Supplementary Material 2

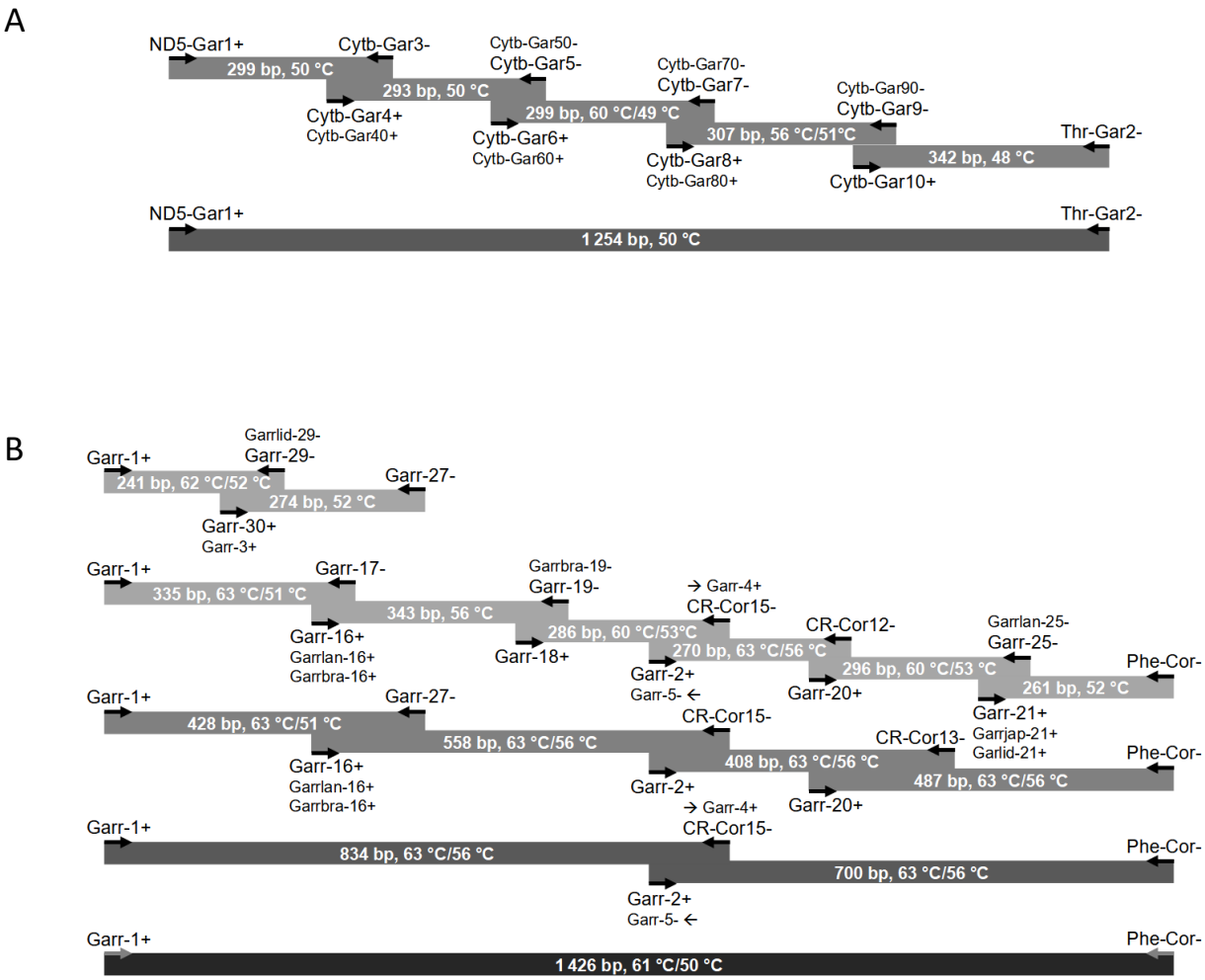

Figure S2.1. Binding sites of **(A)** *cytb* and **(B)** *CR* primers and resulting PCR fragments with lengths in base pairs (bp), referring to the individual Gglacor-2, as well as respective annealing temperatures in °C. For two step PCRs both annealing temperatures, separated by a slash, are given.

