Supplementary materials

The D614G mutation in SARS-CoV-2 Spike increases transduction of multiple human cell types

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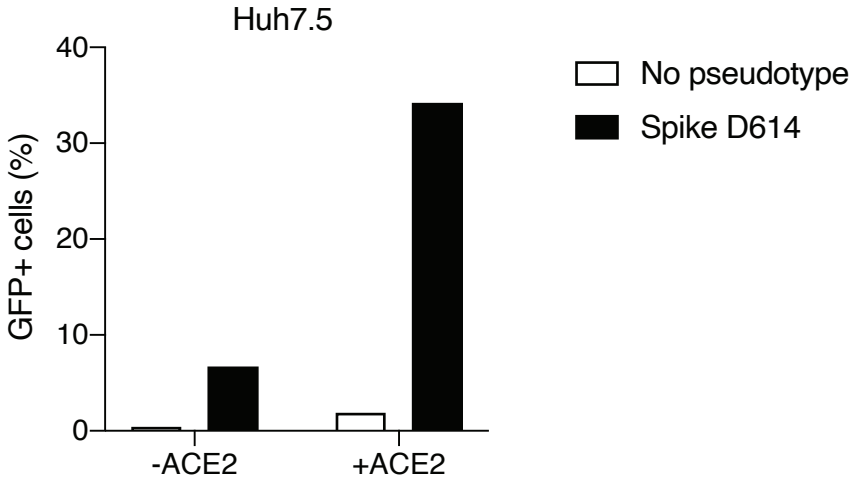
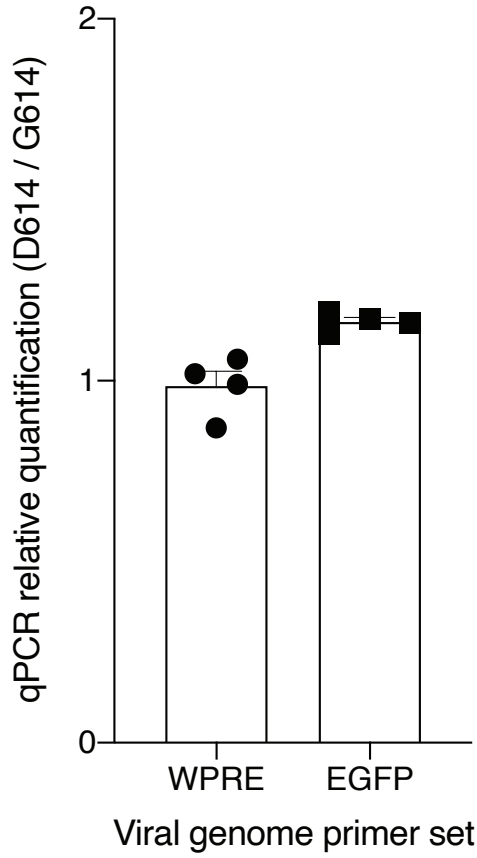
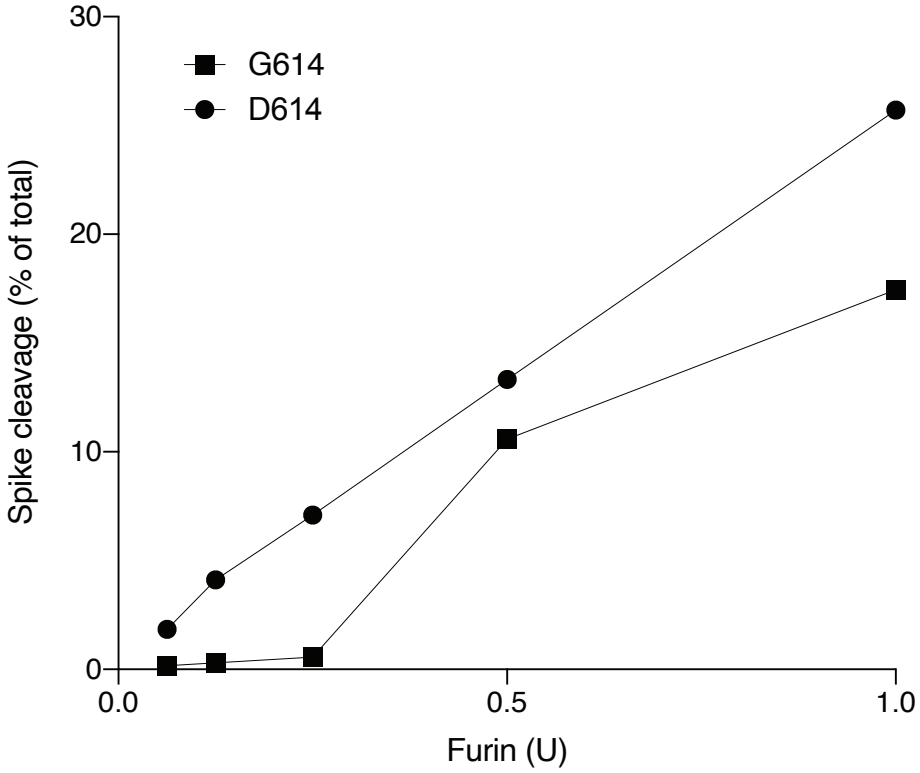


