Table S-2: Descriptions of the 98 markers used in this study. The second column indicates whether markers belong to the first genotyped set (69 markers) or the second “saturating” set (29 markers in four linkage groups). Next columns indicate the PCR primers and the annealing temperatures. The table also shows the range (base pairs) of the PCR products, the diversity estimates (AR: allelic richness, Ho: Observed heterozygosity, He: Expected heterozygosity, EA: Effective number of alleles), the intra-individual allelic correlations (FIS) and the expected frequencies of null alleles, for

Locus	LG	Dataset	Motif	Forward primer	Reverse primer	Annealing Temperature
FIR073	1	1st	TA	TCGCTGAGAAAAGAAACAAAAA	GAATTTCTGGGAAAGCGTGA	59
VIT026	1	1st	CCA	CCACCTAAACCAAACCCTCA	TGTTGCCAATACCGATTCCT	61
POR040	1	1st	GA	CATCATACGACCCGAAAACC	TCTTCTGCTCCTCTCCCCTA	59
VIT007	1	1st	TC	ACCCTTTCCTCTTCCCAAAG	GGAAATCGGAAATCGGAAAT	60
WAG011	1	1st	CT	AAAAACCCCATTTCACCCTC	TTTGAGAAACTTTGGCCACC	59
FIR040	1	1st	GGA	GAAACGGAAACGCAAACG	GAGCAGAGGGCTAAACTCCA	59
VIT020	2	1st	CT	CCAAACACGGCTTACAAAGAA	CCGCTCGAGGCTTTTCTAGT	61
FIR065	2	1st	CTT	ATTCCCATGCATCAAAATCC	TCCTTCAGTTTGAGAGCTCCTT	59
ZQP104	2	2nd	AG	CACCACTACCGCTGTGAGATAG	GATGGTACAGTAGCAACATTC	59
ZQR87	2	1st	AG	TCCCACCACTTTGGTCTCTCA	GTTGTCAGCAGTGGGATGGGTA	55.5
FIR112	2	2nd	CT	TCTCTTCTATAATCCTCTCTCAAGGTC	GCGCCAGAGTGAAACAAAGT	59
ZQP36	2	2nd	AG	GATCAAAATTTGGAATATTAAGAGAG	ACTGTGGTGGTGAGTCTAACATGTAG	59
WAG019	2	2nd	TTC	ACAGAACACGGAGGAGTTGG	CTGCAAAATCGGCTTAGCTC	59
FIR048	2	2nd	CT	TGCACCAAAATTGGAGGATG	TTGATGCAAGGTGCAGTTTC	59
PIE136	2	2nd	TG	TTATCCACTCTGCGGACATG	ATACACAGCCAGACCCATCC	59
POR041	2	2nd	CT	TGAAACCCAGAGGCAGAGAT	CCAATTGCCAAAGAAAAGAG	59
WAG054	2	2nd	CCA	AACAGCTCATCCAAGATGCC	AGGACGAGGCTTCTTGTTCC	59
ZQP119	2	1st	AG	GATCAGTGATAGTGCCTCTC	GATCAACAAGCCCAAGGCAC	55.5
WAG032	2	2nd	CT	GGGGACTCTGGAGTTGTGC	AGGCTGTGTGAGAAGGTTGG	59
POR038	2	1st	CT	GCCTGCTTTTTGTTCCAGAT	CGAGCTGTTCTTGAAGGTTG	59
PIE197	2	1st	CTA	CAAGTACCACACCCACAACC	GAAAGAGCACTGCCTCCAAC	59
FIR016	2	2nd	CTT	AAATGTGTGCTTGTTGTATGCAG	CCCAACAAATGATAATTAGAAGCA	59
FIR032	2	2nd	TA	TGAAACTGGTCTCAGATTTTGTG	ACACTACACACACTTGCTCTTTTT	59

