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Shifting national surveillance of Shigella infections toward geno-serotyping by the development of a tailored Luminex assay and NGS workflow

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Abstract

The phylogenetically closely related Shigella species and enteroinvasive Escherichia coli (EIEC) are responsible for millions of episodes of bacterial dysenteriae worldwide. Given its distinct epidemiology and public health relevance, only Shigellae are subject to mandatory reporting and follow-up by public health authorities. However, many clinical laboratories struggle to differentiate non-EIEC, EIEC, and Shigella in their current workflows, leading to inaccuracies in surveillance and rising numbers of misidentified E. coli samples at the National Reference Centre (NRC). In this paper, we describe two novel tools to enhance Shigella surveillance. First, we developed a lowcost Luminex-based multiplex assay combining five genetic markers for species identification with 11 markers for serotype prediction for S. sonnei and S. flexneri isolates. Using a test panel of 254 clinical samples, this assay has a sensitivity of 100% in differentiation of EIEC/Shigella pathotype from non-EIEC strains, and 68.7% success rate in distinction of Shigella and EIEC. A novel, and particularly successful marker was a Shigella-specific deletion in the spermidine acetyltransferase gene speG, reflecting its metabolic decay. For Shigella serotype prediction, the multiplex assay scored a sensitivity and specificity of 96.6% and 98.4%, respectively. All discrepancies were analyzed with whole-genome sequencing and shown to be related to causative mutations (stop codons, indels, and promoter mutations) in glycosyltransferase genes. This observation spurred the development of an in silico workflow which extracts the Shigella serotype from Next-Generation Sequencing (NGS) data, taking into account gene functionality. Both tools will be implemented in the workflow of the NRC, and will play a major role in the shift from phenotypic to genotyping-based surveillance of shigellosis in Belgium.

KEYWORDS

Luminex, multiplex, public health surveillance, sequencing, Shigella

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1 | INTRODUCTION

Shigellae are facultative intracellular pathogens and the etiological agents of bacillary dysentery or shigellosis (Croxen et al., 2013; Gomes et al., 2016). Shigellosis affects annually 164.7 million people, and results in a high mortality among children aged 1–4 years in low- and middle-income countries (Kotloff, Riddle, Platts-Mills, Pavlinac, & Zaidi, 2017). In western countries, *Shigella* infections were traditionally mostly travel-related, but recent surveillance data from the United Kingdom indicate a shift to domestically circulating strains (Aragón et al., 2007; Baker et al., 2015), some of which are increasingly resistant to ciprofloxacin and azithromycin.

The Shigella genus is subdivided into four species based on their antigenic properties: S. sonnei, S. boydii, S. dysenteriae, and S. flexneri, each having different subtypes based on variations in the O-antigen of the LPS layer (Edwards & Ewing, 1986). This classification does not reflect its evolutionary history as phylogenetic analyses clearly cluster Shigella species within the Escherichia coli species (Chen et al., 2014; Edwards, Logan, Langham, Swift, & Gharbia, 2012; Escobar-Páramo, Giudicelli, Parsot, & Denamur, 2003; Pettengill, Pettengill, & Binet, 2016). In particular, enteroinvasive E. coli (EIEC) lineages have been identified as the direct evolutionary ancestor of Shigella, by having acquired a large F-type plasmid (pINV) that encodes the molecular machinery required for invasion, survival, and diffusion of the bacterium within the host (Sansonetti, Kopecko, & Formal, 1982; Yang et al., 2005). Phylogenetic studies suggest this acquisition occurred multiple times in independent events (Hazen et al., 2016; Pettengill et al., 2016), upon which Shigella spp. evolved to a strictly human pathogen because of intense gene decay. This is reflected by decreased metabolic activity, increased disease severity, and decreased infectious dose (DuPont et al., 1971; Prosseda et al., 2012). Specific surveillance and differentiation of Shigella spp. from non-EIEC remains therefore warranted from a medical and public health perspective.

National surveillance in Belgium is performed by the National Reference Centre for Shigellosis (NRCS), which receives annually approximately 400 *Shigella* cultures on a voluntary basis from

peripheral laboratories (Figure 1a). Of the 2,066 confirmed Shigella strains received in the period 2013-2018, 72.1% were S. sonnei, 21.9% S. flexneri, 4.3% S. boydii, and 1.7% S. dysenteriae with a serotype distribution that has been stable for more than a decade (Figure 1b). Notably, the number of false-positive Shigella cultures has increased substantially since 2015 as clinical laboratories increasingly rely on MALDI-TOF for bacterial identification, which fails to properly differentiate Shigella from E. coli (Figure 1c, Khot & Fisher, 2013). Shigella spp. are traditionally typed using biochemical, mobility and serological assays, which are time consuming and error prone through possible cross-reactions of O-antigens between E. coli and Shigella (Liu et al., 2008; Sun et al., 2011). Molecular PCR methods have been described for identification and geno-serotyping of Shigella spp. (Dutta et al., 2001; Gentle, Ashton, Dallman, & Jenkins, 2016; Li, Cao, et al., 2009; Sun et al., 2011), but either have limited resolution or are not cost-effective to be implemented in routine surveillance. Some western countries have introduced whole-genome sequencing (WGS) for Shigella surveillance, delivering SNP-level discriminatory power (Chattaway et al., 2017; Dallman et al., 2016; McDonnell et al., 2013). However, wide implementation of Next-Generation Sequencing (NGS) in national surveillance programs is hampered by budgetary limitation, a lack of bioinformatics expertise, and the extensive validation which is required at NRCs which are working under a quality system (Rossen, Friedrich, & Moran-Gilad, 2018).

Here, we present a novel two-step surveillance approach for *Shigella* surveillance. First, we developed a low-cost Luminex-based multiplex that combines species identification and subtyping of *S. flexneri* in a single test, allowing feedback to the clinical lab within 48 hr for 95% of submitted samples. This method is based on a modular multiplex oligonucleotide ligation-PCR procedure (MOL-PCR), using commercially available MagPlex[™]-TAG microspheres for detection (Appendix 1; Ceyssens et al., 2016; Wuyts, Roosens, Bertrand, Marchal, & De Keersmaecker, 2015). Additionally, we present a workflow for extraction of *Shigella* spp. serotypes based on NGS data. We validated both arms by retrospectively analyzing 254 serotyped isolates, 16 confirmed EIEC strains, and publicly available sequence data.



FIGURE 1 Key statistics of the Belgian National Reference Centre for Shigellosis. (a) Evolution of submitted samples in absolute numbers for the period 2006–2017. (b) *Shigella* species distribution in 2016–2017, as compared to 2006–2007. (c) Annual percentage of submitted samples that were confirmed as not being *Shigella* spp. by lack of agglutination and biochemical testing for the period 2013–2018 (data until September 2018)

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2 | METHODS

2.1 | Bacterial strains, traditional typing, and genomic DNA extraction

In Belgium, peripheral clinical laboratories collect Shigella isolates from human patients and send them voluntarily to the NRCS for identification using Triple Sugar Iron Agar (TSI, Biotrading, NL) and serotyping by slide agglutination using commercially available monovalent antisera (Denka Seiken CO, UK; Appendix 2). Confirmed EIEC isolates were acquired from the "Centre for Infectious Disease Control" (RIVM, The Netherlands). Bacterial cultures were grown overnight at 37°C on Mueller-Hinton agar (Bio-Rad). For DNA extraction, either a single colony was added to 200 µl of InstaGene™ Matrix (Bio-Rad) and placed in a thermal cycler (56°C for 25 min, 99°C for 8 min, cooled to 4°C). The mixture was spun (14,000 g, 1 min) and the supernatant was used immediately or stored at -20°C. Alternatively, gDNA was extracted semi-automatically using the MgC Bacterial DNA Kit[™] with 60 µl elution volume (Atrida, NL), according to the manufacturer's instructions for gram-negative bacteria.

2.2 | MOL-PCR using Luminex xTAG beads

For all targeted genes, upstream and downstream probes were designed targeting 35–45 bp conserved regions with maximal conservation and accessibility using OligoAnalyzer 3.1 (Table 1). Upstream probes are equipped with an internal anti-TAG sequence compatible with the anti-TAG of the MagPlex[™] beads, while universal T7 and T3 primer sequences were added to the 5' and 3' ends of upstream and downstream probes, respectively. Downstream probes were 5'-phosphorylated.

Our MOL-PCR approach has been described in detail elsewhere (Wuyts et al., 2015). Briefly, all reactions were assembled in cooled 96-well plates in a 10 μ l reaction volume containing 2 nM of each probe, 2 U of Taq DNA Ligase (New England Biolabs, Ipswich, MA), 1× Taq DNA ligase buffer, 2 μ l of DNA template, and nuclease-free water. Ligation was performed by initial denaturation (95°C, 10 min), followed by 25 cycles of ligation (58°C, 30 s) and denaturation (96°C, 25 s). Three microliters of the ligation product was amplified in a 10 μ l PCR containing 0.25 U of HotStartTaq DNA polymerase (Qiagen, Hilden, Germany), 1× DNA polymerase buffer, 125 nM T7 primer, 500 nM 5'-biotin-T3 primer, and 200 μ M dNTPs. Reaction conditions were 15 min of denaturation at 95°C, followed by 35 cycles of 94°C (30 s), 60°C (30 s), and 72°C (30 s), and a final extension step at 72°C for 5 min.

Hybridization of the PCR product to colored microspheres was performed in a volume of 20 μ l per reaction, with MagPlexTM-TAG microspheres (750 beads/target) added to 0.1 M Tris-HCl, pH 8.0/0.2 M NaCl/0.08% Triton-X. To this mixture, 5 μ l of PCR product was added, followed by a denaturation step (90 s at 96°C) and 30 min of hybridization at 37°C. Subsequently, 100 μ l of a reporter mix containing 4 μ g/ml streptavidin-R-phycoerythrin (Life Technologies) was added, and the samples were incubated for 15 min at 37°C in the dark. Subsequent read-out was performed at 37°C using 100 μ l of these samples, on a MAGPIX device with a minimal bead count of 50 microspheres/target (Wuyts et al., 2015). For each marker, the signal-to-noise (S/N) ratios were calculated by dividing the median fluorescence intensity (MFI) by the corresponding MFI of the NC. During assay design, an S/N ratio \geq 2.0 indicated positive identification.

2.3 | Whole genome sequencing and in silico serotyping

Genomic DNA was prepared using MgC Bacterial DNA Kit[™] with 60 µl elution volume (Atrida, NL), following the manufacturer's instructions. Sequencing libraries were constructed using the Illumina Nextera XT DNA sample preparation kit and subsequently sequenced on an Illumina MiSeq instrument with a 250-bp paired-end protocol (MiSeq v3 chemistry) according to the manufacturer's instructions.

Sequence variants were collected for wzx1-5, wzx6, gtrl, gtrll, gtrlV, gtrV,gtrX,gtr1c,oac,andopt,andalsofortheipaHandrfcgenesequences. Raw reads were trimmed using Trimmomatic v0.36 (Bolger, Lohse, & Usadel, 2014) with the following settings: "ILLUMINACLIP: NexteraPE-PE.fa:2:30:10," "LEADING:10," "TRAILING:10," "SLIDINGWINDOW: 4:20" and "MINLEN:40." Afterward SRST2 v0.2.0 using default settings was employed to detect the presence of genes using trimmed reads as input against the constructed sequence database (Inouye et al., 2014). A variant calling-based approach was then used to specifically detect stop and frameshift mutations leading to inactivation in the detected genes as follows. Trimmed reads were mapped against the sequence of every identified gene using bowtie2 v2.3.0 with the "-very-sensitive-local" option enabled (Langmead & Salzberg, 2012). The resulting SAM file was then converted into an indexed BAM file using SAMtools view v1.3.1, followed by SAMtools sort and SAMtools index (Li, Handsaker, et al., 2009). Afterward, a pileup was generated using SAMtools mpileup with output format set to "VCF," followed by variant calling by BCFtools call v1.6 with the following options: "-consensus-caller," "-variants-only," and "-ploidy 1" (Li, 2011). Variants that were covered by <10 reads or variants that were not covered by at least one forward and one reverse read were removed using BCFtools filter (Danecek & McCarthy, 2017). Indels were normalized and duplicates removed using BCFtools norm with the option "-rm-dup both." Finally, the functional effect of the mutations was determined using BCFtools csq v1.9.30 (commit: g983f7da) with the option "-local-csq" enabled. Genes that contained a stop codon and/or a frameshift were considered to be not expressed for the determination of the serotype. Mutations in the gtr promotor were detected similarly by first mapping trimmed reads against a 381 bases-long region covering the gtr promotor and initial coding sequence (accession number KT988057.1). Read mapping and variant calling were done as described before but variant filtering was slightly more strict: minimal depth 10×, minimal forward depth 1×, minimal reverse depth 1×, minimal SNP quality 25, minimal mapping quality 30, minimal Z-score of 1.96, and minimal Ymultiplier of 10 as described elsewhere (Kaas, Leekitcharoenphon, WILEY_MicrobiologyOpen

Aarestrup, & Lund, 2014). The promotor was considered to be wild type if there were no filtered mutations inside the -35 box or the -10 TA box. Otherwise the *gtrX* promoter was considered as not wild type and the *gtrX* gene as not expressed for the determination of the sero-type. The profiles described in Sun et al. (2011) were then used as a decision system to classify the serotype.

3 | RESULTS

3.1 | Multiplex target selection and design

To introduce molecular testing in national Shigella surveillance, we designed a specific multiplex assay for identification, differentiation, and subtyping of Shigella spp. from cultured strains. Our strategy was based on converting known molecular markers into a MOL-PCR assay with read-out on a Luminex MAGPIX[®] platform, allowing multiplex detection of up to 50 genes in a single well (Table 1). For identification of the EIEC/Shigella pathotype, we targeted the invasive plasmid antigen H (ipaH) and the plasmid invC (Ojha, Yean, Ismail, & Singh, 2013; Venkatesan, Buysse, & Hartman, 1991). To distinguish EIEC from Shigella, we inferred the presence of lacY (Pavlovic et al., 2011), cadA (Prosseda et al., 2007) and a Shigella-specific deletion 19_20delGT in speG (Prosseda G, personal communication). Next, we included probes targeting wbgZ and rfc for identification of S. sonnei and S. flexneri, respectively (Ojha et al., 2013). Finally, we adapted a previously described multiplex PCR assay for serotyping of S. flexneri that targets genes for O-antigen synthesis or modification (Gentle et al., 2016; Sun et al., 2011) into to a Luminex-compatible format (Table 1). A decision tree to interpret the results of the final assay can be found in Figure 2a. A probe targeting the opt gene, responsible for addition of phosphoethanolamine to L-rhamonse II or III, leading to Flexneri variants 4av, Xv, and Yv (Sun et al., 2012), was not included as no positive control samples were present in our collection. Genetic serotyping of S. boydii and S. dysenteriae was omitted from the current assay as this would have required the inclusion of 31 additional targets, substantially increasing the reaction cost to cover only a minority of samples submitted in Belgium (<5%, Figure 1b).

3.2 | Luminex-based species identification

To validate the assay and assess its performance in distinguishing *Shigella* from either non-EIEC and EIEC, we retrospectively analyzed 215 samples sent to the Belgian NRC between 2013 and 2018 that had been routinely typed using traditional biochemical and serological methods (Appendix 2). We randomly selected isolates of Sonnei (n = 31, of which 26 Phase I Sonnei), Flexneri 1b (n = 30), 2a (n = 30), 2b (n = 19), 3a (n = 33), 3b (n = 11), 4a (n = 11), and 6 (n = 30). Serotypes 1c (n = 7), 4b (n = 1), 5a/b (n = 1), X (n = 8), and Y (n = 4) are underrepresented in the NRCS collection in comparison to other serotypes, and all available isolates which had a negative identification for *Shigella* spp., 16 confirmed EIEC strains, and six untypable isolates exhibiting nonspecific agglutination reactions.

(Continues) Venkatesan et al. (1991) Barbagallo et al. (2011) Ceyssens et al. (2016) Prosseda et al. (2007) Ojha et al. (2013) Ojha et al. (2013) Kristiansen, and -øbersli, Wester, Brandal (2016) Reference MTAG A066 A075 A044 A012 A038 A014 A074 ZATACGACTCACTATAGGGAGTAAGTGTTAGATAGTATTGAATCATGGCAACGACAAATTAAAGG IAATACGACTCACTATAGGGATTGTGAAGAAGAAGGAAGAAAATTGTAATGTACTCGGTTCTTCGG 'AATACGACTCACTATAGGGAATGTAAAGTAAAGAAAGTGATGAGTATGTTATTGGCGTTTTCCTG AATACGACTCACTATAGGGTTTGTTAGAATGAGAAGATTTATGTCCATCAGGCATCWGAAGGC 'AATACGACTCACTATAGGGAATGAAATAGTGTTAAATGAGTGTATGCCAAGCGCCCACAGTG IAATACGACTCACTATAGGGAGTAGAAGTTGAAATTGATTATGCTGCCCAGTTTCTTCATACG CTTTTCGATAATGATACCGGCTCCCTTTAGTGAGGGTTAAT 3CTCTGTCGTGCCGTTGTTTGTCCCTTTAGTGAGGGTTAA1 CGAAGTAGAAACCATTGCGCTCCCTTTAGTGAGGGTTAAT CAAGTCGGCCGTGGATTATTTCCCTTTAGTGAGGGTTAAT 3AGACTGCCAGTGATAACTCCCTTTAGTGAGGGTTAAT TTAAGCTACGCCCGCTGGATCCCTTTAGTGAGGGTTAAT CACCTACGATGTTTTTGATCCCTTTAGTGAGGGTTAAT Sequence Luminex probes designed using published targets Down Down Down Down Down Down Down Probe d٢ ٩ d٢ d٢ d٢ Чp d٢ gene 16S rRNA Targeted wbgZ ipaH invC speG cadA lacY S. sonnei geno-serotyping spp. and differentiation dentification of Shigella DNA extraction control from Escherichia coli **TABLE 1** Purpose

Purpose	Targeted gene	Probe	Sequence	MTAG	Reference
S. flexneri	rfc	Up	TAATACGACTCACTATAGGGAGTGAATGTATATGTATTTGCTTTACATGGTCGGATCAC	A013	Ojha et al. (2013)
geno-serotyping		Down	GCAGTGAAGATTCTGACTCTTTCCCTTTAGTGAGGGTTAAT		
	WZX1-5	Up	TAATACGACTCACTATAGGGTTTTGTGTGTTATTGTAATTGAGATTTCGGCGAAAAGTGGAACAG	A067	Gentle et al. (2016)
		Down	CATTATTCCGGTGCTGCAATTCCCTTTAGTGAGGGTTAAT		
	wzxó	Up	TAATACGACTCACTATAGGGTTTGTTGTTAGTATGTGGGGGGGG	A063	Gentle et al. (2016)
		Down	GGTAATTCTAACTATATTGGGC7CCC7177GFGGGGGG77AAT		
	gtrl	Up	TAATACGACTCACTATAGGGTTGTTAAGAGTTGTTTAATTGCTAACAGCCCAATTGTATG	A036	Gentle et al. (2016)
		Down	GAGGCATATTTTAGAGAATGGTCCCTTTAGTGAGGGTTAAT		
	gtrll	Up	TAATACGACTCACTATAGGG <u>TTTTAAGTGAGTTATAGAAGTAGTA</u> GACTCAGGAAATATGCTCTC	A029	Gentle et al. (2016)
		Down	CATGAGCGCAGACACTTTTGGTCCCTTTAGTGAGGGTTAAT		
	gtrIV	Up	TAATACGACTCACTATAGGGTGAGTTAGTTTGTATGTTTAAGTAGGCCATAACACCTTTCATGAATG	A065	Gentle et al. (2016)
		Down	GGATCAGACAGTTCTCACATGTCCCTTTAGTGAGGGTTAAT		
	gtrV	Up	TAATACGACTCACTATAGGGAGGTATTAGTAGTAGTTATTGTAAGTTAACTTGCTCTTTCCACC	A057	Gentle et al. (2016)
		Down	CGTAATCTGGGGGGTAATCCCTTTAGTGAGGGTTAAT		
	gtrX	Up	TAATACGACTCACTATAGGGAATTAGAAGTAAGTAGGAGTTTAAGGTCCAAGCCCAATATAACAAATG	A056	Gentle et al. (2016)
		Down	CTCACTGGTATTTATCATTGTCCCTTTAGTGAGGGTTAAT		
	gtr1c	Up	TAATACGACTCACTATAGGGAAATGAGAAAGGAGAAAATGATAGGTCATACGCTTTCTCACGAAC	A072	Gentle et al. (2016)
		Down	CTTAGGTTCAAATGGGTTACTCCCTTTAGTGAGGGTTAAT		
	oac	Up	TAATACGACTCACTATAGGGATTAAGTAAGAATTGAGAGTTTGAAACTGCTTTGACACGGCAAGG	A021	Gentle et al. (2016)
		Down	CTTGTGGCAGCTATGATGGTTTCCCTTTAGTGAGGGTTAAT		
Note. The universal T7 and	T3 primer sequence	es are indicat	ed in italics. Anti-TAG sequences compatible with the indicated MagPlex-TAG Microspheres (MTAG) a	e underlined.	

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FIGURE 2 In-house molecular (MOL)-PCR-based Luminex assay for *Shigella* typing. (a) Decision tree for the developed MOL-PCR assay for detection and subtyping of *Shigella* spp. (b) Graphical representation of raw Luminex data for tested species and serotypes during test validation. The read-out is scored as the median fluorescence intensity, which is converted to signal-to-noise ratios (S/N) for allele calling. The single available isolate of *S. flexneri* 5 was confirmed as *Escherichia coli* based on whole-genome sequencing

During the test phase of the assay, we detected false-positive signals in 5.1% (13/254) of the tested isolates, due to an elevated background (Appendix 2), which disappeared upon re-extraction of their gDNA (data not shown). In 12 of 13 cases, elevated backgrounds were observed in samples extracted by the MgC Bacterial DNA Kit[™], suggesting a better compatibility of the InstaGene[®] Matrix extraction method with Luminex-based read-out. Secondly, in 14.1% (36/254) of the tested samples, an elevated background signal in the No Template Control (NTC) sample lead to false-negative results (Appendix 2). This elevated signal disappeared upon replacing the NTC with 10 pg of *S. enterica* DNA (data not shown). As an additional measure to increase the test robustness, S/N values with of at least twice the baseline value of other probes in the same sample were considered positive throughout the study.

After these optimizations, all samples confirmed as S. sonnei or S. flexneri by traditional methods (215/215) were positive for either the ipaH (99.5%) or the invC (95.2%) probe, and negative for speG, lacY, and cadA. Similarly, all 39 isolates not identified as Shigella (i.e., including untypable samples) were negative for ipaH and invC. These strains were positive for either speG (37/39), lacY (19/39), and/ or cadA (21/39) (Figure 2). One isolate negative for the speG probe (S13BD01340) was identified as Citrobacter freundii by MALDI-TOF, leading to a sensitivity of 97.4% for this probe in identifying E. coli in our test set. The other speG negative isolate (S17BD01771) tested positive for cadA, leading to 100% sensitivity in detecting E. coli with all probes combined. Not unexpectedly, the 16 examined EIEC strains gave an intermediate profile in the multiplex (Appendix 2, Figure 2). Two EIEC reference strains and 13 of 14 clinical EIEC isolates were positive for ipaH and invC, while the presence of speG, lacY, and cadA was detected in 11/16, 6/16, and 0/16 of strains, respectively.

