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Estimating the prevalence of mixed-type gonococcal infections in Queensland, Australia

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Supplementary table 1. Design summary of *porB* group oligonucleotide primers and probe; porB-grpA-F and porB-grpA-R primers were designed to detect sequences belonging to group-A *porB* strains using the consensus probe porB-grps-conTM probe (table 1A below), porB-grpB-F and porB-grpBC-R primers were designed to detect sequences belonging to group-B *porB* (table 1B below) and porB-grpC-F and porB-grpBC-R primers designed to detect sequences belonging to group-C *porB* (table 1B below) along with consensus probe porB-grps-conTM (table 1A).

1A

porB Sequence type (number of isolates)	grpA-F (5' to 3') GTTTAAGCAACATTGCCCAACCC	grpA-R (5' to 3') GAACCTGGTGTTTCTCAGTCGTG	grps-conTM (5' to 3') ACGCTACGATTCTCCCGAATTTGC
147 (n=4)	.....	.....	.....
90 (n=9)	.....	.....	.....
161 (n=1)	.....	.....	.....
251 (n=1)	.....	.....	.....
407 (n=8)	.....	.....	.....
820 (n=1)	.....	.....	.....
2759 (n=2)	.....	.....	.....
4101 (n=45)	.....	.....	.....
4104 (n=26)	.....	.....	.....
4150 (n=1)	.....	.....	.....
4689 (n=3)	.....	.....	.....
4802 (n=2)	.....	.....	.....
4313 (n=4)	.....	.....	.....
402 (n=3)	.....	...T.....	.....
3402 (n=1)	.....	...T.....	.....
1840 (n=1)	.....G....	...T.....	.....
227 (n=4)	AAA.C.....A..G...GG..GG	CGTAT.C.AT...T.T...GCCT	.....
262 (n=2)	AAA.C.....A..G...AG..GG	CGTAT.C.AT...T.T...GCCT	.....
263 (n=2)	AAA.C.....A..G...AG..GG	CGTAT.C.AT...T.T...GCCT	.....
105 (n=3)	AAA.C.....A..G...AG..GG	CGTAT.C.AT...T.T...GCCT	.....
2656 (n=1)	AAA.C.....A..G...AG..GG	CGTAT.C.AT...T.T...GCCT	.....
4072 (n=2)	AAA.C.....A..G...AG..GG	CGTAT.C.AT...T.T...GCCT	.....
8 (n=1)	AAA.C.....A..G...G...GG	CGTAT.C.AT...T.T...GCCT	.....
4393 (n=1)	AAA.C.....A..G...G...GG	CGTAT.C.AT...T.T...GCCT	.....
4391 (n=1)	AAA.C.....A..G...G...GG	CGTAT.C.AT...T.T...GCCT	.....
4687 (n=1)	AAA.C.....A..G...G...GG	CGTAT.C.AT...T.T...GCCT	.....
30 (n=2)	AAA.C.....A..G...GG..GG	..CTA.C.AT...T.T...GCCT	.....
4292 (n=1)	AAA.C.....A..G...GG..GG	..CTA.C.AT...T.T...GCCT	.....
279 (n=1)	AAA.C.....A..G...AG..GG	..CTA.C.AT...T.T...GCCT	.....
2569 (n=14)	AAA.CG....A..G...GG..GG	CGTAT.C.AT...T.T...GCCT	.....
2893 (n=2)	AAA.C.....A..G...GG..GG	AGC.T.C.AT...T.T...GCCT	.....
1808 (n=29)	AAA.C.....A..G...GG..GG	AGTAT.C.AT...T.T...GCCT	.....
3494 (n=2)	AAA.C.....A..G...GG..GG	AGTAT.C.AT...T.T...GCCT	.....
4148 (n=9)	AAA.C.....A..G...GG..GG	AGTAT.C.AT...T.T...GCCT	.....
4397 (n=1)	AAA.C.....A..G...GG..GG	AGTAT.C.AT...T.T...GCCT	.....
4906 (n=1)	AAA.C.....A..G...GG..GG	AGTAT.C.AT...T.T...GCCT	.....
4446 (n=1)	AAA.C.....A..G...GG..GG	AGTAT.C.AT...T.T...GCCT	.....

