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**Supplementary Fig. S1.** Percentage of individuals classified as putative hybrids in response to the chosen level of the probability criterion (based on the relative genome size) in each of the populations. Vertical dashed line denotes the criterion value used in the study (0.85). Dots represent the individuals with the known ITS sequence (*U. kioviensis* – orange, *U. dioica* – blue, hybrids – gray), other individuals are represented as crosses.









