

Supplementary Tables and Figures - Rapid Detection of Antimicrobial Resistance Genes in Critically Ill Children Using a Custom TaqMan Array Card

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Table S1: Targets on the antimicrobial resistance gene TaqMan array card

AMR gene target	Assay name	Assay number	Forward primer 1000nM	Reverse primer 1000nM	6FAM MGB probe 250nM
<i>bla</i> _{CTX-M-1}	Ba04646149_s1	10, 34			
	N/A	22	ATGTGCAGYACCAGTAARGTKATGGC	ATCACKCGGRTCGCCIGGRAT	CCCGACAGCTGGGAGACGAAACGT
<i>bla</i> _{CTX-M-2}	Ba04646142_s1	12, 35			
<i>bla</i> _{CTX-M-8/25}	Ba04646154_s1	13, 36			
<i>bla</i> _{CTX-M-9}	Ba04646127_s1	14, 37			
<i>bla</i> _{CTX-M}	N/A	23	ATGTGCAGYACCAGTAARGTKATGGC	ATCACKCGGRTCGCCIGGRAT	CGAYAATACNGCCATGAA
<i>ermB</i>	Pa04230913_s1	15, 38			
<i>bla</i> _{FOX (ampC)}	Ba04646126_s1	2, 26			
<i>bla</i> _{GES}	Ba04646151_s1	3, 27			
<i>bla</i> _{IMP}	N/A	47	CCCACGTATGCATCTGWATTAACAAA	CCAAACCACTACGTTATCTKGAGTG	AAGACGGTAAGGTNCAAGCYA
	N/A	48	CCCACGTATGCATCTGWATTAACAAA	CCAAACCACTACGTTATCTKGAGTG	AATCCGGTAAGGTNCAAGCYA
<i>bla</i> _{IMP-1}	Ba04646131_s1	5, 29			
<i>bla</i> _{KPC}	Ba04646152_s1	4, 28			
	N/A	44	GCAGCGGCAGCAGTTTGTGATT	GTAGACGGCCAACACAATAGGTGC	CAGTCGGAGACAAAACCGGA
<i>mecA</i>	N/A	20	TGGTATGTGGAAGTTAGATTGGGAT	AGATACATTCTTTGGAACGATGCCTA	CCAGGAATGCAGAAAGACCA
<i>mecA/C</i>	N/A	21	CAAGCAATAGAATCATCAGAYAACAT	CCRTAACCTGAATCWGCTAATAATATTTC	CCRAGTGATTATCCMTT
<i>bla</i> _{NDM}	N/A	46	CAGCAAATGGAACTGGCGAC	ATCCAGTTGAGGATCTGGGC	CCGAATGTCTGGCAGCACACT
<i>bla</i> _{NDM-1}	Ba04931076_s1	6, 30			
<i>bla</i> _{OXA-48}	N/A	43	ATTCGGGCTAAAACKGGATACTCGRCT	GATGTGGGCATATCCATATTCATCGCA	ACCAGCCAATCTTAGGTTTCGAT
	Ba04930816_s1	7, 31			
<i>bla</i> _{OXA-1}	Ba04646133_s1	1, 25			
<i>bla</i> _{PER-1}	Ba04646140_s1	8, 32			
<i>qnrA</i>	Ba04646160_s1	16, 39			
<i>qnrS</i>	Ba04646145_s1	17, 40			
<i>vanA</i>	N/A	24	GGGCAGAGTATTGACTTCGT	CCCGTGTGGATATGTTTTTACAAG	CCGCATTGTACTGAACG
<i>vanB</i>	N/A	42	TCCGGTCGAGGAACGAAA	GCCCTCTGCATCCAAGCA	ACGGCAAAGAAAGTATATCGG
<i>bla</i> _{VEB}	Ba04646153_s1	9, 33			
<i>bla</i> _{VIM}	Ba04646155_s1	18, 41			
	N/A	45	GCAAATTGGACTTCCYGTAACGC	CCCGAAGGACATCAACGCC	ACGCACTTTCATGACGACCG
18S rRNA gene	N/A	11			
<i>MS2</i>	N/A	19	TGGCACTACCCCTCTCCGTATTCACG	GTACGGGCGACCCACGATGAC	TCGATAGATCAAGGTGCCT

