**Supplemental Digital Cotent 1**

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| **SUPPLEMENTARY TABLE 1**. Susceptibility of recombinant viruses to HGS004 | | |
| V3 loop sequences of recombinant viruses | HGS004 | |
|  | IC50 (95% CI) | FC |
| 07J-W0 backbone |  |  |
| CTRPGNNTRKSTRIGPGQTFFATGDIIGDIRQAHC\* | 1.06 (0.78, 1.45) | 1.00 |
| S306P | 0.08 (0.06, 0.1) | 0.08 |
| F318I | 0.13 (0.11, 0.15) | 0.12 |
| G321E | 0.24 (0.2, 0.28) | 0.23 |
| T307I/T320R | 1.40 (1.0, 1.98) | 1.32 |
| T307I/F318I/T320R/G321E | 0.09 (0.07, 0.11) | 0.08 |
| K305R/S306P/T307I/F318I/T320R/G321E | 0.11 (0.09, 0.13 | 0.10 |
| 07J-W28 backbone |  |  |
| CTRPGNNTRRPIRIGPGQTFIAREDIIGDIRQAYC† | 0.39 (0.33, 0.45) | 0.38 |
| 305R🡪K | 0.19 (0.14, 0.26) | 0.18 |
| 306P🡪S | 0.35 (0.30, 0.40) | 0.33 |
| *Note:* CI = Confidence intervals, FC = Fold change in IC50compared to 07J-W0  \* Full-length 07J-W0 envelope; amino acid V3 sequence shown (starting at HXB2 position 296)  † Full-length envelope from 017-W28; amino acid V3 sequence shown | | |