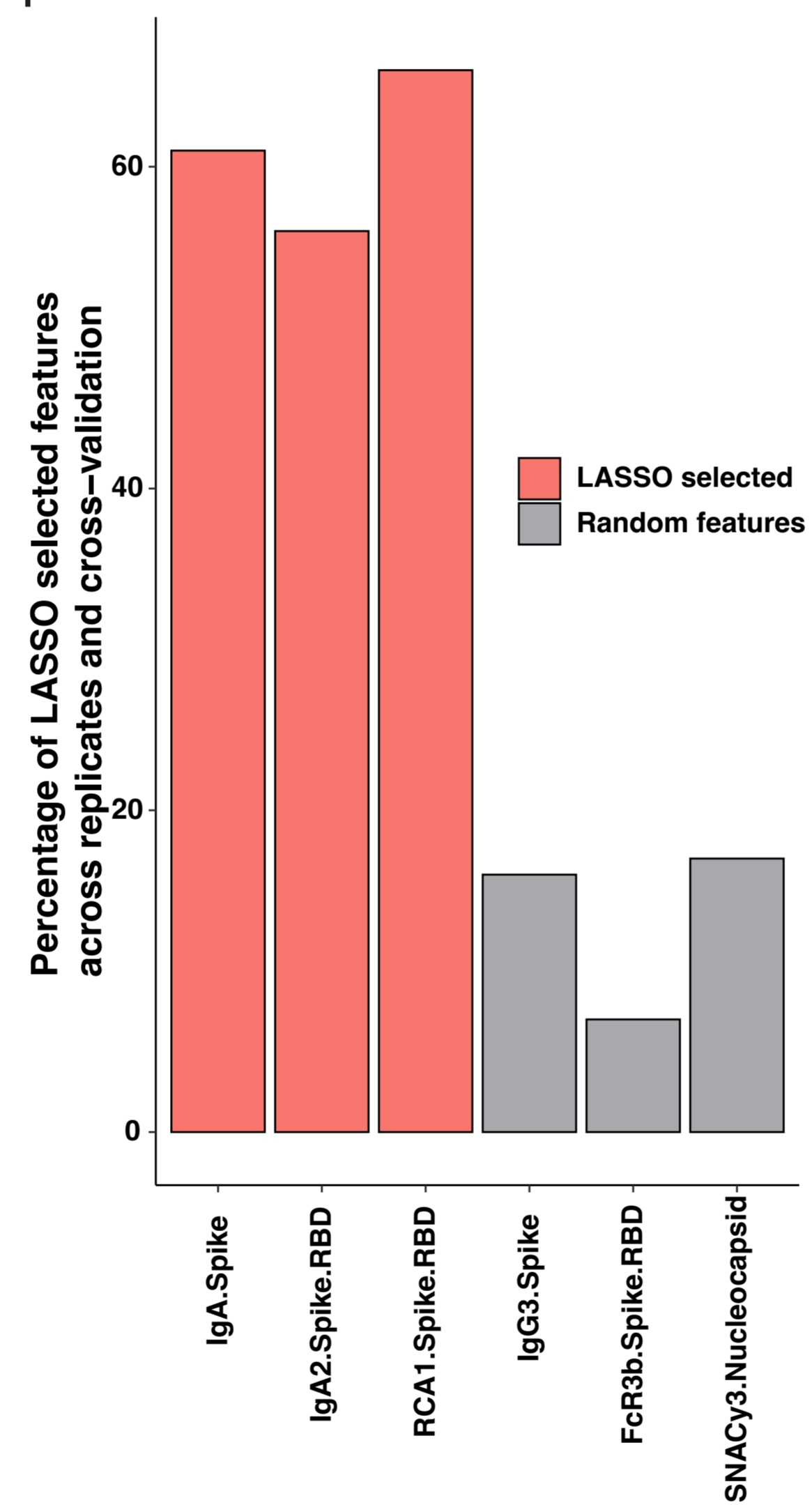
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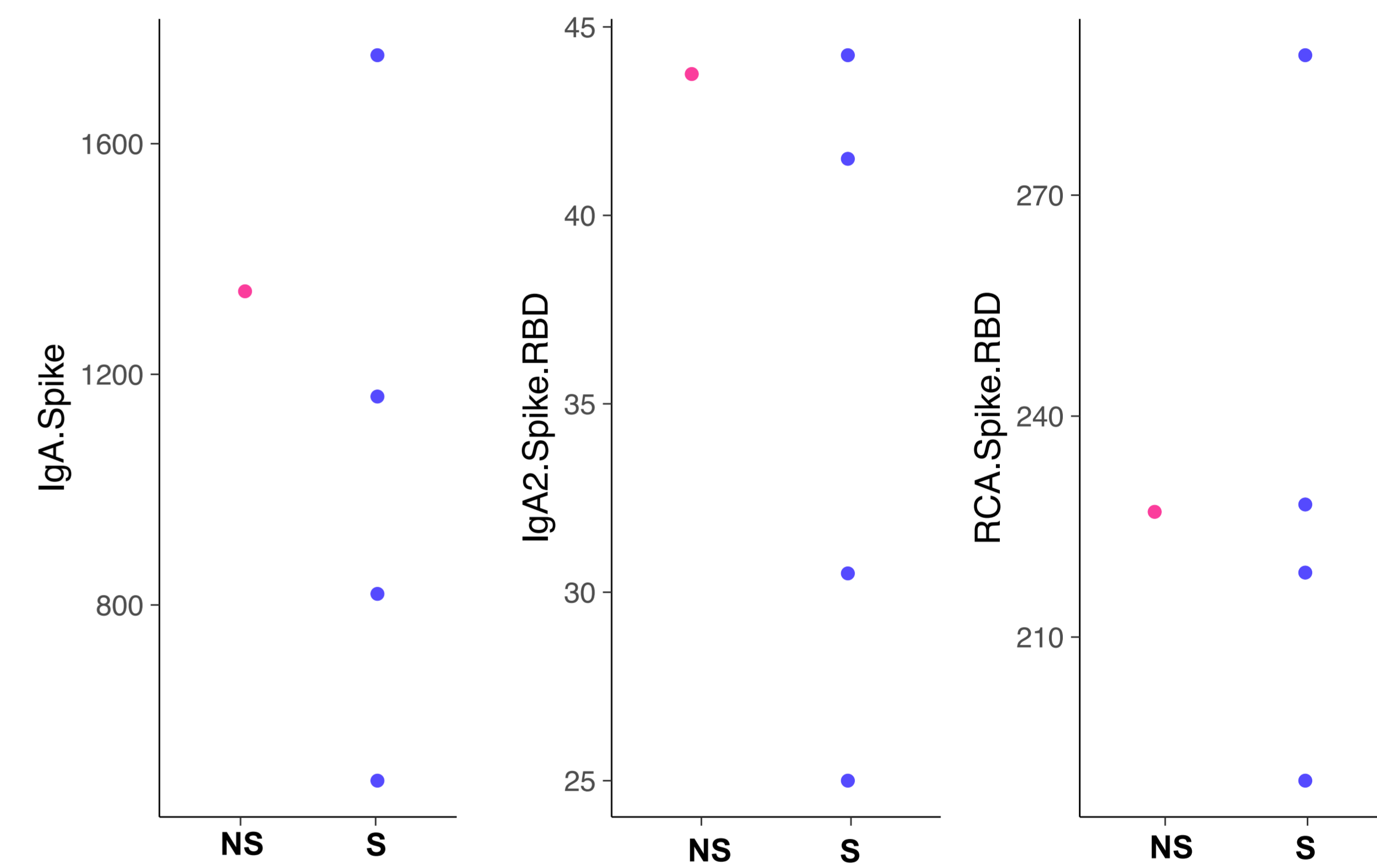
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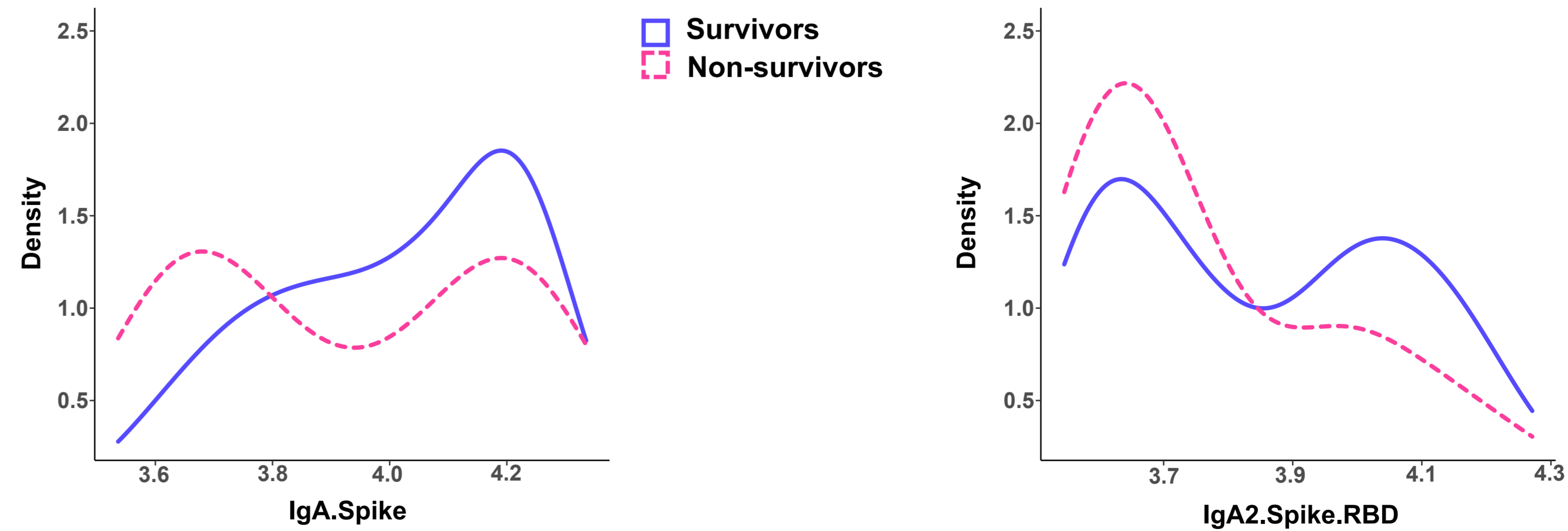
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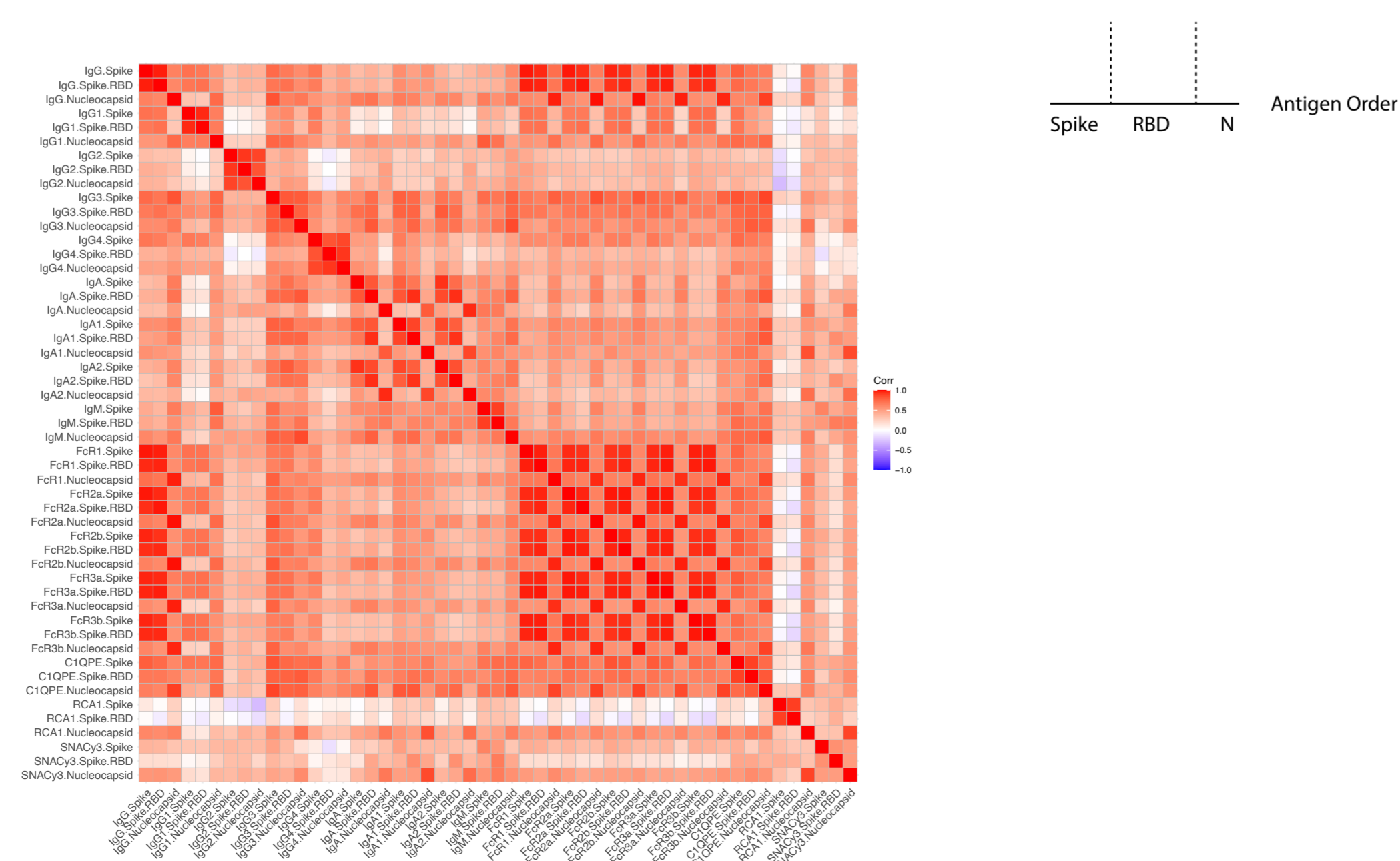
U