Table S2: Validation of antimicrobial resistance gene TaqMan array card with plasmids and ZeptoMetrix NATtrol panel

Validation	AMR genes present in validation sample	AMR-TAC Ct value(s)
VAP plasmid 1	<i>bla</i> _{CTX-M-1}	<i>bla</i> _{CTX-M-1} : 24/24
	<i>bla</i> _{OXA-48}	<i>bla</i> _{CTX-M} : 27
	<i>bla</i> _{IMP}	<i>bla</i> _{OXA-48} : 26/27/26
		<i>bla</i> _{IMP} : 26/25
VAP plasmid 2	<i>bla</i> _{CTX-M}	<i>bla</i> _{CTX-M-9} : 27/28
	<i>bla</i> _{NDM}	<i>bla</i> _{NDM} : 27
	<i>vanA</i>	<i>vanA</i> : 26
	<i>bla</i> _{VIM}	<i>bla</i> _{VIM} : 32/28/21
VAP plasmid 3	<i>bla</i> _{KPC}	<i>bla</i> _{KPC} : 19
	<i>mecC</i>	<i>mecA/C</i> : 25
	<i>vanB</i>	<i>vanB</i> : 18
ZeptoMetrix pool 1	<i>bla</i> _{IMP}	<i>bla</i> _{IMP-1} : 30/31
	<i>bla</i> _{OXA-48-like}	<i>bla</i> _{IMP} : 33
	<i>bla</i> _{CTX-M}	<i>bla</i> _{OXA-1} : 22/22
		<i>bla</i> _{OXA-48} : 22/23/23
		<i>bla</i> _{CTX-M-1} : 22.5/22
		<i>bla</i> _{CTX-M} : 25
ZeptoMetrix pool 2	<i>bla</i> _{KPC}	<i>bla</i> _{KPC} : 24/25/21
	<i>bla</i> _{VIM}	<i>bla</i> _{OXA-1} : 27/27
		<i>bla</i> _{VIM} : 28/30/28
ZeptoMetrix pool 3	<i>bla</i> _{NDM}	<i>bla</i> _{NDM-1} : 22/22
	<i>bla</i> _{CTX-M}	<i>bla</i> _{NDM} : 21
	<i>mecA/C</i> , MREJ	<i>bla</i> _{OXA-1} : 24/23
		<i>bla</i> _{CTX-M-1} : 20/19
		<i>bla</i> _{CTX-M} : 23
		<i>mecA</i> : 27
		<i>mecA/C</i> : 28
ZeptoMetrix pool 4	N/A	Nil
ZeptoMetrix pool 5	N/A	Nil

Table S3: Inter-assay reproducibility of an antimicrobial resistance gene TaqMan array card using faecal sewage