3.3 | Luminex-based serotyping and discrepance analysis

The algorithm for deriving Shigella serotypes from the multiplex data is shown in Figure 2a. The multiplex assay determined correctly the serotype of 26/26 S. sonnei Phase I and 176/185 (95.1%) S. flexneri samples, with 100% concordance between genotyping and classical typing for Flexneri Types 1b, 1c, 2a, 2b, 3a, 6, and Y (Appendix 2). As expected, isolates belonging to Sonnei Phase II (5/5) could not be detected. We employed NGS to evaluate the 10 discordant Flexneri isolates in more detail (Table 2), which allowed to characterize the genes responsible for O-antigen synthesis or modification at a much higher resolution. We identified explanatory indels and frameshift mutations in oac, gtrl, and gtrlV in six strains, impeding their function (Gentle et al., 2016). Moreover, we detected promoter mutations upstream of the gtr operon in four strains, suggesting decreased expression levels resulting in the S. flexneri 3b serotype. A peculiar result was observed for strain S16BD02240, which was previously typed as the only S. flexneri 5 isolate in Belgium. While the species identification panel detected speG and not ipaH or invC, the serotype probes rfc and gtrV were positive (Appendix 2). Closer inspection of sequencing results revealed the insertion of a phage-encoded gtrV

protein in an *E. coli* background, leading to the *E. coli* O13/O135:H11 serotype (Knirel et al., 2016).

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3.4 | NGS-based serotyping

To enhance future workflows, we designed a WGS-based workflow for automated extraction of Shigella serotypes from NGS data that includes detection of opt, wzx, wzy, and other known glycosyltransferase genes, enabling the detection of all currently described variants of the O-antigen from S. boydii, S. sonnei, S. dysenteriae, and S. flexneri (Li, Cao, et al., 2009). To account for observed differences between phenotypes and genotypes described previously, we included the detection of TAG stop codon and frameshifts in all analyzed genes, and promotor mutations in the gtr operon (Figure 3). The algorithm was tested on publicly available NGS data from 135 globally collected S. flexneri strains (Connor et al., 2015), leading to identical serotype predictions in 127 of 135 (94.1%) of tested strains (Appendix 3). Interestingly, frameshifts (17%) and amber mutations (2.9%) were regularly detected among the 127 correctly predicted serotypes, thus showing frequent inactivation of glycosyltransferase genes. Next, we analyzed the eight deviating results using the CLC Bio Genome Workbench. In two samples, we observed low (<5×) coverage of the opt gene, hinting at plasmid loss in a subpopulation of the culture. Given the minimal coverage set at 10×, these genes were below our detection limit. In 3 of 8 cases, our NGS workflow failed to call gtr operon promoter mutations (n = 1), and indels in gtrX (n = 1) and oac (n = 1). In the three remaining cases, no obvious explanation of the discrepancy could be detected.

4 | DISCUSSION AND CONCLUSION

Many clinical laboratories struggle to differentiate non-EIEC, EIEC, and *Shigella* spp. in their current workflows, although their discrimination is important for public health surveillance as only *Shigella* is subject to mandatory reporting (van den Beld et al., 2018). In order to address rising numbers of misidentified *E. coli* samples at the NRCs and to speed up the *Shigella* subtyping process, we developed a Luminex-based multiplex assay combining species identification and serotype prediction for *S. sonnei* and *S. flexneri* isolates.

While successful positive identification of *Shigella*/EIEC is based on the well-known target of *ipaH* (99.5% among tested strains), we describe in this study a particularly successful SNP for which a high negative predictive value (99.6%) and sensitivity (97.4%) were observed for non-EIEC *E. coli*. This SNP causes a frameshift mutation in *speG*, encoding the enzyme spermidine acetyltransferase responsible for the conversion of spermidine into N-acetylspermidine. It has been demonstrated that a higher level of spermidine increases *Shigella* survival within macrophages and confers higher resistance to oxidative stress (Barbagallo et al., 2011), indicating that the loss of *speG* function is an emerging trait. As predicted, EIEC have an intermediate position as active N-acetylspermidine is still present in most EIEC strains (68.7% in our dataset), yet intracellular spermidine tends WILFY_MicrobiologyOpen

	Serotype		
Strain ID	Phenotype	Luminex	Remarks
S15BD09453	flexneri 3b	flexneri 1b	Indel detected in <i>gtr</i> I at position 340
\$13BD04017	flexneri 3b	flexneri 3a	Gtr operon promoter mutations at positions -6, -7, -12, -13, -14, -17, -18, and -19
S14BD01714	flexneri 3b	flexneri 3a	Gtr operon promoter mutations at positions -6, -7, -12, -13, -14, -17, -18, and -19
S15BD06353	flexneri 3b	flexneri 3a	Gtr operon promoter mutations at positions -6, -7, -12, -13, -14, -17, -18, and -19
S15BD08204	flexneri 3b	flexneri 3a	Gtr operon promoter mutations at positions -6, -7, -12, -13, -14, -17, -18, and -19
S16BD02240	flexneri 5	flexneri 5a/coli	gtrV/rfc detected, ipaH absent
S14BD02502	flexneri x	flexneri 3a	Indel detected in <i>oac</i> at position 543
S17BD07654	flexneri x	flexneri 3a	Indel detected in <i>oac</i> at position 718
S14BD01142	flexneri x	flexneri 3a	Frameshift detected in <i>oac</i> at position 346
S14BD01131	flexneri x	flexneri 3a	Frameshift detected in <i>oac</i> at position 346

TABLE 2NGS analysis of Shigellaflexneri strains with discrepant resultsbetween serotyping and Luminex-basedtyping

to be higher as compared to commensal *E. coli* (Campilongo et al., 2014). Interestingly, among all non-*Shigella* strains that were sent to the NRCS by peripheral Belgian laboratories, not a single strain with defective *speG* was detected (Appendix 2), strongly suggesting that the large majority are non-EIEC strains.

A weakness of the current assay is the low positive predictive value for EIEC strains. A first option to cope with this is to expand the biochemical typing of ipaH positive strains, as described by van den Beld et al. (2018). Alternatively, the discriminatory power of the molecular assay can be increased by incorporating additional markers published by Australian researchers during the review process of this article (Dhakal, Wang, Lan, Howard, & Sintchenko, 2018). Their large-scale genome comparisons identified six genetic loci separating Shigella from EIEC, which combined presence/absence led to 95.1% sensitivity. Due to the flexibility of the Luminex-based MOL-PCR methodology, the expansion of our assay from a 17- to a 23-plex is expected to go swiftly with minimal impact on cost and handling time.

In addition to species identification, the presented Luminex assay simultaneously detects S. sonnei Phase I and S. flexneri serotypes. Two published reports on molecular geno-serotyping report 92.6% and 97.8% concordant results between phenotypic serotyping and PCR (Gentle et al., 2016; Sun et al., 2011), comparable with the 95.1% observed in our MOL-PCR based assay. As reported also in these studies, we also observed a robust correlation between the phenotypes and genotypes for S. sonnei and S. flexneri serotypes 1b, 1c, 2a, 2b, 3a, F6, and Y. Discrepancies are commonly caused by amber mutations, insertions, and deletions in O-antigen synthesis or modification genes, rendering these phenotypically inactive. In our test set, these accounted for 5.4% of deviating results among tested S. flexneri. In the global collection of Flexneri strains analyzed by Connor et al. (2015), 19.9% of strains contained such mutations, making a strong case for using WGS data in serotype prediction instead of PCR-based methods that only take a part of the gene into account. As a note,





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opt-mediated O-antigen modification was not detectable in our assay, and should be part of future updates.

In all Shigella species, genes for O-antigen synthesis and modification are typically encoded on mobile elements like prophages and plasmids, and hence are unstable phenotypic markers (Connor et al., 2015; Sun et al., 2013). Recent genomic studies showed evidence of high levels of recombination among genes responsible for serotypes, limiting their use in transmission and epidemiological studies (Connor et al., 2015; Dallman et al., 2016). Therefore, it has little doubt that epidemiological surveillance of Shigella infections will increasingly shift to NGS, as long as allocated budgets allow this transition. Our NGS workflow is able to accurately perform serotype predictions from sequence data, and will be incorporated in future bioinformatic pipelines to allow backwards compatibility with historical results and with traditionally typed strains. In the meantime, the presented Luminex MAGPIX[®]-based assay can provide a cost-effective solution for fast detection and subtyping of the most prevalent Shigella spp. This multiplex surpasses limitations of traditional typing, and is readily implementable in clinical and public health laboratories.

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CONFLICT OF INTEREST

All authors report no conflict of interest.

AUTHORS CONTRIBUTION

E.V. performed wet lab experiments; B.B. and K.V. performed bioinformatics; W.M., S.D.K., and N.R. provided technical expertise; P.C. designed the experiments and wrote the paper. All authors read and approved the manuscript.

ETHICS STATEMENT

None required.

DATA ACCESSIBILITY

Raw sequence data were submitted to the European Nucleotide Archive (ENA; EMBL-EBI, Cambridge, UK) as accession number PRJEB30509 and study name ena-STUDY-Sciensano-21-12-2018-12:27:07:718-355. Accession numbers of publicly available NGS data used in this study, and raw Luminex data are listed in Appendix 3.

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Schematic representation of the MOL-PCR method. When a target allele or SNP is present in the DNA extract of a bacterial strain under study, two sequence-specific probes will be ligated in 25 consecutive cycles of denaturation and annealing. The upstream probes carry a 24 nucleo-tide sequence (shown in red) which binds to the anti-TAG covalently attached to the MagPlex-TAG microspheres (Luminex). Using universal T7 and 5'-biotin labeled T3 primers (shown in blue), the ligated oligonucleotides are amplified, denatured, and hybridized to the corresponding beads. After short exposure to streptavidin-R-phycoerythrin, the luminescent signal is read by the MAGPIX[®] machine, and S/N ratios are calculated using negative control samples. This figure is modified from Ceyssens et al. (2016).

APPENDIX 2

Overview of selected strains and Luminex results. Genomic DNA was isolated using either Instagene[®] Matrix (IM) or the MgC Bacterial DNA Kit[™] (MC). For extraction control, we included a probe targeting 16S rRNA; The result was expressed as positive ("pass") if the resulting MFI surpassed 500 units. Shown in the "species identification" and "serotype prediction" tabs are signal-to-noise (S/N) values of the different probes, using a *S. enterica* strain as negative control. A signal is considered positive if the S/N exceeds 2.0 (cells highlighted in green), or if the S/N value of the probe has a least twice the baseline value of other probes in the same sample (cells highlighted in orange). False-positive signals caused by elevated background signals are indicated in blue. Strains marked with an asterisk gave discrepant results between serotyping and Luminex analysis, and were analyzed using NGS.

			D EXTRA	NA ACTION	si	PECIES	DENTI	FICATIO	ON				SI	EROTYF	PE PREI	остю	N			
SAMPLE ID	SEROTYPE	GENO- SEROTYPE	EXTRACTION METHOD	16S RNA	ІраН	InvC	speG	ІасҮ	cadA	rfc	wbgZ	oac	gtrll	gtrl	gtrX	gtrV	wzx6	gtrlV	wzx1-5	gtrlC
S15BD00065	S. flexneri 1b	S. flexneri 1b	IM	Pass	2.6	3.6	1.0	1.3	1.4	4.2	0.9	4.3	1.3	3.1	1.2	1.4	1.4	1.3	2.6	1.5
S16BD08334	S. flexneri 1b	S. flexneri 1b	IM	Pass	2.5	3.8	1.0	1.2	1.2	3.9	1.0	4.0	1.3	2.9	1.3	1.3	1.4	1.4	2.4	1.4
S17BD04619	S. flexneri 1b	S. flexneri 1b	мс	Pass	4.3	4.9	1.2	0.6	0.9	7.1	1.2	7.9	1.8	4.9	1.6	1.6	1.6	1.4	4.8	1.3
S15BD07389	S. flexneri 1b	S. flexneri 1b	мс	Pass	3.5	1.0	1.2	1.7	1.9	5.8	1.1	6.5	1.6	3.8	1.5	1.4	1.5	1.7	3.0	1.3
S17BD05412	S. flexneri 1b	S. flexneri 1b	MC	Pass	4.1	5.0	1.1	0.6	0.6	7.9	1.2	8.5	1.2	4.7	1.2	1.2	1.3	1.4	4.8	1.3
S17BD00920	S. flexneri 1b	S. flexneri 1b	MC	Pass	4.4	5.0	1.0	0.5	0.8	6.9	1.1	7.1	1.5	5.0	1.4	1.2	1.4	1.3	4.8	1.3
S17BD02926	S. flexneri 1b	S. flexneri 1b	MC	Pass	4.2	1.2	1.1	0.6	0.8	8.0	1.2	8.3	1.6	5.0	1.5	1.3	1.5	1.3	5.0	1.2
S15BD09705	S. flexneri 1b	S. flexneri 1b	IM	Pass	2.5	3.5	0.9	1.0	1.2	3.8	0.8	3.9	1.1	2.8	1.1	1.1	1.2	1.1	2.3	1.2
S16BD01793	S. flexneri 1b	S. flexneri 1b	IM	Pass	2.2	3.4	0.9	1.1	1.0	4.0	0.8	4.1	0.9	2.8	1.1	1.2	1.2	1.1	2.1	1.2
S1/BD04615	S. flexneri 1b	S. flexneri 1b	IM	Pass	4.1	5.1	1.0	0.6	0.6	7.0	1.1	7.4	1.5	4.5	1.4	1.2	1.3	1.2	4.4	1.2
\$15BD06964	S. flexneri 1b	S. flexneri 1b		Pass	2.4	1.2	1.0	1.1	1.5	4.1	0.9	4.3	1.2	3.1		1.2	1.2	1.1	2.5	1.1
\$16BD05857	S flexneri 1b	S flexneri 1b	IM	Pass	4.5	3.5	1 1	1.1	1.5	7.9	1.0	6.8	1.2	2.0	1.1	1.2	1.2	1.1	4.5	1.0
S16BD03590	S. flexneri 1b	S. flexneri 1b	IM	Pass	2.2	3.1	0.9	0.7	1.0	3.7	0.7	3.7	0.9	2.7	0.9	0.9	1.0	0.9	2.1	1.0
S18BD00494	S. flexneri 1b	S. flexneri 1b	IM	Pass	2.2	3.3	0.8	0.8	0.9	3.6	0.7	3.8	0.9	2.7	1.0	0.9	1.1	0.9	2.1	1.0
S16BD00463	S. flexneri 1b	S. flexneri 1b	IM	Pass	2.2	3.4	0.8	0.7	0.7	3.6	0.7	3.9	0.6	2.7	0.7	0.9	1.1	0.9	2.0	1.0
S17BD03190	S. flexneri 1b	S. flexneri 1b	мс	Pass	3.2	3.6	1.0	0.5	0.5	6.3	1.2	6.7	1.0	3.5	1.1	1.0	1.0	1.1	3.7	1.0
S17BD04692	S. flexneri 1b	S. flexneri 1b	MC	Pass	3.8	4.4	0.9	0.9	1.0	5.3	0.9	5.8	1.1	3.3	1.1	1.1	1.0	1.0	3.8	0.9
S15BD06461	S. flexneri 1b	S. flexneri 1b	IM	Pass	1.9	3.1	0.7	0.6	0.7	3.4	0.6	3.5	0.5	2.4	0.7	0.7	0.9	0.7	1.7	0.9
S15BD03178	S. flexneri 1b	S. flexneri 1b	IM	Pass	1.9	3.1	0.7	0.6	0.6	3.2	0.6	3.5	0.5	2.2	0.6	0.7	0.9	0.7	1.7	0.9
S16BD04361	S. flexneri 1b	S. flexneri 1b	IM	Pass	2.2	3.5	0.7	0.6	0.7	3.5	0.6	3.5	0.6	2.7	0.7	0.8	0.9	0.7	2.0	0.9
S15BD00048	S. flexneri 1b	S. flexneri 1b	IM	Pass	2.2	3.2	0.7	0.7	1.0	3.7	0.6	3.7	0.8	2.5	0.8	0.8	0.9	0.8	2.1	0.9
S16BD08182	S. flexneri 1b	S. flexneri 1b	IM	Pass	1.9	3.0	0.7	0.7	0.7	3.6	0.6	3.7	0.6	2.4	0.7	0.7	0.8	0.7	1./	0.8
S18BD02135	S. flexneri 1b	S. flexneri 1b		Pass	2.1	2.9	0.7	0.7	0.7	3.0	0.6	3.8	0.7	2.8	0.7	0.8	0.8	0.8	2.1	0.8
\$17BD02502	S flexneri 1b	S flexneri 1b	MC	Pass	1.0	5.0	1.0	0.0	0.5	5.7	0.0	5.5	0.4	4.3	0.5	0.0	0.0	1.0	4.1	0.8
S15BD06812	S flexneri 1b	S flexneri 1b	IM	Pass	1.4	3.1	0.7	0.6	0.5	3.4	0.5	3.4	0.5	2.4	0.5	0.5	0.9	0.7	17	0.8
S15BD05398	S. flexneri 1b	S. flexneri 1b	IM	Pass	1.8	2.8	0.6	0.6	0.5	3.1	0.5	3.2	0.5	2.1	0.5	0.6	0.7	0.6	1.6	0.7
\$17BD00642	S. flexneri 1b	S. flexneri 1b	MC	Pass	3.4	4.0	1.4	1.5	1.8	4.9	1.4	5.5	1.8	3.3	1.7	1.7	1.7	1.7	2.5	1.5
S16BD00982	S. flexneri 1b	S. flexneri 1b	IM	Pass	2.9	3.7	1.1	1.0	1.4	5.3	1.1	5.8	1.0	2.9	1.1	1.2	1.0	1.1	2.4	1.0
S15BD02726	S. flexneri 1c	S. flexneri 1c	IM	Pass	4.0	5.0	1.2	0.6	0.7	7.8	1.3	1.3	1.5	4.4	1.4	1.3	1.3	1.3	4.6	4.7
S16BD07709	S. flexneri 1c	S. flexneri 1c	MC	Pass	3.9	1.1	1.1	0.6	0.7	7.4	1.1	1.2	1.6	4.5	1.2	1.1	1.2	1.1	4.1	4.6
S15BD06370	S. flexneri 1c	S. flexneri 1c	MC	Pass	3.9	1.4	1.2	0.8	1.0	7.4	1.3	1.6	1.9	4.9	1.7	1.4	1.6	1.6	4.8	4.2
S16BD01515	S. flexneri 1c	S. flexneri 1c	MC	Pass	3.8	3.7	1.0	0.6	0.6	7.0	1.1	1.2	1.4	4.4	1.3	1.2	1.2	1.2	4.4	4.2
S16BD04652	S. flexneri 1c	S. flexneri 1c	IM	Pass	4.0	4.7	1.0	1.0	1.2	8.1	1.0	1.0	0.9	3.6	1.0	1.0	0.9	1.0	4.3	4.0
S15BD02866	S. flexneri 1c	S. flexneri 1c	MC	Pass	4.0	4.9	0.9	0.5	0.6	6.5	1.0	1.0	1.2	4.1	1.1	1.1	1.1	1.0	4.2	3.6
\$17BD02677	S. flexneri 2a	S flexneri 2a	MC	Pass	4.5	4.0	1.1	1.2	1.4	5.7	1.0	1.1	5.7	3.0	1.2	1.2	1.2	1.2	4.5	2.0
\$17BD02077	S flexneri 2a	S flexneri 2a	MC	Pass	4.4	5.1	1.2	0.6	0.7	6.8	1.5	1.5	6.7	1.3	1.5	1.4	1.7	1.4	4.0	1.4
S17BD05047	S. flexneri 2a	S. flexneri 2a	MC	Pass	4.0	5.0	1.1	0.5	0.8	7.8	1.1	1.2	7.1	1.2	1.2	1.2	1.2	1.2	4.7	1.2
S17BD04274	S. flexneri 2a	S. flexneri 2a	мс	Pass	4.4	5.5	1.0	0.6	0.8	7.4	1.1	1.2	7.3	1.6	1.2	1.2	1.4	1.2	4.9	1.1
S17BD02190	S. flexneri 2a	S. flexneri 2a	мс	Pass	4.3	5.5	1.0	0.6	0.7	7.6	1.1	1.2	7.3	1.4	1.2	1.1	1.2	1.2	5.0	1.1
S17BD04237	S. flexneri 2a	S. flexneri 2a	MC	Pass	4.0	5.1	1.0	0.5	0.7	7.0	1.0	1.1	6.8	1.3	1.2	1.1	1.2	1.1	4.5	1.1
S17BD07894	S. flexneri 2a	S. flexneri 2a	MC	Pass	4.1	4.9	0.9	0.6	0.7	7.0	1.0	1.1	6.7	1.2	1.2	1.1	1.2	1.1	4.5	1.0
S15BD09735	S. flexneri 2a	S. flexneri 2a	IM	Pass	4.7	5.7	1.1	1.1	1.2	7.5	1.0	1.0	6.2	1.0	1.1	1.0	1.0	1.0	4.2	1.0
S17BD00526	S. flexneri 2a	S. flexneri 2a	MC	Pass	2.8	3.5	1.2	0.5	0.5	4.9	1.0	1.0	5.6	1.0	1.1	1.0	1.0	1.0	2.5	1.0
S1/BD05130	S. flexneri 2a	S. flexneri 2a	INC	Pass	3.5	4.6	1.0	0.9	1.0	6.5	0.9	1.0	5.3	1.0	0.9	1.1	1.1	1.1	3./	0.9
\$18BD00646	S. flexneri 2a	S flexneri 2a		Pass	2.0	3.4	1.0	1.0	1.5	3.0	0.0	1.1	3.1	1.0	1.0	1.1	1.2	1.2	2.0	1.5
\$16BD00040	S flexneri 2a	S flexneri 2a	IM	Pass	1.7	2.0	1.0	1.2	1.5	2.5	0.8	1.2	23	1.2	1.2	1.4	1.4	0.8	2.5	1.5
S15BD02368	S. flexneri 2a	S. flexneri 2a	IM	Pass	2.0	2.7	0.9	1.0	0.9	2.8	0.8	0.8	2.5	0.8	0.9	0.9	0.9	0.8	1.9	1.0
S16BD07626	S. flexneri 2a	S. flexneri 2a	IM	Pass	2.0	2.6	0.7	0.8	0.9	2.8	0.7	0.8	2.5	0.7	0.8	0.8	0.8	0.8	1.8	0.8
S18BD00647	S. flexneri 2a	S. flexneri 2a	IM	Pass	2.2	3.5	0.8	0.8	1.1	3.7	0.6	0.8	3.2	0.9	0.9	0.9	1.0	0.9	2.1	0.8
S18BD00305	S. flexneri 2a	S. flexneri 2a	IM	Pass	1.7	2.3	0.9	1.3	1.0	2.7	0.6	0.9	2.1	1.0	0.9	1.0	0.7	1.0	2.0	0.8
S18BD00080	S. flexneri 2a	S. flexneri 2a	IM	Pass	1.8	2.6	0.8	0.8	0.8	2.8	0.7	0.8	2.4	0.7	0.8	0.7	0.8	0.7	1.7	0.8
S18BD00940	S. flexneri 2a	S. flexneri 2a	IM	Pass	2.2	3.6	0.7	0.6	0.8	3.7	0.5	0.7	3.2	0.6	0.7	0.7	0.8	0.7	2.1	0.8
S18BD01471	S. flexneri 2a	S. flexneri 2a	IM	Pass	1.5	2.3	0.8	1.1	0.8	2.6	0.7	0.9	2.1	0.8	0.9	0.9	0.8	0.6	1.5	0.8
S18BD00639	S. flexneri 2a	S. flexneri 2a	IM	Pass	1.5	2.4	0.9	1.1	0.7	2.6	0.5	0.6	2.2	0.7	0.9	1.0	0.9	0.6	1.4	0.7
S18BD01126	S. flexneri 2a	S. flexneri 2a		Pass	1./	2.1	0.7	0.9	0.8	2.7	0.5	0.6	2.1	0.9	0.8	0.7	0.7		1.4	0.6
S15BD07040	S. flexneri 2a	S. flexneri 2a	IM	Pass	1.5	2.2	0.0	0.0	0.7	2.7	0.0	0.7	2.2	0.7	0.7	0.0	0.7	0.0	1.4	0.0
11000000000		1						1 0.7	1 0. 7				2.0						1 1.0	1 0.0