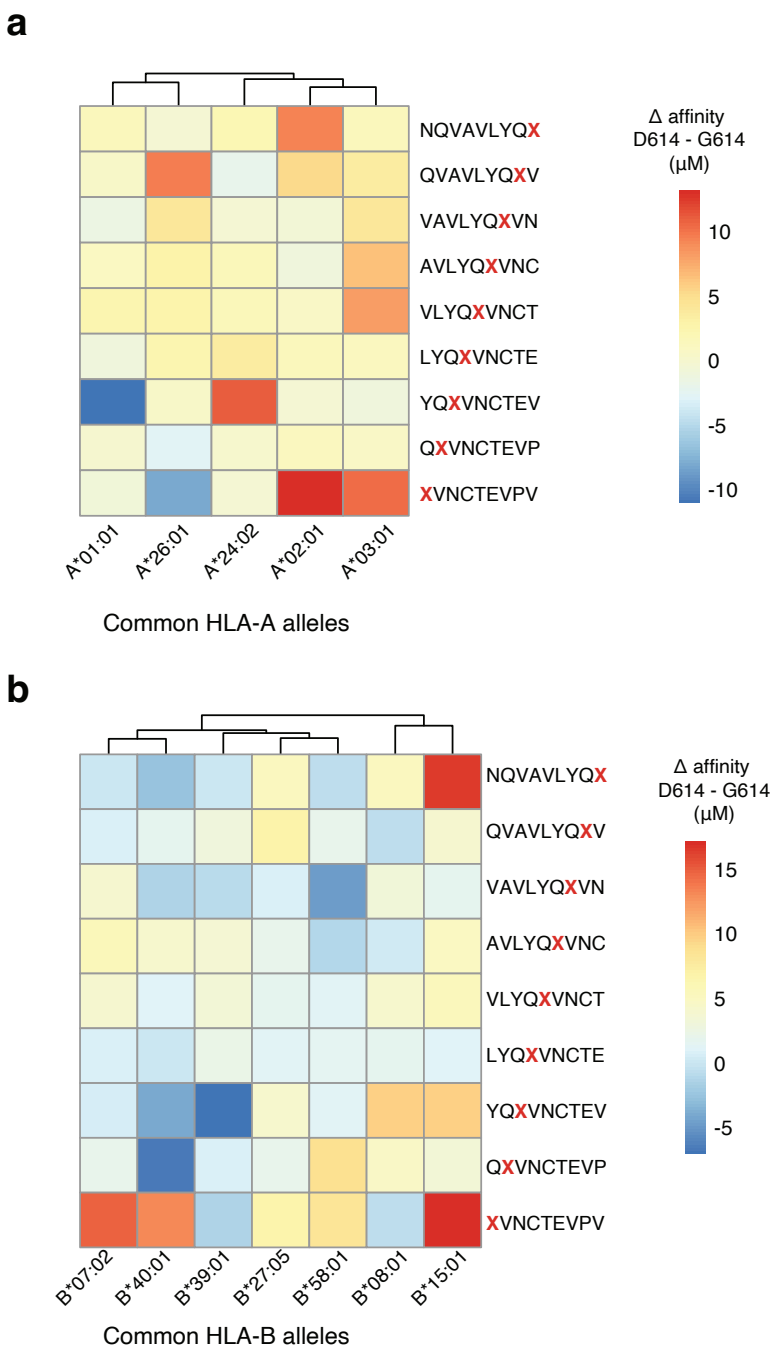
Supplementary Figure 1. Increased transduction of SARS-CoV-2 Spike pseudotyped lentivirus in human cells that constitutively overexpress the human ACE2 receptor. Percent of EGFP+ cells at 6 days post-transduction with 100 μL of supernatant SARS-CoV-2 spike (D614) pseudotyped lentivirus and unpseudotyped lentivirus in human liver Huh7.5 with and without ACE2 overexpression.



Supplementary Figure 2. Quantitative PCR of viral RNA from SARS-CoV-2 Spike pseudotyped lentiviruses. Relative quantification ($\Delta\Delta C_t$) of viral RNA from SARS-CoV-2 Spike pseudotyped lentiviruses. The primers amplify the Woodchuck Hepatitis Virus posttranscriptional regulatory element (WPRE) or the EGFP gene in the viral RNA genome.



Supplementary Figure 3. On-bead furin digestion of immunoprecipitated SARS-CoV-2 Spike variants. Quantification of cleaved Spike (S2) fragment as a percent of total Spike after 1 hour digestion at 37°C with furin protease.



Supplementary Figure 4. Change in MHC binding affinity for peptides near the D614G mutation in the SARS-CoV-2 spike protein. Predicted change in binding affinity for common HLA-A alleles (a) and common HLA-B alleles (b). Predictions were computed using the NetMHC software package.