

Additional file 7. Putative gene conversion tracts between pairs of the C-repeat sequences in 13 IGS sequences from four species of the *Daphnia pulex* complex were computed in GENECONV v. 1.81. BC = Bonferroni corrected. KA = Karlin-Altschul. Num Poly = the number of polymorphic sites within the fragment. Tot Difs = the total number of sites at which the two sequences differ.

Global inner fragments	Simulated P-value	BC KA P-value	Aligned Begin	Offsets End	Length	Num Poly	Tot Difs
DpxE3aC1; Dpc2C2	0.0135	> 1.0	80	197	118	9	7
DpxE3aC1; DpxNA3C2	0.0135	> 1.0	80	197	118	9	7