V



P



Supplementary Figure 1 – Related to Figure 1.

A-O. Dot plots showing deep humoral profiles against canonical (S/RBD/N) Ag specificities for survivors, non-survivors, and healthy controls (A-IgG, B-IgG1, C-IgG3, D-IgA, E-IgA1, F-IgA2, G-IgM, H-Galactose, I-Sialic acid, J-FcR2a, K-FcR3a, L-FcR3b, M-FcR1, N-FcR2b, O-C1Q).

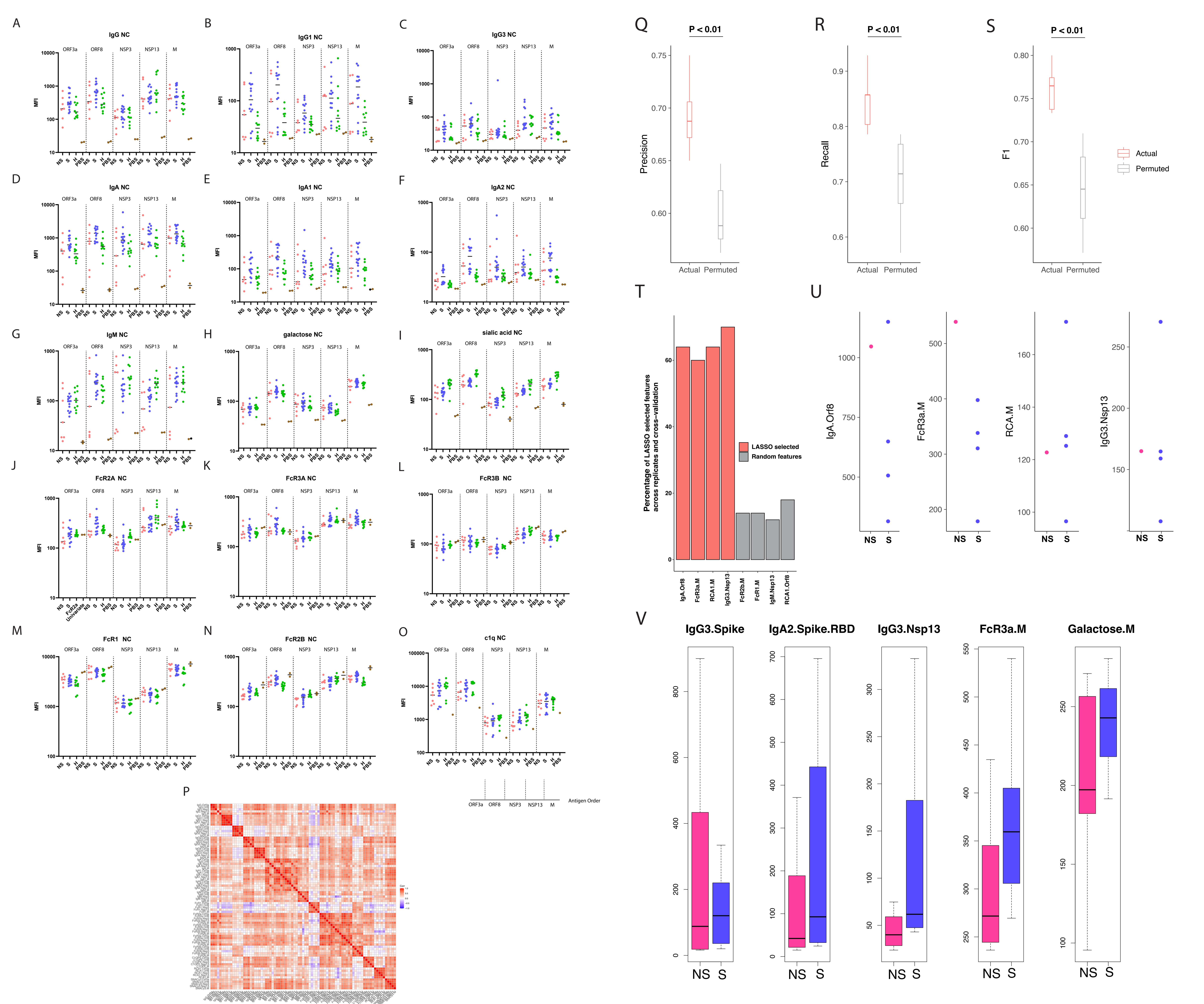
P. Correlation heatmap showing all corresponding pairwise feature correlations (Spearman) across non-survivors and survivors.

Q-S. Performance of LASSO model (precision, recall, F1 score respectively) to discriminate between survivors and non-survivors built using deep humoral profiles against canonical Ag specificities. Model performance is measured in a k-fold cross-validation framework with permutation testing. Actual denotes the performance of the model, built on real data. Permuted denotes performance of the model on shuffled data in a matched cross-validation framework (negative control).

T. Frequency of the 3 LASSO-selected featured and 3 random features across folds and replicates of k-fold cross-validation.

U. Dot-plots showing distributions of the 3 LASSO-selected features in 5 non-COVID-19 ARDS subjects (1 non-survivor, 4 survivors).

V. IgA.Spike and IgA2.Spike.RBD in survivors and non-survivors



Supplementary Figure 2 – Related to Figure 2.