PIE135	3	1st	CT	TTGTCTACCTTTATCAAACATCATTG	CAAATACGAGAATACCACAGCAAC	59
GOT021	3	1st	AT	AGAAAGTTCCAGGGAAAGCA	CTTCGTCCCCAGTTGAATGT	59
PIE021	3	2nd	TC	CACCTCTCTTTCCTTCTTTAGCA	CCCAGATAAGAGAACCCCATA	59
PIE198	3	2nd	CAT	GGTGCTGTGTTGGTAACTGC	GTTCGAAGCCGAATCCATAC	59
FIR075	3	2nd	GA	GCAAGCAGCAGACTGTGTGT	CTCAAACTCACTTGGGAATCG	59
POR011	3	1st	CTT	ATCCTTCAACGCCCTTTAGC	GGCAAGCTTAGAAACGGAGA	59
PIE051	3	1st	ACCAAC	TCAAAACCAAAGCCAAAACC	GCAGCTTCCAAAAGATCACC	61
VIT084	3	2nd	CAG	AGCCACAACAGTCTCAGCAA	GTCGGATCCCCCTATTCTGT	59
VIT107	3	2nd	TA	TGATCACAGATTGGAGCTTAACA	CCCCCACTTAGGAAAGAAGC	59
PIE088	4	1st	TCTTTC	AGAATGGCCTGTACTTTCCTG	CATACTGGAGTCCTGGCAGAG	58
VIT043	4	1st	CA	GATGGGTTGAGCGGACTATC	CAACCAAAATGGAAACATCG	59
PIE082	4	1st	CAGCAA	GAATTCGATTTTTGATCGAAGC	GAGCAGAGTCCGGTTGTGAC	59
POR029	4	1st	ACC	TGGGTTGTGTCTCTCAATGG	AAGCCTGCAATGAAGCTGAT	61
VIT003	4	1st	TA	GCAGTATCCAAACAGACCCTAA	GCTTTGCTCTAAACAGCAACTT	59
VIT017	4	1st	CGG	GATCCGAATCCGAAACTGAA	GTTACGAGCGAGGACGTTGT	59
PIE002	4	1st	AG	CTCCTCCATTTCCCAATTCA	TCGCTTGTGGTACATCTTGG	59
WAG043	5	1st	AG	GCCCACAGGCAAATAACAAC	AACTCAGGCATGGGCTACAG	59
POR014	5	1st	CT	TTCCCACACATCAATTTTTCC	TGAGACGTAAGAGCCAATCCT	59
GOT065	5	1st	TT (comple	AATGCAGGCATGACCTCTCT	TCAACCCGACTACGGAGAAC	59
VIT023	5	1st	ATA	AATGCGAACGACATGAACAA	CTCTCGTCGGAGACTCAACC	58
POR039	5	1st	CCT	CGAAGGAAAAGCCAAAGAA	GCATTCAGTGCAACAAGTCC	59
VIT021	5	1st	GA	GCCGATCCTCGATCTGATAC	CGCTGAGACCTTCTTCAACC	59
POR024	6	1st	AG	GCCCCGGATTTATTTCTCTG	TGAGCCTCAACCAAAACAAA	61
POR034	6	1st	TTC	TGCGTCTCAATCACTCTCTCTT	TCGATCCGTGAAAATCTGAA	61
VIT028	6	1st	AG	CGGAGTTGGTAGGCTCGAT	CTCTCCCTCACTCTCCCTCA	59
POR027	6	1st	GA	AGGCCCAGTTCATCCTTACA	TGGTAATCCAACTCCAAGCTG	59
PIE071	6	1st	TATTTT	GTCGGCGATGAGAGGAAAG	GGAGACATAGTTCCAACTCAAGC	58
PIE137	7	1st	TC	TCTCCTACCACCAAAACAAGG	CACTTCTCTAACCCCATCAGC	59
VIT046	7	1st	CT	ACATCACATGCTGGGGAAAT	GCCAAGTGCTATCAGTGCAA	59
FIR030	7	1st	AG	GGACATATTTATCTAGGAGACGAGGT	ATGTCCCATAGCACAGAGCA	59
PIE127	7	1st	ACACCA	CTTTTGGGGATGATCTGTTG	AGGATCCTTTGAATGGGAAG	59