4803 (n=1)	AAA.C.....A..G...GG..GG	AGTAT.C.AT...T.T...GCCT	.....
601 (n=1)	AAA.C.....A..G...AG..AG	CGTAT.C.AT...T.T...GCCT	.....
4143 (n=9)	AAA.C.....A..G...AG..GG	AGC.T.C.AT...T.T...GCCT	.....
4389 (n=1)	AAA.C.....A..G...GG..GG	ATC.T.CCAT...T.T...GCCT	.....
4781 (n=1)	AAA.C.....A..G...AG..GG	CGTAT.C.AT..CT.T...GCCT	.....
2280 (n=2)	AAA.C.....A..G.....GG	CGTAT.C.AT...T.T...GCCT	.....
193 (n=1)	AAA.C...GGA..G.....GG	TGTAT.C.AT...T.T...GCCT	.....
289 (n=2)	AAA.C...GGA..G.....GG	TGTAT.C.AT...T.T...GCCT	.....
301 (n=5)	AAA.C...GGA..G...G...GG	CGTAT.C.AT...T.T...GCCT	.....
785 (n=1)	AAA.C...GGA..G...G...GG	CGTAT.C.AT...T.T...GCCT	.....
316 (n=1)	AAA.C....GA..G.....GG	ATC.T.CCAT...T.T...GCCT	.....
463 (n=1)	AAA.C...GGA..G.....GG	CGTAT.C.AT...T.T...GCCT	.....
18 (n=1)	AAA.C...GGA..G.....GG	CGTAT.C.AT...T.T...GCCT	.....
904 (n=2)	AAA.C...GGA..G.....GG	CGTAT.C.AT...T.T...GCCT	.....
952 (n=1)	AAA.C...GGA..G.....GG	CGTAT.C.AT...T.T...GCCT	.....
4099 (n=24)	AAA.C...GGA..G.....GG	CGTAT.C.AT...T.T...GCCT	.....
4128 (n=1)	AAA.C...GGA..G.....GG	CGTAT.C.AT...T.T...GCCT	.....
4149 (n=9)	AAA.C...GGA..G.....GG	CGTAT.C.AT...T.T...GCCT	.....
4392 (n=1)	AAA.C...GGA..G.....GG	CGTAT.C.AT...T.T...GCCT	.....
4394 (n=3)	AAA.C...GGA..G.....GG	CGTAT.C.AT...T.T...GCCT	.....
4395 (n=1)	AAA.C...GGA..G.....GG	CGTAT.C.AT...T.T...GCCT	.....
4399 (n=1)	AAA.C...GGA..G.....GG	CGTAT.C.AT...T.T...GCCT	.....
4400 (n=1)	AAA.C...GGA..G.....GG	CGTAT.C.AT...T.T...GCCT	.....
4443 (n=6)	AAA.C...GGA..G.....GG	CGTAT.C.AT...T.T...GCCT	.....
4631 (n=1)	AAA.C...GGA..G.....GG	CGTAT.C.AT...T.T...GCCT	.....
4656 (n=1)	AAA.C...GGA..G.....GG	CGTAT.C.AT...T.T...GCCT	.....
4672 (n=1)	AAA.C...GGA..G.....GG	CGTAT.C.AT...T.T...GCCT	.....
4688 (n=1)	AAA.C...GGA..G.....GG	CGTAT.C.AT...T.T...GCCT	.....
4782 (n=1)	AAA.C...GGA..G.....GG	CGTAT.C.AT...T.T...GCCT	.....
488 (n=1)	AAA.C...GGA..G...A...GG	CGTAT.C.AT...T.T...GCCT	.....
4 (n=3)	AAA.C...GGA..G...A...GG	CGTAT.C.AT...T.T...GCCT	.....
14 (n=33)	AAA.C...GGA..G...A...GG	CGTAT.C.AT...T.T...GCCT	.....
543 (n=2)	AAA.C...GGA..G...A...GG	CGTAT.C.AT...T.T...GCCT	.....
591 (n=1)	AAA.C...GGA..G...A...GG	CGTAT.C.AT...T.T...GCCT	.....
1445 (n=1)	AAA.C...GGA..G...A...GG	CGTAT.C.AT...T.T...GCCT	.....
1489 (n=2)	AAA.C...GGA..G...A...GG	CGTAT.C.AT...T.T...GCCT	.....
1678 (n=1)	AAA.C...GGA..G...A...GG	CGTAT.C.AT...T.T...GCCT	.....
2923 (n=1)	AAA.C...GGA..G...A...GG	CGTAT.C.AT...T.T...GCCT	.....
3377 (n=1)	AAA.C...GGA..G...A...GG	CGTAT.C.AT...T.T...GCCT	.....
4396 (n=2)	AAA.C...GGA..G...A...GG	CGTAT.C.AT...T.T...GCCT	.....
4668 (n=1)	AAA.C...GGA..G...A...GG	CGTAT.C.AT...T.T...GCCT	.....
4779 (n=1)	AAA.C...GGA..G...A...GG	CGTAT.C.AT...T.T...GCCT	.....
4780 (n=1)	AAA.C...GGA..G...A...GG	CGTAT.C.AT...T.T...GCCT	.....
4783 (n=1)	AAA.C...GGA..G...A...GG	CGTAT.C.AT...T.T...GCCT	.....
4784 (n=1)	AAA.C...GGA..G...A...GG	CGTAT.C.AT...T.T...GCCT	.....
4804 (n=1)	AAA.C...GGA..G...A...GG	CGTAT.C.AT...T.T...GCCT	.....
4872 (n=1)	AAA.C...GGA..G...A...GG	CGTAT.C.AT...T.T...GCCT	.....
4905 (n=1)	AAA.C...GGA..G...A...GG	CGTAT.C.AT...T.T...GCCT	.....
908 (n=15)	AAA.C...GGA..G.....GG	C.TATCCT.CCA.T.T...GCCT	.....
3669 (n=2)	AAA.C...GGA..G.....GG	C.TATCCT.CCA.T.T...GCCT	.....
912 (n=3)	AAA.C...GGA..G...A...GG	CGTAT.C.AT...T.....GCCT	.....