APPENDIX 2 (continued)

S16BD06168	S. flexneri 2a	S. flexneri 2a	IM	Pass	1.5	2.3	0.6	0.5	0.4	2.5	0.6	0.5	2.1	0.5	0.5	0.5	0.6	0.5	1.3	0.6
6450004007	6 11 12	C (I) 2				2.2	0.0	0.4		2.2	0.0	0.5	2.0	0.5	0.5	0.4	0.5	0.5	4.2	0.0
S15BD04237	S. flexneri za	S. flexneri Za	IIVI	Pass	1.4	2.2	0.6	0.4	0.4	2.3	0.6	0.5	2.0	0.5	0.5	0.4	0.5	0.5	1.3	0.6
S17BD03809	S. flexneri 2a	S. flexneri 2a	MC	Pass	3.4	4.2	1.3	1.3	1.6	4.8	1.2	1.3	5.1	1.4	1.3	1.2	1.3	1.3	2.5	1.3
C170D04222	C flaurani 2a	C flaurani 2a		Deer	2.0	A.C.	1.0	17	2.4	F 0	1.0	1 5	5.0	1.0	1.0	2.2	1.0	2.0	2.1	1 7
S1/BD04223	S. flexneri za	S. flexneri Za	IVIC	Pass	3.9	4.6	1.6	1.7	2.4	5.8	1.0	1.5	5.9	1.9	1.9	Z.Z	1.8	2.0	3.1	1.7
S17BD00627	S. flexneri 2a	S. flexneri 2a	IM	Pass	3.2	4.1	1.2	1.3	1.3	5.0	1.3	1.2	5.0	1.3	1.3	1.2	1.2	1.4	2.4	1.3
C170D042E0	C flownori 2o	C flownori 2o	18.4	Dace	2 5	4.4	11	1 2	1 1	E 2	11	1 2	E 2	1 2	1 2	11	1 2	1.4	27	1 1
31/0004330	5. Ilexileri za	3. Ilexilen za	1141	FdSS	5.5	4.4	1.1	1.5	1.4	5.5	1.1	1.5	J.2	1.5	1.2	1.1	1.2	1.4	2.7	1.1
S16BD06531	S. flexneri 2b	S. flexneri 2b	MC	Pass	4.4	5.2	1.3	1.3	1.6	5.7	1.1	1.3	5.4	1.6	4.6	1.4	1.6	1.5	4.4	1.3
\$14BD05301	S flexneri 2h	S flexneri 2h	IM	Pass	20	31	12	12	10	3.0	13	12	26	11	22	11	13	13	22	13
5140005501	5. ficklici 25	S. flexifient 26		1 4 5 5	2.0	5.1	1.2	1.2	1.0	5.0	1.5	1.2	2.0	1.1	2.2	1.1	1.5	1.5	2.2	1.5
S16BD06778	S. flexneri 2b	S. flexneri 2b	MC	Pass	4.6	5.6	1.2	0.7	0.9	7.6	1.3	1.4	7.1	1.8	6.5	1.3	1.6	1.4	5.0	1.3
\$15BD02683	S flexneri 2h	S flexneri 2h	MC	Pass	43	55	12	0.6	0.8	75	13	13	73	14	6.6	13	14	13	49	13
C450000740	C (1) 21	C (I))			4.5			0.0	0.0	7.4	4.4	4.0	7.0		6.0	4.0		4.2		4.0
S15BD00742	S. flexneri 2b	S. flexneri 2b	IVIC	Pass	4.5	5.5	1.1	0.6	0.8	7.4	1.1	1.3	1.2	1.6	6.2	1.3	1.5	1.3	4.9	1.3
S16BD06115	S. flexneri 2b	S. flexneri 2b	IM	Pass	4.8	5.9	1.0	1.1	1.3	7.5	1.0	1.0	6.0	1.2	4.8	1.1	1.1	1.1	4.4	1.0
C170006622	C flownori 2h	C flownori 3h	MC	Dace	20	10	0.0	10	1 1 1	6.0	10	1 2	E 1	1 2	E O	11	1 2	1 1	20	10
31/000032	5. Hexhen 20	5. Hexnen 2D	IVIC	Pass	5.0	4.0	0.9	1.0	1.1	0.0	1.0	1.2	5.1	1.2	5.5	1.1	1.2	1.1	5.0	1.0
S14BD00770	S. flexneri 2b	S. flexneri 2b	IM	Pass	2.2	3.8	1.0	1.0	1.0	3.5	0.9	1.0	2.4	1.1	2.7	1.1	1.0	0.9	2.1	0.9
\$1/IBD05312	S flexneri 2h	S flavnari 2h	114	Pace	10	29	07	0.8	00	2.1	0.7	07	25	0.8	2.1	0.8	0.8	0.7	10	0.8
5140005512	J. Hexnell 25	5. Hexiteri 26		1 4 3 3	1.5	2.5	0.7	0.0	0.5	3.1	0.7	0.7	2.5	0.0	2.1	0.0	0.0	0.7	1.5	0.0
S13BD01721	S. flexneri 2b	S. flexneri 2b	IM	Pass	1.7	2.5	0.8	0.8	0.7	2.8	0.8	0.7	2.3	0.7	1.9	0.7	0.7	0.6	1.6	0.8
S14BD04450	S flexneri 2h	S flexneri 2h	IM	Pass	18	26	0.8	0.8	0.8	27	07	07	24	07	2.0	07	07	0.8	16	0.8
0110001100				1 455	1.0	2.0	0.0	0.0	0.0	2	0.7	0.7		0.7	2.0	0.7	0.7	0.0	1.0	0.0
S14BD05382	S. flexneri 2b	S. flexneri 2b	IIVI	Pass	1.6	2.6	0.7	0.8	0.7	2.6	0.7	0.6	2.1	0.7	1.9	0.7	0.7	0.8	1.8	0.8
S14BD05300	S. flexneri 2b	S. flexneri 2b	IM	Pass	1.6	2.5	0.7	0.6	0.6	2.8	0.7	0.6	2.3	0.6	2.1	0.6	0.7	0.6	1.6	0.7
	C flownori 2h	C flownori 2h	18.4	Dace	10	2 5	0.7	0.7	0.7	26	0.7	0.6	2.2	0.6	1.0	0.7	0.7	0.7	1 5	07
314DD00390	5. Hexhen 20	5. Hexhen 20	1111	Pass	1.0	2.5	0.7	0.7	0.7	2.0	0.7	0.0	2.5	0.0	1.9	0.7	0.7	0.7	1.5	0.7
S14BD04113	S. flexneri 2b	S. flexneri 2b	IM	Pass	1.6	2.4	0.6	0.6	0.6	2.5	0.6	0.6	2.3	0.6	1.8	0.6	0.6	0.6	1.5	0.7
\$13BD00439	S flexneri 2h	S flevneri 2h	IM	Pass	15	22	07	0.6	0.5	24	0.6	0.5	2.0	0.6	15	0.6	0.6	0.5	13	07
5150000455	5. flexifient 26	J. HEAHEH ZD	1141	1 4 3 3	1.5	2.2	0.7	0.0	0.5	2.4	0.0	0.5	2.0	0.0	1.5	0.0	0.0	0.5	1.5	0.7
S13BD02812	S. flexneri 2b	S. flexneri 2b	IM	Pass	1.8	2.7	0.7	0.5	0.7	2.9	0.6	0.6	2.4	0.6	1.9	0.7	0.7	0.5	1.7	0.6
S14BD00220	S. flexneri 2b	S. flexneri 2b	IM	Pass	1.7	2.4	0.6	0.5	0.5	3.0	0.5	0.5	2.4	0.5	2.0	0.5	0.5	0.5	1.6	0.6
C1CDD0700C	C flaura ari 2h	C. flaura et 21a	10.4	D	2.2	4.1	1.0	1.0	1.4	5.0	1.0	1 1		1.2	2.0	1.2	1 1	1.1	2.5	1 1
2108001000	S. flexneri 20	S. Tiexneri 2D	IIVI	Pass	3.3	4.1	1.0	1.0	1.4	5.0	1.0	1.1	5.0	1.2	3.8	1.2	1.1	1.1	2.5	1.1
S16BD05937	S. flexneri 3a	S. flexneri 3a	MC	Pass	4.3	5.0	1.4	0.9	1.2	8.2	1.6	9.4	2.3	2.0	7.4	1.7	2.0	1.7	5.1	1.9
\$16BD02801	S flexneri 3a	S flovnori 3a	MC	Pace	51	5.8	16	21	25	71	16	8.2	21	25	6.0	10	21	21	30	1 9
5100002001	5. flexifient 5a	J. HEAHEH Ja	IVIC	1 4 3 3	5.1	5.0	1.0	2.1	2.5	/.1	1.0	0.2	2.4	2.5	0.0	1.5	2.4	2.1	5.5	1.5
S16BD02637	S. flexneri 3a	S. flexneri 3a	MC	Pass	4.6	5.3	1.4	1.6	1.8	6.0	1.3	7.4	1.8	1.7	4.9	1.4	1.7	1.5	4.7	1.4
S16BD05105	S. flexneri 3a	S. flexneri 3a	MC	Pass	4.5	5.1	1.3	0.7	1.0	7.4	1.4	9.0	1.7	1.8	6.2	1.4	1.6	1.7	4.9	1.4
C1000004C2	C. flaumani 2a	C flaura ani 2a	140	D	4.5	F 0	1.2	1 5	17	6.0	1.2	7 1	1.0	10	4.0	1.2	17	1.2	4.5	1.2
310000402	5. Hexnen 5a	5. Hexnen 5a	IVIC	Pass	4.5	5.0	1.2	1.5	1.1	0.0	1.2	/.1	1.0	1.0	4.9	1.5	1./	1.5	4.5	1.5
S15BD04350	S. flexneri 3a	S. flexneri 3a	MC	Pass	3.8	4.6	1.0	0.6	0.7	6.8	1.1	8.0	1.3	1.2	5.5	1.3	1.3	1.2	4.0	1.2
\$15BD00004	S flexneri 3a	S flevneri 3a	мс	Pass	41	48	11	05	07	67	11	76	12	13	52	12	12	11	42	11
010000000	o fi i o			1 455				0.5	0.7	0.7	1.1			1.0	5.2		1.2			
210BD01/10	S. flexneri 3a	S. flexneri 3a	IVIC	Pass	4.1	5.1	1.0	0.6	0.7	6.9	1.2	8.3	1.3	1.1	5.9	1.4	1.3	1.1	4.5	1.1
S15BD04586	S. flexneri 3a	S. flexneri 3a	IM	Pass	3.7	4.2	1.0	1.0	1.3	5.5	0.9	5.8	1.4	1.2	4.1	1.2	1.2	1.1	3.0	1.1
\$188D00964	S flexneri 3a	S flovnori 3a	MC	Pace	30	17	11	11	11	61	10	73	12	15	18	12	11	13	10	11
510000004	5. flexifient 5a	J. HEAHEH Ja	IVIC	1 4 3 3	5.5	4.7	1.1	1.1	1.4	0.1	1.0	7.5	1.2	1.5	4.0	1.5	1.4	1.5	4.0	1.1
S17BD06364	S. flexneri 3a	S. flexneri 3a	IM	Pass	3.6	4.4	1.1	1.1	1.3	5.5	1.0	6.7	1.3	1.3	4.8	1.2	1.3	1.1	3.5	1.1
S15BD09335	S. flexneri 3a	S. flexneri 3a	IM	Pass	4.6	5.1	1.1	1.1	1.3	6.8	1.0	6.3	1.2	1.3	3.9	1.2	1.1	1.1	4.4	1.1
\$150D06521	S flovnori 2a	S flovnori 2a	154	Dace	26	12	11	0.0	1 2	55	10	E 0	12	11	26	11	12	11	20	1 1
5150000551	5. flexifient 5a	J. HEAHEH Ja	1141	1 4 3 3	5.0	4.2	1.1	0.5	1.2	5.5	1.0	5.0	1.2	1.1	5.0	1.1	1.2	1.1	5.0	1.1
S16BD05103	S. flexneri 3a	S. flexneri 3a	IM	Pass	2.7	3.4	1.1	1.1	1.3	4.9	1.1	5.6	1.0	1.1	3.9	1.1	1.0	1.1	2.1	1.0
S15BD06285	S. flexneri 3a	S. flexneri 3a	IM	Pass	3.6	4.1	0.9	1.1	1.2	5.2	0.9	5.7	1.1	1.1	3.5	1.1	1.1	1.1	2.9	1.0
											1 1		1 4 9					1.0	4.0	
\$17BD03234	S flexneri 3a	S flexneri 3a	IM	Pass	40	51	11	11	13	70		63	1 1 2	11	48	11	11	1 1 ()	40	10
S17BD03234	S. flexneri 3a	S. flexneri 3a	IM	Pass	4.0	5.1	1.1	1.1	1.3	7.0	1.1	6.3	1.2	1.1	4.8	1.1	1.1	1.0	4.0	1.0
S17BD03234 S15BD00481	S. flexneri 3a S. flexneri 3a	S. flexneri 3a S. flexneri 3a	IM MC	Pass Pass	4.0 4.4	5.1 4.7	1.1 2.0	1.1 2.1	1.3 2.7	7.0 5.7	1.1	6.3 6.8	1.2 2.5	1.1 2.5	4.8 5.0	1.1 2.2	1.1 2.4	2.5	4.0 3.3	1.0 1.9
S17BD03234 S15BD00481 S16BD09112	S. flexneri 3a S. flexneri 3a S. flexneri 3a	S. flexneri 3a S. flexneri 3a S. flexneri 3a	IM MC MC	Pass Pass Pass	4.0 4.4 3.1	5.1 4.7 3.2	1.1 2.0 2.1	1.1 2.1 1.7	1.3 2.7 3.4	7.0 5.7 5.4	1.1 1.7 1.5	6.3 6.8 5.9	1.2 2.5 1.6	1.1 2.5 1.6	4.8 5.0 5.0	1.1 2.2 1.7	1.1 2.4 1.6	1.0 2.5 1.9	4.0 3.3 2.5	1.0 1.9 1.4
S17BD03234 S15BD00481 S16BD09112 S16BD05677	S. flexneri 3a S. flexneri 3a S. flexneri 3a S. flexneri 3a	S. flexneri 3a S. flexneri 3a S. flexneri 3a S. flexneri 3a	IM MC MC IM	Pass Pass Pass Pass	4.0 4.4 3.1 3.1	5.1 4.7 3.2 3.8	1.1 2.0 2.1	1.1 2.1 1.7 1.3	1.3 2.7 3.4	7.0 5.7 5.4 4 9	1.1 1.7 1.5 1 1	6.3 6.8 5.9 5.9	1.2 2.5 1.6 1.3	1.1 2.5 1.6 1.2	4.8 5.0 5.0 4.0	1.1 2.2 1.7 1.2	1.1 2.4 1.6 1.1	1.0 2.5 1.9 1.2	4.0 3.3 2.5 2.5	1.0 1.9 1.4 1.0
S17BD03234 S15BD00481 S16BD09112 S16BD05677	S. flexneri 3a S. flexneri 3a S. flexneri 3a S. flexneri 3a	S. flexneri 3a S. flexneri 3a S. flexneri 3a S. flexneri 3a	IM MC MC IM	Pass Pass Pass Pass Pass	4.0 4.4 3.1 3.1	5.1 4.7 3.2 3.8	1.1 2.0 2.1 1.1	1.1 2.1 1.7 1.3	1.3 2.7 3.4 1.5	7.0 5.7 5.4 4.9	1.1 1.7 1.5 1.1	6.3 6.8 5.9 5.9	1.2 2.5 1.6 1.3	1.1 2.5 1.6 1.2	4.8 5.0 5.0 4.0	1.1 2.2 1.7 1.2	1.1 2.4 1.6 1.1	1.0 2.5 1.9 1.2	4.0 3.3 2.5 2.5	1.0 1.9 1.4 1.0
S17BD03234 S15BD00481 S16BD09112 S16BD05677 S15BD05434	S. flexneri 3a S. flexneri 3a S. flexneri 3a S. flexneri 3a S. flexneri 3a	S. flexneri 3a S. flexneri 3a S. flexneri 3a S. flexneri 3a S. flexneri 3a	IM MC MC IM IM	Pass Pass Pass Pass Pass	4.0 4.4 3.1 3.1 2.3	5.1 4.7 3.2 3.8 3.0	1.1 2.0 2.1 1.1 1.3	1.1 2.1 1.7 1.3 1.3	1.3 2.7 3.4 1.5 1.3	7.0 5.7 5.4 4.9 3.3	1.1 1.7 1.5 1.1 1.1	6.3 6.8 5.9 5.9 3.6	1.2 2.5 1.6 1.3 1.3	1.1 2.5 1.6 1.2 1.3	4.8 5.0 5.0 4.0 2.5	1.1 2.2 1.7 1.2 1.2	1.1 2.4 1.6 1.1 1.2	1.0 2.5 1.9 1.2 1.3	4.0 3.3 2.5 2.5 2.3	1.0 1.9 1.4 1.0 1.3
S17BD03234 S15BD00481 S16BD09112 S16BD05677 S15BD05434 S14BD03414	S. flexneri 3a S. flexneri 3a S. flexneri 3a S. flexneri 3a S. flexneri 3a S. flexneri 3a	S. flexneri 3a S. flexneri 3a S. flexneri 3a S. flexneri 3a S. flexneri 3a S. flexneri 3a	IM MC IM IM IM	Pass Pass Pass Pass Pass Pass	4.0 4.4 3.1 3.1 2.3 2.0	5.1 4.7 3.2 3.8 3.0 2.9	1.1 2.0 2.1 1.1 1.3 1.2	1.1 2.1 1.7 1.3 1.3 1.1	1.3 2.7 3.4 1.5 1.3 1.1	7.0 5.7 5.4 4.9 3.3 3.2	1.1 1.7 1.5 1.1 1.1 1.2	6.3 6.8 5.9 5.9 3.6 3.7	1.2 2.5 1.6 1.3 1.3 1.1	1.1 2.5 1.6 1.2 1.3 1.1	4.8 5.0 5.0 4.0 2.5 2.5	1.1 2.2 1.7 1.2 1.2 1.0	1.1 2.4 1.6 1.1 1.2 1.1	1.0 2.5 1.9 1.2 1.3 1.2	4.0 3.3 2.5 2.5 2.3 2.6	1.0 1.9 1.4 1.0 1.3 1.2
S17BD03234 S15BD00481 S16BD09112 S16BD05677 S15BD05434 S14BD03414 S15BD06815	S. flexneri 3a S. flexneri 3a S. flexneri 3a S. flexneri 3a S. flexneri 3a S. flexneri 3a S. flexneri 3a	S. flexneri 3a S. flexneri 3a S. flexneri 3a S. flexneri 3a S. flexneri 3a S. flexneri 3a S. flexneri 3a	IM MC IM IM IM IM	Pass Pass Pass Pass Pass Pass Pass Pass	4.0 4.4 3.1 2.3 2.0 1.3	5.1 4.7 3.2 3.8 3.0 2.9 2.1	1.1 2.0 2.1 1.1 1.3 1.2 0.9	1.1 2.1 1.7 1.3 1.3 1.1 0.6	1.3 2.7 3.4 1.5 1.3 1.1 0.7	7.0 5.7 5.4 4.9 3.3 3.2 2.4	1.1 1.7 1.5 1.1 1.1 1.2 1.1	6.3 6.8 5.9 5.9 3.6 3.7 2.9	1.2 2.5 1.6 1.3 1.3 1.1 0.5	1.1 2.5 1.6 1.2 1.3 1.1 0.7	4.8 5.0 5.0 4.0 2.5 2.5 2.0	1.1 2.2 1.7 1.2 1.2 1.0 0.6	1.1 2.4 1.6 1.1 1.2 1.1 0.8	1.0 2.5 1.9 1.2 1.3 1.2 0.8	4.0 3.3 2.5 2.5 2.3 2.6 2.4	1.0 1.9 1.4 1.0 1.3 1.2 1.0
S17BD03234 S15BD00481 S16BD09112 S16BD05677 S15BD05434 S14BD03414 S15BD06545	S. flexneri 3a S. flexneri 3a S. flexneri 3a S. flexneri 3a S. flexneri 3a S. flexneri 3a S. flexneri 3a	S. flexneri 3a S. flexneri 3a S. flexneri 3a S. flexneri 3a S. flexneri 3a S. flexneri 3a S. flexneri 3a	IM MC IM IM IM IM	Pass Pass Pass Pass Pass Pass Pass Pass	4.0 4.4 3.1 2.3 2.0 1.3	5.1 4.7 3.2 3.8 3.0 2.9 2.1	1.1 2.0 2.1 1.1 1.3 1.2 0.9	1.1 2.1 1.7 1.3 1.3 1.1 0.6 1.0	1.3 2.7 3.4 1.5 1.3 1.1 0.7	7.0 5.7 5.4 4.9 3.3 3.2 2.4 2.4	1.1 1.7 1.5 1.1 1.1 1.2 1.1	6.3 6.8 5.9 3.6 3.7 2.9	1.2 2.5 1.6 1.3 1.3 1.1 0.5	1.1 2.5 1.6 1.2 1.3 1.1 0.7	4.8 5.0 5.0 4.0 2.5 2.5 2.0 2.4	1.1 2.2 1.7 1.2 1.2 1.0 0.6	1.1 2.4 1.6 1.1 1.2 1.1 0.8 0.9	1.0 2.5 1.9 1.2 1.3 1.2 0.8	4.0 3.3 2.5 2.5 2.3 2.6 2.4 2.1	1.0 1.9 1.4 1.0 1.3 1.2 1.0
S17BD03234 S15BD00481 S16BD09112 S16BD05677 S15BD05434 S14BD03414 S15BD06815 S15BD05949	S. flexneri 3a S. flexneri 3a	S. flexneri 3a S. flexneri 3a	IM MC IM IM IM IM	Pass Pass Pass Pass Pass Pass Pass Pass	4.0 4.4 3.1 2.3 2.0 1.3 2.2	5.1 4.7 3.2 3.8 3.0 2.9 2.1 2.9	1.1 2.0 2.1 1.1 1.3 1.2 0.9 0.9	1.1 2.1 1.7 1.3 1.3 1.1 0.6 1.0	1.3 2.7 3.4 1.5 1.3 1.1 0.7 1.0	7.0 5.7 5.4 4.9 3.3 3.2 2.4 3.3	1.1 1.7 1.5 1.1 1.1 1.2 1.1 1.0	6.3 6.8 5.9 3.6 3.7 2.9 3.8	1.2 2.5 1.6 1.3 1.3 1.1 0.5 1.0	1.1 2.5 1.6 1.2 1.3 1.1 0.7 0.9	4.8 5.0 5.0 4.0 2.5 2.5 2.0 2.4	1.1 2.2 1.7 1.2 1.2 1.0 0.6 0.9	1.1 2.4 1.6 1.1 1.2 1.1 0.8 0.9	1.0 2.5 1.9 1.2 1.3 1.2 0.8 0.9	4.0 3.3 2.5 2.5 2.3 2.6 2.4 2.1	1.0 1.9 1.4 1.0 1.3 1.2 1.0 1.0