Assay	Cycle threshold value							Mean (SD)
	Card 1	Card 2	Card 3	Card 4	Card 5	Card 6	Card 7	
1 <i>bla</i> _{OXA-1}	21.4	21.0	22.1	23.8	23.2	24.6	21.7	22.6 (1.3)
2 <i>ampC</i>	24.5	24.2	24.7	27.2	26.4	28.3	24.7	25.7 (1.6)
3 <i>bla</i> _{GES}	19.1	19.0	19.7	21.1	20.3	21.8	19.2	20.0 (1.1)
4 <i>bla</i> _{KPC}	26.0	25.9	26.4	26.0	26.3	27.4	25.5	26.2 (0.6)
5 <i>bla</i> _{IMP-1}	22.3	22.3	23.4	24.3	24.9	24.8	22.5	23.5 (1.2)
6 <i>bla</i> _{NDM-1}	22.2	21.5	22.3	24.3	23.9	24.7	21.5	22.9 (1.3)
7 <i>bla</i> _{OXA-48}	26.2	25.5	27.4	27.6	27.0	27.8	26.1	26.8 (0.9)
8 <i>bla</i> _{PER-1}	24.6	24.6	25.1	25.9	24.9	25.6	25.2	25.1 (0.5)
9 <i>bla</i> _{VEB}	25.1	25.5	26.4	27.1	26.9	28.1	25.5	26.4 (1.1)
10 <i>bla</i> _{CTX-M-1}	28.3	28.0	28.4	26.5	26.5	26.6	27.7	27.4 (0.9)
11 18S rRNA gene	16.6	16.5	17.0	16.7	15.6	16.3	15.6	16.3 (0.5)
12 <i>bla</i> _{CTX-M-2}	-	-	-	-	-	-	-	
13 <i>bla</i> _{CTX-M-8/25}	-	-	-	-	-	-	-	
14 <i>bla</i> _{CTX-M-9}	33.3	32.4	34.9	33.4	33.1	34.5	31.6	33.3 (1.1)
15 <i>ermB</i>	20.9	21.5	22.8	21.7	21.1	21.6	21.1	21.5 (0.6)
16 <i>qnrA</i>	23.9	23.3	24.2	26.7	26.3	27.1	23.2	25.0 (1.7)
17 <i>qnrS</i>	35.3	33.5	33.6		34.0	34.5	32.5	33.9 (1.0)
18 <i>bla</i> _{VIM}	26.5	27.0	30.4	27.3	25.2	27.5	26.4	27.2 (1.6)
19 MS2	29.7	29.4	31.0	30.0	27.2	30.5	27.6	29.3 (1.4)
20 <i>mecA</i>	30.9	-	36.2	32.7	-	32.2	-	33.0 (2.3)
21 <i>mecA/C</i>	34.8	35.0	36.7	33.3	35.9	33.8	33.9	34.8 (1.2)
22 <i>bla</i> _{CTX-M}	31.4	32.1	33.6	27.9	29.5	29.6	30.5	30.7 (1.9)
23 <i>bla</i> _{CTX-M}	!	!	!	!	!	!	!	
24 <i>vanA</i>	25.3	26.4	27.0	26.3	25.8	26.1	25.8	26.1 (0.5)
25 <i>bla</i> _{OXA-1}	21.2	21.4	22.2	23.7	23.2	24.4	22.0	22.6 (1.2)
26 <i>ampC</i>	25.1	24.8	25.5	27.9	26.5	28.4	24.6	26.1 (1.5)
27 <i>bla</i> _{GES}	18.3	18.5	19.6	20.7	20.5	21.6	19.3	19.8 (1.2)
28 <i>bla</i> _{KPC}	26.1	26.1	23.4	26.2	26.3	27.5	25.3	25.9 (1.3)
29 <i>bla</i> _{IMP-1}	23.2	22.7	23.6	25.4	24.9	25.0	22.6	23.9 (1.2)
30 <i>bla</i> _{NDM-1}	22.3	22.2	22.1	24.7	24.1	24.4	21.6	23.1 (1.3)
31 <i>bla</i> _{OXA-48}	25.6	26.9	28.6	27.8	26.9	28.1	26.7	27.2 (1.0)
32 <i>bla</i> _{PER-1}	25.0	24.9	25.3	25.6	25.2	25.8	25.2	25.3 (0.3)
33 <i>bla</i> _{VEB}	25.7	25.6	26.1	27.5	26.8	27.4	25.2	26.3 (0.9)
34 <i>bla</i> _{CTX-M-1}	28.4	28.1	28.3	26.4	26.4	26.2	27.5	27.3 (1.0)
35 <i>bla</i> _{CTX-M-2}	-	-	-	-	-	-	-	
36 <i>bla</i> _{CTX-M-8/25}	-	-	-	-	-	-	-	
37 <i>bla</i> _{CTX-M-9}	34.4	33.5	33.7	35.4	35.6	33.0	32.7	34.0 (1.2)
38 <i>ermB</i>	21.6	21.4	21.7	21.6	21.3	22.3	21.0	21.6 (0.4)
39 <i>qnrA</i>	23.8	23.3	23.5	26.4	26.5	26.4	23.1	24.7 (1.6)
40 <i>qnrS</i>	36.6	35.0	36.1		37.7	34.9	33.1	35.6 (1.6)
41 <i>bla</i> _{VIM}	25.7	27.2	29.4	28.6	25.1	27.1	26.1	27.0 (1.5)
42 <i>vanB</i>	25.7	27.7	29.0	24.9	24.8	25.9	27.4	26.5 (1.6)

