

Table S1. Bayesian latent class models with different covariance terms for estimating the cut-off value and diagnostic performances for five tests for *Enterocytozoon hepatopenaei* (EHP) nucleic acid in samples from Penaeid shrimp populations in Vietnam and Ecuador.

Model	Covariance terms included	DIC	PD
M ₀ (Saturated)	$\rho D^{+,12}$ $\rho D^{-,12}$ $\rho D^{+,13}$ $\rho D^{-,13}$ $\rho D^{+,14}$ $\rho D^{-,14}$ $\rho D^{+,15}$ $\rho D^{-,15}$ $\rho D^{+,16}$ $\rho D^{-,16}$ $\rho D^{+,23}$ $\rho D^{-,23}$ $\rho D^{+,24}$ $\rho D^{-,24}$ $\rho D^{+,25}$ $\rho D^{-,25}$ $\rho D^{+,26}$ $\rho D^{-,26}$ $\rho D^{+,34}$ $\rho D^{-,34}$ $\rho D^{+,35}$ $\rho D^{-,35}$ $\rho D^{+,36}$ $\rho D^{-,36}$ $\rho D^{+,45}$ $\rho D^{-,45}$ $\rho D^{+,46}$ $\rho D^{-,46}$	108.0	32.1
M ₁	M ₀ minus $\rho D^{+,25}$ $\rho D^{-,34}$	104.0	29.4
M ₂	M ₁ minus $\rho D^{-,14}$ $\rho D^{-,25}$	104.8	30.6
M ₃	M ₂ minus $\rho D^{+,26}$ $\rho D^{+,45}$	104.5	30.8
M ₄	M ₀ reformulated with sp5 = sp6	109.4	34.5

DIC = deviance information criterion (lower implies better model fit); PD = effective number of parameters. Correlation terms represented as $\rho D^{+,12}$ for the correlation in results between tests 1 and 2 in samples that were truly infected with *Enterocytozoon hepatopenaei* (EHP). Tests: 1 = PTP2G PCR, 2 = SWP26G PCR, 3 = PTP2 Wang PCR, 4 = Shrimp MultiPath EHP, 5 = Nested PCR in Vietnam, 6 = Nested PCR in Ecuador.

Table S2. Estimated correlation terms between tests from a Bayesian latent class model for five assays in one population (PTP2G, SWP26G, PTP2_Wang, SMP EHP and nested SWP1)).

Correlation	Posterior median (95% CrI)	Prior distribution
$\rho D^{+,12}$	0.255 (0.059, 0.460)	Uniform(-1, 1)
$\rho D^{+,13}$	0.127 (-0.005, 0.313)	Uniform(-1, 1)
$\rho D^{+,14}$	0.097 (-0.040, 0.259)	Uniform(-1, 1)
$\rho D^{+,15}$	0.062 (-0.186, 0.360)	Uniform(-1, 1)
$\rho D^{+,16}$	-0.099 (-0.306, 0.017)	Uniform(-1, 1)
$\rho D^{+,23}$	0.135 (-0.027, 0.347)	Uniform(-1, 1)
$\rho D^{+,24}$	0.072 (-0.070, 0.254)	Uniform(-1, 1)
$\rho D^{+,26}$	-0.047 (-0.246, 0.119)	Uniform(-1, 1)
$\rho D^{+,34}$	0.178 (0.003, 0.455)	Uniform(-1, 1)
$\rho D^{+,35}$	0.157 (-0.097, 0.446)	Uniform(-1, 1)
$\rho D^{+,36}$	-0.219 (-0.515, -0.016)	Uniform(-1, 1)
$\rho D^{+,45}$	0.072 (-0.170, 0.347)	Uniform(-1, 1)
$\rho D^{+,46}$	-0.204 (-0.482, -0.018)	Uniform(-1, 1)
$\rho D^{-,12}$	0.055 (-0.891, 0.846)	Uniform(-1, 1)
$\rho D^{-,13}$	0.115 (-0.818, 0.875)	Uniform(-1, 1)
$\rho D^{-,14}$	-0.017 (-0.874, 0.58)	Uniform(-1, 1)
$\rho D^{-,15}$	0.173 (-0.839, 0.927)	Uniform(-1, 1)
$\rho D^{-,16}$	0.110 (-0.915, 0.935)	Uniform(-1, 1)
$\rho D^{-,23}$	0.166 (-0.783, 0.835)	Uniform(-1, 1)
$\rho D^{-,24}$	0.063 (-0.682, 0.566)	Uniform(-1, 1)
$\rho D^{-,25}$	-0.041 (-0.934, 0.907)	Uniform(-1, 1)
$\rho D^{-,26}$	-0.161 (-0.957, 0.902)	Uniform(-1, 1)
$\rho D^{-,35}$	0.265 (-0.837, 0.945)	Uniform(-1, 1)
$\rho D^{-,36}$	0.210 (-0.879, 0.951)	Uniform(-1, 1)
$\rho D^{-,45}$	-0.333 (-0.958, 0.240)	Uniform(-1, 1)
$\rho D^{-,46}$	-0.180 (-0.945, 0.683)	Uniform(-1, 1)

Correlation terms represented as $\rho D^{+,12}$ for the correlation in results between tests 1 and 2 in samples that were truly infected with *Enterocytozoon hepatopenaei* (EHP). Tests: 1 = PTP2G PCR, 2 = SWP26G PCR, 3 = PTP2 Wang PCR, 4 = Shrimp MultiPath EHP5 = Nested PCR in Vietnam, 6 = Nested PCR in Ecuador. Model deviance information criterion (DIC) = 104.0.

Table S3. SWP26 sequence variation between Vietnam and Ecuador EHP SWP26 genes focused on consensus positions. Sequence variation at codon position 514 bp leads to amino acid change from Serine (polar) to Alanine (non-polar) in the predicted AA sequence.

CONSENSUS POSITION ¹	81	117	120	135	198	258	354	501	514
MN604022_SWP26_CDS	C	C	C	A	T	A	G	A	T
Vietnam SWP26 ²	C	C	C	A	T	A	G	A	T
Ecuador SWP26 ²	T	T	T	G	C	G	T	G	G
CODON (IUPAC)	ACY	TAY	TCY	CAR	AAY	GCR	GCK	AAR	TCA / GCA
AMINO ACID	T	Y	S	Q	N	A	A	K	S / A

¹Consensus position measured from ATG start codon MN604022 (CDS length is 687bp). Sequencing coverage from base 33 to base 605.

²Number of direct amplicon sequencing traces EHP SWP26 from Vietnam (7) and Ecuador (10)

Table S4. PTP2 sequence variation between Vietnam and Ecuador EHP PTP2 genes focused on consensus positions.

CONSENSUS POSITION ¹	516	597	654
MT249228_PTP2_CDS	A	C	C
Vietnam PTP2 ²	A	C	C
Ecuador PTP2 ²	G	T	T
CODON (IUPAC)	TTR	ATY	TGY
AMINO ACID	L	I	C

¹Consensus position measured from ATG start codon MN604022 (CDS length is 855bp). Sequencing coverage from base 69 to base 771.

²Number of direct amplicon sequencing traces EHP SWP26 from Vietnam (7) and Ecuador (9)