A-O. Dot plots showing deep humoral profiles against non-canonical (orf3a/orf8/nsp3/nsp13/M) Ag specificities for survivors, non-survivors, and healthy controls (A-IgG, B-IgG1, C-IgG3, D-IgA, E-IgA1, F-IgA2, G-IgM, H-Galactose, I-Sialic acid, J-FcR2a, K-FcR3a, L-FcR3b, M-FcR1, N-FcR2b, O-C1Q).

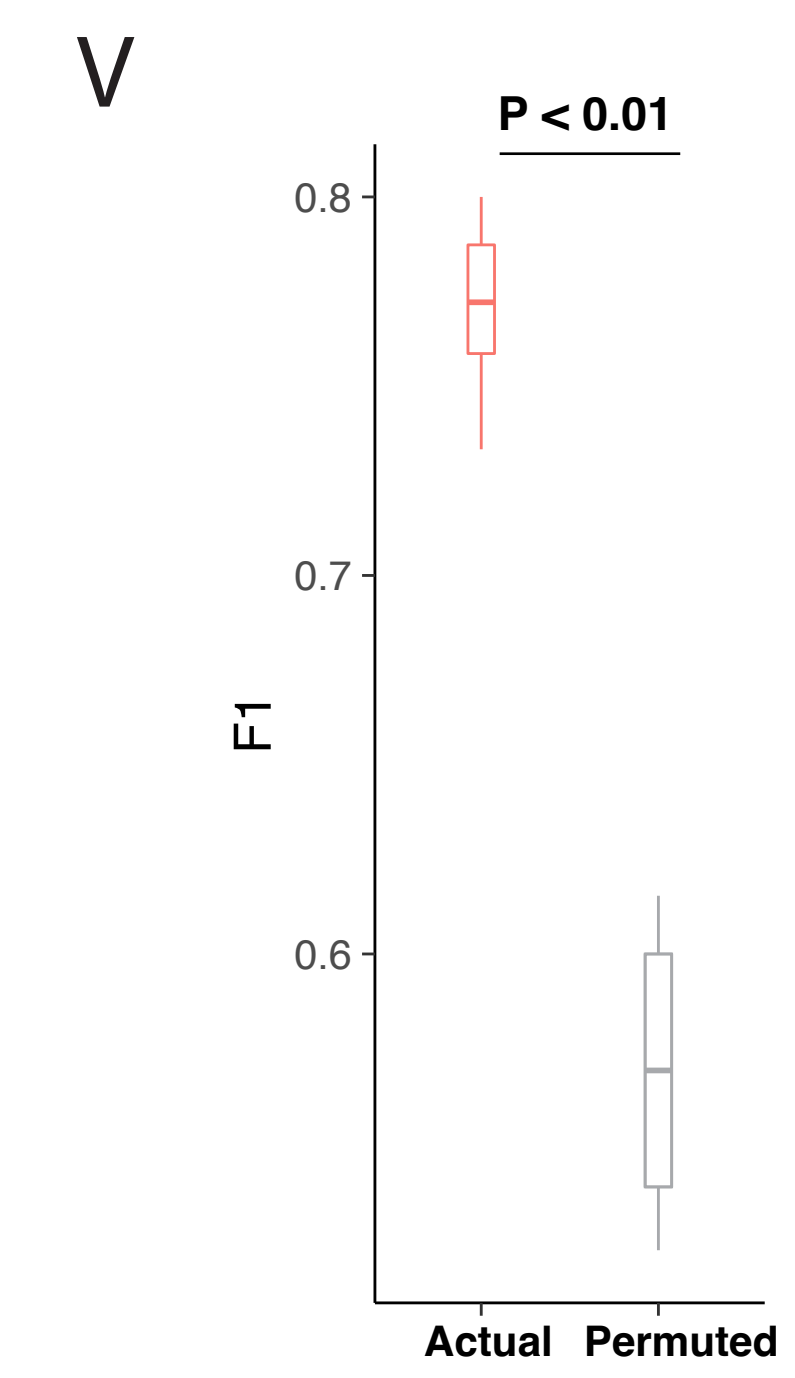
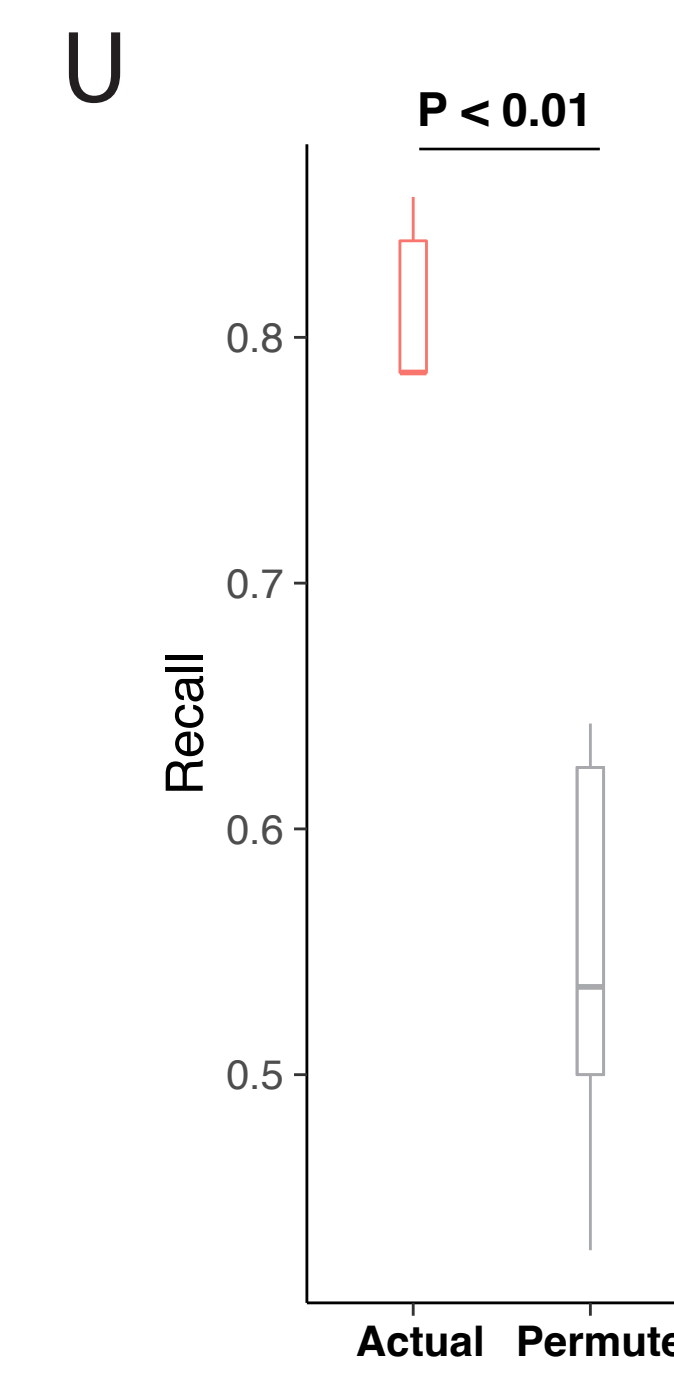
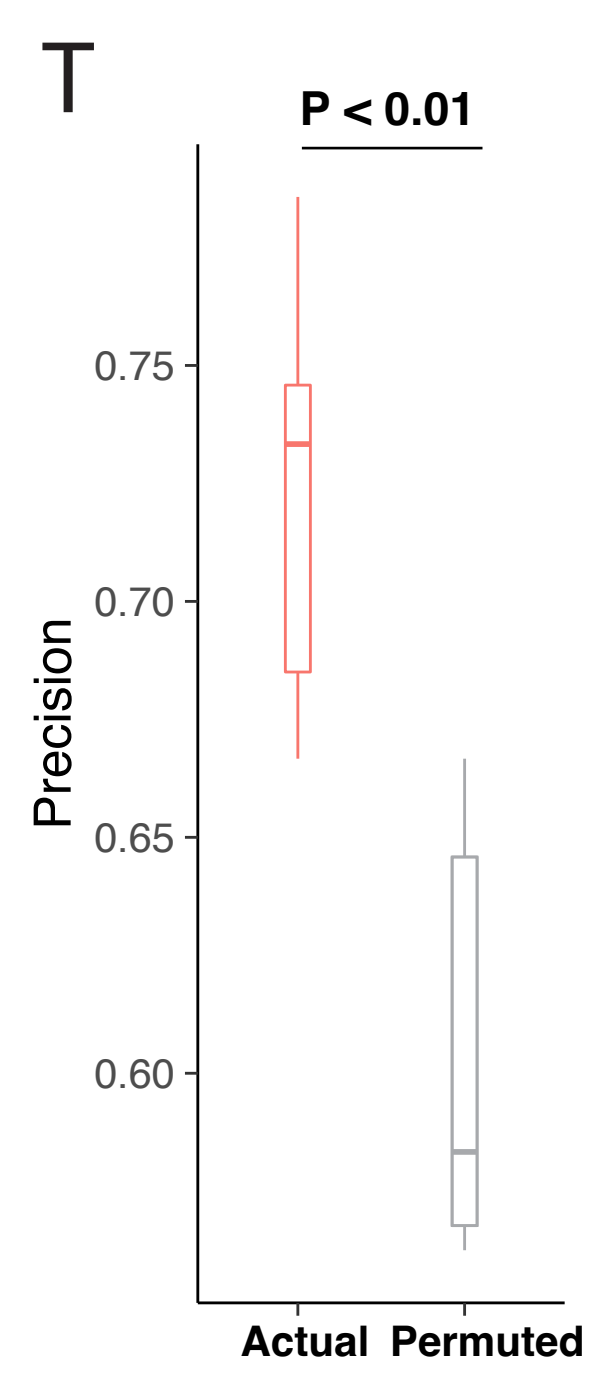
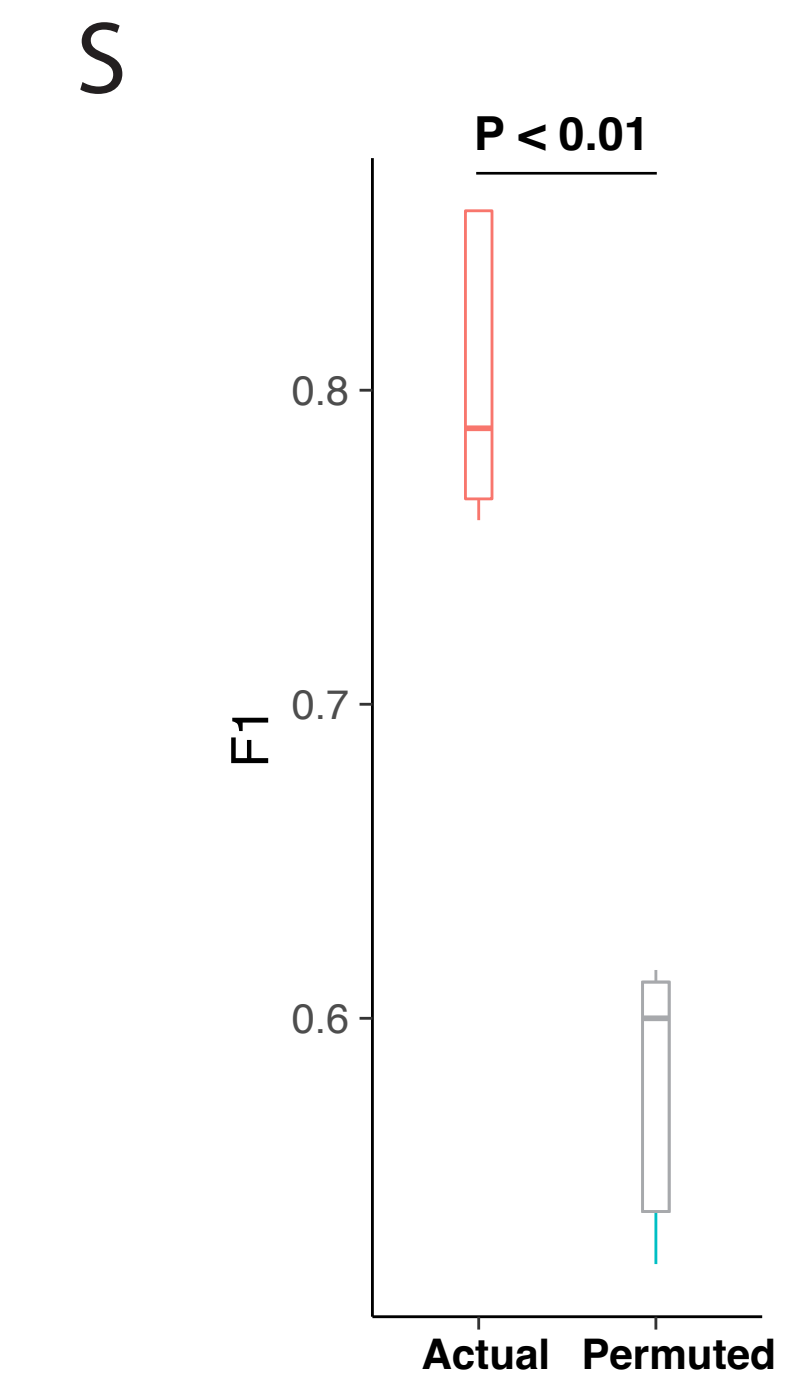
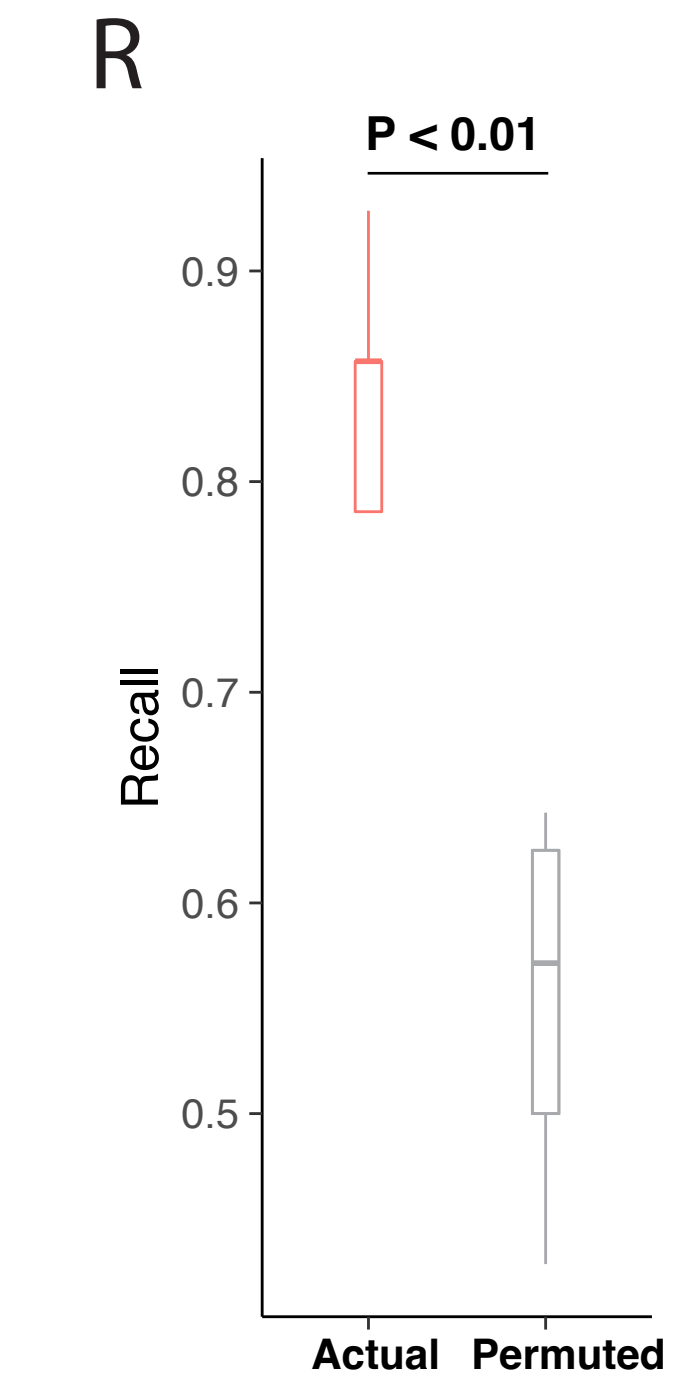