POR025	7	1st	TC	CACACAAACCCATATGATCTGAA	TCTCTTTCGATCCCTTCTGC	59
VIT009	7	1st	AG	CTGCTGCTGCTTCTTCCTCT	GCGATCCGTAGGGTTAGGTC	59
PIE011	8	2nd	AT	CACCAAAAATTTCTTCGCTTATG	TGAGCTACAAGGTTTACATCCCTA	59
PIE023	8	1st	AG	GGTCTCTCTTATTTTCTCTTTCTTCG	TGTGAAGAAGAACAAGACCCTTT	59
PIE054	8	2nd	GGTACG	AGCTAGCCCTGATCGATGTC	CTGTGAAAGTGCCACTGGAG	59
POR008	8	2nd	GTG	AGGGGTCATCAGAGTTGGTG	ATCCCTCAGTCTTCCCGAAC	59
PIE101	8	1st	AT	GCGACAGTCACAATTAAGCTAC	CACCCAATTTTCAATCTGTG	59
FIR046	8	1st	AT	GTTTTGGGGCATTTTGTGAC	GGCTAGTCTAGTGTGGGGCTTT	59
VIT013	8	1st	AAC	GCCATGGCTTACACCACTTC	ATCAACAGAGCGGGTTTGTC	59
PIE090	8	2nd	CAGCAA	GAAACGTTCCTGTTGGAGGA	GGAAAGCTGGGAAACCAAG	59
WAG014	8	2nd	GAA	CCGAGCTTCAATTCTTCGAG	TCTTATGCAGAAGTGGGATGG	59
PIE249	8	2nd	AG	GCTTTCACCTTTGAGAGAACTTG	TGGCTATGAACTCAGCAATCC	59
VIT031.1	8	1st	NA	GCCACCCACCACTTTACAA	TTGAAGCTTGGAGGAGATGAA	59
VIT031.2	8	1st	CT	GCCACCCACCACTTTACAA	TTGAAGCTTGGAGGAGATGAA	59
PIE155	8	1st	GA	CCAGAAAATCAAGGCTGCTC	ACAACTCACTCATCACCACTGA	59
VIT099	8	2nd	TA	TGAGGTTGCTGATTCGTCAC	TGAAAATCCAAAACCCTAACC	59
PIE259	9	1st	AC	TGGCTTTATGACACCTTTCG	CCTTTGGCATTTAGCATCAAA	59
PIE059	9	1st	GAGCAC	GAGAGATGGAGCACGAGCA	GGGTCAGGACCATCTTCTTGT	59
FIR005	9	1st	CAA	GGCAACAAGGCCTTAAATCA	GGCAAGGGTTAAGGTGAACA	59
PIE081	9	1st	GACAGG	GCAGAAGAACGGAAGAAGCA	ATCCCGACTACCTCGAGCAT	59
POR028	10	1st	AAT	TCTTCAAAACCCCTTCAACG	TGAGGATGCCATAACCATCA	59
ZQR96	10	1st	AG	CCCAGTCACATCCACTACTGTCC	GGTTGGGAAAAGGAGATCAGA	59
PIE148	10	1st	GA	GGTGTTGAAGTTTTTGTTTCC	ATCCTTTGGTGGGTGTGG	55.5
ZQR11	10	1st	AG	CCTTGAACTCGAAGGTGTCCTT	GTAGGTCAAAACCATTGGTTGACT	59
PIE186	10	1st	TAA	CCATCACAAAACTGCGCTATC	CACGCTCATATACACCCAAATG	58
PIE187	10	1st	ACA	TTCTCAGCCCTTCGATCAAC	TTTGTGGTGGTCTTTGTTGG	58
PIE144	11	1st	CT	TGCAAGGTGGGAACTTTGAT	CGGCATTAAAAGAGCCTTCTC	59
PIE257	11	1st	CT	GCCAACGAGAGCTAAGTTGC	GCAAGGTCAAGGTCAGGGTA	59
WAG079	11	1st	CT	CAAAACGACAAGGAAGGAGC	CTAACACTGGCTGCTGTTGC	58
FIR104	11	1st	GGT	TTAACTCGGTTTGCGACTCA	AGCACGTGACTCGACCTGTA	61
PIE102	11	1st	AG	ACCTTCCATGCTCAAAGATG	GCTGGTGATACAAGTGTTTGG	59
PIE202	11	1st	GAA	GGGAAGAGAGAAAGAGATGGAAG	CATTTCTGAAAAGCCCAATATG	59