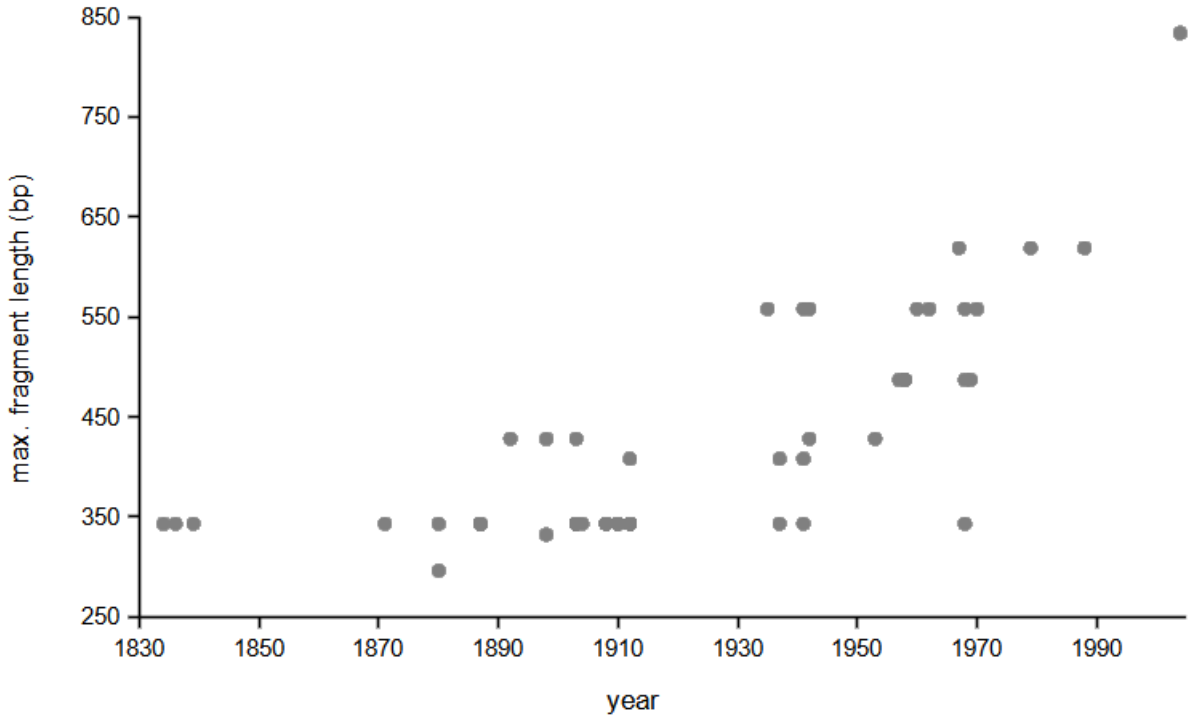

Figure S2.2. Maximum length, in base pairs (bp), of successfully sequenced *CR* fragments from DNA extracted from foot pad samples of 49 specimens with year of collection.