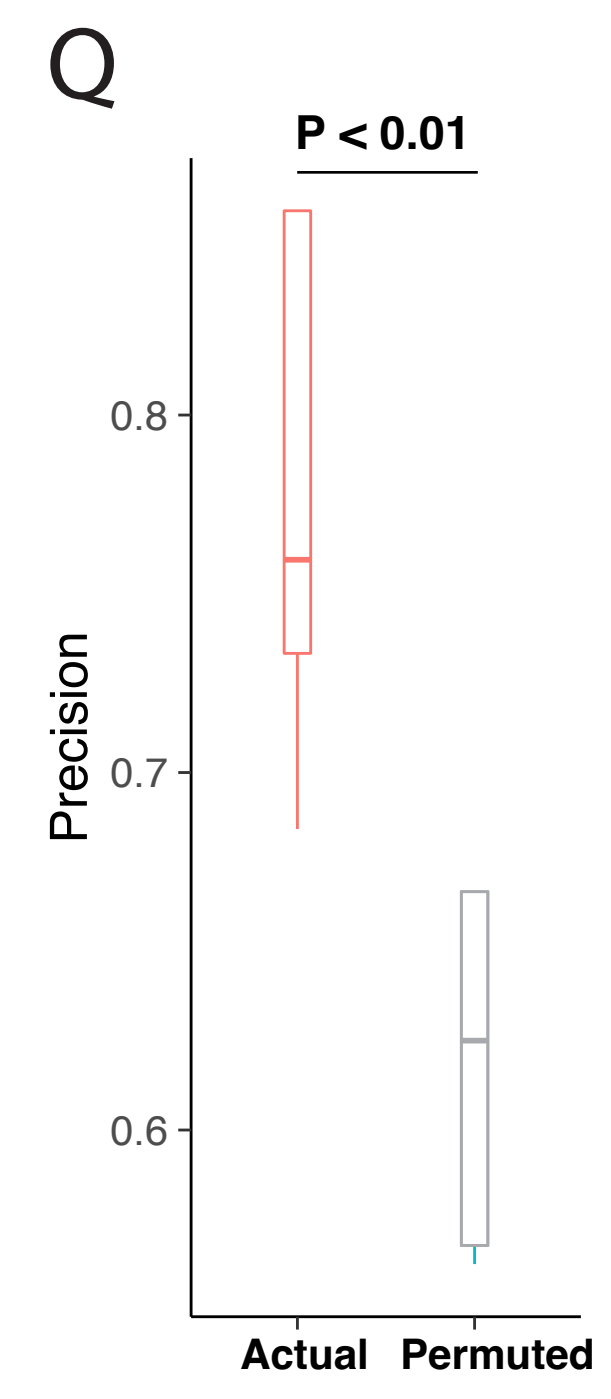
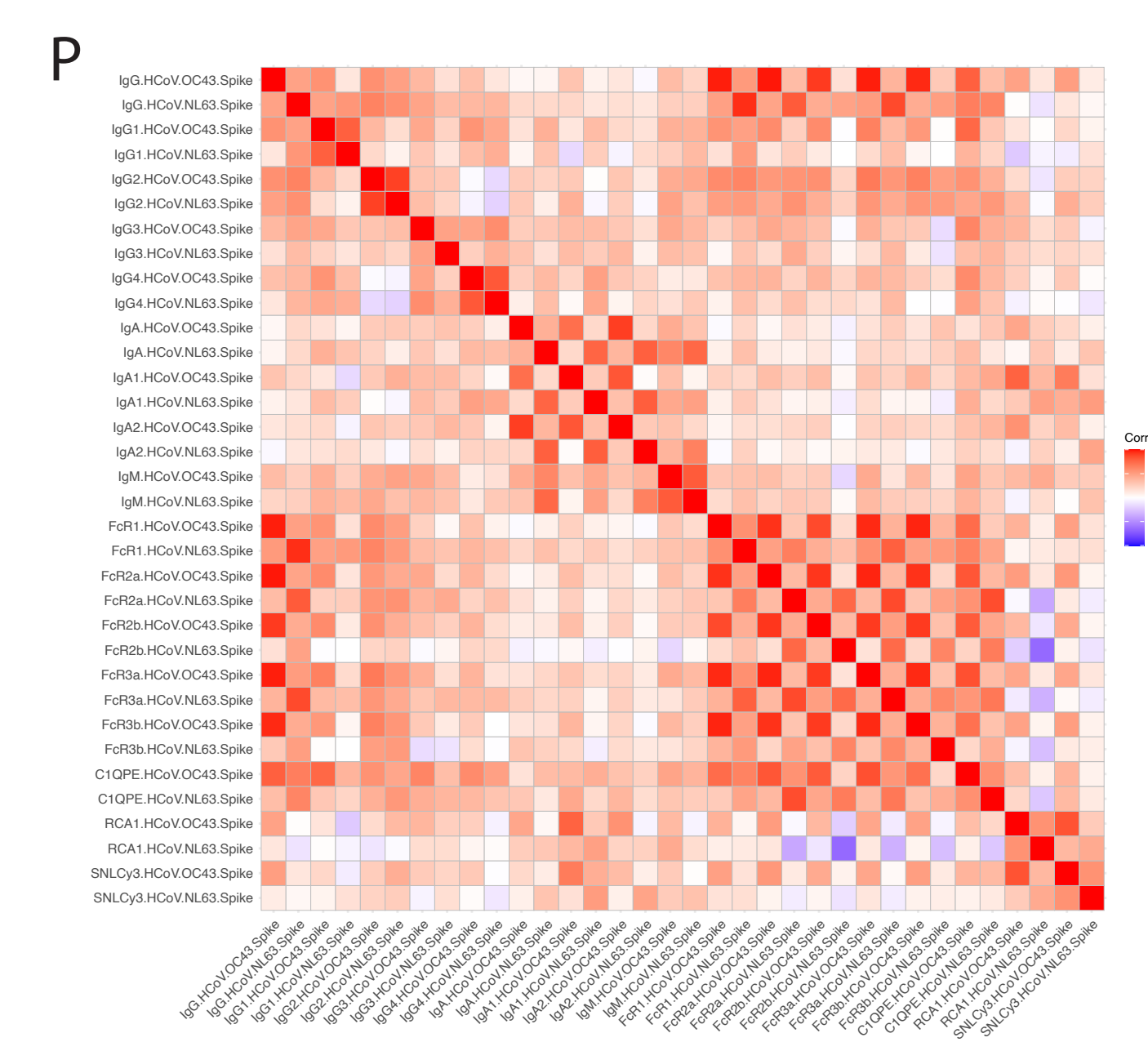
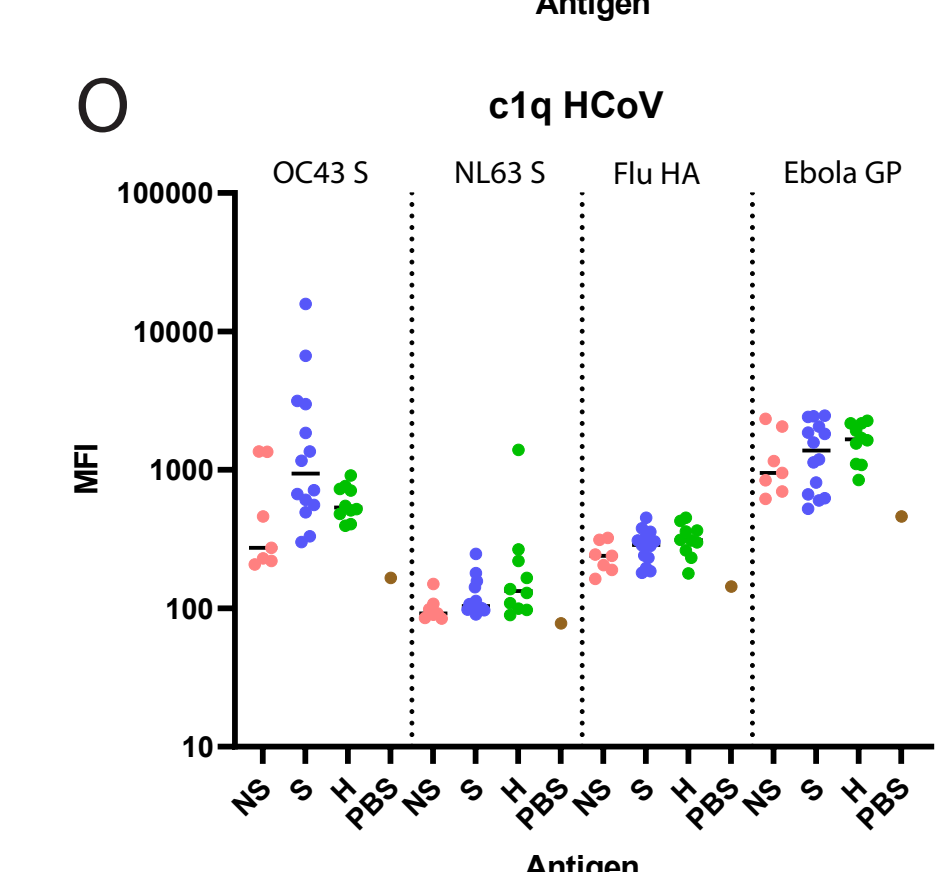
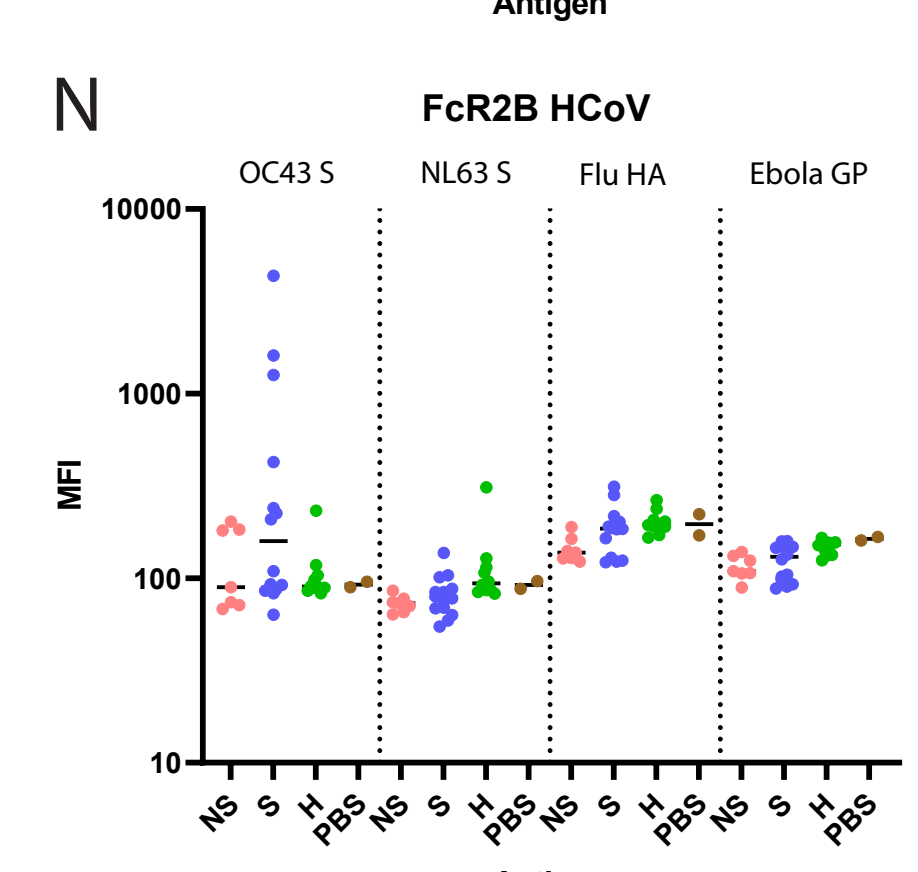
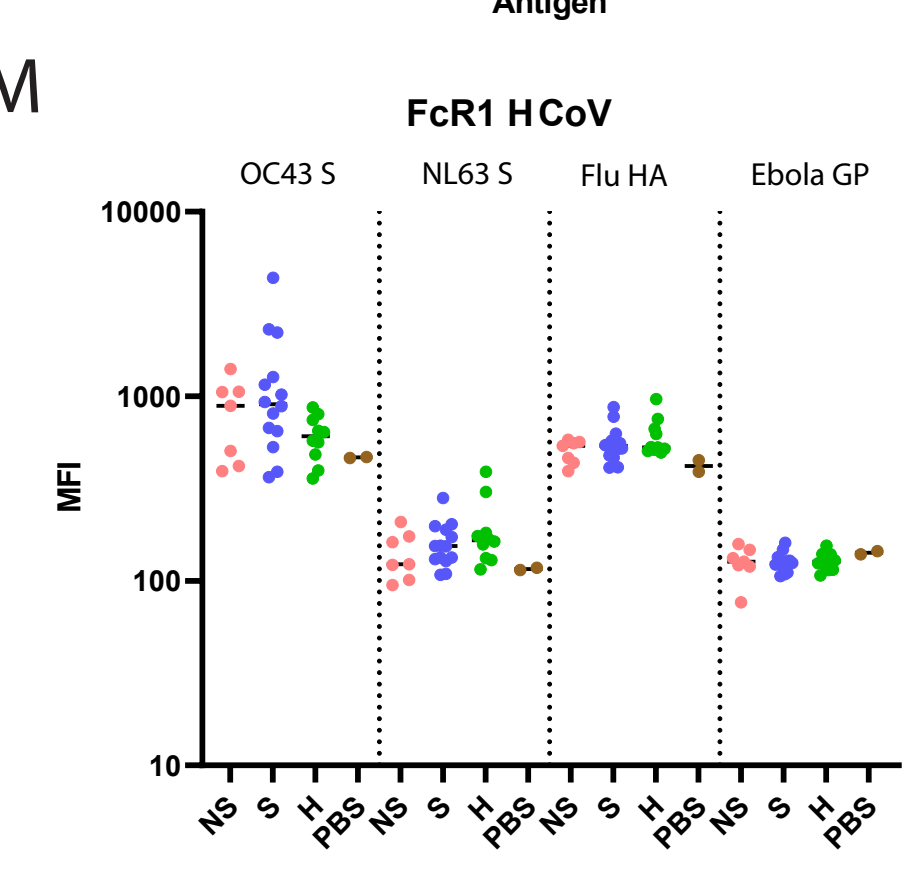
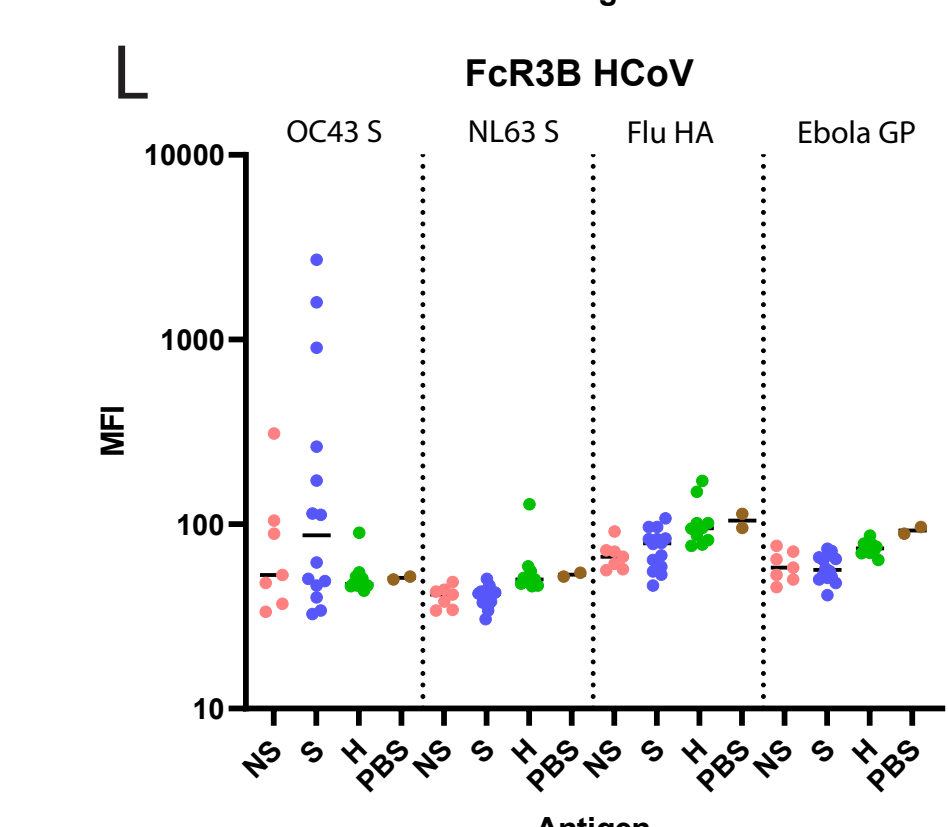