PIE089	12	1st	TTAGGG	CGCCCTTAGACCAGGATTTT	TTGAGTCTTGCTTGCCATTG	59
GOT009	12	2nd	TC	CACCTCACTAAGCAACCTGTCA	TTTTGGAGGCGGAGATAATG	59
VIT010	12	1st	TC	CACGTGCATGTAAAGGTGCT	CTGTGTCTGTGATGCGTGTTT	59
PIE126	12	2nd	AATCCG	ACCGAAAGAAAAGCAGTGAG	TAGTCGCGGAAGAAAGAGAG	59
GOT032	12	2nd	AT	TTACAGCCATTCCCTTTGCT	AGACGAGGCTGAGCAAGTGT	59
PIE196	12	2nd	GTG	GTCTGCGTGTCTCAACTTCG	CACAGCACTCTCACCACAGC	59
VIT037	12	1st	TC	GAAGCCACCAAAAGCTCTGT	GAGTGGAAATGAAAAACCCAGA	59
PIE236	12	1st	GAA	TCAATCCCATCTTCCTGCTC	TCTATGCGATTCCGCTTACC	59
ZQR112	12	1st	AG	TTCTTGCTTTGGTGCGCG	GTGGTCAGAGACTCGGTAAGTATTC	59
POR020	12	2nd	GAT	CAAATCCGCTCAACTTGTCA	ACCATCGTCTCCAACATCAA	59
ZQR30	12	1st	AG	TGCTCCGTCATAATCTTGCTCTGA	GCAATCCTATCATGCACATGCACAT	59
VIT050	12	2nd	ATTTTG	TGGTTCCCTCAAGGTTGGT	TGGTTTCAAACACAAACCAG	59
AVERAGE						

1: Observed sizes, including the M13-tail

2: Allelic richness based on a sample size of 75 diploid individuals

3: Observed heterozygosity estimated from the number of heterozygotes.

4: Expected heterozygosity (Nei, 1987).

5: Effective-Number of Alleles (Crow & Kimura, 1964)