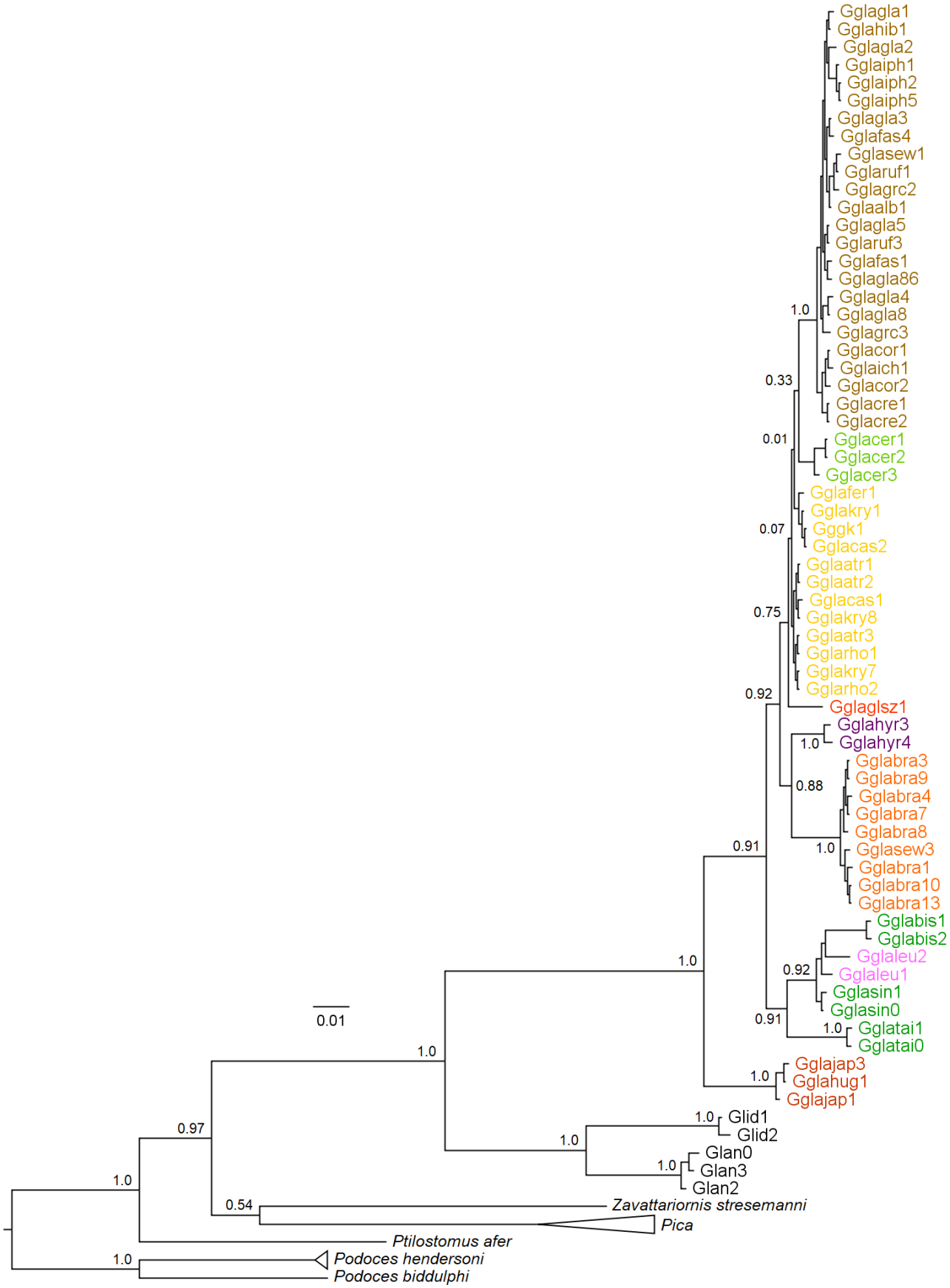

Figure S2.3. Bayesian tree of the genus *Garrulus* based on 76 *cytb* sequences (1143 bp). Posterior probability values of major nodes are shown. The colours correspond to subspecies groups.

