**Supplementary Table 2**

**Examination of possible confounding factors of codon usage analysis: relative frame of *de novo* genes compared to ancestral genes, and relative age of de novo frames.**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Genus | Ancestral frame | *De novo frame* | P< | Relative frame | “relative age” of novel frame according to taxonomic distribution(1) |
| *Noro* | Capsid | VF1 | 0.001 | +1 | Intermediate |
| *Omegatetra* | Capsid | p17 | 0.005 | +1 | Intermediate |
| *Dependo* | VP2 | AAP | 0.005 | +1 | Intermediate |
| *Carmo* (replicase/p23) | Replicase | p23 | 0.005 | +1 | Young |
| *Luteo* | P5 | P4 | 0.005 | +1 | Old |
| *Tymo* | Replicase | MP | 0.01 | +2 | Intermediate |
| *Aquabirna* | VP2 | VP5 | 0.01 | +2 | Old |
| *Capillo* | MP | Replicase | 0.025 | +1 | Intermediate |
| *Mandari* | Capsid | NABP | 0.025 | +2 | not applicable(2) |
| *Carmo* (capsid/p25) | Capsid | p25 | 0.025 | +1 | Young |
| *Betatetra* | Capsid | Replicase | 0.05 | +2 | not applicable(2) |
| *Gyro* | VP2 | Apoptin | 0.05 | +1 | Intermediate |
| *Potex* | TGBp2 | TGBp3 | 0.05 | +1 | Young |
| *Parvo* | VP2 | SAT |  | +1 | Intermediate |
| *Begomo* | Replicase | AC4 |  | +2 | Old |
| *Orthobunya* | N | NSs |  | +1 | Intermediate |
| *Tombus* | p22 | p19 |  | +2 | Old |
| *Denso* | NS1 | NS2 |  | +1 | Old |
| *Apara* | Capsid | Pog |  | +1 | Intermediate |
| *Orthohepadna* (pol/L) | Pol | L |  | +1 | Old |
| *Umbra* | ORF4 | ORF3 |  | +2 | Intermediate |
| *Hordei* | TGBp2 | TGBp3 |  | +1 | Old |
| *Orthohepadna* (pol/X) | Pol | X |  | +2 | Intermediate |
| *Brevidenso* | NS1 | NS2 |  | +1 | Intermediate |
| *Tricho* | Capsid | MP |  | +2 | Intermediate |

(1): We used taxonomic distribution as a very approximate, empirical proxy to estimate comparative ages of the overlaps. *De novo* frames found only in one species are considered “young” (provided there are several species in the genus considered, see note 2 below); overlaps found in more than one species but less than one genus are considered of “intermediate” age, and overlaps found in more than one genus are considered “old”. The taxonomic distribution of *de novo* frames is taken from Supplementary Table S1

(2): We excluded cases where there was insufficient taxonomic sampling, such as the *betatetravirus* overlap, since the *betatetravirus* genus comprises only ones species.