**Table S6. Complete heterosubtypic coverage and resistance hedging when only full-length viral segment sequences were analysed**

|  |  |  |  |
| --- | --- | --- | --- |
| A | Target sequences | *5-S* | *3-S* |
| **Segment** | **Counts** | **Counts** |
| **1** | 156 (156) | 2,722 (2,722) |
| **2** | 243 (243) | 279 (279) |
| **3** | 49 (49) | 493 (493) |
| **5** | 107 (107) | 281 (281) |
| **7** | 594 (594) | 1,695\* (1,696) |
| **8** | 34 (34) | 52 (52) |
| **Total** | **1,183 (1,183)** | **5,522 (5,523)** |

|  |  |  |  |
| --- | --- | --- | --- |
| B | Effective *Duals* | *5-S* | *3-S* |
| **Segment** | **Counts** | **Counts** |
| **1** | 957 (943) | 15,363 (15,363) |
| **2** | 36 (36) | 42 (42) |
| **3** | 156 (96) | 28,676 (6,971) |
| **5** | 21\*\* (0) | 4,939\* (4,167) |
| **7** | 1,230 (587) | 4,249 (2,578) |
| **8** | – | 3 (3) |
| **Total** | **2,400 (1,662)** | **53,272 (29,124)** |

**C**

|  |  |  |  |
| --- | --- | --- | --- |
|  | Effective *Doubles* | *5-S* | *3-S* |
| **Segment** | **2** | **3** | **5** | **7** | **8** | **2** | **3** | **5** | **7** | **8** |
| **1** | 528(510) | 696(645) | 6.827(6,821) | 5,853(5,853) | 285(117) | 7,598(7,598) | 103,917(102,840) | 38,471(36,287) | 75,816\*(63,335) | 6,137(4,831) |
| **2** |  | 414(414) | 2,280(2,280) | 3,114(2,634) | 162(72) |  | 6,402(4,107) | 4,482(4,482) | 4,524(3,828) | 312(162) |
| **3** |  |  | 3,687(3,687) | 969(879) | 276(108) |  |  | 35,761(28,971) | 15,235(11,710) | 3,469(2,233) |
| **5** |  |  |  | 8,322(2,946) | 468(468) |  |  |  | 14,538\*(6,807) | 1,449(1,404) |
| **7** |  |  |  |  | 1,749(1,029) |  |  |  |  | 3,631\*(1,756) |
| **Total** | **35,630 (28,463)** | **321,742 (280,351)** |

|  |  |  |  |
| --- | --- | --- | --- |
| D | Graphs size distribution | *5-S* | *3-S* |
| **Graph size** | **Counts** | **Counts** |
| **1** | – | 497,386,251 (0) |
| **2** | – | 7,356,828,159 (539,518,482) |
| **3** | – | 13,311,685,395 (1,359,713,196) |
| **4** | – | 25,446,077,829 (2,268,239,631) |
| **5** | – | 41,395,204,197 (4,150,228,191) |
| **6** | 31,050 (0) | 58,605,029,064 (5,972,694,501) |
| **7** | 403,380 (0) | 65,331,607,806 (7,372,942,287) |
| **8** | 1,275,156 (0) | 57,289,184,010 (6,130,754,955) |
| **9** | 2,995,488 (0) | 41,714,899,560 (5,769,792,072) |
| **10** | 9,397,134 (126,360) | 28,921,666,005 (4,280,931,897) |
| **11** | 18,730,980 (909,792) | 16,146,455,949 (2,916,639,192) |
| **12** | 24,155,280 (1,794,312) | 7,458,580,143 (1,610,712,312) |
| **13** | 15,426,612 (4,245,696) | 2,014,509,366 (575,618,256) |
| **14** | 8,505,864 (3,790,800) | 302,888,754 (89,329,752) |
| **15 \*** | 808,704 (808,704) | 7,056,072 (3,944,376) |
| **Total** | **81,729,648 (11,675,664)** | **365,799,058,560 (43,041,059,100)** |

11% of the total unique internal segment sequences that are non-full-length were removed. Counts from the all-length segment sequence analysis are given in parentheses for comparison. **(A)** Target sequences. No target sequence can achieve 100% heterosubtypic coverage in the all-genome analysis. No single target sequence can achieve 100% heterosubtypic coverage in the full-length analysis. \* Except for one target sequence in segment 7 in the 3-S set, the target sequences in both 5-S and 3-S sets are identical in both full- and all-length analyses. **(B)** Effective *Duals*. \* Except for five effective *Duals* in segment 7 in the 3-S set, all effective *Duals* from the all-length analysis are complete subset of those from the full-length analysis. \*\* 21 effective *Duals* in segment 5 were obtained in the full-length analysis whereas there was none in the all-length analysis. **(C)** Effective *Doubles*. \* Except for six S1-S7, 45 S5-S7, and three S7-S8 effective *Doubles* in the 3-S set, all effective *Doubles* from the all-length analysis are complete subset of those from the full-length analysis. **(D)** Size distribution of all 6-vertices segment partner graphs formed by a target sequence (whose *NSP = 5*) from each of the six internal segments (Fig. 3C and Fig. S9B). \*Complete graphs of size 15.