Table S 7 Variety of domain d apical loop sequence in genomes of *Enterovirus G, H* and *J* species.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **N** | **Loop and flanking base pairs sequence** | **Abundance** | **Abundance in filtered set of genomes** | **Sequence of RNA-binding tripeptide** |
| **Enterovirus G** | | | | |
|  | uauUACGgua | 5 | 3 | STGK |
|  | uauUGCGgua | 1 | 1 | STGK |
|  | auuUGCGgau | 1 | 1 | STGK |
|  | uauCGCGgua | 1 | 1 | STGK |
|  | uauCACGgua | 1 | 1 | STGK |
|  | cacGUUAgug | 1 | 1 | SMGK |
| **Total** | | **10** | **8** | -- |
| **Enterovirus H** | | | | |
|  | uauUGCGgua | 1 | 1 | TTGK |
|  | uauUACGgua | 2 | 1 | TTGR |
| **Total** | | **3** | **2** | -- |
| **Enterovirus J** | | | | |
|  | uauUACGgua | 3 | 2 | ATGK |
|  | uauCAAGgua | 3 | 1 | ATGK |
|  | uauCACGgua | 2 | 2 | ATGK |
| **Total** | | **8** | **5** | -- |