6: n.s.: non-significant; *: $p<0.05$

7: Null-Alleles Frequency

Quercus faginea							*Quercus pyrenaica*						
Obs. Size[1]	*AR*[2]	*H*o[3]	*H*e[4]	*EA*[5]	*F*is[6]	NAF[7]	Obs. Size[1]	*AR*[2]	*H*o[3]	*H*e[4]	*EA*[5]	*F*is[6]	NAF[7]
146-189	23.89	0.72	0.93	14.71	0.22 *	0.11	145-192	23.18	0.73	0.93	13.51	0.21 *	0.10
251-268	13.46	0.52	0.80	4.88	0.35 *	0.15	255-268	11.65	0.46	0.77	4.39	0.41 *	0.18
159-209	19.04	0.87	0.90	9.71	0.03 n.s.		167-207	19.65	0.91	0.90	10.00	-0.01 n.s.	
117-145	16.95	0.67	0.90	9.62	0.25 *	0.11	122-145	11.76	0.73	0.80	4.98	0.09 *	0.05
234-249	9.04	0.41	0.50	2.00	0.18 *	0.08	234-253	12.99	0.72	0.77	4.41	0.07 n.s.	0.03
169-195	5.566	0.55	0.60	2.48	0.07 n.s.	0.02	181-193	4.90	0.56	0.67	3.04	0.17 *	0.06
130-165	18.78	0.89	0.92	12.05	0.03 n.s.	0.03	127-162	16.69	0.79	0.86	7.35	0.09 *	0.06
186-198	4.95	0.45	0.53	2.11	0.15 n.s.		186-203	4.71	0.59	0.65	2.83	0.09 n.s.	
201-254	26.19	0.86	0.94	15.38	0.08 *	0.04	200-251	23.14	0.70	0.94	15.87	0.25 *	0.12
118-162	12.05	0.56	0.62	2.60	0.10 n.s.		110-191	19.93	0.84	0.85	6.80	0.02 n.s.	
234-269	16.74	0.76	0.89	8.85	0.15 *	0.06	224-263	21.35	0.70	0.84	6.13	0.17 *	0.08
216-250	16.13	0.49	0.75	4.03	0.34 *	0.12	220-258	18.07	0.83	0.91	10.75	0.09 *	0.03
218-245	13.45	0.64	0.81	5.35	0.21 *	0.11	218-247	11.29	0.57	0.72	3.60	0.21 *	0.10
196-221	8.49	0.24	0.26	1.36	0.10 n.s.	0.03	186-226	18.73	0.73	0.82	5.65	0.12 *	0.05
244-273	8.57	0.60	0.78	4.46	0.22 *	0.10	234-267	9.76	0.57	0.56	2.25	-0.03 n.s.	0.04
137-161	15.62	0.66	0.75	3.92	0.11 *	0.04	132-161	15.66	0.75	0.87	7.75	0.14 *	0.06
289-336	12.26	0.69	0.76	4.10	0.09 n.s.		282-333	12.11	0.55	0.64	2.74	0.12 n.s.	
72-147	28.14	0.58	0.91	11.11	0.36 *	0.17	74-158	30.35	0.94	0.94	16.95	0.00 n.s.	0.01
179-199	10.58	0.84	0.79	4.65	0.02 n.s.		179-199	11.60	0.74	0.75	4.02	0.02 n.s.	
130-176	18.28	0.94	0.93	13.51	-0.01 n.s.		130-180	16.87	0.82	0.86	6.94	0.04 n.s.	
192-208	2.00	0.58	0.49	1.98	-0.17 n.s.		188-207	4.71	0.40	0.45	1.80	0.10 n.s.	
209-238	18.79	0.82	0.89	9.35	0.08 *	0.04	210-240	17.13	0.67	0.82	5.41	0.18 *	0.06
164-193	17.97	0.77	0.82	5.43	0.05 n.s.		161-200	21.15	0.89	0.91	10.53	0.01 n.s.	