43	<i>bla</i> _{OXA}	22.4	21.1	22.5	23.6	23.1	24.3	21.8	22.7 (1.1)
44	<i>bla</i> _{KPC}	27.1	26.6	26.7	27.4	26.2	26.0	25.6	26.5 (0.6)
45	<i>bla</i> _{VIM}	23.6	22.8	23.1	23.5	22.1	23.0	22.2	22.9 (0.6)
46	<i>bla</i> _{NDM}	24.7	21.4	24.4	27.7	26.1	27.6	23.9	25.1 (2.2)
47	<i>bla</i> _{IMP}	24.9	23.9	26.7	26.5	27.5	28.3	26.0	26.3 (1.5)
48	<i>bla</i> _{IMP}	26.3	31.5	33.2	30.0	31.9	30.8	29.9	30.5 (2.2)

! :failed assay; - :negative

Table S4: Antimicrobial resistance genes identified on samples with phenotypic resistance

Validation sample	Sample ID	Bacteria	Known phenotypic/genotypic resistance	AMR gene card result	Concordant with AMR-TAC
1	102074	<i>S. aureus</i>	MRSA	<i>mecA/C</i> : 16	☉
2	102073	<i>S. aureus</i>	MRSA	<i>mecA/C</i> : 16	☉
3	102072	<i>S. aureus</i>	MRSA	<i>mecA</i> : 31 <i>mecA/C</i> : 32	☉
4	SA227	<i>S. aureus</i>	<i>MecC</i>	<i>mecA/C</i> : 16	☉
5	LGA 706(2)	<i>S. aureus</i>	<i>MecC</i>	<i>mecA/C</i> : 21	☉
6	160002 MU50	<i>S. aureus</i>	MSSA	-	☉
7	73048 eMRSA 3	<i>S. aureus</i>	MRSA	<i>mecA</i> : 15 <i>mecA/C</i> : 15	☉
8	17077 France 5	<i>S. aureus</i>	MRSA	<i>mecA</i> :13 <i>mecA/C</i> : 15	☉
9	17098 CA - MRSA MLST ST80	<i>S. aureus</i>	MRSA	<i>mecA</i> : 15 <i>mecA/C</i> : 16	☉
10	07045 Australia Sydney	<i>S. aureus</i>	MRSA	<i>mecA</i> : 13 <i>mecA/C</i> : 15	☉
11	WIS21093 19	<i>S. aureus</i>	MRSA	<i>mecA</i> : 14 <i>mecA/C</i> : 15	☉
12	17061 Japan 8	<i>S. aureus</i>	MRSA	<i>mecA</i> : 15 <i>mecA/C</i> : 16 <i>ermB</i> : 15/14	☉/?
13	NCTC 13379	<i>E. faecalis</i>	<i>vanHBX</i> <i>ermB</i> <i>aac(6')-aph(2'')</i> [§] <i>ant(6)-Ia</i> [§] <i>aph(3')-III</i> [§] <i>Isa(A)</i> [§] <i>qacZ</i> [§] <i>cat(pC233)</i> [§]	<i>vanB</i> : 16 <i>ermB</i> : 17/16	☉
14	NCTC 12952	<i>E. faecium</i>	<i>vanHBX</i> <i>msr(C)</i> [§] <i>tet(M)</i> [§] <i>aac(6')-II</i> [§]	<i>vanB</i> : 17	☉
15	73082 France 2	<i>S. aureus</i>	MRSA	<i>mecA</i> :16 <i>mecA/C</i> : 17	☉
16	73047 - 4	<i>S. aureus</i>	MRSA	<i>mecA</i> : 13 <i>mecA/C</i> : 15	☉
17	17069 Denmark DLL4916 - 7	<i>S. aureus</i>	MRSA	<i>mecA</i> : 16 <i>mecA/C</i> : 18	☉
18	17048 UK early strain RL13136	<i>S. aureus</i>	MRSA	<i>mecA</i> : 15 <i>mecA/C</i> : 18	☉
19	07060 Atlanta USA 80760R7	<i>S. aureus</i>	MRSA	<i>mecA</i> : 18 <i>mecA/C</i> : 18	☉
20	07059 - SF40R6LA	<i>S. aureus</i>	MRSA	<i>mecA</i> : 15 <i>mecA/C</i> : 16	☉
21	* Anonymised *VRE	<i>E. faecium</i>	<i>vanA</i>	<i>vanA</i> : 20 <i>ermB</i> : 18/18	☉/?
22	* Anonymised * VRE	<i>E. faecium</i>	<i>vanA</i>	<i>vanA</i> : 22 <i>ermB</i> : 20/20	☉/?
23	* Anonymised * VRE	<i>E. faecium</i>	<i>vanA</i>	<i>vanA</i> : 21	☉