S17BD03234 S15BD00481 S16BD09112 S16BD05677 S15BD05434 S14BD03414 S15BD06815 S15BD05949 S15BD01389	S. flexneri 3a S. flexneri 3a	S. flexneri 3a S. flexneri 3a	IM MC IM IM IM IM IM	Pass Pass Pass Pass Pass Pass Pass Pass	4.0 4.4 3.1 2.3 2.0 1.3 2.2 2.2	5.1 4.7 3.2 3.8 3.0 2.9 2.1 2.9 2.9 2.9	1.1 2.0 2.1 1.1 1.3 1.2 0.9 0.9 1.0	1.1 2.1 1.7 1.3 1.3 1.1 0.6 1.0 1.0	1.3 2.7 3.4 1.5 1.3 1.1 0.7 1.0 1.1	7.0 5.7 5.4 4.9 3.3 3.2 2.4 3.3 3.2	1.1 1.7 1.5 1.1 1.1 1.2 1.1 1.0 1.0	6.3 6.8 5.9 3.6 3.7 2.9 3.8 3.8	1.2 2.5 1.6 1.3 1.3 1.1 0.5 1.0 1.1	1.1 2.5 1.6 1.2 1.3 1.1 0.7 0.9 0.9	4.8 5.0 5.0 4.0 2.5 2.5 2.0 2.4 2.4	1.1 2.2 1.7 1.2 1.2 1.0 0.6 0.9 0.9	1.1 2.4 1.6 1.1 1.2 1.1 0.8 0.9 0.9	1.0 2.5 1.9 1.2 1.3 1.2 0.8 0.9 1.0	4.0 3.3 2.5 2.5 2.3 2.6 2.4 2.1 2.1	1.0 1.9 1.4 1.0 1.3 1.2 1.0 1.0 1.0
S17BD03234 S15BD00481 S16BD09112 S16BD05677 S15BD05434 S14BD03414 S15BD05815 S15BD05949 S15BD01372	S. flexneri 3a S. flexneri 3a	S. flexneri 3a S. flexneri 3a	IM MC IM IM IM IM IM IM	Pass Pass Pass Pass Pass Pass Pass Pass	4.0 4.4 3.1 3.1 2.3 2.0 1.3 2.2 2.2 1.7	5.1 4.7 3.2 3.8 3.0 2.9 2.1 2.9 2.9 2.9 2.9 2.6	1.1 2.0 2.1 1.1 1.3 1.2 0.9 0.9 1.0 1.0	1.1 2.1 1.7 1.3 1.3 1.1 0.6 1.0 1.0 0.8	1.3 2.7 3.4 1.5 1.3 1.1 0.7 1.0 1.1 0.8	7.0 5.7 5.4 4.9 3.3 3.2 2.4 3.3 3.2 2.9	1.1 1.7 1.5 1.1 1.1 1.2 1.1 1.0 1.0 1.0	6.3 6.8 5.9 3.6 3.7 2.9 3.8 3.8 3.8 3.4	1.2 2.5 1.6 1.3 1.3 1.1 0.5 1.0 1.1 0.7	1.1 2.5 1.6 1.2 1.3 1.1 0.7 0.9 0.9 0.8	4.8 5.0 5.0 4.0 2.5 2.5 2.0 2.4 2.4 2.2	1.1 2.2 1.7 1.2 1.2 1.0 0.6 0.9 0.9 0.8	1.1 2.4 1.6 1.1 1.2 1.1 0.8 0.9 0.9 0.9 0.8	1.0 2.5 1.9 1.2 1.3 1.2 0.8 0.9 1.0 0.9	4.0 3.3 2.5 2.5 2.3 2.6 2.4 2.1 2.1 1.9	1.0 1.9 1.4 1.0 1.3 1.2 1.0 1.0 1.0 1.0
S17BD03234 S15BD00481 S16BD09112 S16BD05677 S15BD05434 S14BD03414 S15BD06815 S15BD05949 S15BD01389 S14BD03172	S. flexneri 3a S. flexneri 3a	S. flexneri 3a S. flexneri 3a	IM MC IM IM IM IM IM IM	Pass Pass Pass Pass Pass Pass Pass Pass	4.0 4.4 3.1 2.3 2.0 1.3 2.2 2.2 1.7 2.0	5.1 4.7 3.2 3.8 3.0 2.9 2.1 2.9 2.9 2.9 2.6 2.7	1.1 2.0 2.1 1.1 1.3 1.2 0.9 0.9 1.0 1.0	1.1 2.1 1.7 1.3 1.3 1.1 0.6 1.0 1.0 0.8 1.0	1.3 2.7 3.4 1.5 1.3 1.1 0.7 1.0 1.1 0.8	7.0 5.7 5.4 4.9 3.3 3.2 2.4 3.3 3.2 2.9 2.1	1.1 1.7 1.5 1.1 1.1 1.2 1.1 1.0 1.0 1.0	6.3 6.8 5.9 3.6 3.7 2.9 3.8 3.8 3.8 3.4 2.5	1.2 2.5 1.6 1.3 1.3 1.1 0.5 1.0 1.1 0.7	1.1 2.5 1.6 1.2 1.3 1.1 0.7 0.9 0.9 0.8 0.8	4.8 5.0 5.0 2.5 2.5 2.0 2.4 2.4 2.2 2.2	1.1 2.2 1.7 1.2 1.2 1.0 0.6 0.9 0.9 0.9 0.8	1.1 2.4 1.6 1.1 1.2 1.1 0.8 0.9 0.9 0.9 0.8	1.0 2.5 1.9 1.2 1.3 1.2 0.8 0.9 1.0 0.9	4.0 3.3 2.5 2.5 2.3 2.6 2.4 2.1 2.1 1.9	1.0 1.9 1.4 1.0 1.3 1.2 1.0 1.0 1.0 1.0
S17BD03234 S15BD00481 S16BD09112 S16BD05677 S15BD05434 S14BD03414 S15BD06815 S15BD05499 S15BD01389 S14BD03172 S15BD04550	S. flexneri 3a S. flexneri 3a	S. flexneri 3a S. flexneri 3a	IM MC IM IM IM IM IM IM	Pass Pass Pass Pass Pass Pass Pass Pass	4.0 4.4 3.1 3.1 2.3 2.0 1.3 2.2 2.2 1.7 2.0	5.1 4.7 3.2 3.8 3.0 2.9 2.1 2.9 2.9 2.9 2.6 2.7	1.1 2.0 2.1 1.1 1.3 1.2 0.9 0.9 1.0 1.0 1.0 0.9	1.1 2.1 1.7 1.3 1.3 1.1 0.6 1.0 1.0 0.8 1.0	1.3 2.7 3.4 1.5 1.3 1.1 0.7 1.0 1.1 0.8 1.0	7.0 5.7 5.4 4.9 3.3 3.2 2.4 3.3 3.2 2.9 3.1	1.1 1.7 1.5 1.1 1.1 1.2 1.1 1.0 1.0 1.0 0.8	6.3 6.8 5.9 3.6 3.7 2.9 3.8 3.8 3.4 3.5	1.2 2.5 1.6 1.3 1.3 1.1 0.5 1.0 1.1 0.7 1.0	1.1 2.5 1.6 1.2 1.3 1.1 0.7 0.9 0.9 0.8 0.9	4.8 5.0 5.0 4.0 2.5 2.5 2.0 2.4 2.4 2.2 2.3	1.1 2.2 1.7 1.2 1.2 1.0 0.6 0.9 0.9 0.9 0.8 0.9	1.1 2.4 1.6 1.1 1.2 1.1 0.8 0.9 0.9 0.9 0.8 0.9	1.0 2.5 1.9 1.2 1.3 1.2 0.8 0.9 1.0 0.9 0.8	4.0 3.3 2.5 2.5 2.3 2.6 2.4 2.1 2.1 1.9 2.0	1.0 1.9 1.4 1.0 1.3 1.2 1.0 1.0 1.0 1.0 0.9
S17BD03234 S15BD00481 S16BD09112 S16BD05677 S15BD05434 S15BD06815 S15BD05949 S15BD01389 S14BD03172 S15BD04550 S15BD05517	S. flexneri 3a S. flexneri 3a	S. flexneri 3a S. flexneri 3a	IM MC IM IM IM IM IM IM IM IM	Pass Pass Pass Pass Pass Pass Pass Pass	4.0 4.4 3.1 2.3 2.0 1.3 2.2 2.2 1.7 2.0 1.8	5.1 4.7 3.2 3.8 3.0 2.9 2.1 2.9 2.9 2.6 2.7 2.6	1.1 2.0 2.1 1.1 1.3 1.2 0.9 0.9 1.0 1.0 0.9 0.9	1.1 2.1 1.7 1.3 1.3 1.1 0.6 1.0 1.0 0.8 1.0 1.0	1.3 2.7 3.4 1.5 1.3 1.1 0.7 1.0 1.1 0.8 1.0 1.2	7.0 5.7 5.4 4.9 3.3 3.2 2.4 3.3 3.2 2.9 3.1 2.9	1.1 1.7 1.5 1.1 1.1 1.2 1.1 1.0 1.0 1.0 0.8 0.9	6.3 6.8 5.9 3.6 3.7 2.9 3.8 3.8 3.4 3.5 3.5	1.2 2.5 1.6 1.3 1.3 1.1 0.5 1.0 1.1 0.7 1.0 0.9	1.1 2.5 1.6 1.2 1.3 1.1 0.7 0.9 0.9 0.8 0.9 0.9 0.9	4.8 5.0 5.0 4.0 2.5 2.5 2.0 2.4 2.4 2.2 2.3 2.6	1.1 2.2 1.7 1.2 1.0 0.6 0.9 0.9 0.8 0.9 0.9 0.9	1.1 2.4 1.6 1.1 1.2 1.1 0.8 0.9 0.9 0.8 0.9 0.9 0.9	1.0 2.5 1.9 1.2 1.3 1.2 0.8 0.9 1.0 0.9 0.8 1.0	4.0 3.3 2.5 2.5 2.3 2.6 2.4 2.1 2.1 1.9 2.0 1.8	1.0 1.9 1.4 1.0 1.3 1.2 1.0 1.0 1.0 0.9 0.9
S17BD03234 S15BD00481 S16BD09112 S16BD05677 S15BD05434 S14BD03414 S15BD06815 S15BD05499 S15BD01389 S14BD03172 S15BD04550 S15BD06154	S. flexneri 3a S. flexneri 3a	S. flexneri 3a S. flexneri 3a	IM MC IM IM IM IM IM IM IM IM	Pass Pass Pass Pass Pass Pass Pass Pass	4.0 4.4 3.1 2.3 2.0 1.3 2.2 2.2 1.7 2.0 1.8 1.9	5.1 4.7 3.2 3.8 3.0 2.9 2.1 2.9 2.9 2.6 2.7 2.6 2.7 2.6 2.6	1.1 2.0 2.1 1.1 1.3 1.2 0.9 0.9 1.0 1.0 1.0 0.9 0.9 0.9 0.8	1.1 2.1 1.7 1.3 1.3 1.1 0.6 1.0 1.0 0.8 1.0 1.0 0.8	1.3 2.7 3.4 1.5 1.3 1.1 0.7 1.0 1.1 0.8 1.0 1.2 0.8	7.0 5.7 5.4 4.9 3.3 3.2 2.4 3.3 3.2 2.9 3.1 2.9 3.0	1.1 1.7 1.5 1.1 1.1 1.1 1.0 1.0 1.0 1.0 0.8 0.9 0.8	6.3 6.8 5.9 3.6 3.7 2.9 3.8 3.8 3.8 3.4 3.5 3.5 3.4	1.2 2.5 1.6 1.3 1.3 1.1 0.5 1.0 1.1 0.7 1.0 0.9 0.7	1.1 2.5 1.6 1.2 1.3 1.1 0.7 0.9 0.9 0.9 0.8 0.9 0.9 0.7	4.8 5.0 5.0 4.0 2.5 2.5 2.0 2.4 2.4 2.2 2.3 2.6 2.2	1.1 2.2 1.7 1.2 1.0 0.6 0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.7	1.1 2.4 1.6 1.1 1.2 1.1 0.8 0.9 0.9 0.8 0.9 0.9 0.9 0.9 0.8	1.0 2.5 1.9 1.2 1.3 1.2 0.8 0.9 1.0 0.9 0.8 1.0 0.8	4.0 3.3 2.5 2.5 2.3 2.6 2.4 2.1 2.1 1.9 2.0 1.8 1.8	1.0 1.9 1.4 1.0 1.3 1.2 1.0 1.0 1.0 1.0 0.9 0.9 0.9
S17BD03234 S15BD00481 S16BD09112 S16BD05677 S15BD05434 S15BD06815 S15BD06815 S15BD06815 S15BD04550 S15BD04550 S15BD04550 S15BD04551 S15BD0454	S. flexneri 3a S. flexneri 3a	S. flexneri 3a S. flexneri 3a	IM MC IM IM IM IM IM IM IM	Pass Pass Pass Pass Pass Pass Pass Pass	4.0 4.4 3.1 3.1 2.3 2.0 1.3 2.2 2.2 1.7 2.0 1.8 1.9	5.1 4.7 3.2 3.8 3.0 2.9 2.1 2.9 2.9 2.6 2.7 2.6 2.6 2.6 2.6	1.1 2.0 2.1 1.1 1.3 1.2 0.9 0.9 1.0 1.0 1.0 0.9 0.9 0.8 0.8	1.1 2.1 1.7 1.3 1.3 1.1 0.6 1.0 1.0 0.8 1.0 1.0 0.8	1.3 2.7 3.4 1.5 1.3 1.1 0.7 1.0 1.1 0.8 1.0 1.2 0.8	7.0 5.7 5.4 4.9 3.3 3.2 2.4 3.3 3.2 2.9 3.1 2.9 3.0 2.2	1.1 1.7 1.5 1.1 1.1 1.2 1.1 1.0 1.0 1.0 0.8 0.9 0.8 0.7	6.3 6.8 5.9 3.6 3.7 2.9 3.8 3.8 3.4 3.5 3.5 3.4 2.6	1.2 2.5 1.6 1.3 1.3 1.1 0.5 1.0 1.1 0.7 1.0 0.9 0.7	1.1 2.5 1.6 1.2 1.3 1.1 0.7 0.9 0.9 0.9 0.9 0.9 0.7 0.7	4.8 5.0 5.0 4.0 2.5 2.5 2.0 2.4 2.4 2.2 2.3 2.6 2.2 2.4	1.1 2.2 1.7 1.2 1.2 1.0 0.6 0.9 0.9 0.9 0.9 0.9 0.9 0.7 0.7	1.1 2.4 1.6 1.1 1.2 1.1 0.8 0.9 0.9 0.9 0.8 0.9 0.9 0.8 0.9 0.8	1.0 2.5 1.9 1.2 1.3 1.2 0.8 0.9 1.0 0.9 0.8 1.0 0.8	4.0 3.3 2.5 2.5 2.3 2.6 2.4 2.1 2.1 1.9 2.0 1.8 1.8	1.0 1.9 1.4 1.0 1.3 1.2 1.0 1.0 1.0 1.0 0.9 0.9 0.9
S17BD03234 S15BD00481 S16BD09112 S16BD05677 S15BD05434 S14BD03414 S15BD05949 S15BD05949 S14BD03172 S15BD04550 S15BD0517 S15BD06154 S18BD01687	S. flexneri 3a S. flexneri 3a	S. flexneri 3a S. flexneri 3a	IM MC IM IM IM IM IM IM IM IM IM	Pass Pass Pass Pass Pass Pass Pass Pass	4.0 4.4 3.1 2.3 2.0 1.3 2.2 2.2 1.7 2.0 1.8 1.9 1.9	5.1 4.7 3.2 3.8 3.0 2.9 2.1 2.9 2.9 2.6 2.7 2.6 2.7 2.6 2.6 2.6	1.1 2.0 2.1 1.1 1.3 1.2 0.9 0.9 1.0 1.0 0.9 0.9 0.8 0.8	1.1 2.1 1.7 1.3 1.3 1.1 0.6 1.0 1.0 0.8 1.0 1.0 0.8 0.8	1.3 2.7 3.4 1.5 1.3 1.1 0.7 1.0 1.1 0.8 1.0 1.2 0.8 0.9	7.0 5.7 5.4 4.9 3.3 3.2 2.4 3.3 3.2 2.9 3.1 2.9 3.0 3.2 3.2	1.1 1.7 1.5 1.1 1.1 1.2 1.1 1.0 1.0 1.0 0.8 0.9 0.8 0.7	6.3 6.8 5.9 3.6 3.7 2.9 3.8 3.8 3.4 3.5 3.5 3.4 3.6	1.2 2.5 1.6 1.3 1.3 1.1 0.5 1.0 1.1 0.7 1.0 0.9 0.7 0.7	1.1 2.5 1.6 1.2 1.3 1.1 0.7 0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.7 0.7	4.8 5.0 5.0 4.0 2.5 2.5 2.0 2.4 2.4 2.2 2.3 2.6 2.2 2.4	1.1 2.2 1.7 1.2 1.2 1.0 0.6 0.9 0.9 0.9 0.9 0.9 0.9 0.7 0.7	1.1 2.4 1.6 1.1 1.2 1.1 0.8 0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.8 0.9 0.8 0.8	1.0 2.5 1.9 1.2 1.3 1.2 0.8 0.9 1.0 0.9 0.8 1.0 0.8 0.8	4.0 3.3 2.5 2.5 2.3 2.6 2.4 2.1 2.1 1.9 2.0 1.8 1.8 1.9	$1.0 \\ 1.9 \\ 1.4 \\ 1.0 \\ 1.3 \\ 1.2 \\ 1.0 \\ 1.0 \\ 1.0 \\ 1.0 \\ 0.9 \\ 0.9 \\ 0.9 \\ 0.8 $
S17RD03234 S15BD00481 S16BD09112 S16BD05677 S15BD05434 S15BD06815 S15BD06815 S15BD06815 S15BD04550 S15BD04550 S15BD04550 S15BD04557 S15BD06154 S18BD01687 S15BD00512	S. flexneri 3a S. flexneri 3a	S. flexneri 3a S. flexneri 3a	IM MC IM IM IM IM IM IM IM IM IM IM	Pass Pass Pass Pass Pass Pass Pass Pass	4.0 4.4 3.1 2.3 2.0 1.3 2.2 2.2 1.7 2.0 1.8 1.9 1.9 1.9	5.1 4.7 3.2 3.8 3.0 2.9 2.1 2.9 2.9 2.9 2.6 2.7 2.6 2.6 2.6 2.6 2.6	1.1 2.0 2.1 1.1 1.3 1.2 0.9 0.9 1.0 1.0 1.0 0.9 0.9 0.9 0.8 0.8 0.8	1.1 2.1 1.7 1.3 1.3 1.1 0.6 1.0 1.0 0.8 1.0 1.0 0.8 0.8 0.8	1.3 2.7 3.4 1.5 1.3 1.1 0.7 1.0 1.1 0.8 1.0 1.2 0.8 0.9 0.9	7.0 5.7 5.4 4.9 3.3 3.2 2.4 3.3 3.2 2.9 3.1 2.9 3.0 3.2 3.2 3.1 2.9 3.0 3.2 3.1	1.1 1.7 1.5 1.1 1.1 1.2 1.1 1.0 1.0 1.0 0.8 0.9 0.8 0.7 0.8	6.3 6.8 5.9 3.6 3.7 2.9 3.8 3.8 3.4 3.5 3.5 3.4 3.6 3.5	1.2 2.5 1.6 1.3 1.3 1.1 0.5 1.0 1.1 0.7 1.0 0.9 0.7 0.7 0.7	1.1 2.5 1.6 1.2 1.3 1.1 0.7 0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.7 0.7 0.7 0.8	4.8 5.0 5.0 4.0 2.5 2.5 2.0 2.4 2.4 2.2 2.3 2.6 2.2 2.4 2.2 2.4 2.2	1.1 2.2 1.7 1.2 1.2 1.0 0.6 0.9 0.9 0.9 0.9 0.9 0.9 0.7 0.7 0.7	1.1 2.4 1.6 1.1 1.2 1.1 0.8 0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.8 0.9 0.8 0.9	1.0 2.5 1.9 1.2 1.3 1.2 0.8 0.9 1.0 0.9 0.8 1.0 0.8 0.8 0.8 0.7	4.0 3.3 2.5 2.5 2.3 2.6 2.4 2.1 2.1 1.9 2.0 1.8 1.8 1.9 1.8	$1.0 \\ 1.9 \\ 1.4 \\ 1.0 \\ 1.3 \\ 1.2 \\ 1.0 \\ 1.0 \\ 1.0 \\ 1.0 \\ 0.9 \\ 0.9 \\ 0.9 \\ 0.8 $
S17BD03234 S15BD00481 S16BD09112 S16BD05677 S15BD05434 S15BD05434 S15BD05849 S15BD05849 S15BD05817 S15BD04550 S15BD05517 S15BD06154 S18BD01687 S15BD05677	S. flexneri 3a S. flexneri 3a	S. flexneri 3a S. flexneri 3a	IM MC IM IM IM IM IM IM IM IM IM	Pass Pass Pass Pass Pass Pass Pass Pass	4.0 4.4 3.1 2.3 2.0 1.3 2.2 2.2 1.7 2.0 1.8 1.9 1.9 1.9 1.9	5.1 4.7 3.2 3.8 3.0 2.9 2.1 2.9 2.6 2.6 2.6 2.6 2.6 2.6 2.6 2.5	1.1 2.0 2.1 1.1 1.3 1.2 0.9 0.9 1.0 1.0 1.0 0.9 0.9 0.8 0.8 0.8 0.8	1.1 2.1 1.7 1.3 1.3 1.1 0.6 1.0 1.0 0.8 1.0 1.0 0.8 0.8 0.8 0.8 0.7	1.3 2.7 3.4 1.5 1.3 1.1 0.7 1.0 1.1 0.8 1.0 1.2 0.8 0.9 0.9 0.7	7.0 5.7 5.4 4.9 3.3 3.2 2.4 3.3 3.2 2.9 3.1 2.9 3.0 3.2 3.1 2.9	1.1 1.7 1.5 1.1 1.1 1.2 1.1 1.0 1.0 1.0 1.0 0.8 0.9 0.8 0.7 0.8 0.7	6.3 6.8 5.9 3.6 3.7 2.9 3.8 3.8 3.4 3.5 3.5 3.4 3.6 3.5 3.3	1.2 2.5 1.6 1.3 1.3 1.1 0.5 1.0 1.1 0.7 1.0 0.9 0.7 0.7 0.7 0.7 0.8	1.1 2.5 1.6 1.2 1.3 1.1 0.7 0.9 0.9 0.9 0.9 0.9 0.7 0.7 0.7 0.8 0.7	4.8 5.0 5.0 4.0 2.5 2.5 2.0 2.4 2.4 2.2 2.3 2.6 2.2 2.4 2.2 2.4 2.2 2.2	1.1 2.2 1.7 1.2 1.0 0.6 0.9 0.9 0.9 0.9 0.9 0.9 0.7 0.7 0.7 0.7 0.7	1.1 2.4 1.6 1.1 1.2 1.1 0.8 0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.8 0.9 0.9 0.8 0.9 0.7	1.0 2.5 1.9 1.2 1.3 1.2 0.8 0.9 1.0 0.9 0.8 1.0 0.8 0.8 0.7 0.7	4.0 3.3 2.5 2.5 2.3 2.6 2.4 2.1 2.1 1.9 2.0 1.8 1.8 1.9 1.8 1.8	1.0 1.9 1.4 1.0 1.3 1.2 1.0 1.0 1.0 1.0 0.9 0.9 0.9 0.8 0.8 0.7