234-260	18.78	0.65	0.94	15.63	0.31 *	0.15	234-262	18.13	0.80	0.89	9.17	0.10 *	0.05
112-130	2.99	0.12	0.14	1.16	0.12 n.s.		112-130	4.71	0.61	0.55	2.20	-0.12 n.s.	
170-223	30.75	0.81	0.94	15.63	0.13 *	0.07	162-225	28.61	0.64	0.95	18.52	0.33 *	0.15
222-244	4.35	0.45	0.44	1.78	-0.02 n.s.		223-229	2.77	0.41	0.41	1.68	-0.02 n.s.	
145-178	13.29	0.66	0.87	7.52	0.23 *	0.10	138-168	12.86	0.44	0.83	5.78	0.47 *	0.21
202-233	12.46	0.61	0.75	3.97	0.18 *	0.07	204-230	9.75	0.93	0.87	7.69	-0.07 n.s.	0.00
179-211	6.78	0.54	0.65	2.87	0.17 *	0.07	181-210	6.77	0.56	0.67	3.02	0.16 *	0.04
136-178	15.77	0.81	0.88	8.20	0.08 *	0.03	144-186	16.33	0.80	0.86	7.35	0.08 *	0.02
143-193	12.49	0.83	0.86	7.35	0.04 n.s.	0.00	147-195	24.09	0.88	0.94	17.54	0.06 *	0.03
184-213	14.82	0.34	0.87	7.52	0.61 *	0.28	183-213	14.62	0.42	0.83	5.95	0.50 *	0.23
107-120	7.47	0.43	0.47	1.88	0.07 n.s.		107-118	6.48	0.48	0.50	2.00	0.03 n.s.	
220-244	4.74	0.53	0.44	1.79	-0.20 n.s.		229-244	3.77	0.53	0.51	2.04	-0.04 n.s.	
131-163	9.56	0.95	0.84	6.25	-0.13 *	0.00	131-160	8.74	0.96	0.84	6.33	-0.15 *	0.00
150-180	17.94	0.61	0.91	10.75	0.32 *	0.15	154-183	17.12	0.58	0.92	12.35	0.37 *	0.18
93-107	5.79	0.33	0.35	1.55	0.07 n.s.		93-110	6.53	0.32	0.33	1.50	0.05 n.s.	
172-195	12.42	0.73	0.79	4.76	0.07 n.s.		172-188	12.39	0.76	0.78	4.57	0.02 n.s.	
272-328	22.40	0.87	0.88	8.62	0.02 n.s.	0.02	273-328	22.34	0.80	0.93	15.15	0.14 *	0.07
159-191	19.15	0.78	0.86	7.14	0.09 *	0.03	162-191	18.38	0.74	0.89	9.01	0.17 *	0.07
248-269	4.78	0.51	0.58	2.39	0.12 n.s.		249-268	9.47	0.63	0.71	3.42	0.11 n.s.	
129-154	12.59	0.48	0.69	3.27	0.31 *	0.11	129-153	12.50	0.55	0.77	4.41	0.28 *	0.12
174-214	5.75	0.67	0.58	2.40	-0.15 n.s.	0.00	185-214	7.93	0.58	0.73	3.66	0.20 *	0.08
155-192	16.75	0.91	0.90	9.71	-0.02 n.s.		153-190	19.36	0.88	0.87	7.81	-0.01 n.s.	
169-212	20.10	0.78	0.89	9.35	0.12 *	0.06	174-200	15.59	0.81	0.86	6.99	0.06 n.s.	0.04
174-198	8.74	0.70	0.73	3.68	0.04 n.s.	0.00	174-200	8.53	0.58	0.72	3.58	0.20 *	0.10
150-172	15.53	0.42	0.81	5.24	0.49 *	0.22	150-178	15.72	0.69	0.87	7.46	0.20 *	0.09
117-131	5.57	0.65	0.62	2.60	-0.06 n.s.	0.00	117-139	8.70	0.45	0.62	2.60	0.27 *	0.12
235-256	14.50	0.67	0.90	10.10	0.26 *	0.12	237-267	14.79	0.68	0.88	8.20	0.23 *	0.10
340-356	8.47	0.48	0.51	2.04	0.06 n.s.		347-354	4.77	0.42	0.45	1.82	0.06 n.s.	
184-199	5.78	0.65	0.72	3.55	0.09 n.s.		184-197	6.76	0.59	0.57	2.33	-0.03 n.s.	
134-193	15.83	0.71	0.77	4.27	0.08 n.s.		134-195	15.97	0.78	0.78	4.55	0.00 n.s.	
139-152	3.00	0.28	0.33	1.49	0.16 n.s.		139-152	3.95	0.34	0.40	1.67	0.15 n.s.	