24	* Anonymised *	<i>E. faecium</i>	<i>vanA</i>	<i>vanA</i> : 22 <i>ermB</i> : 19/19	⊙/?
25	* Anonymised *	<i>E. faecalis</i>	<i>vanA</i>	<i>vanA</i> : 19 <i>ermB</i> : 18/18	⊙/?
26	* Anonymised *	<i>E. faecalis</i>	<i>vanA</i>	<i>vanA</i> : 20 <i>ermB</i> : 19/19	⊙/?
27	* Anonymised *	<i>E. faecium</i>	Fully susceptible	-	⊙
28	NCTC 13439	<i>K. pneumoniae</i>	<i>qnrS1</i> <i>bla_{VIM-1}</i> <i>fosA</i> ^s <i>aac(6')-Ib3</i> ^s <i>aac(6')-Ib-cr</i> ^s <i>OqxB</i> ^s <i>OqxA</i> ^s <i>dfrA14</i> ^s <i>blaSHV-178</i> ^s <i>bla_{SHV-36}</i> ^s <i>bla_{SHV-80}</i> ^s <i>bla_{SHV-12}</i> ^s	<i>qnrS</i> : 21/22 <i>bla_{VIM}</i> : 28/28/23	⊙

29	NCTC 13443	<i>K. pneumoniae</i>	<i>bla</i> _{NDM-1} <i>bla</i> _{CTX-M-15} <i>bla</i> _{OXA-1} <i>msr</i> (E) ^s <i>fosA</i> ^s <i>aac</i> (3)- <i>IId</i> ^s <i>aph</i> (6)- <i>Id</i> ^s <i>aac</i> (6')- <i>Ib</i> ^s <i>aadA1</i> ^s <i>aac</i> (6')- <i>Ib-cr</i> ^s <i>aac</i> (3)- <i>IIa</i> ^s <i>armA</i> , <i>aph</i> (3'')- <i>Ib</i> ^s <i>ere</i> (A) ^s <i>msr</i> (E) ^s <i>mph</i> (E) ^s <i>OqxA</i> ^s <i>OqxB</i> ^s <i>dfrA1</i> ^s <i>sul2</i> ^s <i>sul1</i> ^s <i>ARR-2</i> ^s <i>aadA1</i> ^s <i>bla</i> _{SHV-70} ^s <i>bla</i> _{SHV-13} ^s <i>bla</i> _{SHV-11} ^s <i>bla</i> _{SHV-28} ^s <i>bla</i> _{SHV-25} ^s <i>bla</i> _{TEM-} <i>1A</i> ^s <i>bla</i> _{DHA-7} ^s <i>bla</i> _{SHV-31} ^s <i>bla</i> _{DHA-24} ^s <i>bla</i> _{SHV-69} ^s <i>bla</i> _{SHV-185} ^s <i>bla</i> _{CMY-4} ^s <i>bla</i> _{DHA-1} ^s <i>bla</i> _{SHV-106} ^s <i>bla</i> _{TEM-} <i>1B</i> ^s <i>qacE</i> ^s <i>catB3</i> ^s <i>catA1</i> ^s <i>cmlA1</i> ^s	<i>bla</i> _{NDM-1} : 17/17 <i>bla</i> _{NDM} : 19 <i>bla</i> _{CTX-M} : 18 <i>bla</i> _{CTX-M-1} : 17/18 <i>qnrS</i> : 18/18	◎/x
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30	NCTC 13442	<i>K. pneumoniae</i>	<i>bla</i> _{OXA-48} <i>aph</i> (3')-Ia ^s <i>fosA</i> ^s <i>ere</i> (A) ^s <i>OqxA</i> ^s <i>OqxB</i> ^s <i>dfrA5</i> ^s <i>sul1</i> ^s <i>dfra14</i> ^s <i>tet</i> (C) ^s <i>bla</i> _{SHV-79} ^s <i>bla</i> _{SHV-89} ^s <i>bla</i> _{SHV-56} ^s <i>bla</i> _{SHV-85} ^s <i>bla</i> _{TEM-1B} ^s <i>bla</i> _{SHV-4} ^s <i>qacE</i> ^s <i>catA1</i> ^s	<i>bla</i> _{OXA-48} : 16/18/17	⊙
31	NCTC 13438	<i>K. pneumoniae</i>	<i>bla</i> _{KPC-3} <i>bla</i> _{OXA-9} ^s <i>aph</i> (3')-Ia ^s <i>aac</i> (6')-Ib ^s <i>aadA2b</i> ^s <i>aadA2</i> ^s <i>fosA</i> ^s <i>mph</i> (A) ^s <i>OqxA</i> ^s <i>OqxB</i> ^s <i>aac</i> (6')-Ib-cr ^s <i>sul1</i> ^s <i>dfrA12</i> ^s <i>bla</i> _{SHV-182} ^s <i>bla</i> _{TEM-1A} ^s <i>qacE</i> ^s <i>catA1</i> ^s	<i>bla</i> _{KPC} : 18/17/19	⊙