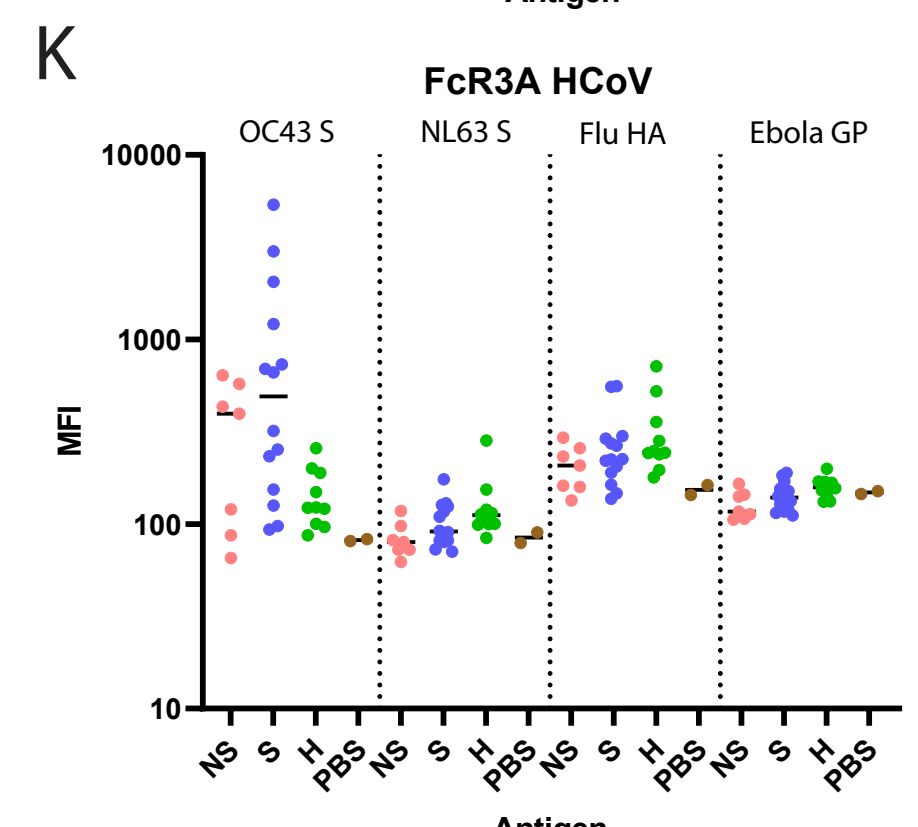
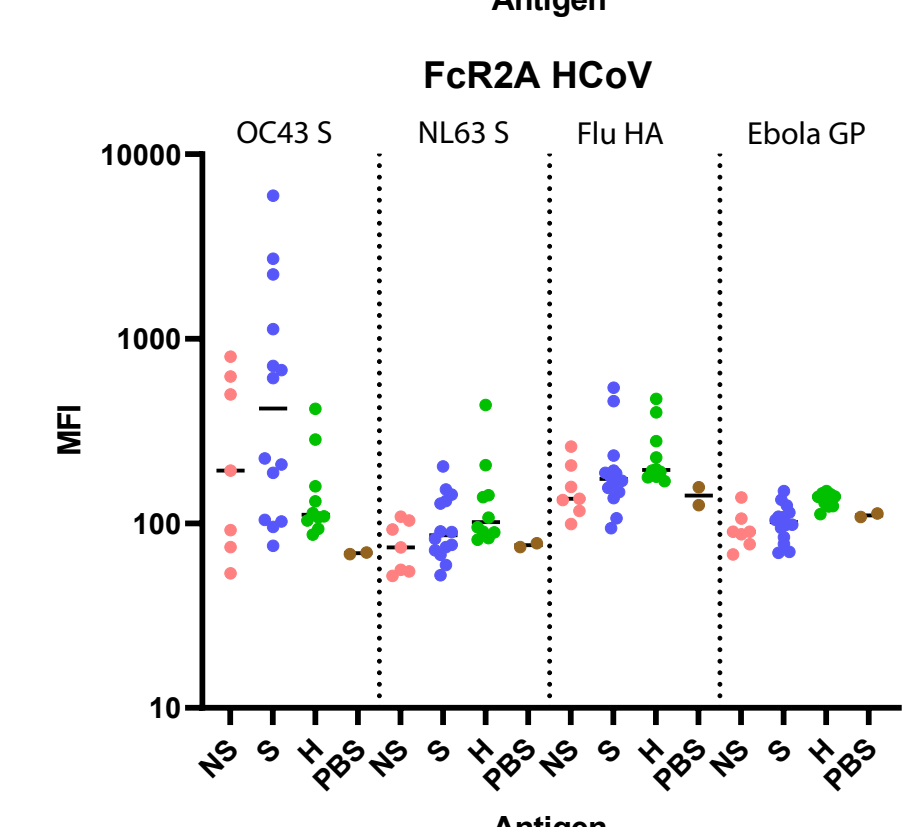
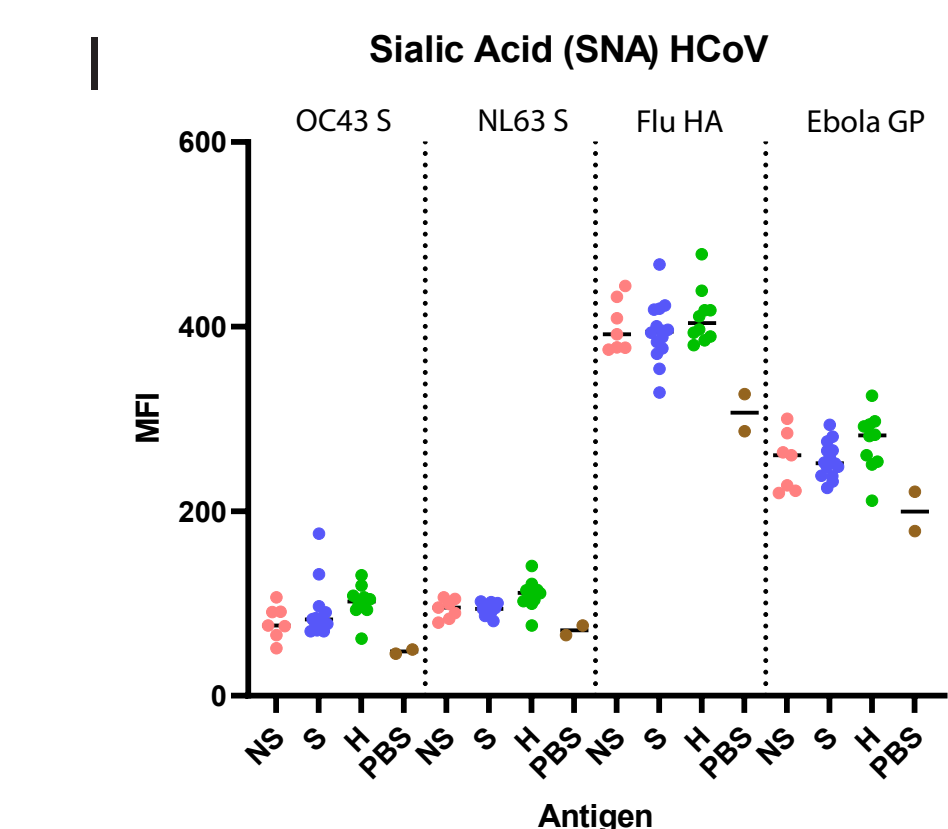
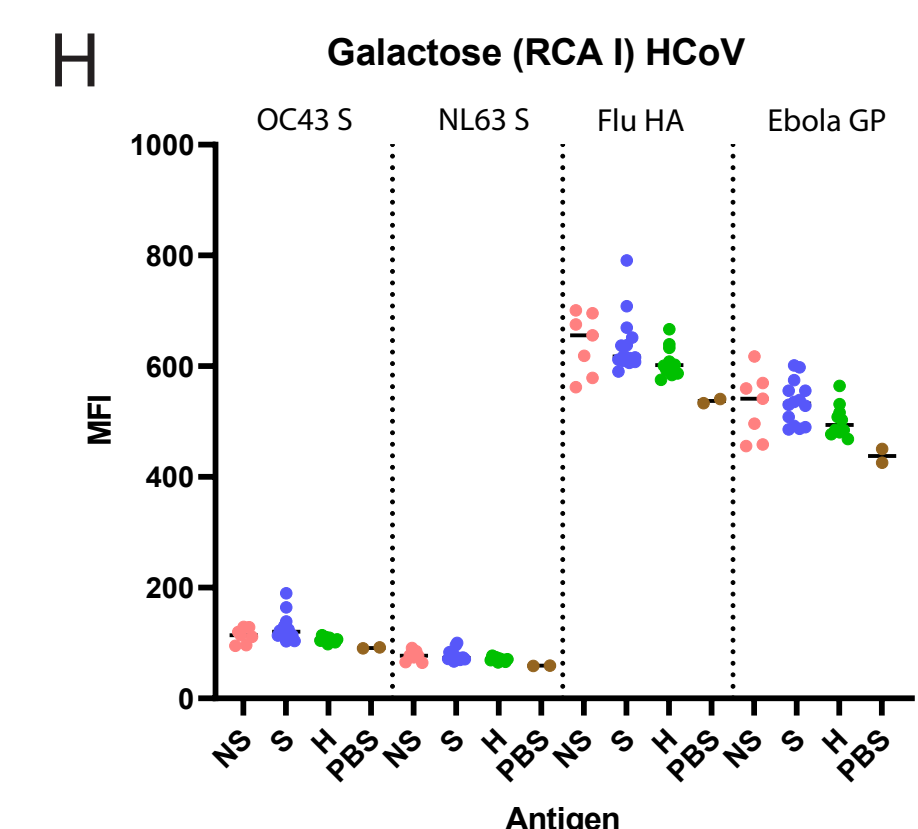
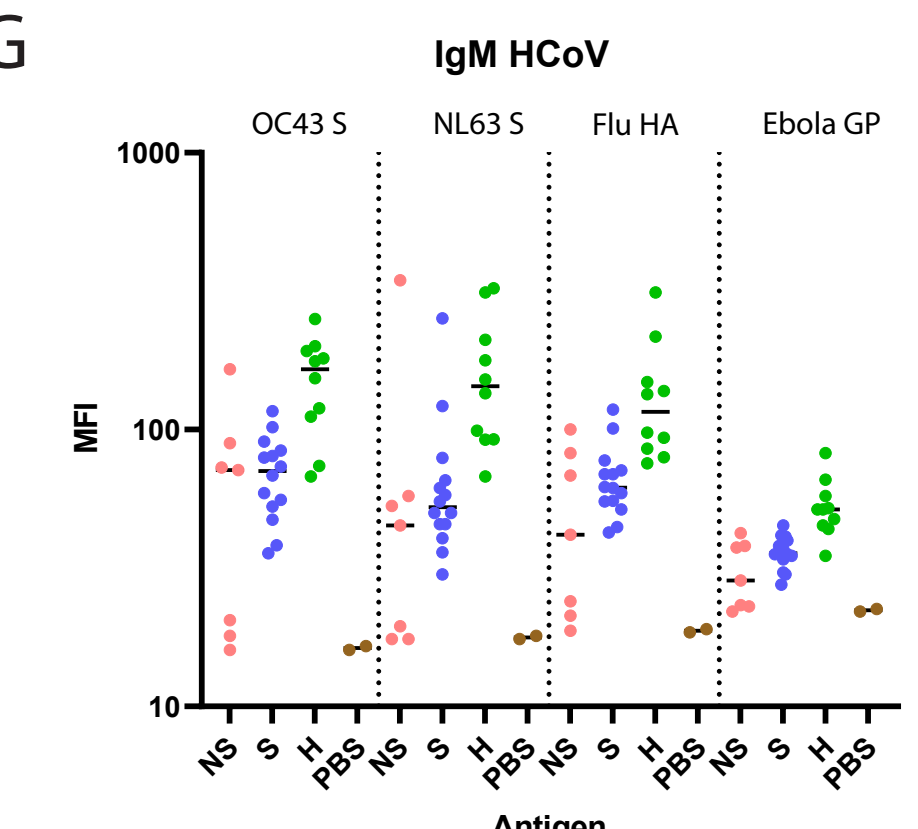
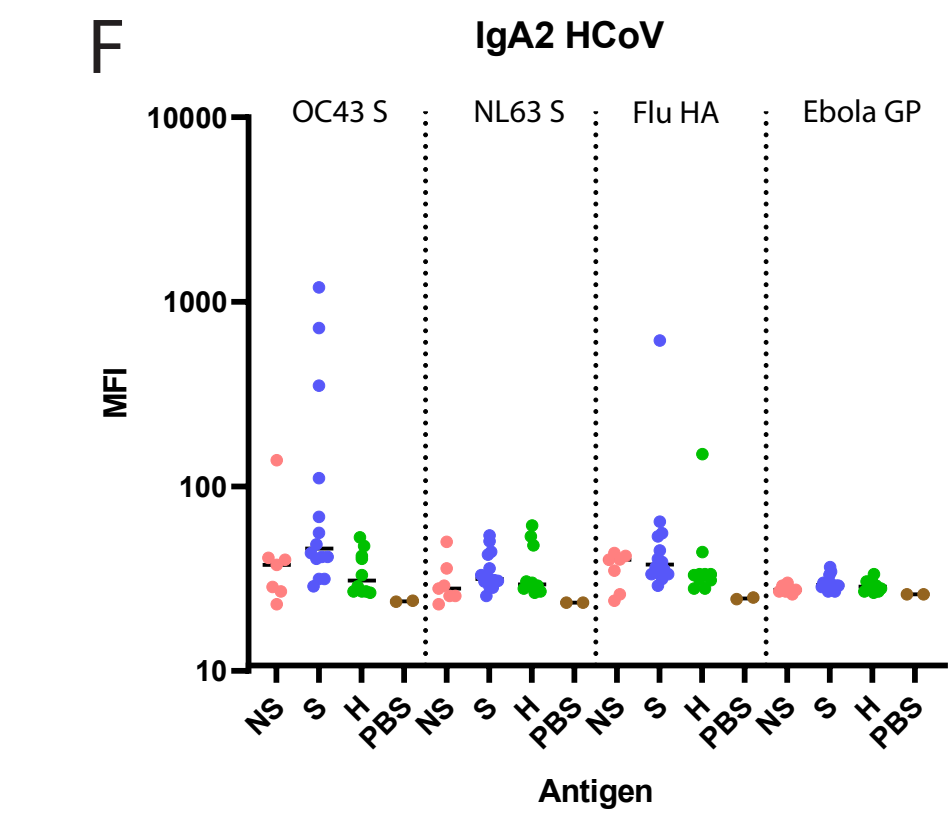