S17BD03234 S15BD00481 S16BD09112 S16BD05677 S15BD05434 S14BD03414 S15BD06815 S15BD0549 S15BD01389 S14BD03172 S15BD04550 S15BD0517 S15BD06154 S18BD01687 S15BD06154 S18BD01687 S15BD0512 S16BD05677	S. flexneri 3a S. flexneri 3a	S. flexneri 3a S. flexneri 3a	IM MC IM IM IM IM IM IM IM IM IM	Pass Pass Pass Pass Pass Pass Pass Pass	4.0 4.4 3.1 3.1 2.3 2.0 1.3 2.2 2.2 1.7 2.0 1.8 1.9 1.9 1.9 1.9	5.1 4.7 3.2 3.8 3.0 2.9 2.1 2.9 2.6 2.7 2.6 2.6 2.6 2.6 2.6 2.5 2.2	1.1 2.0 2.1 1.1 1.3 1.2 0.9 0.9 1.0 1.0 0.9 0.9 0.9 0.8 0.8 0.8 0.8 0.8	1.1 2.1 1.7 1.3 1.3 1.1 0.6 1.0 1.0 0.8 1.0 1.0 0.8 0.8 0.8 0.8 0.7 0.6	1.3 2.7 3.4 1.5 1.3 1.1 0.7 1.0 1.1 0.8 1.0 1.2 0.8 0.9 0.9 0.7 0.7	7.0 5.7 5.4 4.9 3.3 3.2 2.4 3.3 3.2 2.9 3.1 2.9 3.0 3.2 3.1 2.9 3.2 3.1 2.9 3.7	1.1 1.7 1.5 1.1 1.1 1.2 1.1 1.0 1.0 1.0 1.0 0.8 0.9 0.8 0.7 0.8 0.7 0.6	6.3 6.8 5.9 3.6 3.7 2.9 3.8 3.8 3.4 3.5 3.5 3.4 3.5 3.4 3.6 3.5 3.4 3.5 3.2	1.2 2.5 1.6 1.3 1.3 1.1 0.5 1.0 1.1 0.7 1.0 0.9 0.7 0.7 0.7 0.7 0.7 0.8 0.6	1.1 2.5 1.6 1.2 1.3 1.1 0.7 0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.7 0.7 0.7 0.8 0.7 0.6	4.8 5.0 5.0 4.0 2.5 2.5 2.0 2.4 2.4 2.2 2.3 2.6 2.2 2.4 2.2 2.2 2.2 2.2	1.1 2.2 1.7 1.2 1.0 0.6 0.9 0.9 0.9 0.9 0.9 0.7 0.7 0.7 0.7 0.6 0.6	1.1 2.4 1.6 1.1 1.2 1.1 0.8 0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.8 0.9 0.9 0.8 0.9 0.9 0.7 0.7	1.0 2.5 1.9 1.2 1.3 1.2 0.8 0.9 1.0 0.9 0.8 1.0 0.9 0.8 1.0 0.8 0.8 0.7 0.7	4.0 3.3 2.5 2.5 2.3 2.6 2.4 2.1 2.1 1.9 2.0 1.8 1.8 1.8 1.8 1.8	1.0 1.9 1.4 1.0 1.3 1.2 1.0 1.0 1.0 1.0 0.9 0.9 0.9 0.8 0.8 0.7 0.7
S17BD03234 S15BD00481 S16BD09112 S16BD05677 S15BD05434 S15BD05815 S15BD05949 S15BD01389 S14BD03172 S15BD04550 S15BD045517 S15BD06154 S18BD01687 S15BD05677 S14BD03746	S. flexneri 3a S. flexneri 3a	S. flexneri 3a S. flexneri 3a	IM MC IM IM IM IM IM IM IM IM IM IM IM	Pass Pass Pass Pass Pass Pass Pass Pass	4.0 4.4 3.1 3.1 2.3 2.0 1.3 2.2 2.2 1.7 2.0 1.8 1.9 1.9 1.9 1.9 1.8 1.5	5.1 4.7 3.2 3.8 3.0 2.9 2.1 2.9 2.9 2.6 2.7 2.6 2.6 2.6 2.6 2.6 2.5 2.2	1.1 2.0 2.1 1.1 1.3 1.2 0.9 0.9 1.0 1.0 0.9 0.9 0.9 0.8 0.8 0.8 0.8 0.8 0.7	1.1 2.1 1.7 1.3 1.3 1.1 0.6 1.0 1.0 0.8 1.0 1.0 0.8 0.8 0.8 0.8 0.7 0.6	1.3 2.7 3.4 1.5 1.3 1.1 0.7 1.0 1.1 0.8 1.0 1.2 0.8 0.9 0.9 0.7 0.9	7.0 5.7 5.4 4.9 3.3 3.2 2.4 3.3 3.2 2.9 3.1 2.9 3.0 3.2 3.1 2.9 3.2 3.1 2.9 3.2	$\begin{array}{c} 1.1\\ 1.7\\ 1.5\\ 1.1\\ 1.1\\ 1.2\\ 1.1\\ 1.0\\ 1.0\\ 1.0\\ 0.8\\ 0.9\\ 0.8\\ 0.7\\ 0.8\\ 0.7\\ 0.8\\ 0.7\\ 0.6\\ \end{array}$	6.3 6.8 5.9 3.6 3.7 2.9 3.8 3.8 3.4 3.5 3.5 3.4 3.5 3.4 3.5 3.5 3.4 3.5 3.2	1.2 2.5 1.6 1.3 1.3 1.1 0.5 1.0 1.1 0.7 1.0 0.9 0.7 0.7 0.7 0.7 0.8 0.6	1.1 2.5 1.6 1.2 1.3 1.1 0.7 0.9 0.9 0.9 0.9 0.9 0.7 0.7 0.7 0.8 0.7 0.6	4.8 5.0 5.0 4.0 2.5 2.5 2.0 2.4 2.4 2.2 2.3 2.6 2.2 2.4 2.2 2.2 2.2 2.3	1.1 2.2 1.7 1.2 1.2 1.0 0.6 0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.7 0.7 0.7 0.7 0.6 0.6	1.1 2.4 1.6 1.1 1.2 1.1 0.8 0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.9	1.0 2.5 1.9 1.2 1.3 1.2 0.8 0.9 1.0 0.9 0.8 1.0 0.8 0.8 0.7 0.7 0.6	4.0 3.3 2.5 2.5 2.5 2.3 2.6 2.4 2.1 2.1 1.9 2.0 1.8 1.8 1.9 1.8 1.8 1.4	$1.0 \\ 1.9 \\ 1.4 \\ 1.0 \\ 1.3 \\ 1.2 \\ 1.0 \\ 1.0 \\ 1.0 \\ 1.0 \\ 0.9 \\ 0.9 \\ 0.9 \\ 0.9 \\ 0.8 \\ 0.7 $
S17BD03234 S15BD00481 S16BD09677 S15BD05677 S15BD05434 S14BD03414 S15BD05845 S15BD05949 S15BD05949 S15BD0517 S15BD06154 S15BD06154 S15BD06154 S15BD06517 S15BD06517 S14BD03746 S15BD06817	S. flexneri 3a S. flexneri 3a	S. flexneri 3a S. flexneri 3a	IM MC IM IM IM IM IM IM IM IM IM IM IM	Pass Pass Pass Pass Pass Pass Pass Pass	4.0 4.4 3.1 3.1 2.3 2.0 1.3 2.2 2.2 1.7 2.0 1.8 1.9 1.9 1.9 1.9 1.9 1.8 1.5 1.7	5.1 4.7 3.2 3.8 3.0 2.9 2.1 2.9 2.6 2.6 2.6 2.6 2.6 2.6 2.6 2.6 2.5 2.2 2.4	1.1 2.0 2.1 1.1 1.3 1.2 0.9 0.9 0.9 0.9 0.9 0.9 0.8 0.8 0.8 0.8 0.8 0.7 0.8	1.1 2.1 1.7 1.3 1.3 1.1 0.6 1.0 1.0 0.8 0.8 0.8 0.8 0.7 0.6 0.6	1.3 2.7 3.4 1.5 1.3 1.1 0.7 1.0 1.1 0.8 0.9 0.9 0.7 0.9 0.7	7.0 5.7 5.4 4.9 3.3 3.2 2.4 3.3 3.2 2.9 3.1 2.9 3.0 3.2 3.1 2.9 3.0 3.2 3.1 2.9 3.2 3.1 2.9 3.0 3.2 3.1 2.9 3.2 3.1 2.9 3.2 2.7 2.6	1.1 1.7 1.5 1.1 1.1 1.2 1.1 1.0 1.0 1.0 0.8 0.9 0.8 0.7 0.8 0.7 0.6 0.7	6.3 6.8 5.9 3.6 3.7 2.9 3.8 3.4 3.5 3.4 3.5 3.4 3.6 3.5 3.3 3.2 3.1	1.2 2.5 1.6 1.3 1.3 1.1 0.5 1.0 1.1 0.7 1.0 0.9 0.7 0.7 0.7 0.7 0.7 0.7 0.8 0.6 0.5	1.1 2.5 1.6 1.2 1.3 1.1 0.7 0.9 0.9 0.9 0.9 0.9 0.7 0.7 0.7 0.7 0.8 0.7 0.6 0.6	4.8 5.0 5.0 4.0 2.5 2.5 2.0 2.4 2.4 2.2 2.3 2.6 2.2 2.4 2.2 2.2 2.2 2.3 1.9	1.1 2.2 1.7 1.2 1.0 0.6 0.9 0.9 0.9 0.9 0.7 0.7 0.7 0.7 0.7 0.6 0.6	1.1 2.4 1.6 1.1 1.2 1.1 0.8 0.9 0.9 0.8 0.9 0.9 0.8 0.9 0.8 0.9 0.7 0.6 0.8	1.0 2.5 1.9 1.2 1.3 1.2 0.8 0.9 1.0 0.9 0.8 1.0 0.8 0.8 0.7 0.7 0.7 0.6 0.6	4.0 3.3 2.5 2.5 2.3 2.6 2.4 2.1 2.1 1.9 2.0 1.8 1.8 1.8 1.8 1.8 1.4 1.5	1.0 1.9 1.4 1.0 1.3 1.2 1.0 1.0 1.0 1.0 0.9 0.9 0.9 0.9 0.9 0.8 0.7 0.7 0.7
S17BD03234 S15BD00481 S16BD09112 S16BD05677 S15BD05434 S15BD06815 S15BD05949 S15BD05949 S15BD04550 S15BD04550 S15BD04550 S15BD045517 S15BD06512 S16BD05677 S14BD03746 S15BD06817 S14BD03502	S. flexneri 3a S. flexneri 3a	S. flexneri 3a S. flexneri 3a	IM MC IM IM IM IM IM IM IM IM IM IM IM IM	Pass Pass Pass Pass Pass Pass Pass Pass	4.0 4.4 3.1 3.1 2.3 2.0 1.3 2.2 2.2 1.7 2.0 1.8 1.9 1.9 1.9 1.9 1.8 1.5 1.7 4.8	5.1 4.7 3.2 3.8 3.0 2.9 2.1 2.9 2.6 2.7 2.6 2.6 2.6 2.6 2.6 2.6 2.6 2.6 2.2 2.4 5 9	1.1 2.0 2.1 1.1 1.3 1.2 0.9 0.9 1.0 1.0 1.0 0.9 0.9 0.8 0.8 0.8 0.8 0.8 0.8 0.7 0.8 1.1	1.1 2.1 1.7 1.3 1.3 1.1 0.6 1.0 1.0 0.8 1.0 1.0 0.8 0.8 0.8 0.8 0.7 0.6 0.6 1.1	1.3 2.7 3.4 1.5 1.3 1.1 0.7 1.0 1.1 0.8 1.0 1.2 0.8 0.9 0.9 0.7 0.9 0.7 1.2	7.0 5.7 5.4 4.9 3.3 3.2 2.4 3.3 3.2 2.9 3.1 2.9 3.0 3.2 3.1 2.9 3.0 3.2 3.1 2.9 2.7 2.6 7 8	1.1 1.7 1.5 1.1 1.1 1.2 1.1 1.0 1.0 1.0 1.0 0.8 0.9 0.8 0.7 0.6 0.7 1.1	6.3 6.8 5.9 5.9 3.6 3.7 2.9 3.8 3.4 3.5 3.4 3.5 3.4 3.5 3.4 3.5 3.2 3.1 7 3	1.2 2.5 1.6 1.3 1.3 1.1 0.5 1.0 1.1 0.7 1.0 0.9 0.7 0.7 0.7 0.7 0.7 0.7 0.7 0.7 0.7 0.7	1.1 2.5 1.6 1.2 1.3 1.1 0.7 0.9 0.9 0.9 0.9 0.9 0.9 0.7 0.7 0.7 0.7 0.7 0.7 0.7 0.7 0.7 0.6 0.6 1.1	4.8 5.0 5.0 2.5 2.5 2.0 2.4 2.4 2.2 2.3 2.6 2.2 2.4 2.2 2.4 2.2 2.3 1.9 4 7	1.1 2.2 1.7 1.2 1.0 0.6 0.9 0.9 0.9 0.9 0.9 0.7 0.7 0.7 0.7 0.7 0.6 0.6 0.6 1.2	1.1 2.4 1.6 1.1 1.2 1.1 0.8 0.9 0.9 0.9 0.9 0.9 0.9 0.8 0.9 0.7 0.6 0.8 1.0	1.0 2.5 1.9 1.2 1.3 1.2 0.8 0.9 1.0 0.9 0.8 1.0 0.8 0.8 0.7 0.7 0.6 0.6 1.1	4.0 3.3 2.5 2.5 2.3 2.6 2.4 2.1 2.1 1.9 2.0 1.8 1.8 1.9 1.8 1.8 1.9 1.8 1.4 1.5 4 5	1.0 1.9 1.4 1.0 1.3 1.2 1.0 1.0 1.0 1.0 0.9 0.9 0.9 0.9 0.9 0.9 0.8 0.7 0.7 0.7 1.1
S17BD03234 S15BD00481 S16BD09677 S15BD05677 S15BD05434 S18BD06815 S15BD05949 S15BD01389 S14BD0372 S15BD06154 S15BD06154 S15BD06154 S15BD06154 S15BD06154 S15BD06154 S15BD0677 S14BD03746 S15BD06817 S14BD03746	S. flexneri 3a S. flexneri 3a	S. flexneri 3a S. flexneri 3a	IM MC IM IM IM IM IM IM IM IM IM IM IM IM IM	Pass Pass Pass Pass Pass Pass Pass Pass	4.0 4.4 3.1 3.1 2.3 2.2 1.7 2.0 1.8 1.9 1.9 1.9 1.9 1.9 1.8 1.5 1.7 4.8	5.1 4.7 3.2 3.8 3.0 2.9 2.1 2.9 2.9 2.6 2.7 2.6 2.7 2.6 2.6 2.6 2.6 2.6 2.5 2.2 2.4 5.9	1.1 2.0 2.1 1.1 1.3 1.2 0.9 0.9 1.0 1.0 0.9 0.9 0.9 0.8 0.8 0.8 0.8 0.8 0.7 0.8 1.1	1.1 2.1 1.7 1.3 1.3 1.1 0.6 1.0 1.0 0.8 1.0 1.0 0.8 0.8 0.8 0.8 0.7 0.6 0.6 1.1 2.2	1.3 2.7 3.4 1.5 1.3 1.1 0.7 1.0 1.1 0.8 1.0 1.2 0.8 0.9 0.9 0.7 0.9 0.7 1.2 2.2	7.0 5.7 5.4 4.9 3.3 3.2 2.4 3.3 3.2 2.9 3.1 2.9 3.0 3.2 3.1 2.9 3.0 3.2 3.1 2.9 3.0 3.2 3.1 2.9 3.0 3.2 3.1 2.9 3.0 3.2 3.1 2.9 3.0 3.2 3.1 2.9 3.0 3.2 3.1 2.9 3.0 3.2 2.4 3.0 3.2 2.4 3.3 3.2 2.4 3.3 3.2 2.4 3.3 3.2 2.4 3.3 3.2 2.4 3.3 3.2 2.4 3.3 3.2 2.4 3.3 3.2 2.4 3.3 3.2 2.4 3.3 3.2 2.4 3.3 3.2 2.4 3.3 3.2 2.4 3.3 3.2 2.5 3.1 2.5 3.1 2.5 3.5 3.2 2.5 3.1 2.5 3.5 3.2 2.5 3.5 3.5 3.5 2.5 3.5 3.5 3.5 3.5 3.5 3.5 3.5 3.5 3.5 3	1.1 1.7 1.5 1.1 1.1 1.2 1.1 1.0 1.0 1.0 1.0 0.8 0.9 0.8 0.7 0.8 0.7 0.8 0.7 0.6 0.7 1.1 1.2 0.7 0.8 0.8 0.7 0.8 0.8 0.8 0.7 0.8 0.7 0.8 0.7 0.8 0.7 0.8 0.7 0.8 0.8 0.7 0.8 0.7 0.8 0.7 0.8 0.7 0.8 0.8 0.8 0.8 0.7 0.8 0.8 0.8 0.7 0.8 0.7 0.8 0.8 0.8 0.8 0.8 0.8 0.8 0.8	6.3 6.8 5.9 3.6 3.7 2.9 3.8 3.8 3.4 3.5 3.5 3.4 3.5 3.4 3.5 3.2 3.1 7.3 3.2 3.1 7.3	1.2 2.5 1.6 1.3 1.3 1.1 0.5 1.0 1.1 0.7 0.7 0.7 0.7 0.7 0.7 0.7 0.7 0.7 0.7	1.1 2.5 1.6 1.2 1.3 1.1 0.7 0.9 0.9 0.9 0.9 0.9 0.9 0.7 0.7 0.7 0.8 0.7 0.6 0.6 1.1	4.8 5.0 5.0 4.0 2.5 2.5 2.0 2.4 2.4 2.2 2.3 2.6 2.2 2.4 2.2 2.2 2.3 1.9 4.7 2.5	1.1 2.2 1.7 1.2 1.0 0.6 0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.7 0.7 0.7 0.7 0.6 0.6 0.6 1.2	1.1 2.4 1.6 1.1 1.2 1.1 0.8 0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.9	1.0 2.5 1.9 1.2 1.3 1.2 0.8 0.9 1.0 0.9 0.8 0.9 1.0 0.9 0.8 0.9 0.8 0.7 0.7 0.6 0.6 1.1	4.0 3.3 2.5 2.5 2.3 2.6 2.4 2.1 2.1 1.9 2.0 1.8 1.8 1.8 1.8 1.8 1.8 1.4 1.5 4.5 2.2	1.0 1.9 1.4 1.0 1.3 1.2 1.0 1.0 1.0 1.0 0.9 0.9 0.9 0.9 0.8 0.7 0.7 0.7 1.1 1.0
S17BD03234 S15BD00481 S16BD09112 S16BD05677 S15BD05434 S15BD06815 S15BD05949 S15BD04550 S15BD04550 S15BD04550 S15BD05517 S15BD06154 S15BD00512 S16BD05677 S14BD03746 S15BD06817 S14BD02502 S14BD01142	S. flexneri 3a S. flexneri 3a	S. flexneri 3a S. flexneri 3a	IM MC IM IM IM IM IM IM IM IM IM IM IM IM IM	Pass Pass Pass Pass Pass Pass Pass Pass	4.0 4.4 3.1 3.1 2.3 2.0 1.3 2.2 2.2 1.7 2.0 1.8 1.9 1.9 1.9 1.9 1.9 1.8 1.5 1.7 4.8 2.9	5.1 4.7 3.2 3.8 3.0 2.9 2.1 2.9 2.6 2.7 2.6 2.6 2.6 2.6 2.6 2.6 2.5 2.2 2.4 5.9 3.7	1.1 2.0 2.1 1.1 1.3 1.2 0.9 0.9 1.0 1.0 0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.8 0.8 0.8 0.8 0.7 0.8 1.1 0.9	1.1 2.1 1.7 1.3 1.3 1.1 0.6 1.0 1.0 0.8 1.0 1.0 0.8 0.8 0.8 0.8 0.7 0.6 0.6 1.1 0.8	1.3 2.7 3.4 1.5 1.3 1.1 0.7 1.0 1.1 0.8 1.0 1.2 0.8 0.9 0.9 0.7 0.9 0.7 1.2 0.8	7.0 5.7 5.4 4.9 3.3 3.2 2.4 3.3 3.2 2.9 3.1 2.9 3.0 3.2 3.1 2.9 2.7 2.6 7.8 4.8	$\begin{array}{c} 1.1\\ 1.7\\ 1.5\\ 1.1\\ 1.1\\ 1.2\\ 1.1\\ 1.0\\ 1.0\\ 1.0\\ 0.8\\ 0.9\\ 0.8\\ 0.7\\ 0.8\\ 0.7\\ 0.8\\ 0.7\\ 0.6\\ 0.7\\ 1.1\\ 0.8 \end{array}$	6.3 6.8 5.9 5.9 3.6 3.7 2.9 3.8 3.7 3.8 3.8 3.4 3.5 3.5 3.4 3.5 3.4 3.5 3.4 3.5 3.4 3.5 3.2 3.1 7.3 5.2	1.2 2.5 1.6 1.3 1.3 1.1 0.5 1.0 1.1 0.7 1.0 0.9 0.7 0.7 0.7 0.7 0.7 0.8 0.6 0.5 1.2 0.7	1.1 2.5 1.6 1.2 1.3 1.1 0.7 0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.7 0.7 0.7 0.7 0.8 0.7 0.6 0.6 1.1 1.0	4.8 5.0 5.0 2.5 2.5 2.0 2.4 2.4 2.2 2.3 2.6 2.2 2.4 2.2 2.2 2.2 2.3 1.9 4.7 3.5	1.1 2.2 1.7 1.2 1.0 0.6 0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.7 0.7 0.7 0.7 0.6 0.6 0.6 1.2 0.9	1.1 2.4 1.6 1.1 1.2 1.1 0.8 0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.9	$\begin{array}{c} 1.0\\ \hline 2.5\\ 1.9\\ 1.2\\ 1.3\\ 1.2\\ 0.8\\ 0.9\\ 1.0\\ 0.9\\ 0.8\\ 1.0\\ 0.8\\ 0.7\\ 0.7\\ 0.6\\ 0.6\\ 1.1\\ 0.9 \end{array}$	4.0 3.3 2.5 2.5 2.3 2.6 2.4 2.1 2.1 1.9 2.0 1.8 1.8 1.9 1.8 1.8 1.9 1.8 1.4 1.5 4.5 2.3	1.0 1.9 1.4 1.0 1.3 1.2 1.0 1.0 1.0 1.0 0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.9 0