32	* Anonymised *	<i>E. cloacae</i>	<i>bla</i> _{IMP}	<i>bla</i> _{IMP} : 20 <i>bla</i> _{IMP-1} : 16/16 <i>qnrA</i> : 16/16	⊙/?
33	* Anonymised *	<i>K. pneumoniae</i>	<i>bla</i> _{NDM}	<i>bla</i> _{NDM} : 17 <i>bla</i> _{NDM-1} : 15/16 <i>bla</i> _{CTX-M} : 18 <i>bla</i> _{CTX-M-1} : 17/17	⊙/?
34	* Anonymised *	<i>E. cloacae</i>	<i>bla</i> _{IMP-1}	<i>bla</i> _{IMP} : 18 <i>bla</i> _{IMP-1} : 15/15 <i>qnrA</i> : 15/15	⊙/?
35	ME21	Unknown	<i>bla</i> _{KPC} <i>bla</i> _{OXA-48}	<i>bla</i> _{KPC} : 18/19/18 <i>bla</i> _{OXA-48} : 35/34/18 <i>bla</i> _{CTX-M-9} : 20/20 <i>qnrA</i> : 18/18 <i>qnrS</i> : 18/17	⊙/?
36	* Anonymised *	<i>P. aeruginosa</i>	Unknown	-	?
37	* Anonymised *	<i>P. aeruginosa</i>	Fully susceptible	-	⊙
38	* Anonymised *	<i>P. aeruginosa</i>	Fully susceptible	-	⊙
39	ESBL15-01	<i>S. marcescens</i>	<i>bla</i> _{IMP-1}	<i>bla</i> _{IMP} : 16/18 <i>bla</i> _{IMP-1} : 19/18	⊙
40	ESBL15-02	<i>E. coli</i>	<i>bla</i> _{OXA-48} <i>bla</i> _{CTX-M-27} (group 9) <i>bla</i> _{TEM-1} §	<i>bla</i> _{OXA-48} : 18/21/20 <i>bla</i> _{CTX-M-9} : 20/22 <i>ermB</i> : 20/20	⊙/?
41	ESBL15-04	<i>K. pneumoniae</i>	<i>bla</i> _{OXA-232} (<i>bla</i> _{OXA-48} -like) <i>bla</i> _{NDM-1} <i>bla</i> _{SHV-28} §	<i>bla</i> _{NDM-1} : 22/22 <i>bla</i> _{NDM} : 25 <i>bla</i> _{OXA-1} : 22/22 <i>bla</i> _{OXA-48} : 20	⊙
42	ESBL15-05	<i>E. cloacae</i>	<i>bla</i> _{CTX-M-15} (group 1) <i>bla</i> _{NDM-1} <i>bla</i> _{TEM-1} § <i>bla</i> _{SHV-12} §	<i>bla</i> _{OXA-1} : 19/18 <i>bla</i> _{CTX-M} : 18 <i>bla</i> _{CTX-M-1} : 16/17 <i>bla</i> _{NDM} : 20 <i>bla</i> _{NDM-1} : 18/17	⊙/?
43	ESBL15-07	<i>E. coli</i>	<i>bla</i> _{CTX-M-55} (group 1) <i>bla</i> _{TEM-1} §	<i>bla</i> _{CTX-M} : 21 <i>bla</i> _{CTX-M-1} : 20/20 <i>bla</i> _{NDM} : 20 <i>bla</i> _{NDM-1} : 18/17	⊙/?
44	ESBL15-09	<i>E. coli</i> / <i>K. pneumoniae</i>	<i>bla</i> _{KPC-3} <i>bla</i> _{OXA-48} <i>bla</i> _{CTX-M-27} (group 9) <i>bla</i> _{TEM-1} § <i>bla</i> _{SHV-11} §	<i>bla</i> _{KPC} : 23/23/24 <i>bla</i> _{OXA-48} : 21/19/21 <i>bla</i> _{CTX-M-9} : 22/22 <i>ermB</i> : 21/21	⊙/?
45	ESBL15-10	<i>Enterobacter aerogenes</i>	<i>bla</i> _{TEM-24} § <i>bla</i> _{SHV-2a} §		⊙
46	ESBL15-11	<i>K. pneumoniae</i>	<i>bla</i> _{CTX-M-14} (group 9) <i>bla</i> _{SHU-76} -like §	<i>bla</i> _{CTX-M-9} : 22/23 <i>qnrS</i> : 21/22	⊙/?
47	GES control (neat)	Unknown	<i>bla</i> _{GES}	<i>bla</i> _{GES} : 15/14	⊙