1389 (n=1)	AAA.C...GGA..G.....GG	ATC.T.CCAT...T.T...GCCT	.....
1903 (n=1)	AAA.C...GGA..G.....GG	C.TATCTT.CCA.T.T...GCCT	.....
4146 (n=5)	AAA.C....GA..G.....GG	CGTAT.C.AT...T.T...GCCT	.....
4907 (n=2)	AAA.C....GA..G.....GG	CGTAT.C.AT...T.T...GCCT	.....
4390 (n=1)	AAA.C...GGA..G...A...GG	CGTAT.C.GT...T.T...GCCT	.....
4398 (n=2)	AAA.C...GGA..G...A...GG	TGTAT.C.AT...T.T...GCCT	.....
4785 (n=1)	AAA.C...GGA..G...A...GG	TGTAT.C.AT...T.T...GCCT	.....
4401 (n=1)	AAA.C...GGA..G...A...AG	CGTAT.C.AT...T.T...GCCT	.....

1B

porB Sequence type number of isolates)	grpB-F (5' to 3') GGCAAATATACCGGCGAGCTT	grpC-F (5' to 3') GGCAAATTTACCGGCAATGTG	grpBC-R (5' to 3') GCCTTCGCCGTATCTTTGGAA
147 (n=4)	..T...------A..T.CTA.	..T...------A..T.CTAT	CGTG.AA.TA.G.....TAT.
90 (n=9)	..T...------A..T.CTA.	..T...------A..T.CTAT	CGTG.AATTA.G.....TAT.
161 (n=1)	..T...------A..T.CTA.	..T...------A..T.CTAT	CGTG.AA.TA.G.....TAT.
251 (n=1)	..T...------A..T.CTA.	..T...------A..T.CTAT	CGTG.AATTA.G.....TAT.
407 (n=8)	..T...------A..T.CTA.	..T...------A..T.CTAT	CGTG.AATTA.G.....TAT.
820 (n=1)	..T...------A..T.CTA.	..T...------A..T.CTAT	CGTG.AATTA.G.....TAT.
2759 (n=2)	..T...------A..T.CTA.	..T...------A..T.CTAT	CGTG.AATTA.G.....TAT.
4101 (n=45)	..T...------A..T.CTA.	..T...------A..T.CTAT	CGTG.AATTA.G.....TAT.
4104 (n=26)	..T...------A..T.CTA.	..T...------A..T.CTAT	CGTG.AATTA.G.....TAT.
4150 (n=1)	..T...------A..T.CTA.	..T...------A..T.CTAT	CGTG.AATTA.G.....TAT.
4689 (n=3)	..T...------A..T.CTA.	..T...------A..T.CTAT	CGTG.AATTA.G.....TAT.
4802 (n=2)	..T...------A..T.CTA.	..T...------A..T.CTAT	CGTG.AATTA.G.....TAT.
4313 (n=4)	..T...------A..T.CTA.	..T...------A..T.CTAT	CGTG.AATTA.G.....TAT.
402 (n=3)	..T...------A..T.CTA.	..T...------A..T.CTAT	CGTG.AATTA.G.....TAT.
3402 (n=1)	..T...------A..T.CTA.	..T...------A..T.CTAT	CGTG.AAT.A.G.....TAT.
1840 (n=1)	..T...------A....ATA.	..T...------A..G.ATAT	CGTG.AATTA.G.....TAT.
227 (n=4)	.....T..	.....A.....G.GT.T	.....
262 (n=2)	.....T..	.....A.....G.GT.T	.....
263 (n=2)	.....T..	.....A.....G.GT.T	.....
105 (n=3)	.....T..	.....A.....G.GT.T	.....
2656 (n=1)	.....T..	.....A.....G.GT.T	.....
4072 (n=2)	.....T..	.....A.....G.GT.T	.....
8 (n=1)	.....T..	.....A.....G.GT.T	.....
4393 (n=1)	.....T..	.....A.....G.GT.T	.....
4391 (n=1)	.....T..	.....A.....G.GT.T	.....
4687 (n=1)	.....T..	.....A.....G.GT.T	.....
30 (n=2)	.....T..	.....A.....G.GT.T	.....
