

**Additional file 2.** Genetic data of host amphipod species. Given are the number of specimens (N), number of haplotypes (H), haplotype diversity (Hd) and genetic diversity ( $\pi$ ); sd = standard deviation.

<b>Indigenous host species</b>	N	H	Hd	sd	$\pi$	sd
<i>G. pulex</i> clade C	117	22	0.868	0.019	0.0035	0.0002
<i>G. pulex</i> clade D	3	3	1.000	0.272	0.0020	0.0007
<i>G. pulex</i> clade E	33	6	0.333	0.105	0.0006	0.0002
<i>G. fossarum</i> type B	23	3	0.170	0.102	0.0003	0.0002
<i>G. roeselii</i>	30	5	0.361	0.109	0.0011	0.0004
<b>Non-indigenous host species</b>						
<i>D. villosus</i>	42	3	0.138	0.071	0.0003	0.0001
<i>D. haemobaphes</i>	21	2	0.524	0.036	0.0008	0.0001
<i>G. tigrinus</i>	30	6	0.545	0.101	0.0085	0.0027
<i>E. berilloni</i>	15	3	0.257	0.020	0.0006	0.0004
<i>E. trichiatus</i>	5	1	0.000	0.000	0.0000	0.0000