48	GES control (1:20)	Unknown	<i>bla_{GES}</i>	<i>bla_{GES}</i> : 13/11	☉
49	FOX control (neat)	Unknown	<i>AmpC</i>	<i>AmpC</i> : 20/10	☉
50	FOX control (1:20)	Unknown	<i>AmpC</i>	<i>AmpC</i> : 23/23	☉
51	<i>bla_{CTX-M-15}</i> control (neat)	Unknown	<i>bla_{CTX-M-15}</i>	<i>bla_{OXA-1}</i> : 20/21 <i>bla_{CTX-M}</i> : 21 <i>bla_{CTX-M-1}</i> : 18/19	☉/?

52	<i>bla</i> _{CTX-M-2} control (neat)	Unknown	<i>bla</i> _{CTX-M-2}	<i>bla</i> _{CTX-M-2} : 22/22	☉
53	<i>bla</i> _{CTX-M-9} control (neat)	Unknown	<i>bla</i> _{CTX-M-9}	<i>bla</i> _{CTX-M-9} : 21/22 <i>qnrA</i> : 22/21	☉/?
54	<i>bla</i> _{CTX-M-14} control (neat)	Unknown	<i>bla</i> _{CTX-M-14}	<i>bla</i> _{CTX-M-9} : 20/22	☉
55	3* Anonymised *	<i>E. faecium</i>	VRE: ampicillin and vancomycin resistant	<i>vanA</i> : 21 <i>ermB</i> : 21/21	☉/?
56	* Anonymised *	<i>E. faecium</i>	VRE: ampicillin and vancomycin resistant	<i>vanA</i> : 22 <i>ermB</i> : 20/22	☉/?
57	NCTC 13437	<i>P. aeruginosa</i>	<i>bla</i> _{VIM-2} <i>bla</i> _{VEB-1} <i>fosA</i> ^{\$} <i>aadA1</i> ^{\$} <i>aph</i> (3')-Iib ^{\$} <i>aac</i> (6')-II ^{\$} <i>ant</i> (2'')-Ia ^{\$} <i>aac</i> (6')-II ^{\$} <i>crpP</i> , <i>sul1</i> ^{\$} <i>dfrB2</i> ^{\$} <i>tet</i> (A) ^{\$} <i>bla</i> _{PAO} ^{\$} <i>bla</i> _{OXA-50} ^{\$} <i>bla</i> _{OXA-10} ^{\$} <i>qacE</i> ^{\$} <i>catB7</i> ^{\$}	<i>bla</i> _{VIM} : 15/19/25 <i>bla</i> _{VEB} : 17/16	☉
58	NCTC 13443	<i>K. pneumoniae</i>	<i>bla</i> _{NDM-1} <i>bla</i> _{OXA-1} <i>bla</i> _{CTX-M-15} <i>msr</i> (E) ^{\$} <i>fosA</i> ^{\$} <i>aac</i> (3)-Iid ^{\$} <i>aph</i> (6)-Id ^{\$} <i>aac</i> (6')-Ib ^{\$} <i>aadA1</i> ^{\$} <i>aac</i> (6')-Ib-cr ^{\$} <i>aac</i> (3)-IIa ^{\$} <i>armA</i> ^{\$} <i>aph</i> (3'')-Ib ^{\$} <i>ere</i> (A) ^{\$} <i>msr</i> (E) ^{\$} <i>mph</i> (E) ^{\$} <i>OqxA</i> ^{\$} <i>OqxB</i> ^{\$} <i>dfrA1</i> ^{\$} <i>sul2</i> ^{\$} <i>sul1</i> ^{\$} <i>ARR-2</i> ^{\$} <i>aadA1</i> ^{\$} <i>bla</i> _{SHV-70} ^{\$} <i>bla</i> _{SHV-13} ^{\$} <i>bla</i> _{SHV-11} ^{\$} <i>bla</i> _{SHV-28} ^{\$} <i>bla</i> _{SHV-25} ^{\$} <i>bla</i> _{TEM-1A} ^{\$}	<i>bla</i> _{NDM} : 23/22/25 <i>bla</i> _{OXA-1} : 20/20 <i>bla</i> _{CTX-M-1} : 17/17/16	☉

