

Additional file 3. Characterisation of redesigned Primer set_B for *Hydrobia ulvae*

Locus	Corresponding A-primer clone name	Primer set	Repeat motif	Exp. allele size (bp) [†]	Primer sequence 5'-3' with 5' label or pigtail* (underlined) [‡]	Pv3 (°C) ^Ψ	T _m (°C)	T _a (°C)	MgCl ₂ (mM)	N	A	Allele range (bp)	H _O	H _E	HWE p-value
<i>Huly-01</i>	66C08	B	GA(CA) ₃ (GACA) ₄ (GA) ₂ (CA) ₂ (GA) ₂₂ CA(GA) ₇ CA(GA) ₄ CA(GA) ₄ CA(GA) ₇	230	F: HEX-GATCTGGGGCACACACAA R: <u>(GTTTCTT)</u> -CACAAATCGGGAGAAGG	59.0 59.0	51.0	2.0	40	24	214 – 338	0.63	0.83	**	
<i>Huly-02</i>	67G01	B	Primers not redesigned due to difficulty in identifying new primer sites												
<i>Huly-03</i>	67H10	B	(A) ₂₃ & CTTACTA(CTTA) ₇	172	F: HEX-GACTCGGGCACTCCACAGTAAA R: <u>(GTTTCTT)</u> -TCAATAGGGAGGGTGAGTCC	63.7 63.6	55.0	2.0	46	16	155 – 177	0.59	0.89	**	
<i>Huly-04</i>	68D02	B	(CA) ₃₀ AACA	172	F: 6-FAM-ACGGGTGTAACAACGACAAT R: <u>(GTTTCTT)</u> -GATCTGCAAGAGAGATGTAAGAACT	57.9 57.5	51.0	2.0	47	27	134 – 204	0.92	0.91	NS	
<i>Huly-05</i>	69C07	B	(GTTA) ₂₁	235	F: 6-FAM-GATCGTAGGGCTACTTACTACCCTG R: <u>(GTTTCTT)</u> -TCTGACCTGGTGTGTCATGT	57.8 57.4	51.0	2.0	44	21	174 – 306	0.59	0.93	**	
<i>Huly-06</i>	60F03	B	(CTAA) ₄ (CTCA) ₁₂	217	F: HEX-CACAAAGCAACAGCTATAACTAA R: <u>(GTTTCTT)</u> -TGATGGTGTGCGTACTGAATC	54.5 54.3	51.0	2.0	40	21	169 – 249	0.33	0.94	**	
<i>Huly-07</i>	69A07	B	(GTTA) ₉	154	F: 6-FAM-CCGCACTACCAATGTAGC R: <u>(GTTTCTT)</u> -ATCAATAATCGGGCTAAAC	55.2 55.1	50.0	2.0	34	20	123 – 236	0.12	0.95	**	

[†]Allele size in sequenced library source individual; [‡]Pigtail: GTTTCTT added to 5' end of reverse primer to reduce stutter bands [33].

Note that in all cases the 7 base pair pigtauls have been incorporated in the allele sizes stated.

^Ψ, Primers designed and melting temperature (T_m) calculated using PRIMER3 (Pv3) [32].

T_a, annealing temperature; N, number of individuals successfully genotyped from the Dyfi estuary, Wales; A, number of alleles observed;

H_O, observed heterozygosity; H_E, expected heterozygosity.

^{}Locus deviates significantly from Hardy-Weinberg equilibrium (p<0.01), estimated using GENEPOP v3.4 [25].

NS, no significant deviation from Hardy-Weinberg equilibrium.