**Supplementary Table 2. Estimates of divergence between each human case and the most closely related sequenced animal cases (as determined by lowest patristic distance between related case and human case).** Patristic distance (substitutions per site) and time between each human case and the named related sequence extracted from the phylogeny. The patristic distance was divided by the average mutation rate (0.000244 substitutions per site per year [1]) and used to estimate the time since the cases diverged (equivalent to an approximate most recent common ancestor). - or + indicates days before or after human cases respectively.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Human case** | **ID of most closely related case(s)** | **Patristic distance**  **(substitution/site)** | **Estimated divergence (year)** | **Time between cases (day)** |
| 1 | KT119642 | 0.0309 | 63.38 | -5447 |
| 2 | OR920307 | 0.0029 | 5.89 | -309 |
| 2 | OR920256 | 0.0070 | 14.41 | +1212 |
| 3 | OR045943 | 0.0034 | 6.92 | -178 |
| 3 | OR920235 | 0.0021 | 4.29 | +758 |
| 4 | OR920236 | 0.0020 | 4.02 | -299 |
| 5 | OR045943 | 0.0027 | 5.47 | -1266 |

Reference

1. Troupin C, Dacheux L, Tanguy M, Sabeta C, Blanc H, Bouchier C, et al. Large-Scale Phylogenomic Analysis Reveals the Complex Evolutionary History of Rabies Virus in Multiple Carnivore Hosts. PLOS Pathog. 2016;12: e1006041. doi:10.1371/journal.ppat.1006041