			<i>bla</i> _{DHA-7} ^{\$} <i>bla</i> _{SHV-31} ^{\$} <i>bla</i> _{DHA-24} ^{\$} <i>bla</i> _{SHV-69} ^{\$} <i>bla</i> _{SHV-185} ^{\$} <i>bla</i> _{CMY-4} ^{\$} <i>bla</i> _{DHA-1} ^{\$} <i>bla</i> _{SHV-106} ^{\$} <i>bla</i> _{TEM-1} ^{\$} <i>qacE</i> ^{\$} <i>qacE</i> ^{\$} <i>catB3</i> ^{\$} <i>catA1</i> ^{\$} <i>cmlA1</i> ^{\$}		
59	NCTC 13438	<i>K. pneumoniae</i>	<i>bla</i> _{KPC-3} <i>bla</i> _{OXA-9} ^{\$} <i>aph(3')-Ia</i> ^{\$} <i>aac(6')-Ib</i> ^{\$} <i>aadA2b</i> ^{\$} <i>aadA2</i> ^{\$} <i>fosA</i> ^{\$} <i>mph(A)</i> ^{\$} <i>OqxA</i> ^{\$} <i>OqxB</i> ^{\$} <i>aac(6')-Ib-cr</i> ^{\$} <i>sul1</i> ^{\$} <i>dfrA12</i> ^{\$} <i>bla</i> _{SHV-182} ^{\$} <i>bla</i> _{TEM-1A} ^{\$} <i>qacE</i> ^{\$} <i>catA1</i> ^{\$}	<i>bla</i> _{KPC} : 19/19/16	⊙
60	NCTC 13476	<i>E. coli</i>	<i>bla</i> _{IMP} <i>aac(3)-IIId</i> ^{\$}	<i>bla</i> _{IMP} : 21/21 <i>bla</i> _{IMP-1} : 20	⊙

⊙ = correlation; ? = unknown correlation; \$ = genes not present on AMR-TAC; MRSA: methicillin resistant *Staphylococcus aureus*; MSSA: methicillin susceptible *Staphylococcus aureus*; VRE: vancomycin resistant *Enterococcus*⊙

Table S5: Concordance of antimicrobial resistance gene TaqMan array card results in faecal and respiratory samples obtained from children with suspected lower respiratory tract infection.

		<i>blaCTX-M-1</i>		
Faecal		Respiratory		
		+	-	
	+	0	1	1
	-	0	66	66
		0	67	

		<i>blaCTX-M-9</i>		
Faecal		Respiratory		
		+	-	
	+	0	1	1
	-	0	66	66
		0	67	

		<i>ermB</i>		
Faecal		Respiratory		
		+	-	
	+	5	30	35
	-	5	27	32
		10	57	

		<i>mecA</i>		
Faecal		Respiratory		
		+	-	
	+	3	6	9
	-	5	53	58
		8	59	

		<i>mecC</i>		
Faecal		Respiratory		
		+	-	
	+	0	2	2
	-	0	65	65
		0	67	

		<i>vanB</i>		
Faecal		Respiratory		
		+	-	
	+	0	1	1
	-	0	66	66
		0	67	

		<i>TOTAL</i>		
Faecal		Respiratory		
		+	-	
	+	8	41	49
	-	10	353	363
		18	394	