S17BD03234 S15BD00481 S16BD09112 S16BD05677 S15BD05434 S18BD05815 S15BD05949 S15BD01389 S14BD0372 S15BD05517 S15BD05517 S15BD05517 S16BD05677 S14BD03746 S15BD06817 S14BD03746 S15BD06817 S14BD03742 S14BD01131	S. flexneri 3a S. flexneri x	S. flexneri 3a S. flexneri 3a	IM MC IM IM IM IM IM IM IM IM IM IM IM IM IM	Pass Pass Pass Pass Pass Pass Pass Pass	4.0 4.4 3.1 2.3 2.0 1.3 2.2 2.2 1.7 2.0 1.8 1.9 1.9 1.9 1.9 1.9 1.9 1.9 1.9 1.9 2.2 2.2 1.7 2.0 1.3 2.2 2.2 1.7 2.0 1.3 2.2 2.2 1.7 2.0 1.3 2.2 2.2 2.2 1.7 2.0 1.3 2.2 2.2 2.2 1.7 2.0 1.3 2.2 2.2 2.2 1.7 2.0 1.3 2.2 2.2 2.2 2.2 1.7 2.0 2.0 1.3 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2	5.1 4.7 3.2 3.8 3.0 2.9 2.1 2.9 2.9 2.6 2.7 2.6 2.6 2.6 2.6 2.6 2.6 2.5 2.2 2.4 5.9 3.7 3.8	1.1 2.0 2.1 1.1 1.3 1.2 0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.9	1.1 2.1 1.7 1.3 1.3 1.1 1.0 0.8 1.0 1.0 0.8 0.8 0.8 0.8 0.8 0.7 0.6 0.6 0.6 0.6 1.1 0.8 0.8	1.3 2.7 3.4 1.5 1.3 1.1 0.7 1.0 1.1 0.8 1.0 1.2 0.8 0.9 0.7 0.9 0.7 0.9 0.7 0.9 0.7 0.9 0.7 0.8 0.8	7.0 5.7 5.4 4.9 3.3 3.2 2.4 3.3 3.2 2.9 3.1 2.9 3.0 3.2 3.1 2.9 3.0 3.2 3.1 2.9 3.0 3.2 4.8 4.9	1.1 1.7 1.5 1.1 1.1 1.2 1.1 1.0 1.0 1.0 1.0 0.8 0.7 0.8 0.7 0.8 0.7 0.8 0.7 0.8 0.7 1.1 0.8 0.7 0.8 0.7 0.6 1.1 1.1 1.1 1.0 1.0 1.0 1.0 1.0	6.3 6.8 5.9 3.6 3.7 2.9 3.8 3.8 3.4 3.5 3.4 3.5 3.5 3.4 3.5 3.2 3.1 7.3 5.2 5.1	1.2 2.5 1.6 1.3 1.3 1.1 0.5 1.0 1.1 0.7 0.7 0.7 0.7 0.7 0.7 0.7 0.8 0.6 0.5 1.2 0.7 0.8	1.1 2.5 1.6 1.2 1.3 1.1 0.7 0.9 0.9 0.9 0.9 0.9 0.7 0.7 0.7 0.7 0.8 0.7 0.7 0.6 0.6 1.1 1.0 1.1	4.8 5.0 5.0 2.5 2.5 2.0 2.4 2.4 2.2 2.3 2.6 2.2 2.4 2.2 2.3 1.9 4.7 3.5 3.3	1.1 2.2 1.7 1.2 1.2 1.0 0.6 0.9 0.9 0.9 0.9 0.9 0.9 0.7 0.7 0.7 0.7 0.7 0.7 0.6 0.6 0.6 0.6 0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.9	1.1 2.4 1.6 1.1 1.2 1.1 0.8 0.9 0.9 0.9 0.9 0.9 0.9 0.8 0.9 0.9 0.9 0.8 0.9 0.9 0.8 0.9 0.9 0.9 0.8 0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.9	1.0 2.5 1.9 1.2 1.3 1.2 0.8 0.9 1.0 0.8 0.8 0.8 0.7 0.6 0.6 0.6 1.1 0.9 1.0	4.0 3.3 2.5 2.5 2.3 2.6 2.4 2.1 2.1 1.9 2.0 1.8 1.8 1.8 1.8 1.8 1.4 1.5 2.3 2.4	1.0 1.9 1.4 1.0 1.3 1.2 1.0 1.0 1.0 1.0 1.0 1.0 0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.9 0
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S178D03234 S158D00481 S168D09112 S168D05677 S158D05434 S148D03414 S158D06815 S158D05949 S158D04550 S158D04550 S158D04550 S158D04550 S158D06154 S158D06154 S158D06154 S158D06817 S148D03746 S158D06817 S148D01746 S158D08204 S168D07706 S168D02884 S168D07706 S168D02884 S168D0714 S168D0714 S158D06188 S148D0332 S158D06188 S148D03114 S158D06353 S138D04017 S158D06353 S138D04017 S158D06353 S158D06353 S158D06353 S158D06353 S158D06353 S158D06353 S158D06353 S158D06353 S158D06353 S158D06353 S158D06353 S158D06353 S158D06355 S168D08316 S178D06331 S158D0094 S178D09431 S158D0094	S. flexneri 3a S. flexneri 3 S. flexneri 3b S. flexneri 4a S. flexneri 4a S. flexneri 4a S. flexneri 4a S. flexneri 4a S. flexneri 4a	S. flexneri 3a S. flexneri 3b S. flexneri 3b S. flexneri 3a S. flexneri 3a S. flexneri 3a S. flexneri 3a S. flexneri 3a S. flexneri 4a S. flexneri 4a S. flexneri 4a S. flexneri 4a S. flexneri 4a S. flexneri 4a S. flexneri 4a	IMC MC IM IM IM IM IM IM IM IM IM IM IM IM IM	Pass Pass Pass Pass Pass Pass Pass Pass	4.0 4.4 3.1 3.1 2.3 2.0 1.3 2.2 2.2 2.2 2.2 2.2 2.0 1.8 1.9 1.9 1.9 1.9 1.9 1.9 1.9 1.9 1.9 1.9	5.1 4.7 3.2 3.8 3.0 2.9 2.9 2.9 2.6 2.6 2.6 2.6 2.6 2.6 2.6 2.6 2.6 2.6	1.1 2.0 2.1 1.1 1.3 1.2 0.9 0.9 0.9 0.9 0.9 0.9 0.0 0.9 0.9 0.0 0.0	1.1 2.1 1.7 1.3 1.3 1.1 1.6 0.6 1.0 1.0 0.8 0.8 0.7 0.6 0.8 0.7 0.6 0.8 0.7 0.6 0.8 0.7 0.6 0.8 0.7 0.6 0.8 0.7 0.6 0.6 1.0 1.0 1.0 0.8 0.8 0.7 1.0 0.8 0.8 0.7 1.0 0.8 0.8 0.7 1.0 0.8 0.8 0.7 1.0 0.8 0.8 0.8 0.7 0.6 0.6 0.0 1.0 0.0 0.8 0.8 0.6 0.6 0.0 1.0 0.0 0.8 0.8 0.7 0.6 0.6 0.0 1.0 0.0 0.8 0.8 0.7 0.6 0.6 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	1.3 2.7 3.4 1.5 1.3 1.1 0.7 1.0 1.1 0.7 0.7 0.9 0.9 0.7 0.9 0.7 0.9 0.7 0.9 0.7 0.9 0.7 0.7 0.9 0.7 0.9 0.7 0.7 1.2 0.8 0.8 0.7 1.2 0.7 1.2 0.8 0.7 1.2 0.7 1.2 0.7 1.2 0.7 1.2 0.7 1.2 0.7 1.2 0.7 0.7 1.2 0.7 0.7 1.2 0.7 0.7 1.2 0.7 0.7 1.2 0.7 0.7 1.2 0.7 0.7 1.2 0.7 0.7 0.7 0.7 0.7 0.9 0.9 0.9 0.9 0.7 0.7 0.7 0.7 0.7 0.7 0.7 0.7 0.7 0.7	7.0 5.7 5.4 4.9 3.3 3.2 2.4 3.3 3.2 2.9 3.0 2.9 3.0 2.9 3.1 2.9 3.0 2.9 3.1 2.9 3.1 2.9 3.0 2.7 7.8 4.8 4.9 6.7 6.7 5.2 6.4 8.5 5.3 5.6 5.3 5.3 5.6 5.3 5.3 5.6 5.3	1.7 1.7 1.7 1.7 1.1 1.1 1.1 1.2 1.1 1.0 1.0 0.8 0.7 0.8 0.7 0.8 0.7 0.8 0.7 0.7 1.1 0.8 1.0 1.2 1.3 1.0 1.2 1.3 1.0 1.2 1.3 1.0 1.2 1.3 1.0 1.2 1.3 1.0 1.2 1.1 1.1 0.0 0.7 0.7 0.7 1.1 1.2 1.1 1.1 0.0 0.8 0.7 0.7 0.7 1.1 0.0 0.7 0.7 1.1 1.2 1.1 1.2 1.1 1.0 0.7 0.7 1.1 0.0 0.7 1.1 0.0 0.7 0.7 1.1 0.0 1.2 1.3 1.0 1.2 1.3 1.0 1.2 1.3 1.0 1.2 1.3 1.0 1.2 1.3 1.0 1.2 1.3 1.0 0.7 0.8 0.7 0.6 0.7 1.1 0.0 1.2 1.3 1.0 0.7 1.2 0.8 0.7 0.6 0.7 1.1 0.0 1.2 1.3 1.0 0.7 1.2 0.8 0.7 0.6 0.7 1.1 0.0 0.7 1.2 0.8 0.7 0.6 0.7 1.1 0.0 0.7 1.2 0.8 0.7 0.7 1.3 1.0 0.7 1.3 1.0 0.7 1.3 1.0 0.7 1.3 1.0 0.7 1.3 1.0 0.7 1.3 1.0 0.7 1.3 1.0 0.7 1.3 1.0 0.7 1.3 1.0 0.7 1.3 1.0 0.7 1.3 1.0 0.7 1.3 1.0 0.7 1.3 1.0 0.7 1.3 1.0 0.7 1.3 1.0 0.7 1.3 1.0 0.7 1.3 1.0 0.7 0.7 0.7 0.7 0.7 0.7 0.7 0	6.3 6.8 6.8 5.9 5.9 3.6 3.7 2.9 3.8 3.7 3.8 3.4 3.5 3.4 3.5 3.4 3.5 3.4 3.5 3.4 3.5 3.4 3.5 3.4 3.5 3.4 3.6 3.5 3.1 7.3 5.2 5.1 7.0 8.0 6.6 5.9 5.7 5.8 5.1 1.4 1.3 1.2 0.8 0.7 0.9 8	1.2 2.5 1.6 1.3 1.3 1.1 0.5 1.0 0.7 1.0 0.7 0.7 0.7 0.7 0.7 0.7 0.7 0.7 0.7 0	1.1 2.5 1.6 1.2 1.3 1.1 0.7 0.9 0.9 0.9 0.9 0.7 0.8 0.9 0.9 0.7 0.8 0.7 0.6 0.6 1.1 1.0 1.1 1.2 1.8 1.3 1.5 1.2 1.1 1.1 1.0 1.2 0.7 0.9 0.9 0.9 0.9 0.9 0.9 0.7 0.7 0.9 0.9 0.9 0.9 0.7 0.7 0.7 0.9 0.9 0.7 0.7 0.7 0.7 0.7 0.7 0.7 0.7 0.7 0.7	4.8 5.0 4.0 2.5 2.5 2.0 2.4 2.2 2.3 2.6 2.2 2.3 2.6 2.2 2.3 2.6 2.2 2.3 2.6 2.2 2.3 2.6 2.2 2.3 2.6 2.2 2.3 3.3 4.8 5.8 5.8 2.1 1.1 1.1 1.1 1.0 0.9 9.7 1.7 1.4 1.5 0.0 0.7 1.7 1.7 1.7 1.7 1.7 1.7 1.7 1.7 1.7 1	1.1 2.2 1.7 1.2 1.2 1.0 0.6 0.9 0.9 0.9 0.9 0.9 0.7 0.7 0.7 0.7 0.7 0.7 0.7 0.7 0.7 0.7	1.1 2.4 1.6 1.1 1.2 1.1 0.8 0.9 0.9 0.9 0.8 0.9 0.9 0.8 0.9 0.9 0.9 0.8 0.9 0.9 0.8 0.9 0.9 0.8 0.9 0.9 0.8 0.9 0.9 0.9 0.8 0.9 0.9 0.8 0.9 0.9 0.9 0.8 0.9 0.9 0.9 0.8 0.9 0.9 0.9 0.8 0.9 0.9 0.8 0.9 0.9 0.8 0.9 0.9 0.8 0.9 0.9 0.8 0.9 0.9 0.8 0.9 0.9 0.8 0.9 0.9 0.8 0.9 0.9 0.9 0.8 0.9 0.9 0.8 0.9 0.9 0.8 0.9 0.9 0.8 0.9 0.9 0.9 0.8 0.9 0.7 7 0.6 1.1 1.1 1.1 1.1 1.1 1.1 1.1 1.1 1.1 1	1.0 2.5 1.9 1.2 1.3 1.2 0.8 0.9 0.8 0.7 0.6 1.1 0.9 0.8 0.7 0.6 1.1 0.9 1.0 0.7 0.6 1.1 0.9 1.0 0.9 0.0 1.3 1.5 1.4 1.2 1.2 1.2 0.9 0.9 0.9 0.8 4.9 4.4 4.3 4.7 4.0 3.2	4.0 3.3 2.5 2.5 2.3 2.5 2.3 2.5 2.3 2.4 2.1 1.9 2.0 1.8 1.8 1.9 1.9 1.8 1.8 1.4 1.5 2.3 2.4 4.5 2.3 2.4 4.5 2.3 2.4 4.5 2.3 2.4 2.5 2.5 2.3 2.4 2.1 2.0 1.9 2.0 1.8 1.9 1.9 2.0 1.8 1.9 1.9 1.9 2.0 1.8 1.9 1.9 1.9 1.9 1.8 1.8 1.4 1.5 2.3 2.4 2.5 2.3 2.4 2.5 2.5 2.5 2.4 2.4 2.5 2.5 2.5 2.4 2.4 2.5 2.5 2.5 2.4 2.4 2.5 2.5 2.5 2.4 2.4 2.5 2.5 2.5 2.5 2.4 2.4 2.5 2.5 2.5 2.5 2.5 2.4 2.4 2.5 2.5 2.5 2.4 2.4 2.5 2.4 2.5 2.3 2.4 2.4 2.5 2.3 2.4 2.5 2.3 2.4 2.5 2.3 2.4 2.5 2.5 2.3 2.4 2.5 2.5 2.4 2.5 2.5 2.5 2.4 2.5 2.5 2.4 2.4 2.5 2.5 2.4 2.4 2.5 2.5 2.4 2.4 2.4 2.4 2.4 2.5 2.4 2.4 2.4 2.4 2.4 2.4 2.4 2.4	1.0 1.9 1.4 1.4 1.0 1.3 1.2 1.0 1.0 1.0 1.0 1.0 0.9 0.9 0.9 0.9 0.9 0.9 0.9 0
S17BD03234 S15BD00481 S16BD09112 S16BD05677 S15BD05434 S15BD05815 S15BD05949 S15BD01389 S15BD04550 S15BD04550 S15BD04550 S15BD05517 S15BD06154 S15BD06517 S16BD05677 S14BD0172 S14BD01142 S14BD01142 S14BD01142 S14BD01142 S14BD01142 S16BD0706 S16BD02884 S16BD0706 S16BD02884 S16BD070654 S16BD070654 S16BD070654 S16BD070654 S16BD0714 S16BD06188 S14BD05332 S15BD01044 S15BD06353 S15BD00319 S16BD06353 S15BD00319 S16BD06316 S17BD06431 S17BD06431 S15BD02902 S14BD01213 S15BD01245	S. flexneri 3a S. flexneri 3 S. flexneri 3 S. flexneri 3 S. flexneri 3b S. flexneri 4a S. flexneri 4a S. flexneri 4a S. flexneri 4a S. flexneri 4a S. flexneri 4a	S. flexneri 3a S. flexneri 4a S. flexneri 4a	INC MC IN IN IN IN IN IN IN IN IN IN IN IN IN	Pass Pass Pass Pass Pass Pass Pass Pass	4.0 4.4 3.1 3.1 2.3 2.0 1.3 2.2 2.2 2.2 1.7 1.9 1.9 1.9 1.9 1.9 1.9 1.9 1.9 1.9 1.9	5.1 4.7 3.2 3.8 3.0 2.9 2.1 2.9 2.9 2.6 2.6 2.6 2.6 2.6 2.6 2.6 2.6 2.5 2.2 2.4 4.7 4.7 3.7 3.8 3.7 4.3 3.7 4.3 3.7 4.2 3.8 3.7 4.2 3.8 3.7 4.2 3.8 3.7 4.2 3.8 3.7 4.2 3.8 3.7 4.2 3.8 3.7 5.4 4.2 3.7 5.4 4.2 5.5 5.4 4.2 5.5 5.4 4.2 5.5 5.4 4.2 5.5 5.4 4.2 5.5 5.4 4.2 5.5 5.4 7.7 5.5 5.5 7.7 5.5 7.7 7.7 7.6 7.7 7.7 7.6 7.7 7.7 7.7 7.7	1.1 2.0 2.1 1.1 1.3 1.2 0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.9	1.1 2.1 1.7 1.3 1.3 1.1 1.6 6 1.0 1.0 0.8 0.8 0.7 0.6 0.6 0.6 0.6 0.6 0.6 0.6 0.6 0.6 0.8 0.7 0.6 0.8 0.8 0.7 0.6 0.8 0.7 0.6 0.8 0.7 0.6 0.8 0.7 1.3 1.3 1.0 0.8 0.8 0.7 0.6 0.8 0.8 0.7 0.6 0.8 0.8 0.7 0.6 0.8 0.8 0.7 0.6 0.0 0.0 0.8 0.8 0.7 0.6 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	1.3 2.7 3.4 1.5 1.3 1.1 0.7 1.0 1.1 0.7 0.7 0.7 0.7 0.9 0.7 0.9 0.7 0.9 0.7 0.9 0.7 0.9 0.7 0.9 0.7 0.9 0.7 0.9 0.7 0.9 0.7 0.7 1.2 0.8 0.8 1.3 1.1 1.1 0.8 8 0.9 0.9 0.7 0.7 1.2 0.8 8 0.9 0.7 0.7 1.2 0.8 8 0.9 0.7 0.7 0.7 0.7 0.7 0.7 0.9 0.7 0.7 0.7 0.7 0.7 0.9 0.9 0.7 0.7 0.7 0.7 0.7 0.7 0.7 0.7 0.9 0.9 0.7 0.7 0.7 0.7 0.7 0.7 0.7 0.7 0.7 0.7	7.0 5.7 5.4 4.9 3.3 3.2 2.4 3.3 3.2 2.9 3.0 3.2 2.9 3.0 3.2 3.1 2.9 3.1 2.9 3.1 2.9 3.1 2.9 3.1 2.9 3.1 2.9 3.2 3.1 2.9 3.2 3.2 3.1 2.9 5.5 6.7 5.5 6.7 5.5 6.7 5.5 5.5 5.5 5.5 5.5 5.5 5.5 5.5 5.5 5	1.7 1.7 1.7 1.5 1.1 1.1 1.2 1.1 1.0 1.0 1.0 0.8 0.7 0.6 0.7 0.6 0.7 0.6 0.7 0.6 0.7 0.8 0.8 0.7 0.8 0.8 0.9 0.8 0.9 0.8 0.9 0.8 0.9 0.8 0.9 0.8 0.9 0.8 0.9 0.8 0.9 0.8 0.9 0.8 0.7 0.1 0.2 1.1 0.1 0.7 0.8 0.9 0.8 0.9 0.8 0.7 0.7 1.1 0.7 0.7 1.1 0.7 0.8 0.9 0.8 0.9 0.8 0.9 0.9 0.7 0.7 1.1 0.7 0.7 1.1 0.7 0.7 1.1 0.7 0.7 1.1 0.7 0.7 1.1 0.7 0.7 1.1 0.7 0.7 1.1 0.7 0.7 0.7 0.7 0.7 0.7 0.7 0.7	6.3 6.8 5.9 3.6 5.9 3.6 3.7 2.9 3.8 3.4 3.5 3.4 3.5 3.4 3.5 3.4 3.5 3.4 3.5 3.4 3.5 3.4 3.5 3.4 3.5 3.4 3.5 3.3 3.2 3.1 7.3 5.2 5.1 7.0 6.0 5.8 5.7 5.8 5.1 1.3 1.3 1.3 1.3 1.3 1.3 1.3 1.3 0.7 0.9 0.8 0.7	1.2 2.5 1.6 1.3 1.3 1.1 0.5 1.0 0.5 1.0 0.7 0.7 0.7 0.7 0.7 0.7 0.7 0.7 0.7 0	1.1 2.5 1.6 1.2 1.3 1.1 0.7 0.9 0.9 0.9 0.9 0.9 0.7 0.7 0.8 0.9 0.9 0.7 0.7 0.8 0.9 0.9 0.7 0.7 0.8 0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.9	4.8 5.0 5.0 4.0 2.5 2.5 2.0 2.4 2.4 2.2 2.3 2.6 2.2 2.2 2.3 2.6 2.2 2.2 2.3 3.5 3.3 4.8 2.1 1.3 1.2 1.1 1.1 1.1 1.0 8.3 4.4 0.09 9.7 7.7	1.1 2.2 1.7 1.2 1.2 1.0 0.6 0.9 0.9 0.9 0.9 0.9 0.9 0.7 0.7 0.7 0.7 0.7 0.7 0.7 0.7 0.7 0.7	1.1 2.4 1.6 1.1 1.2 1.1 0.8 0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.9	1.0 2.5 1.9 1.2 1.3 1.2 0.8 0.9 1.0 0.8 1.0 0.8 1.0 0.8 1.0 0.8 1.0 0.8 1.0 0.7 0.6 1.1 0.9 1.0 0.9 1.0 0.9 1.2 1.0 0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.8 4.4 4.3 4.4 3.8 3.2	4.0 3.3 2.5 2.5 2.3 2.6 2.4 2.1 2.1 2.0 1.8 1.8 1.4 1.9 1.8 1.8 1.4 1.5 2.3 2.4 2.0 1.8 1.8 1.4 1.5 4.5 2.3 2.3 2.4 2.5 2.3 2.0 2.0 1.8 1.8 1.8 1.8 1.4 1.5 2.3 2.3 2.3 2.4 2.0 1.8 1.8 1.8 1.8 1.8 1.8 1.4 1.5 2.3 2.3 2.3 2.4 2.0 1.8 1.8 1.8 1.8 1.8 1.8 1.5 2.3 2.4 2.3 2.4 2.5 2.3 2.4 2.0 1.8 1.8 1.8 1.8 1.5 2.3 2.4 2.3 2.4 2.5 2.3 2.4 2.5 2.3 2.4 2.5 2.3 2.4 2.5 2.3 2.4 2.5 2.3 2.4 2.5 2.3 2.4 2.5 2.3 2.4 2.5 2.3 2.4 2.5 2.3 2.4 2.5 2.3 2.4 2.5 2.3 2.4 2.5 2.3 2.4 2.2 3.1 2.4 2.6 2.7 2.4 2.6 2.7 2.4 2.6 2.7 2.4 2.6 2.7 2.4 2.6 2.7 2.4 2.6 2.7 2.4 2.6 2.7 2.4 2.4 2.7 2.4 2.4 2.6 2.7 2.4 2.4 2.6 2.7 2.4 2.7 2.8 2.8 2.7 2.8 2.8 2.7 2.8 2.8 2.7 2.8 2.8 2.7 2.8 2.8 2.7 2.8 2.8 2.7 2.8 2.8 2.7 2.1 2.0 2.1 2.0 2.1 2.0 2.1 2.0 2.1 2.1 2.1 2.1 2.1 2.1 2.1 2.1	1.0 1.9 1.4 1.0 1.3 1.2 1.0 1.0 1.0 1.0 1.0 0.9 0.9 0.9 0.9 0.9 0.9 0.9 0

