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| --- | --- | --- | --- | --- | --- |
| **Target** | **DNA or RNA** | **Primer/Probe** | **Sequence (5’-3’)** | **Genomic Target** | **References** |
| Sapovirus | RNA | Sav1F | TTG GCC CTC GCC ACC TAC | Junction of polymerase and capsid |  |
| Sav5F | TTT GAA CAA GCT GTG GCA TGC TAC |
| Sav124F | GAY CAS GCT CTC GCY ACC TAC |
| Sav124R | CCC TCC ATY TCA AAC ACT A |
| Sav124TPa (Probe) | FAM-CCR CCT ATR AAC CA-MGB-NFQ |
| Sav5TPa (Probe) | FAM-TGC CAC CAA TGT ACC A-MGB-NFQ |
| Rotavirus Type A | RNA | NSP3-F | ACC ATC TWC ACR TRA CCC TCT ATG AG | Non-structural Protein 3 |  |
| NSP3-R | GGT CAC ATA ACG CCC CTA TAG C |
| NSP3-Pa (Probe) | VIC-AGT TAA AAG CTA ACA CTG TCA AA-MGB-NFQ |
| Adenovirus 40/41 | DNA | AdV-F | GCC TGG GGA ACA AGT TCA G | Hexon |  |
| AdV-R | ACG GCC AGC GTA AAG CG |
| AdV-Pa (Probe) | NED-ACC CAC GAT GTA ACC AC-MGB-NFQ |
| Astrovirus | RNA | Ast-F | AAG CAG CTT CGT GAR TCT GG | Junction of polymerase and capsid |  |
| Ast-R | GCC ATC RCA CTT CTT TGG TCC |
| Ast-Pb (Probe) | Cy5-CAC AGA AGA GCA ACT CCA TCG CAT TTG-Tao-IBDRQ |
| GI | RNA | Cog1F-flap | AATAAATCATAACGYTGGATGCGNTTYCATGA | Norovirus GI |  |
| Cog1R-flap | AATAAATCATAACTTAGACGCCATCATCATTYAC |
| Ring1a.2 (Probe) | 6-FAM- AGATYGCGR/ZEN/ TCYCCTGTCCA -IBFQ |
| GII | RNA | Cog2F-flap | AATAAATCATAACARGARBCNATGTTYAGRTGGAT GAG | Norovirus GII |  |
| Cog2R-flap | AATAAATCATAATCGACGCCATCTTCATTCACA |
|  |
| Ring 2.2 (Probe) | JOE - TGGGAGGGY/ZEN/ GATCGCAATCT - IBFQ |  |
| CrAssphage | DNA | CrAss-F | CAG AAG TAC AAA CTC CTA AAA AAC GTA GAG | Genomic base pair region: 14731 bp-14856 bp |  |  |
| CrAss-R | GAT GAC CAA TAA ACA AGC CAT TAG C |  |
| CrAss-P (Probe) | FAM-AAT AAC GAT TTA CGT GAT GTA AC |  |
| Pepper Mild Mottle Virus | RNA | PMMV-FP1-rev | GAG TGG TTT GAC CTT AAC GTT TGA | 1878 bp-1901 bpa  and |  |  |
| 1945 bp-1926 bpa |  |  |
| PMMV-RP1 | TTG TCG GTT GCA ATG CAA GT |  |  |  |
| PMMV-P (Probe) | FAM-CCT ACC GAA GCA AAT G-MGB-NFQ |  |  |  |
| *Escherichia coli* | DNA | uidA\_784F | GTG TGA TAT CTA CCC GCT TCG C |  |  |  |
| uidA\_866R | AGA ACG GTT TGT GGT TAA TCA GGA | *uidA* |  |  |
| EC807d probe | FAM-TCGGCATCCGGTCAGTGGCAGT-BHQ1 |  |  |  |
| aCorresponding nucleotide position of GenBank accession number M81413 (PMMoV strain S)  dQuencher: Iowa Black fluorescent | | | | | |  |
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