Supplementary

Table S1: Pinna nobilis *DNA samples PCR amplified with HapF1-HapR2 primers for Sanger sequencing.*

Sample/ amplicon size	[DNA] (ng/µL)	A_{260}/A_{280}	Origin
PN4 (300 pb)	19,4	1,68	Faeces
PN9 (300 pb)	41,9	1,68	Necropsy mantle and digestive gland *Pinna nobilis*
PN13 (300 pb)	37,6	1,81	
PN14 (300 pb)	56,5	1,8	

Table S2: Pinna nobilis *DNA samples PCR amplified with COIH1-COIL1 primers.*

Sample/ amplicon size	[DNA] (ng/µL)	A_{260}/A_{280}	Origin
PN1 (710 pb)	16,7	1,88	Mantle biopsy *Pinna nobilis*
PN2 (710 pb)	57	1,78	
PN3 (710 pb)	37,1	1,71	

Table S3: Blast analysis for Sanger sequences obtained from PCR positive Pinna nobilis samples

Sample	Most similar species (BLAST)	Query Cover	Identity
PN1	*Pinna nobilis* (KY321790.1)	87%	95.77%
PN2	*Pinna nobilis* (KY321794.1)	66%	84.14%
PN3	*Pinna nobilis* (JX854841.1)	100%	100%

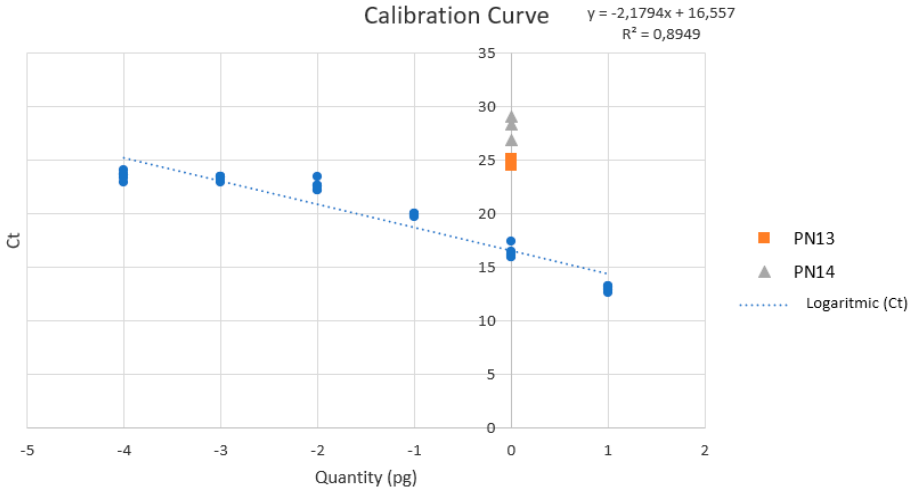

Figure S1: Calibration curve for qPCR for quantification of Haplosporidium pinnae.