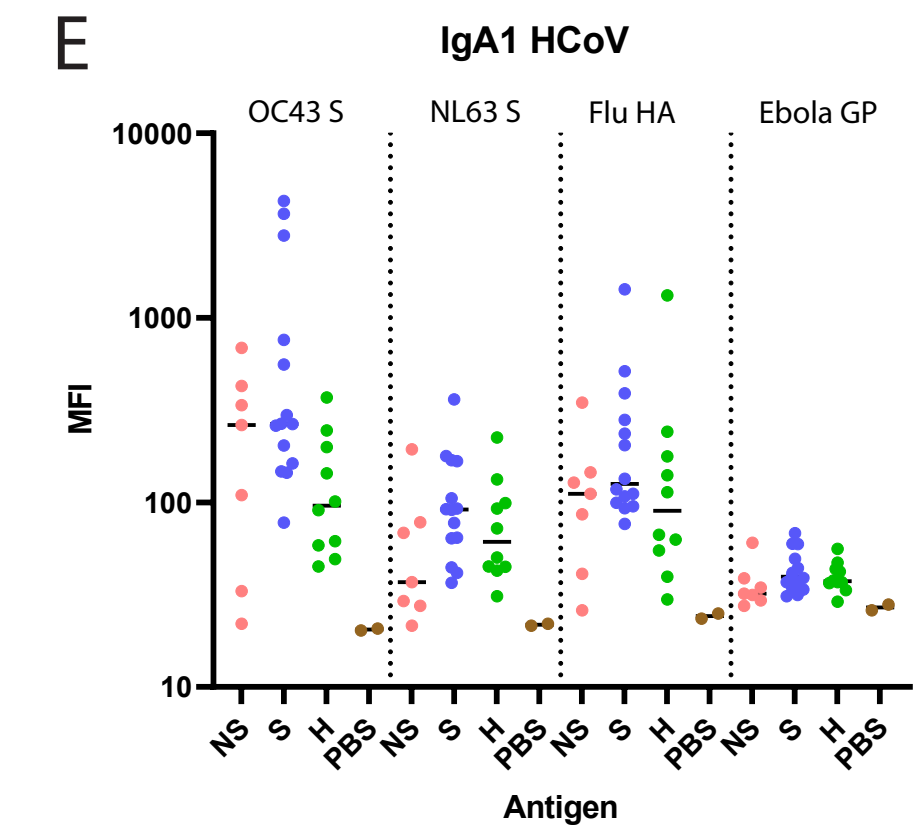
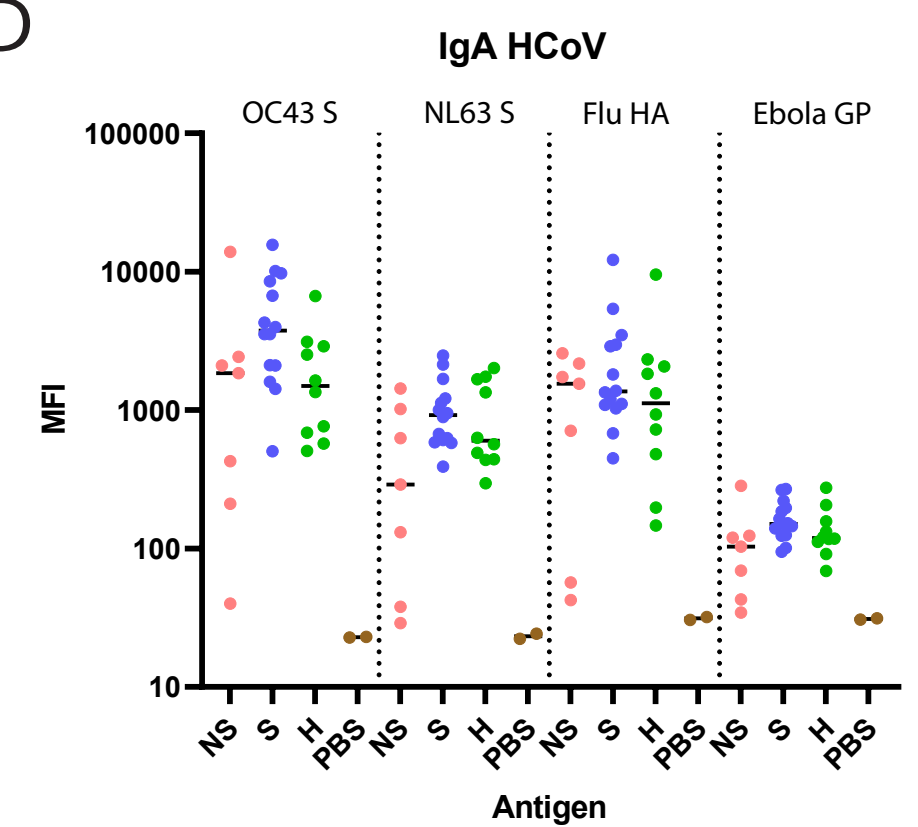
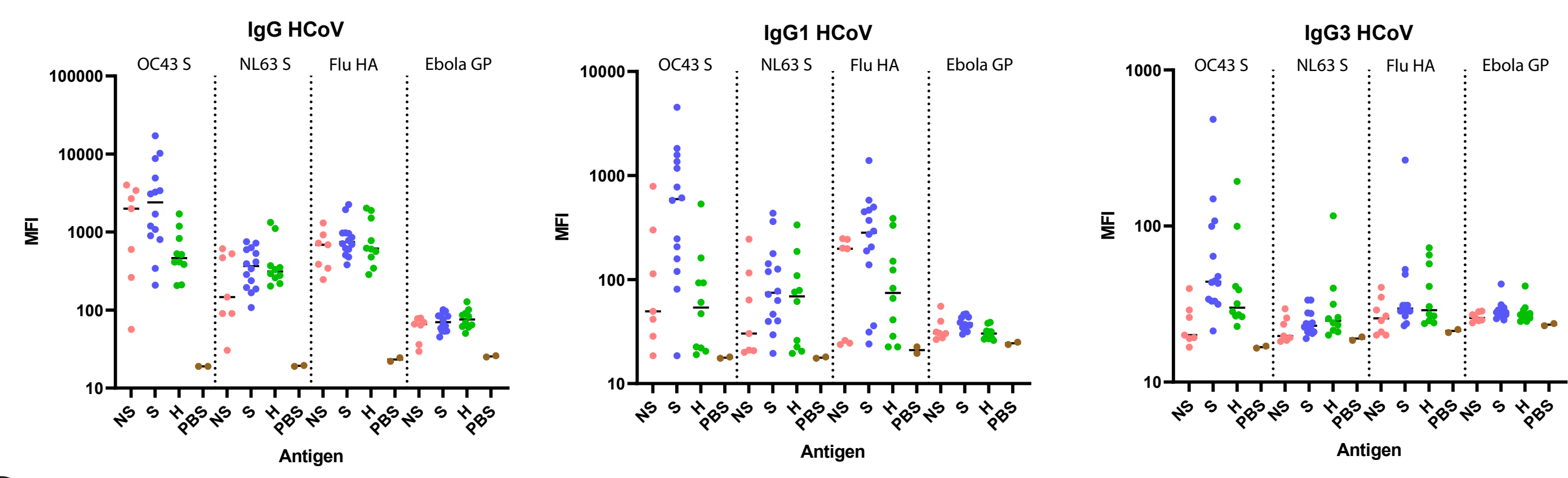
P. Correlation heatmap showing all corresponding pairwise feature correlations (Spearman) across non-survivors and survivors.

