Supplementary Figure S1: Maximum likelihood phylogenetic trees for different plastid haplotypes of *S. vulgaris* a based on all sites of the plastid genome except for homopolymer sites larger than five nucleotides; b plastid coding regions only. *Silene latifolia* was used as outgroup. Long branches were shortened by 50%, indicated with two diagonal slashes. Indels were coded after Simmon & Ochoterena (2000). The scale bar indicates the number of substitutions per site. Branches with bootstrap support below 60% were collapsed to polytomies. Phylogenetic trees were computed through the CIPRES webportal with RAxML v. 8.2.10 using 1000 bootstraps and the GTRGAMMA model.