Table S 5 Variety of domain d apical loop sequence in genomes of *Enterovirus D* species.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **N** | **Loop sequence** | **Serotype** | **Abundance** | **Abundance in filtered set of genomes** | **Diversity of 3 flanking base pairs** | **Diversity of 3 flanking base pairs in filtered set of genomes** |
|  | UUCG | HEV68 | 404 | 50 | 5 | 3 |
|  | UUUG | HEV68 | 4 | 1 | 1 | 1 |
|  | CUCG | HEV68 | 3 | 2 | 1 | 1 |
|  | CCCG | HEV70 | 3 | 1 | 1 | 1 |
|  | CUUG | HEV68 | 3 | 2 | 1 | 1 |
|  | CACG | HEV94 | 1 | 1 | 1 | 1 |
|  | UUGG | HEV68 | 1 | 0 | 1 | 0 |
| **Total** | | | 419 | 57 | 11 | 8 |