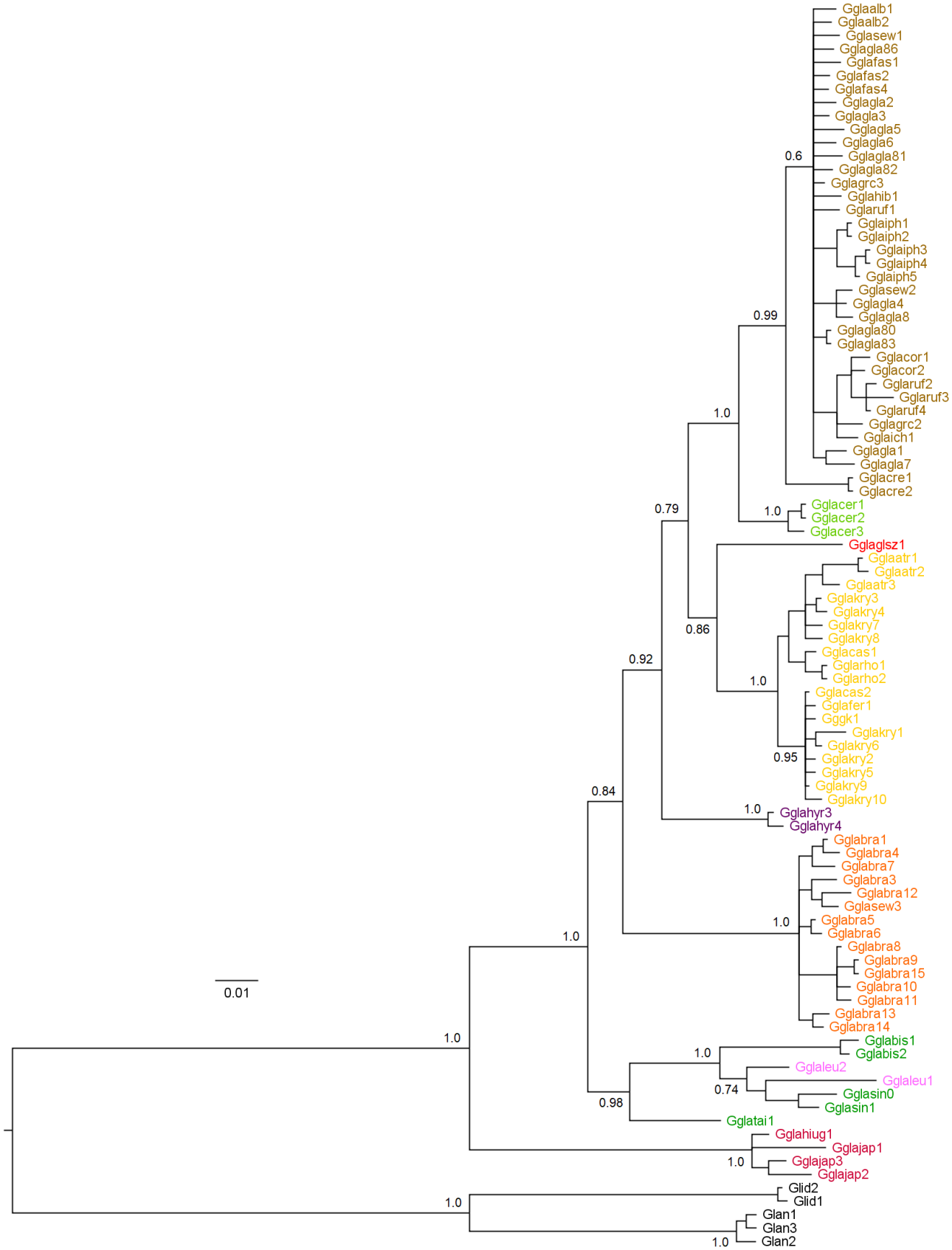

Figure S2.4. Bayesian tree based on 93 *CR* sequences (1340 alignment sites) of the genus *Garrulus*. Posterior probability values of selected nodes are shown, major clades as well as some additional individuals of the *Garrulus glandarius* complex are denoted by different colours.

Figure S2.5. Sampled specimens of *Garrulus glandarius hyrcanus* (Gglahyr-3, Gglahyr-4) and „*Garrulus glandarius caspius*“ (Gglacas-1, Gglacas-2).

Table S2.1. Genetic *p*-distances (in %) between *G. glandarius* subspecies groups as well as selected genetically distinct subspecies and species, calculated from the *cytochrome b* alignment. Mean *p*-distances are shown below the diagonal, the diagonal depicts sequence variability within each group/taxon (*in italics*) and the range of *p*-distances between groups/taxa is given above the diagonal.