4292 (n=1)	.....T..	.....A.....G.GT.T	.....
279 (n=1)	.....T..	.....A.....G.GT.T	.....
2569 (n=14)	.....T..	.....A.....G.GT.T	.....
2893 (n=2)	.....	.....A.....G.GC.T	.....
1808 (n=29)	.....	.....A.....G.GC.T	.....
3494 (n=2)	.....G.....	.....GA.....G.GC.T	.....

4148 (n=9)	.....	.....A.....G.GC.T	.....
4397 (n=1)	A.....	A.....A.....G.GC.T	.....
4906 (n=1)	.....	.....A.....G.GC.T	.....
4446 (n=1)	.....	.....A.....G.GC.T	.....
4803 (n=1)	.....	.....A.....G.GC.T	.....
601 (n=1)	.....T..	.....A.....G.GT.T	.....
4143 (n=9)	.....	.....A.....G.GC.T	.....
4389 (n=1)	.....T..	.....A.....G.GT.T	.....
4781 (n=1)	.....T..	.....A.....G.GT.T	.....
2280 (n=2)	.....T..	.....A.....G.GT.T	.....
193 (n=1)	.....T.....A.TG.G	.....	.....
289 (n=2)	.....T.....A.TG.G	.....	.....
301 (n=5)	.....T.....A.TG.G	.....	.....
785 (n=1)	.....T.....A.TG.G	.....	.....
316 (n=1)	.....T.....A.TG.G	.....	.....
463 (n=1)	.....T.....A.TG.G	.....	.....
18 (n=1)	.....T.....A.TG.G	.....	.....
904 (n=2)	.....T.....A.TG.G	.....	.....
952 (n=1)	.....T.....A.TG.G	.....	.....
4099 (n=24)	.....T.....A.TG.G	.....	.....
4128 (n=1)	.....T.....A.TG.G	.....	.....
4149 (n=9)	.....T.....A.TG.G	.....	.....
4392 (n=1)	.....T.....A.TG.G	.....	.....
4394 (n=3)	.....T.....A.TG.G	.....	.....
4395 (n=1)	.....T.....A.TG.G	.....	.....
4399 (n=1)	.....T.....A.TG.G	.....	.....
4400 (n=1)	.....T.....A.TG.G	.....	.....
4443 (n=6)	.....T.....A.TG.G	.....	.....
4631 (n=1)	.....T.....A.TG.G	.....	.....
4656 (n=1)	.....T.....A.TG.G	.....	.....
4672 (n=1)	.....T.....A.TG.G	.....	.....
4688 (n=1)	.....T.....A.TG.G	.....	.....
4782 (n=1)	.....T.....A.TG.G	.....	.....
488 (n=1)	.....T.....A.TG.G	.....	.....
4 (n=3)	.....T.....TG.G	.....G.....	.....
14 (n=33)	.....T.....TG.G	.....G.....	.....
543 (n=2)	.....T.....A.TG.G	.....	.....
591 (n=1)	.....T.....A.TG.G	.....	.....
1445 (n=1)	.....T.....A.TG.G	.....	.....
1489 (n=2)	.....T.....TG.G	.....G.....	.....
1678 (n=1)	.....T.....TG.G	.....G.....	.....
2923 (n=1)	.....T.....A.TG.G	.....	.....
3377 (n=1)	.....T.....A.TG.G	.....	.....
4396 (n=2)	.....T.....TG.G	.....G.....	.....
4668 (n=1)	.....T.....TG.G	.....G.....	.....
4779 (n=1)	.....T.....A.TG.G	.....	.....
4780 (n=1)	.....T.....A.TG.G	.....	.....
4783 (n=1)	.....T.....TG.G	.....G.....	.....
4784 (n=1)	.....T.....A.TG.G	.....	.....T.....
4804 (n=1)	.....T.....TG.G	.....G.....	.....
4872 (n=1)	.....T.....A.TG.G	.....	.....

