

Table S4. Validity of the STH-PAS tool

1. *yaiO* gene

	Outcome +	Outcome -	Total
Test +	99	0	99
Test -	3	37	40
Total	102	37	139

Point estimates and 95% CIs:

Apparent prevalence *	0.71 (0.63, 0.79)
True prevalence *	0.73 (0.65, 0.81)
Sensitivity *	0.97 (0.92, 0.99)
Specificity *	1.00 (0.91, 1.00)
Positive predictive value *	1.00 (0.96, 1.00)
Negative predictive value *	0.92 (0.80, 0.98)
Positive likelihood ratio	Inf (NaN, Inf)
Negative likelihood ratio	0.03 (0.01, 0.09)
False T+ proportion for true D- *	0.00 (0.00, 0.09)
False T- proportion for true D+ *	0.03 (0.01, 0.08)
False T+ proportion for T+ *	0.00 (0.00, 0.04)
False T- proportion for T- *	0.07 (0.02, 0.20)
Correctly classified proportion *	0.98 (0.94, 1.00)

* Exact CIs

2. *khe* gene

	Outcome +	Outcome -	Total
Test +	10	0	10
Test -	0	129	129
Total	10	129	139

Point estimates and 95% CIs:

Apparent prevalence *	0.07 (0.04, 0.13)
True prevalence *	0.07 (0.04, 0.13)
Sensitivity *	1.00 (0.69, 1.00)
Specificity *	1.00 (0.97, 1.00)
Positive predictive value *	1.00 (0.69, 1.00)
Negative predictive value *	1.00 (0.97, 1.00)
Positive likelihood ratio	Inf (NaN, Inf)
Negative likelihood ratio	0.00 (0.00, NaN)
False T+ proportion for true D- *	0.00 (0.00, 0.03)
False T- proportion for true D+ *	0.00 (0.00, 0.31)
False T+ proportion for T+ *	0.00 (0.00, 0.31)
False T- proportion for T- *	0.00 (0.00, 0.03)
Correctly classified proportion *	1.00 (0.97, 1.00)

* Exact CIs