Taxon	gla	cre	glsz	cer	atr	hyr	bra	bis	sin	leu	tai	jap	Glan	Glid	Zstr	Ppic
***glandarius* group** (n=22)	*0.3*	0.1-0.3	1.4-1.7	0.9-1.2	0.5-0.9	1.8-2.0	2.1-2.6	3.2-3.4	2.3-2.5	2.5-3.2	3.1-3.3	4.2-4.5	11.0-11.5	11.4-11.8	13.2-13.5	14.3-14.5
G. g. cretorum (n=2)	0.3	*0.0*	1.3	0.9-1.0	0.5-0.7	1.8	2.2-2.4	3.2	2.3-2.4	2.4-3.1	3.1	4.2-4.4	11.1-11.4	11.3-11.5	13.1	14.4
G. g. glaszneri (n=1)	1.6	1.3	*/*	1.5-1.7	1.0-1.1	2.4	2.5-2.7	3.5	2.4-2.5	2.5-2.8	3.4	4.5-4.6	10.8-11.0	11.3-11.5	13.0	14.3
***cervicalis* group** (n=3)	1.1	1.0	1.6	*0.3*	0.5-0.9	1.8-2.0	2.0-2.3	3.2	2.2-2.4	2.4-3.1	3.0-3.1	4.2-4.5	11.1-11.4	11.6-11.8	12.8-13.1	14.4
***atricapillus* group** (n=12)	0.7	0.6	1.0	0.7	*0.3*	1.3-1.6	1.7-2.0	2.9-3.0	1.8-2.0	2.1-2.6	2.6-2.7	3.8-4.1	10.8-11.3	11.4-11.7	12.8-13.1	14.1-14.3
***hyrcanus* group** (n=1)	1.9	1.8	2.4	2.0	1.5	*/*	2.3-2.4	3.8	3.0-3.1	3.2-3.5	3.4	4.6-5.0	11.0-11.3	12.2-12.3	13.2	14.6
***brandtii* group** (n=9)	2.4	2.3	2.6	2.1	1.8	2.4	*0.3*	3.7-3.9	2.8-3.1	3.1-3.7	3.8-3.9	4.4-4.6	10.9-11.5	11.7-12.2	12.6-12.9	13.8-14.2
G. g. bispecularis (n=2)	3.3	3.2	3.5	3.2	2.9	3.8	3.8	*0.2*	1.4-1.5	1.5-1.7	3.2-3.4	4.6-5.2	10.5-10.9	10.8-10.9	12.2	13.0-13.2
G. g. sinensis (n=2)	2.4	2.3	2.5	2.3	1.9	3.0	3.0	1.4	*0.1*	0.4-1.0	2.5-2.6	4.3-4.5	10.8-11.1	10.8-11.0	12.7-12.8	13.6
***leucotis* group** (n=2)	2.9	2.8	2.7	2.8	2.3	3.4	3.4	1.6	0.7	*1.0*	2.8-2.9	4.5-5.0	10.6-11.2	10.7-10.9	12.6-12.8	13.5-13.6
G. g. taivanus (n=2)	3.3	3.2	3.4	3.1	2.7	3.4	3.9	3.4	2.6	2.8	*0.2*	5.1-5.3	11.4-11.6	11.5-11.8	12.9-13.1	13.9
***japonicus* group** (n=3)	4.4	4.3	4.5	4.4	4.0	4.8	4.5	4.9	4.4	4.8	5.2	*0.3*	10.8-11.1	11.3-11.5	13.6-13.9	13.6-13.8
G. lanceolatus (n=3)	11.3	11.2	10.9	11.2	11.0	11.1	11.2	10.7	10.9	10.9	11.5	10.9	*0.5*	5.8-6.2	14.0-14.2	12.4-12.8
G. lidthi (n=2)	11.6	11.4	11.4	11.7	11.5	12.2	12.0	10.8	10.9	10.8	11.6	11.4	6.0	*0.3*	13.7-14.2	13.3-13.4
Z. stresemanni (n=1)	13.3	13.1	13.0	12.9	13.0	13.2	12.7	12.2	12.7	12.7	13.0	13.7	14.1	14.0	*/*	12.1
P. pica pica (n=1)	14.4	14.4	14.3	14.4	14.2	14.6	14.0	13.1	13.6	13.5	13.9	13.7	12.6	13.3	12.1	*/*

Table S2.2. Genetic *p*-distances (in %) between *G. glandarius* subspecies groups as well as selected genetically distinct subspecies and species, calculated from the *Control Region* alignment. Mean *p*-distances are shown below the diagonal, the diagonal depicts sequence variability within each group/taxon (*in italics*) and the range of *p*-distances between groups/taxa is given above the diagonal.