Q-S. Performance of LASSO model (precision, recall, F1 score respectively) to discriminate between survivors and non-survivors built using deep humoral profiles against non-canonical Ag specificities. Model performance is measured in a k-fold cross-validation framework with permutation testing. Actual denotes the performance of the model, built on real data. Permuted denotes performance of the model on shuffled data in a matched cross-validation framework (negative control).

T. Frequency of the 4 LASSO-selected featured and 4 random features across folds and replicates of k-fold cross-validation.

U. Dot-plots showing distributions of the 4 LASSO-selected features in 5 non-COVID-19 ARDS subjects (1 non-survivor, 4 survivors).

V. LASSO-selected features from model built using deep humoral profiles against canonical and non-canonical Ag specificities.



Antigen Order
OC43 S NL63 S Flu HA Ebola GP

Supplementary Figure 3 – Related to Figure 3.

A-O. Dot plots showing deep humoral profiles against non-SARS-CoV2 (HCoVOC43, HCoVNL63) Ag specificities for survivors, non-survivors, and healthy controls (A-IgG, B-IgG1, C-IgG3, D-IgA, E-IgA1, F-IgA2, G-IgM, H-Galactose, I-Sialic acid, J-FcR2a, K-FcR3a, L-FcR3b, M-FcR1, N-FcR2b, O-C1Q).

P. Correlation heatmap showing all corresponding pairwise feature correlations (Spearman) across non-survivors and survivors.

Q-S. Performance of LASSO model (precision, recall, F1 score respectively) to discriminate between survivors, non-survivors and healthy controls built using deep humoral profiles against canonical and non-canonical Ag specificities. Model performance (3-way) is measured in a k-fold cross-validation framework with permutation testing. Actual denotes the performance of the model, built on real data. Permuted denotes performance of the model on shuffled data in a matched cross-validation framework (negative control).

T-V. Performance of LASSO model (precision, recall, F1 score respectively) to discriminate between survivors, non-survivors and healthy controls built using deep humoral profiles against non-SARS-CoV2 Ag specificities. Model performance is measured in a k-fold cross-validation framework with permutation testing for outcome prediction between survivors, non-survivors, and healthy controls (3-way). Actual denotes the performance of the model, built on real data. Permuted denotes performance of the model on shuffled data in a matched cross-validation framework (negative control).