APPENDIX 2 (continued)

S17BD01719	S. flexneri 4a	S. flexneri 4a	IM	Pass	1.9	2.6	0.7	0.7	0.8	3.0	0.7	0.6	0.7	0.6	0.7	0.6	0.7	2.5	1.8	0.7
S17BD01539	S. flexneri 4a	S. flexneri 4a	мс	Pass	3.4	4.3	0.8	0.8	0.8	5.5	0.8	0.8	0.8	0.8	0.8	0.8	0.8	3.9	3.5	0.7
S17BD06406	S. flexneri 4b	S. flexneri 4b	IM	Pass	3.9	5.4	1.3	1.4	1.4	6.7	1.3	6.4	1.3	1.2	1.3	1.4	1.3	4.7	3.7	1.3
	S. flexneri 5	S. flexneri	IM	Pass																
S16BD02240	-	5/coli*			1.3	1.1	6.5	1.1	5.6	8.1	1.1	1.2	1.2	1.2	1.1	7.0	1.1	1.2	1.3	1.1
S16BD06481	S. flexneri 6	S. flexneri 6	мс	Pass	4.1	5.2	1.3	0.7	1.0	1.5	1.3	1.6	1.9	2.0	1.5	1.7	3.6	1.4	1.8	1.8
S17BD03420	S. flexneri 6	S. flexneri 6	MC	Pass	4.1	5.4	1.3	0.8	0.9	1.9	1.6	1.8	2.1	2.0	1.7	1.7	3.9	1.8	1.9	1.7
S17BD08337	S. flexneri 6	S. flexneri 6	MC	Pass	3.9	5.0	1.1	0.7	0.8	1.3	1.2	1.3	1.6	1.7	1.6	1.3	3.4	1.5	1.5	1.4
S17BD08093	S. flexneri 6	S. flexneri 6	NIC	Pass	3.9	5.0	1.2	0.6	0.7	1.4	1.2	1.3	1.5	1.4	1.5	1.3	3.4	1.3	1.5	1.4
S1/BD0061/	S. flexneri 6	S. flexneri 6	INC	Pass	4.2	5.1	1.3	1.3	1.5	1.2	1.1	1.2	1.4	1.4	1.4	1.2	3.2	1.4	1.6	1.1
S14BD04017	S. flexneri 6	S. flexneri 6		Pass	3.1	4.5	1.0	1.0	1.1	1.1	1.0	1.1	1.2	1.2	1.1	1.0	4.7	1.2	1.0	1.1
S1/BD08/04	S. flexneri 6	S. flexneri 6	IVIC	Pass	3.5	4.7	1.0	0.5	1.0	1.1	1.1	1.2	1.1	1.1	1.2	1.0	3.1	1.1	1.2	1.1
S15BD07174	S. floxnori 6	S. floxpori 6		Pass	5.5	4.0	1.0	1.0	1.0	1.0	1.0	1.1	1.0	1.0	1.0	1.0	4.7	1.0	0.9	1.1
S16BD00004	S flevneri 6	S flexneri 6		Pace	4.0	5.4	1.0	0.6	0.6	1.0	1.0	1.0	1.0	1.0	1.0	1.0	2.0	1.0	1.1	1.1
S15BD09868	S. flexneri 6	S flexneri 6	IM	Pass	33	47	1.0	0.0	0.0	1.1	0.9	1.2	0.8	1.5	0.9	0.9	47	1.2	0.8	1.1
S15BD05808	S flexneri 6	S flexneri 6	IM	Pass	29	4.7	0.9	0.5	0.0	0.9	0.5	0.9	0.0	0.8	0.5	0.5	4.7	0.8	0.8	1.0
\$15BD03143	S. flexneri 6	S flexneri 6	IM	Pass	3.1	4.4	0.9	0.5	1.0	1.0	0.0	0.9	1.0	11	10	0.9	4.6	1.0	0.0	0.9
S14BD03684	S. flexneri 6	S. flexneri 6	IM	Pass	3.2	4.6	0.9	0.9	0.8	1.0	0.9	1.0	0.9	1.0	1.0	0.9	4.7	0.9	0.8	0.9
S17BD01720	S. flexneri 6	S. flexneri 6	MC	Pass	3.8	5.0	1.0	0.9	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	3.0	1.0	1.0	0.9
S15BD07159	S. flexneri 6	S. flexneri 6	IM	Pass	2.9	4.2	0.8	0.8	0.8	0.9	0.8	0.9	0.8	0.9	0.9	0.8	4.2	0.9	0.8	0.9
S15BD06239	S. flexneri 6	S. flexneri 6	IM	Pass	2.8	4.0	0.9	0.8	0.7	0.9	0.9	0.9	0.8	0.8	0.9	0.8	4.1	0.8	0.7	0.9
S16BD07009	S. flexneri 6	S. flexneri 6	ім	Pass	3.0	4.4	0.9	0.8	0.9	1.0	0.8	0.9	0.9	0.9	1.0	0.9	4.6	0.9	0.9	0.9
S16BD05985	S. flexneri 6	S. flexneri 6	IM	Pass	4.1	5.5	0.6	0.7	0.9	0.7	0.5	0.7	0.7	0.7	0.9	0.8	3.7	0.8	1.1	0.9
S16BD00745	S. flexneri 6	S. flexneri 6	IM	Pass	3.0	4.2	0.8	0.7	0.7	0.8	0.7	0.8	0.7	0.8	0.9	0.8	4.1	0.8	0.7	0.8
S18BD00434	S. flexneri 6	S. flexneri 6	IM	Pass	3.1	4.4	0.8	0.7	0.7	0.8	0.8	0.8	0.6	0.8	0.8	0.7	4.5	0.7	0.7	0.8
S14BD02795	S. flexneri 6	S. flexneri 6	IM	Pass	4	4.2	0.7	0.7	1	0.7	0.5	0.7	0.8	0.7	0.9	0.8	4.8	0.7	1.0	0.8
S16BD07329	S. flexneri 6	S. flexneri 6	IM	Pass	2.6	4.0	0.7	0.6	0.6	0.7	0.8	0.8	0.5	0.7	0.8	0.6	4.0	0.8	0.5	0.8
S18BD01383	S. flexneri 6	S. flexneri 6	IM	Pass	2.8	4.2	0.8	0.7	0.6	0.8	0.8	0.8	0.6	0.8	0.8	0.8	4.0	0.8	0.6	0.8
S14BD01717	S. flexneri 6	S. flexneri 6	IM	Pass	2.7	3.9	0.8	0.7	0.7	0.9	0.7	0.8	0.7	0.8	0.8	0.7	4.1	0.7	0.6	0.8
S14BD02851	S. flexneri 6	S. flexneri 6	IM	Pass	3.0	4.3	0.7	0.6	0.5	0.7	0.7	0.7	0.5	0.7	0.7	0.6	4.4	0.6	0.5	0.7
S16BD06271	S. flexneri 6	S. flexneri 6	IM	Pass	2.8	3.9	0.7	0.6	0.7	0.7	0.7	0.7	0.6	0.8	0.8	0.7	4.1	0.7	0.6	0.7
S17BD03083	S. flexneri 6	S. flexneri 6	MC	Pass	3.2	4.2	1.2	1.3	1.5	1.2	1.2	1.2	1.4	1.3	1.3	1.3	2.7	1.4	1.0	1.2
S17BD03431	S. flexneri 6	S. flexneri 6	MC	Pass	3.7	4.4	1.3	1.4	2.0	1.4	1.2	1.3	1.6	1.6	1.6	1.6	3.1	1.4	1.3	1.4
S17BD08081	S. flexneri 6	S. flexneri 6	MC	Pass	3.4	4.4	1.2	1.3	1.8	1.2	1.1	1.1	1.3	1.3	1.3	1.2	2.8	1.4	1.1	1.1
S15BD04220	S. flexneri x	S. flexneri x	NIC	Pass	4.0	5.0	1.2	0.6	0.7	6.6 7.2	1.3	1.4	1.4	1.5	5.9	1.3	1.4	1.3	4.3	1.3
S16BD02856	S. flexneri x	S. flexneri x	IVIC	Pass	4.5	5.5	1.1	1.5	1.5	7.3 0.2	1.1	1.2	1.5	1.4	5.8	1.5	1.4	1.3	3.7	1.2
S10BD01789	S. flexneri x	S. flexneri x		Pass	4.0	5.0	1.2		1.2	8.2 6.2	1.1	1.2	1.2	0.5	4.7	1.1	1.1		4.9	1.1
S15BD05064	S. floxnori v	S. floxnori v		Pass	5.4	4.4	1.0	0.0	0.0	0.2	0.9	1.0	1.0	1.0	4.0	0.0	1.0	1.0	2.0	0.9
S1/BD03094	S flexneri v	S flexneri v	MC	Pace	4.0	5.0	1.0	1.1	1.1	5.9	0.9	1.0	1.0	1.0	1.0	1.5	1.0	1.0	4.4	1.8
S18BD00191	S flexneri v	S flexneri v	MC	Pass	4.J 5.1	6.0	1.0	1.5	2.1	7.6	1.4	1.4	1.5	1.0	1.0	1.5	1.9	1.0	4.5	1.0
\$17BD04960	S. flexneri y	S flexneri v	IM	Pass	3.0	3.8	11	1.0	13	5.4	11	1.0	11	1.5	11	11	1.0	11	2.4	1.0
S17BD00384	S. sonnei	S. sonnei	MC	Pass	4.0	4.0	1.5	1.5	1.6	1.4	5.6	1.6	1.5	1.9	1.6	1.7	1.8	1.5	1.5	1.5
S17BD02087	S. sonnei	S. sonnei	MC	Pass	4.1	4.5	1.3	1.4	1.5	1.4	6.8	1.3	1.4	1.5	1.4	1.2	1.5	1.4	1.4	1.3
S18BD01729	S. sonnei	S. sonnei	ім	Pass	2.4	2.8	1.2	1.2	1.2	1.1	3.0	1.2	1.2	1.2	1.2	1.3	1.2	1.4	1.1	1.3
S18BD02156	S. sonnei	S. sonnei	IM	Pass	2.4	3.1	1.1	1.2	1.2	1.1	3.5	1.0	1.2	1.3	1.1	1.1	1.2	1.2	1.1	1.3
S17BD00522	S. sonnei	S. sonnei	мс	Pass	4.0	3.6	1.1	1.2	1.4	1.2	4.7	1.1	1.3	1.3	1.3	1.2	1.5	1.3	1.3	1.2
S17BD02253	S. sonnei	S. sonnei	мс	Pass	3.8	3.9	1.1	1.4	1.4	1.3	5.5	1.2	1.4	1.4	1.4	1.2	1.4	1.3	1.3	1.2
S17BD05216	S. sonnei	S. sonnei	MC	Pass	4.1	3.7	1.1	1.4	1.5	1.4	4.8	1.2	1.5	1.4	1.4	1.3	1.4	1.3	1.4	1.2
S17BD00324	S. sonnei	S. sonnei	MC	Pass	4.0	3.0	1.1	1.2	1.3	1.2	4.0	1.2	1.3	1.3	1.5	1.2	1.2	1.2	1.4	1.2
S16BD00696	S. sonnei	S. sonnei	IM	Pass	3.8	2.3	1.2	1.1	1.3	1.2	2.4	1.2	1.2	1.2	1.3	1.1	1.1	1.1	1.2	1.2
S17BD02897	S. sonnei	S. sonnei	MC	Pass	3.9	3.9	1.1	1.1	1.4	1.2	5.3	1.1	1.2	1.2	1.3	1.1	1.3	1.3	1.2	1.1
S17BD00697	S. sonnei	S. sonnei	MC	Pass	4.1	4.3	1.1	1.1	1.4	1.2	6.4	1.1	1.2	1.2	1.2	1.2	1.2	1.2	1.3	1.1
S17BD00325	S. sonnei	S. sonnei	MC	Pass	3.8	3.1	1.1	1.1	1.2	1.1	4.1	1.2	1.2	1.2	1.2	1.1	1.3	1.1	1.2	1.1
S18BD02050	S. sonnei	S. sonnei	IM	Pass	2.3	3.2	0.9	0.8	1.0	1.0	4.0	0.8	0.9	0.9	0.9	1.0	1.0	0.9	0.8	1.0
S1/BD05856	S. sonnei	S. sonnei	INIC	Pass	3.4	3.1	1.0	1.0	1.2	1.1	4.6	1.1	1.0	1.0	1.1	1.1	1.2	1.1	1.0	1.0
S15BD09298	S. sonnei	S. sonnei		Pass	3.3	3.4	1.1	0.9	1.0	1.0	3.5	1.0	1.0	0.6	0.9	0.9	0.9	0.9	0.9	1.0
S17BD02104	S. sonnoi	S. sonnoi	MC	Pace	2.6	2.4	1.1		1.2	1.1	4.7 E 0	1.1	1.2	1.1	1.2	1.1	1.2	1.2	1.1	1.0
\$18BD01725	S sonnei	S sonnei	IM	Pass	2.1	2.6	0.9	0.9	0.9	0.9	2.4	0.9	0.9	0.8	0.8	1.0	1.0	0.9	0.7	0.9
S18BD01826	S. sonnei	S. sonnei	IM	Pass	2.1	2.8	0.9	0.9	0.8	0.8	3.2	0.8	0.7	0.9	0.8	1.0	1.0	0.9	0.8	0.9
S18BD00724	S. sonnei	S. sonnei	MC	Pass	3.3	3.8	1.0	0.8	0.9	0.9	5.8	0.9	0.9	1.0	0.9	0.9	0.9	1.0	0.9	0.9
S18BD01943	S. sonnei	S. sonnei	IM	Pass	2.0	2.9	0.8	0.8	0.8	0.8	3.3	0.8	0.9	0.7	0.7	0.8	0.9	0.9	0.7	0.9
S18BD01827	S. sonnei	S. sonnei	IM	Pass	2.2	2.3	0.9	0.8	0.6	0.8	2.7	0.8	0.7	0.9	0.7	0.8	0.9	0.8	0.7	0.9
S16BD07521	S. sonnei	S. sonnei	IM	Pass	3.2	3.9	1.0	0.8	0.9	0.9	4.5	1.0	0.9	0.4	0.9	0.9	0.9	0.9	0.8	0.8
S17BD00521	S. sonnei	S. sonnei	MC	Pass	3.1	2.9	0.9	0.8	0.9	0.9	3.5	0.9	0.7	0.9	0.9	0.9	0.9	0.9	0.8	0.8
S17BD00581	S. sonnei	S. sonnei	мс	Pass	4.3	4.5	1.4	1.8	1.9	1.7	5.9	1.5	1.5	1.4	1.6	1.6	1.7	1.8	1.5	1.6
S17BD02088	S. sonnei phase II	Shigella	MC	Pass	3.5	1.0	1.0	1.0	1.2	1.1	1.0	1.1	1.1	1.1	1.1	1.2	1.2	1.2	1.1	1.0
S15BD04402	S. sonnei phase II	Shigella	IM	Pass	3.0	0.8	0.9	0.7	0.9	0.8	0.7	0.7	0.7	0.6	0.7	0.7	0.7	0.8	0.7	0.7
S18BD02200	S. sonnei phase II	Shigella	IM	Pass	2.2	1.1	1.1	1.0	0.8	1.0	1.1	0.9	0.8	1.0	0.8	0.9	1.1	1.0	0.7	1.1
S17BD02526	S. sonnei phase II	Shigella	мс	Pass	3.6	1.0	1.0	1.0	1.4	1.1	1.0	0.9	1.1	1.0	1.1	1.1	1.2	1.0	1.1	1.0
\$18BD00011	S. sonnei phase II	Shigella	MC	Pass	3.0	0.9	0.9	0.9	1.0	0.9	0.9	1.0	0.9	1.0	0.9	1.0	1.0	0.9	0.9	0.9
S17BD05970	No Shigella	E. coli	MC	Pass	1.7	1.6	7.2	7.5	5.5	1.9	1.4	1.6	1.8	1.7	1.6	1.8	1.9	1.7	1.9	1.8
S18BD00012	No Shigella	E. coli	MC	Pass	1.6	1.7	7.5	7.9	3.5	1.8	1.4	1.5	1.6	1.7	1.7	1.8	1.7	1.7	3.2	1.7
S1/BD07964	No Shigella	E. coli	MC	Pass	1.7	1.7	8.0	1.8	3.6	1.8	1.6	1.6	1.9	1.7	1.7	1.7	1.8	1.7	2.1	1.6
S1/BDU8236	No Shigella	E. COII		Pass	1.0	1.0	8.6	1.6	2.4	1.0	1.5	1.5	1.0	1.b 1 r	1.0	1./	1.0	1.5	2.4	1.5
517BD04904	No Shigolla	E. COII		Pass	1.5 1.6	1.5	7.3	7.0	3.5	1.5	1.3 1.2	1.4	1.5 1.6	1.5 1.7	1.4	1.0	1.4	1.4	5.3 1.9	1.4 1.2
S1/8000/80	· · · · · · · · · · · · · · · · · · ·	L. COII	1 11/1	rdss	1.0	1.2	0.9	0.0	5.7	T.2	1.4	1.2	1.0	1./	1.5	1.5	1.4	1.2	1.0	1.5
210000133	No Shigollo	E coli	164	Pace	00	1.0	/10	26	11/	11		10	00	1 1 1			1 2	1 1 2	1 5	
\$18800000	No Shigella	E. coli	IM	Pass	0.9	1.2	4.9	3.6	1./	1.1	1.1	1.0	0.9	1.1	1.0	1.2	1.3	1.3	1.5	1.3
S18BD00008 S15BD05104	No Shigella No Shigella No Shigella	E. coli E. coli E. coli	IM IM IM	Pass Pass Pass	0.9 1.5 1.2	1.2 1.1 1.1	4.9 6.2 6.4	3.6 1.3 7.4	1.7 5.0 1.5	1.1 1.3 1.3	1.1 1.2 1.1	1.0 1.1 1.1	0.9 1.5 1.4	1.1 1.5 1.4	1.0 1.2 1.2	1.2 1.2 1.2	1.3 1.3 1.2	1.3 1.2 1.1	1.5 1.6 1.4	1.3 1.2 1.1
S18BD00008 S15BD05104 S18BD01590	No Shigella No Shigella No Shigella No Shigella No Shigella	E. coli E. coli E. coli E. coli E. coli	IM IM IM IM	Pass Pass Pass Pass	0.9 1.5 1.2 0.9	1.2 1.1 1.1 1.3	4.9 6.2 6.4 5.6	3.6 1.3 7.4 1.0	1.7 5.0 1.5 1.1	1.1 1.3 1.3 1.1	1.1 1.2 1.1 1.1	1.0 1.1 1.1 1.0	0.9 1.5 1.4 1.0	1.1 1.5 1.4 1.1	1.0 1.2 1.2 1.1	1.2 1.2 1.2 1.1	1.3 1.3 1.2 1.3	1.3 1.2 1.1 1.2	1.5 1.6 1.4 1.3	1.3 1.2 1.1 1.1