Taxon	gla	cre	glsz	cer	atr	hyr	bra	bis	sin	leu	tai	jap	Glan	Glid
***glandarius* group** (n=35)	*1.3*	1.1-1.5	2.2-2.8	1.3-2.1	2.0-3.2	1.6-3.2	3.1-4.1	3.5-4.2	3.1-4.1	3.4-4.2	2.9-3.5	5.1-6.3	10.5-11.1	10.9-11.1
cretorum (n=2)	1.3	*0.0*	2.8	1.5	2.4-2.8	2.0-2.8	3.3-3.6	4.1-4.2	3.5-3.9	3.4-3.7	3.0	5.7-6.2	10.8-11.0	11.0-11.1
glaszneri (n=1)	2.5	2.8	*/*	2.5-2.6	2.1-2.7	2.2-3.2	3.2-3.8	3.6-3.8	3.5-3.9	3.7-3.9	3.3	5.1-5.8	11.3-11.4	10.8-10.9
***cervicalis* group** (n=3)	1.6	1.5	2.6	*0.2*	2.1-2.7	1.6-2.5	3.1-3.7	3.6-3.9	3.2-3.9	3.4-3.8	2.4	5.3-6.2	10.9-11.1	11.0-11.1
***atricapillus* group** (n=19)	2.5	2.5	2.3	2.2	*1.2*	1.0-2.3	3.0-4.0	3.8-4.5	3.2-3.8	3.4-4.0	2.8-3.2	5.1-6.2	10.8-11.3	10.4-10.9
***hyrcanus* group** (n=2)	2.4	2.4	2.7	2.0	1.7	*0.1*	3.0-4.2	3.4-4.1	2.3-3.1	2.6-3.3	2.2-2.7	4.7-6.2	10.3-10.8	10.3-11.1
***brandtii* group** (n=15)	3.5	3.5	3.4	3.4	3.5	3.5	*1.2*	3.6-4.1	3.4-3.9	3.5-4.2	3.5-3.9	5.2-6.2	11.0-11.5	10.6-11.3
Bispecularis (n=2)	3.8	4.2	3.7	3.8	4.0	3.8	3.9	*0.2*	2.1-2.4	1.9-2.8	3.2	5.4-5.6	10.6-10.7	10.4-10.5
sinensis (n=2)	3.5	3.7	3.7	3.6	3.4	2.7	3.5	2.3	*0.6*	1.0-1.9	2.5-2.9	4.5-5.2	11.0-11.2	11.0-11.2
leucotis (n=2)	3.7	3.5	3.8	3.7	3.6	2.9	3.8	2.3	1.4	*1.8*	2.5-3.0	4.7-5.9	11.0-11.2	11.0-11.2
taivanus (n=1)	3.2	3.0	3.3	2.4	2.9	2.4	3.6	3.2	2.7	2.8	*/*	5.4-5.7	10.5-10.6	10.5-10.6
***japonicus* group** (n=4)	5.8	6.0	5.5	5.9	5.7	5.4	5.7	5.5	4.9	5.3	5.6	*1.5*	10.7-11.5	11.6-12.1
G. lanceolatus (n=3)	10.8	10.9	11.3	11.0	11.1	10.6	11.3	10.8	11.1	11.1	10.5	11.1	*0.3*	5.9-6.0
G. lidthi (n=2)	11.0	11.1	10.8	11.0	10.6	10.7	10.8	10.5	11.1	11.1	10.5	11.8	6.0	*0.1*