**Supplemental Digital Content 7:** Real time PCR assays on TaqMan Array Card used in SHINE

All the assays have been described previously and extensively validated1-3. Nucleic acid was extracted with the QIAamp Fast DNA Stool mini kit (Qiagen, Hilden, Germany) with pre-treatment steps that included bead beating. AgPath One Step RT-PCR reagents were used for qPCR reactions, which were performed on ViiA 7 systems. Quantification cycles (Cqs) are the PCR cycle values at which fluorescence from amplification exceeds the background, which acts as an inverse metric of quantity of nucleic acid. Valid results required proper functioning of controls (the negative results of a sample are valid only when its external control MS2 is positive, Cq ≤ 35; the positive results are valid only when the corresponding extraction blank is negative for the relevant targets, Cq > 35), and excluded data flagged by the real time PCR software, i.e. BADROX in combination with NOISE or SPIKE.

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| --- | --- | --- |
|  | **Pathogen** | **Gene** |
| **Viruses** | Adenovirus 40/41 | Fiber gene |
|  | Astrovirus | Capsid |
|  | Norovirus GI/GII | GI ORF1-2 and GII ORF1-2 |
|  | Rotavirus | *NSP3* |
|  | Sapovirus | *RdRp* |
| **Bacteria** | EAEC\* | *aaiC, aatA, aggR* |
|  | Atypical EPEC\* | *eae* |
|  | Typical EPEC\*# | *bfpA* |
|  | ETEC\* | *LT, STh* and *STp* |
|  | STEC\*# | *stx1, stx2* |
|  | *Aeromonas*# | Aerolysin |
|  | *Campylobacter spp.* | *cadF* and *cpn60* |
|  | *Helicobacter pylori*# | *ureC* |
|  | *Plesiomonas shigelloides*# | *gyrB* |
|  | *Salmonella*# | *ttr* |
|  | *Shigella*/EIEC | *ipaH* |
|  | *Vibrio cholerae*# | *hlyA* |
| **Fungi** | *Enterocytozoon bieneusi*# | *ITS* |
|  | *Encephalitozoon intestinalis*# | SSU rRNA |
| **Protozoa** | *Cryptosporidium* | 18S rRNA |
|  | *Cyclospora* *cayetanensis*# | 18S rRNA |
|  | *Cystoisospora belli*# | 18S rRNA |
|  | *Entamoeba histolytica*# | 18S rRNA |
|  | *Giardia* | 18S rRNA |
| **Helminth** | *Ancylostoma* *duodenale*# | *ITS2* |
|  | *Ascaris* *lumbricoides*# | *ITS1* |
|  | *Necator* *americanus*# | *ITS2* |
|  | *Strongyloides* *stercoralis*# | Dispersed repetitive sequence |
|  | *Trichuris* *trichiura*# | 18S rRNA |
| **Controls** | MS2 | *MS2g1* |
|  | PhHV | *gB* |

*\* E. coli* pathotypes were defined as follows: EAEC (*aaiC*, or *aatA*, or both), atypical EPEC (*eae* without *bfpA*, *stx1*, and *stx2*), typical EPEC (*bfpA*), ETEC (STh, STp, or LT), STEC (*eae* without *bfpA* and with *stx1*, *stx2*, or both).

# 17 pathogens with less than 1% overall prevalence were omitted from individual pathogen analyses but retained in the composite pathogen burden measures.