APPENDIX 2 (continued)

S17BD08884	No Shigella	E. coli	ім	Pass	1.3	1.0	7.7	1.2	4.0	1.2	1.1	1.2	1.3	1.2	1.1	1.2	1.1	1.1	1.9	1.1
S16BD01018	No Shigella	E. coli	IM	Pass	1.0	1.2	6.3	6.6	2.3	1.1	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	2.0	1.1
S18BD00385	No Shigella	E. coli	IM	Pass	0.9	1.0	4.9	3.7	1.9	1.1	0.9	1.0	0.9	1.0	0.9	1.1	1.1	1.0	1.0	1.1
S18BD01710	No Shigella	E. coli	ім	Pass	0.9	1.0	4.4	3.5	2.8	4.3	0.8	0.9	0.9	0.9	2.7	1.0	1.1	0.9	1.0	1.1
S18BD01102	No Shigella	E. coli	ім	Pass	0.9	1.2	5.4	1.0	1.0	1.1	1.0	1.0	0.9	1.0	0.9	1.0	1.1	1.1	0.9	1.1
S14BD02777	No Shigella	E. coli	IM	Pass	1.0	1.0	9.2	9.1	3.4	1.1	1.0	1.1	1.0	1.0	1.0	1.0	1.1	1.1	1.3	1.1
S18BD01973	No Shigella	E. coli	ім	Pass	0.7	1.0	4.6	3.5	1.2	1.1	1.2	0.8	0.7	0.9	0.8	1.0	1.0	0.9	0.7	1.0
S15BD06369	No Shigella	E. coli	IM	Pass	1.0	1.0	6.4	6.4	3.4	1.0	1.0	1.0	0.9	0.9	1.0	1.0	1.0	1.0	0.7	0.9
S18BD00689	No Shigella	E. coli	ім	Pass	0.5	0.7	4.7	3.4	1.4	0.7	0.8	0.7	0.6	0.8	0.7	0.7	0.9	0.8	0.7	0.9
S18BD00811	No Shigella	E. coli	IM	Pass	0.5	0.7	4.3	3.1	2.3	0.6	0.6	0.6	0.5	0.6	0.6	0.7	0.8	0.7	0.6	0.8
S18BD01228	No Shigella	E. coli	ім	Pass	0.5	0.8	5.1	0.7	2.7	0.7	0.8	0.7	0.5	0.7	0.6	0.8	0.8	0.7	0.7	0.8
S18BD01042	No Shigella	E. coli	ім	Pass	0.6	0.7	4.6	3.3	2.4	0.6	0.6	0.7	0.6	0.6	0.6	0.7	0.9	0.7	0.5	0.8
		Citrobacter		_																
S13BD01340	No Shigella	(MALDI)	IM	Pass	0.8	0.8	1.0	0.9	0.7	0.7	0.9	0.7	0.8	0.7	0.7	0.7	0.7	0.7	0.8	0.7
S17BD04899	No Shigella	E. coli	мс	Pass	1.8	1.5	4.4	2.4	1.9	1.4	1.2	1.5	1.8	1.7	1.6	1.5	1.8	1.6	1.8	1.6
S17BD08176	No Shigella	E. coli	мс	Pass	1.5	1.2	8.2	1.4	1.9	1.3	1.2	1.3	1.4	1.5	1.6	1.3	1.5	1.5	1.5	1.6
S17BD02630	No Shigella	E. coli	мс	Pass	1.5	1.4	7.8	1.4	1.8	1.5	1.2	1.2	1.6	1.6	1.5	1.5	1.6	1.5	2.3	1.5
S18BD00270	No Shigella	E. coli	мс	Pass	1.7	1.4	7.7	7.4	1.8	1.5	1.2	1.3	1.7	1.7	1.7	1.4	1.7	1.5	2.3	1.4
S17BD05007	No Shigella	E. coli	мс	Pass	1.5	1.3	4.3	1.4	1.4	1.4	1.1	1.1	1.4	1.5	1.4	1.3	1.5	1.3	1.4	1.2
S17BD01771	No Shigella	E. coli	мс	Pass	1.3	1.4	1.1	1.1	2.7	1.4	1.2	1.4	1.4	1.6	1.2	1.3	1.5	1.3	1.7	1.2
S17BD08254	No Shigella	E. coli	мс	Pass	1.1	1.1	8.8	1.0	1.3	1.1	1.1	1.2	1.1	1.3	1.2	1.2	1.3	1.2	1.2	1.1
S17BD00385	No Shigella	E. coli	мс	Pass	1.4	1.1	6.9	1.2	4.6	1.2	1.0	1.2	1.3	1.3	1.1	1.2	1.4	1.1	1.5	1.0
S17BD02040	No Shigella	E. coli	мс	Pass	1.2	1.0	8.2	1.0	1.4	1.1	0.9	1.0	1.2	1.1	1.1	1.1	1.2	1.1	1.1	0.9
S15BD02268	Untypable	E. coli	IM	Pass	0.9	0.9	6.1	0.8	2.3	0.9	1.0	0.9	0.7	1.0	1.0	0.9	1.1	0.9	1.7	1.0
S15BD06515	Untypable	E. coli	IM	Pass	0.7	0.9	6.0	4.5	0.9	0.9	1.0	1.0	0.7	0.9	1.0	0.9	1.0	0.9	1.7	1.0
S15BD04401	Untypable	E. coli	мс	Pass	1.7	1.8	5.2	1.9	2.0	1.7	1.8	1.8	2.0	1.7	1.8	1.7	2.0	1.8	2.6	1.8
S16BD08716	Untypable	E. coli	мс	Pass	1.4	1.2	5.5	1.2	1.7	1.1	0.9	1.3	1.4	1.3	1.4	1.3	1.6	1.3	2.4	1.4
S16BD03147	Untypable	E. coli	IM	Pass	0.9	1.0	6.4	1.0	1.4	1.0	1.0	1.0	0.9	0.9	1.0	0.9	0.9	1.0	1.4	1.0
S17BD07122	Untypable	E. coli	мс	Pass	0.9	0.9	7.1	7.1	4.4	6.9	1.0	1.1	0.9	1.0	1.1	1.1	1.0	1.1	1.2	1.0
Q12-047	EIEC (EQA 2012)	EIEC	IM	Pass	4.3	3.8	4.2	1.2	0.7	0.8	0.7	0.8	1.1	0.7	1.2	0.8	0.9	1.0	1.4	1.0
13FP1902	EIEC (EQA 2013)	EIEC	IM	Pass	4.1	3.6	5.0	1.0	0.7	0.6	0.6	0.7	1.0	0.6	1.1	0.7	0.8	0.8	1.5	0.8
BD09-00375	EIEC	Shigella spp.	IM	Pass	4.2	3.7	0.7	1.1	0.6	0.7	0.7	0.8	1.1	0.7	1.1	0.7	0.8	0.9	4.0	0.9
BD12-00018	EIEC	EIEC	IM	Pass	3.8	3.4	4.1	4.9	0.6	0.6	0.7	0.8	1.1	0.7	1.1	0.7	0.8	0.9	1.1	0.9
EW227	EIEC	EIEC	IM	Pass	4.0	3.6	4.3	1.1	0.7	0.7	0.7	0.8	1.0	0.6	1.1	0.7	0.8	0.9	1.4	0.8
BD11-00138	EIEC	EIEC	IM	Pass	3.9	3.7	4.0	5.1	0.7	0.8	0.8	0.9	1.2	0.8	1.4	0.9	1.0	1.1	3.7	1.0
BD13-00007	EIEC	EIEC	IM	Pass	3.7	3.5	3.9	1.1	0.6	0.7	0.7	0.8	0.9	0.7	1.1	0.7	0.8	0.9	1.3	0.8
1111-55	EIEC	EIEC	IM	Pass	4.1	3.3	4.1	5.1	0.8	0.8	0.8	0.9	1.2	0.8	1.3	0.8	1.0	1.1	1.3	1.0
1624-56	EIEC	EIEC	IM	Pass	4.1	3.5	4.1	2.0	0.7	0.7	0.7	0.8	1.0	0.7	1.2	0.7	0.8	0.9	3.5	0.9
BD09-00443	EIEC	Shigella spp.	IM	Pass	4.1	3.6	0.7	1.0	0.6	0.6	0.7	0.7	1.0	0.6	1.0	0.6	0.8	0.8	1.0	0.8
1184-68	EIEC	EIEC	IM	Pass	3.5	2.8	3.9	5.0	0.8	0.7	0.7	0.9	1.1	0.7	1.2	0.7	1.0	1.0	3.5	0.9
BD13-00213	EIEC	Shigella spp.	IM	Pass	3.8	3.6	0.7	1.2	0.7	0.7	0.7	0.9	1.1	0.7	1.2	0.7	0.9	1.0	3.4	1.0
145/46	EIEC	E. coli	IM	Pass	1.0	0.8	4.3	4.9	0.7	0.6	0.7	0.7	0.9	0.6	1.0	0.6	0.7	0.9	1.0	0.8
L119B-103	EIEC	EIEC	IM	Pass	3.0	2.4	3.7	4.4	0.6	0.6	0.7	0.8	1.0	0.7	1.1	0.7	0.9	1.0	3.0	0.9
BD13-00037	EIEC	Shigella spp.	IM	Pass	4.4	3.8	1.0	1.6	0.9	1.0	1.0	1.1	1.4	0.9	1.7	1.0	1.1	1.3	1.7	1.2
BD11-00028	EIEC	Shigella spp.	IM	Pass	4.3	3.7	1.0	1.5	0.9	0.9	1.0	1.2	1.5	0.9	1.6	1.0	1.2	1.4	1.6	1.3

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In silico workflow results

	NGS algorit	thm								
Sample ID	Flexneri type ^a	ipaH present	rfc present	Detected genes	Wild type P _{gtr} ^b	Amber mutation	Frameshift	Result	Match	Comment
ERR042839	×	TRUE	TRUE	gtrX, opt, wzx1_5	TRUE	Ι	I	۸۷	FALSE	opt detected in low (4.7×) coverage
ERR042840	۲v	TRUE	TRUE	gtrX, opt, wzx1_5	TRUE	I	I	۸۷	FALSE	gtr promoter mutations not called
ERR048322	5a	TRUE	TRUE	gtrll, wzx1_5	TRUE	I	I	2a	FALSE	No obvious cause for discrepancy detected
ERR127048	4a	TRUE	TRUE	gtrlV, opt, wzx1_5	TRUE	I	I	4av	FALSE	No obvious cause for discrepancy detected
ERR217013	۲v	TRUE	TRUE	gtrX, opt, wzx1_5	TRUE	I	I	۸۷	FALSE	Indel in gtrX not detected
ERR832473	×	TRUE	TRUE	gtrX, oac, wzx1_5	TRUE	Ι	Ι	3a	FALSE	indel oac not detected
ERR832480	5a	TRUE	TRUE	gtrV, wzx1_5	TRUE	gtrV	I	≻	FALSE	No obvious cause for discrepancy detected
ERR832481	7	TRUE	TRUE	opt, wzx1_5	TRUE	I	I	¥	FALSE	opt detected in low (2.6×) coverage
ERR048265	5b	TRUE	TRUE	gtrV, gtrX, oac, wzx1_5	TRUE	I	oac	5b	TRUE	
ERR127042	5b	TRUE	TRUE	gtrV, gtrX, oac, wzx1_5	TRUE	I	oac	5b	TRUE	
ERR127044	5b	TRUE	TRUE	gtrV, gtrX, oac, wzx1_5	TRUE	I	oac	5b	TRUE	
ERR217033	1cv	TRUE	TRUE	gtrl, gtrlC, gtrX, opt, wzx1_5	TRUE	I	gtrX	1cv	TRUE	
ERR042796	۸۷	TRUE	TRUE	gtrX, opt, wzx1_5	TRUE	I	I	×	TRUE	
ERR042797	×	TRUE	TRUE	gtrX, wzx1_5	TRUE	I	I	×	TRUE	
ERR042799	2a	TRUE	TRUE	gtrll, wzx1_5	TRUE	Ι	Ι	2a	TRUE	
ERR042803	2a	TRUE	TRUE	gtrll, wzx1_5	TRUE	I	Ι	2a	TRUE	
ERR042806	2b	TRUE	TRUE	gtrll, gtrX, wzx1_5	TRUE	I	I	2b	TRUE	
ERR042810	1b	TRUE	TRUE	gtrl, oac, wzx1_5	TRUE	I	I	1b	TRUE	
ERR042811	3a	TRUE	TRUE	gtrX, oac, wzx1_5	TRUE	I	I	3a	TRUE	
ERR042814	2a	TRUE	TRUE	gtrll, wzx1_5	TRUE	I	I	2a	TRUE	
ERR042816	×	TRUE	TRUE	wzx1_5	TRUE	I	I	×	TRUE	
ERR042819	3b	TRUE	TRUE	oac, wzx1_5	TRUE	I	I	3b	TRUE	
ERR042821	2a	TRUE	TRUE	gtrll, wzx1_5	TRUE	I	I	2a	TRUE	
ERR042824	2a	TRUE	TRUE	gtrll, wzx1_5	TRUE	I	1	2a	TRUE	
ERR042825	2a	TRUE	TRUE	gtrll, wzx1_5	TRUE	I	I	2a	TRUE	
ERR042831	~	TRUE	TRUE	wzx1_5	TRUE	I	I	≻	TRUE	

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																																(Continues)
1	Comment																															
	Match	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	
	Result	1a	Зa	1a	2a	Зa	×	1c	1b	2b	1c	Зa	2a	×	¥	1b	Зa	1b	2a	NA	Зa	2a	1c	2a	4bv	1b	Зa	1b	5a	≻	1b	
	Frameshift	I	I	I	Ι	I	I	I	I	I	I	Ι	I	I	I	Ι	I	I	Ι	I	Ι	Ι	Ι	I	Ι	I	I	Ι	oac	gtrX	I	
	Amber mutation	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	Ι	Ι	I	I	I	I	I	I	I	Ι	I	
	Wild type P _{gtr} b	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	
	Detected genes	gtrl, wzx1_5	gtrX, oac, wzx1_5	gtrl, wzx1_5	gtrll, wzx1_5	gtrX, oac, wzx1_5	gtrX, opt, wzx1_5	gtrl, gtrlC, wzx1_5	gtrl, oac, wzx1_5	gtrll, gtrX, wzx1_5	gtrl, gtrlC, wzx1_5	gtrX, oac, wzx1_5	gtrll, wzx1_5	gtrX, opt, wzx1_5	opt, wzx1_5	gtrl, oac, wzx1_5	gtrX, oac, wzx1_5	gtrl, oac, wzx1_5	gtrll, wzx1_5	gtrll, opt, wzx1_5	gtrX, oac, wzx1_5	gtrll, wzx1_5	gtrl, gtrlC, wzx1_5	gtrll, wzx1_5	gtrIV, oac, opt, wzx1_5	gtrl, oac, wzx1_5	gtrX, oac, wzx1_5	gtrl, oac, wzx1_5	gtrV, oac, wzx1_5	gtrX, wzx1_5	gtrl, oac, wzx1_5	
	rfc present	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	
ithm	ipaH present	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	
NGS algori	Flexneri type ^a	1a	За	1a	2a	За	×	1c	1b	2b	1c	За	2a	Xv	۲۷	1b	За	1b	2a	NA	Зa	2a	1c	2a	4bv	1b	За	1b	5a	×	1b	
	Sample ID	ERR042835	ERR042837	ERR042841	ERR042842	ERR042843	ERR042845	ERR042849	ERR042851	ERR042852	ERR042853	ERR042855	ERR042860	ERR042861	ERR042863	ERR047236	ERR047239	ERR047294	ERR047306	ERR047307	ERR047396	ERR047406	ERR048234	ERR048246	ERR048259	ERR048261	ERR048285	ERR048286	ERR048287	ERR048288	ERR048290	

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	NGS algori	thm								
Sample ID	Flexneri type ^a	ipaH present	rfc present	Detected genes	Wild type P _{gtr} b	Amber mutation	Frameshift	Result	Match	Comment
ERR048295	2b	TRUE	TRUE	gtrll, gtrX, wzx1_5	TRUE	1	I	2b	TRUE	
ERR048296	3a	TRUE	TRUE	gtrX, oac, wzx1_5	TRUE	I	I	3a	TRUE	
ERR048300	3a	TRUE	TRUE	gtrX, oac, wzx1_5	TRUE	Ι	I	3a	TRUE	
ERR048302	2a	TRUE	TRUE	gtrll, wzx1_5	TRUE	Ι	Ι	2a	TRUE	
ERR048304	2a	TRUE	TRUE	gtrll, wzx1_5	TRUE	I	I	2a	TRUE	
ERR048306	2a	TRUE	TRUE	gtrll, wzx1_5	TRUE	I	I	2a	TRUE	
ERR048313	2b	TRUE	TRUE	gtrll, gtrX, wzx1_5	TRUE	I	I	2b	TRUE	
ERR048315	2a	TRUE	TRUE	gtrll, wzx1_5	TRUE	I	I	2a	TRUE	
ERR048316	1b	TRUE	TRUE	gtrl, oac, wzx1_5	TRUE	I	I	1b	TRUE	
ERR048319	1a	TRUE	TRUE	gtrl, wzx1_5	TRUE	I	I	1a	TRUE	
ERR048320	×	TRUE	TRUE	gtrX, wzx1_5	TRUE	Ι	Ι	×	TRUE	
ERR048331	~	TRUE	TRUE	wzx1_5	TRUE	I	I	≻	TRUE	
ERR048339	2b	TRUE	TRUE	gtrll, gtrX, wzx1_5	TRUE	I	I	2b	TRUE	
ERR049152	3a	TRUE	TRUE	gtrV, gtrX, oac, wzx1_5	TRUE	gtrV	I	3a	TRUE	
ERR126958	2a	TRUE	TRUE	gtrll, wzx1_5	TRUE	I	I	2a	TRUE	
ERR127015	2a	TRUE	TRUE	gtrll, wzx1_5	TRUE	I	I	2a	TRUE	
ERR127017	2a	TRUE	TRUE	gtrll, wzx1_5	TRUE	I	I	2a	TRUE	
ERR127019	3a	TRUE	TRUE	gtrX, oac, wzx1_5	TRUE	Ι	I	3a	TRUE	
ERR127032	1a	TRUE	TRUE	gtrl, wzx1_5	TRUE	Ι	I	1a	TRUE	
ERR127034	1c	TRUE	TRUE	gtrl, gtrlC, wzx1_5	TRUE	Ι	I	1c	TRUE	
ERR127035	2a	TRUE	TRUE	gtrll, wzx1_5	TRUE	I	I	2a	TRUE	
ERR127036	2b	TRUE	TRUE	gtrll, gtrX, wzx1_5	TRUE	I	I	2b	TRUE	
ERR127037	3a	TRUE	TRUE	gtrX, oac, wzx1_5	TRUE	I	I	3a	TRUE	
ERR127038	Зb	TRUE	TRUE	oac, wzx1_5	TRUE	I	I	3b	TRUE	
ERR127039	Зb	TRUE	TRUE	oac, wzx1_5	TRUE	Ι	I	3b	TRUE	
ERR127040	4a	TRUE	TRUE	gtrIV, wzx1_5	TRUE	I	I	4a	TRUE	
ERR127041	4b	TRUE	TRUE	gtrIV, oac, wzx1_5	TRUE	Ι	I	4b	TRUE	
ERR127043	5a	TRUE	TRUE	gtrV, oac, wzx1_5	TRUE	Ι	oac	5a	TRUE	
ERR127046	×	TRUE	TRUE	gtrX, wzx1_5	TRUE	Ι	I	×	TRUE	
ERR127047	~	TRUE	TRUE	wzx1_5	TRUE	Ι	I	≻	TRUE	
ERR200344	1b	TRUE	TRUE	gtrl, oac, wzx1_5	TRUE	ł	I	1b	TRUE	

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																															(Continues)
I	Comment																														
	Match	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE
	Result	2a	2a	2a	2a	2b	2b	За	За	3a	3a	5a	×	×	≻	×	≻	≻	×	×	≻	×	1c	1c	4av	4av	2a	5a	2a	2a	5а
	Frameshift	I	I	Ι	Ι	Ι	Ι	Ι	Ι	gtrV	gtrV	oac	gtrX	gtrX	gtrX	gtrX	gtrX	gtrX	gtrX	gtrX	gtrX	gtrX	Ι	Ι	Ι	Ι	Ι	I	Ι	I	oac
	Amber mutation	I	I	Ι	Ι	Ι	Ι	I	Ι	gtrV	gtrV	I	Ι	I	Ι	I	Ι	I	I	I	Ι	I	Ι	I	Ι	I	Ι	I	I	I	I
	Wild type P _{gtr} ^b	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE
	Detected genes	gtrll, wzx1_5	gtrll, wzx1_5	gtrll, wzx1_5	gtrll, wzx1_5	gtrll, gtrX, wzx1_5	gtrll, gtrX, wzx1_5	gtrX, oac, wzx1_5	gtrX, oac, wzx1_5	gtrV, gtrX, oac, wzx1_5	gtrV, gtrX, oac, wzx1_5	gtrV, oac, wzx1_5	gtrX, opt, wzx1_5	gtrX, opt, wzx1_5	gtrX, wzx1_5	gtrX, opt, wzx1_5	gtrX, wzx1_5	gtrX, wzx1_5	gtrX, opt, wzx1_5	gtrX, opt, wzx1_5	gtrX, wzx1_5	gtrX, opt, wzx1_5	gtrl, gtrlC, wzx1_5	gtrl, gtrlC, wzx1_5	gtrIV, opt, wzx1_5	gtrIV, opt, wzx1_5	gtrll, wzx1_5	gtrV, wzx1_5	gtrll, wzx1_5	gtrll, wzx1_5	gtrV, oac, wzx1_5
	rfc present	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE
ithm	ipaH present	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE
NGS algor	Flexneri type ^a	2a	2a	2a	2a	2b	2b	За	За	За	3a	5a	۲v	۲v	≻	۲v	¥	≻	۲v	۲v	≻	۲v	1c	1c	4av	4av	2a	5a	2a	2a	5a
	Sample ID	ERR200360	ERR200365	ERR200370	ERR200378	ERR200390	ERR200392	ERR200393	ERR200402	ERR200403	ERR200405	ERR200413	ERR200414	ERR217015	ERR217016	ERR217023	ERR217024	ERR217026	ERR217028	ERR217030	ERR217031	ERR217032	ERR217047	ERR217080	ERR217081	ERR217084	ERR559526	ERR832453	ERR832456	ERR832457	ERR832459

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	NGS algorit	thm								
Sample ID	Flexneri type ^a	ipaH present	rfc present	Detected genes	Wild type P _{gt} ^b	Amber mutation	Frameshift	Result	Match	Comment
ERR832461	2b	TRUE	TRUE	gtrll, gtrX, wzx1_5	TRUE	I	I	2b	TRUE	
ERR832462	2a	TRUE	TRUE	gtrll, wzx1_5	TRUE	I	I	2a	TRUE	
ERR832464	5a	TRUE	TRUE	gtrV, oac, wzx1_5	TRUE	I	oac	5a	TRUE	
ERR832465	3b	TRUE	TRUE	oac, wzx1_5	TRUE	I	I	3b	TRUE	
ERR832467	2a	TRUE	TRUE	gtrll, wzx1_5	TRUE	I	I	2a	TRUE	
ERR832468	2a	TRUE	TRUE	gtrll, wzx1_5	TRUE	Ι	Ι	2a	TRUE	
ERR832470	1b	TRUE	TRUE	gtrl, oac, wzx1_5	TRUE	I	I	1b	TRUE	
ERR832474	X۷	TRUE	TRUE	gtrX, opt, wzx1_5	TRUE	Ι	Ι	۸۷	TRUE	
ERR832477	3a	TRUE	TRUE	gtrX, oac, wzx1_5	TRUE	I	I	3a	TRUE	
ERR832483	1a	TRUE	TRUE	gtrl, wzx1_5	TRUE	I	I	1a	TRUE	
ERR832485	~	TRUE	TRUE	gtrll, wzx1_5	TRUE	I	gtrll	≻	TRUE	
ERR832486	2b	TRUE	TRUE	gtrll, gtrX, wzx1_5	TRUE	Ι	Ι	2b	TRUE	
ERR832487	2a	TRUE	TRUE	gtrll, wzx1_5	TRUE	I	I	2a	TRUE	
ERR832489	2a	TRUE	TRUE	gtrll, wzx1_5	TRUE	I	Ι	2a	TRUE	
ERR832490	4bv	TRUE	TRUE	gtrlV, oac, opt, wzx1_5	TRUE	I	I	4bv	TRUE	
ERR832491	1b	TRUE	TRUE	gtrl, oac, wzx1_5	TRUE	Ι	Ι	1b	TRUE	
ERR832492	3b	TRUE	TRUE	oac, wzx1_5	TRUE	I	I	3b	TRUE	
ERR832494	×	TRUE	TRUE	gtrX, wzx1_5	TRUE	I	I	×	TRUE	
S14BD02502	×	TRUE	TRUE	gtrX, oac, wzx1_5	TRUE	I	I	3a	FALSE	oac indel not detected
S15BD08204	3b	TRUE	TRUE	gtrX, oac, wzx1_5	TRUE	Ι	Ι	3a	FALSE	promoter mutations not found
S13BD04017	3b	TRUE	TRUE	gtrX, oac, wzx1_5	TRUE	I	I	3a	FALSE	promoter mutations not found
S14BD01131	×	TRUE	TRUE	gtrX, oac, wzx1_5	TRUE	Ι	oac	×	TRUE	
S14BD01142	×	TRUE	TRUE	gtrX, oac, wzx1_5	TRUE	I	oac	×	TRUE	
S14BD01714	3b	TRUE	TRUE	gtrX, oac, wzx1_5	FALSE	I	I	Зb	TRUE	
S15BD06353	3b	TRUE	TRUE	gtrX, oac, wzx1_5	TRUE	I	I	3a	FALSE	promoter mutations not found
S15BD09453	3b	TRUE	TRUE	gtrl, oac, wzx1_5	TRUE	I	I	1b	FALSE	Indel in gtrl at position 340 not detected
S16BD02240	5	FALSE	TRUE	gtrV, wzx1_5	TRUE	I	I		TRUE	
S17BD07654	×	TRUE	TRUE	gtrX, oac, oac, wzx1_5	TRUE	Ι	I	3a	FALSE	oac indel not detected
^a As determined by c	lassical seroty	ping metho	ids. ^b Based c	in comparison with the gtr promoter	(accession nur	nber KT9880.	57.1).			

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