4905 (n=1)	.....T.....A.TG.G	.....	.....
908 (n=15)	.....T.....A.TG.G	.....	.....
3669 (n=2)	.....T.....A.TG.G	.....	.....
912 (n=3)	.....T.....TG.G	.....G.....	.....
1389 (n=1)	.....T.....A.TG.G	.....	.....
1903 (n=1)	.....T.....A.TG.G	.....	.....
4146 (n=5)	.....T.....A.TG.G	.....	.....
4907 (n=2)	.....T.....A.TG.G	.....	.....
4390 (n=1	.....T.....TG.G	.....G.....	.....
4398 (n=2)	.....T.....A.TG.G	.....	.....
4785 (n=1)	.....T.....A.TG.G	.....	.....
4401 (n=1)	.....T.....TG.G	.....G.....	.....

Supplementary table 2. *porB* group PCR validation summary. Cycle threshold values are provided in parentheses.

NGMAST	tbpB	porB	porB group assay	No. isolate	porB-grpA	porB-grpB	porB-grpC
758	**29**	**90**	grpA	1	DT (17.7)	nd	nd
3228	**294**	**90**	grpA	1	DT (17.5)	nd	nd
4990	**1044**	**90**	grpA	2	DT (16.12;27.82)	nd	nd
6876	**1330**	**4101**	grpA	2	DT (18.12;18.8)	nd	nd
6886	**1334**	**4104**	grpA	2	DT (16.59;17.34)	nd	nd
6937	**1329**	**4104**	grpA	2	DT (19.42;23.26)	nd	nd
6938	**1343**	**407**	grpA	2	DT (18.86;19.33)	nd	nd
7705	**349**	**4101**	grpA	2	DT (24.53;30.38)	nd	nd
8021	**1330**	**4689**	grpA	1	DT (17.42)	nd	nd
190	**26**	**227**	grpB	1	nd	16.6	nd
2992	**29**	**1808**	grpB	4	nd	DT (17.4-19.9; mean 18.47)	nd
4186	**241**	**2569**	grpB	4	nd	DT (17.54-29.24; mean 21.25)	nd
4768	**3**	**105**	grpB	2	nd	DT (19.29;20.73)	nd
5031	**32**	**227**	grpB	1	nd	DT (19.04)	nd
6946	**29**	**4148**	grpB	3	nd	DT (20.34-31.68; mean 27.46)	nd
21	**33**	**14**	grpC	7	nd	nd	DT (18.78-25.64; mean 21.6)
1407	**110**	**908**	grpC	1	nd	nd	DT (17.37)

6879	**349**	**4099**	grpC	4	nd	nd	DT (17.12-18.97; mean 17.81)
7413	**349**	**4443**	grpC	3	nd	nd	DT (25.17-28.31; mean 26.53)

DT = detected; nd = not detected