118-156	18.93	0.75	0.84	6.06	0.11 *	0.05	118-154	19.55	0.84	0.91	10.87	0.08 *	0.04
126-184	19.26	0.83	0.85	6.58	0.02 n.s.	0.01	123-182	17.52	0.81	0.89	9.35	0.09 *	0.05
234-265	19.68	0.63	0.89	9.09	0.29 *	0.13	236-267	19.24	0.91	0.91	10.87	0.00 n.s.	0.01
188-192	2.78	0.16	0.19	1.23	0.16 n.s.		190-198	4.84	0.22	0.23	1.31	0.05 n.s.	
248-277	9.05	0.17	0.31	1.45	0.45 *	0.13	240-277	10.94	0.43	0.62	2.60	0.30 *	0.12
147-158	4.73	0.18	0.19	1.24	0.05 n.s.		151-154	2.00	0.12	0.11	1.12	-0.06 n.s.	
154-174	9.56	0.52	0.81	5.21	0.36 *	0.16	154-178	10.53	0.59	0.83	5.75	0.29 *	0.13
211-241	19.03	0.58	0.93	14.29	0.38 *	0.18	210-239	20.92	0.68	0.92	12.66	0.26 *	0.12
151-188	6.77	0.55	0.63	2.70	0.12 n.s.	0.02	151-166	5.00	0.43	0.74	3.82	0.42 *	0.18
198-209	3.78	0.28	0.44	1.79	0.37 *	0.15	198-205	3.00	0.29	0.53	2.13	0.46 *	0.18
295-324	14.02	0.70	0.72	3.58	0.03 n.s.	0.00	300-327	13.54	0.82	0.89	9.17	0.08 *	0.04
282-301	10.42	0.65	0.74	3.79	0.12 *	0.05	281-299	11.16	0.64	0.70	3.34	0.08 n.s.	0.03
93-103	7.99	0.55	0.81	5.26	0.32 *	0.15	97-104	4.94	0.13	0.55	2.24	0.76 *	0.27
104-114	6.98	0.54	0.78	4.50	0.30 *	0.13	106-121	6.71	0.65	0.74	3.82	0.11 *	0.04
245-281	16.98	0.77	0.87	7.63	0.11 *	0.04	246-283	20.22	0.84	0.87	7.46	0.03 n.s.	0.01
134-165	15.21	0.83	0.86	6.94	0.03 n.s.		138-167	14.13	0.81	0.85	6.45	0.04 n.s.	
135-162	11.56	0.70	0.87	7.58	0.19 *	0.08	135-162	8.76	0.44	0.83	6.02	0.48 *	0.22
164-189	5.78	0.65	0.66	2.97	0.02 n.s.		164-195	9.72	0.78	0.75	4.03	-0.03 n.s.	
161-184	6.95	0.83	0.73	3.75	-0.13 *	0.00	161-178	7.94	0.72	0.70	3.34	-0.02 n.s.	0.01
175-200	5.69	0.22	0.24	1.32	0.11 n.s.		180-200	5.76	0.46	0.52	2.09	0.12 n.s.	
118-139	15.45	0.56	0.89	8.85	0.37 *	0.17	117-140	14.51	0.42	0.90	10.10	0.53 *	0.25
148-197	18.31	0.87	0.91	11.63	0.05 n.s.		156-205	18.08	0.78	0.83	5.85	0.05 n.s.	
182-217	20.30	0.88	0.93	13.33	0.04 n.s.		184-217	23.33	0.90	0.93	14.93	0.04 n.s.	
264-297	15.41	0.34	0.76	4.18	0.56 *	0.24	264-295	16.54	0.50	0.84	6.41	0.41 *	0.19
185-211	13.79	0.77	0.87	7.41	0.11 *	0.03	185-214	18.86	0.87	0.93	14.29	0.06 *	0.03
213-229	5.82	0.68	0.70	3.37	0.03 n.s.		217-229	4.93	0.65	0.61	2.54	-0.07 n.s.	
235-271	19.61	0.94	0.93	13.89	-0.01 n.s.		235-269	19.75	0.87	0.92	12.99	0.06 n.s.	
163-191	12.52	0.93	0.87	7.94	-0.06 n.s.		167-191	11.52	0.93	0.87	7.81	-0.07 n.s.	
302-338	18.56	0.78	0.89	8.93	0.12 *	0.04	301-339	19.48	0.79	0.75	4.03	-0.05 n.s.	0.00
216-250	12.43	0.87	0.84	6.41	-0.03 n.s.		216-247	10.28	0.76	0.77	4.35	0.01 n.s.	
162-187	12.68	0.84	0.82	5.68	-0.02 n.s.		152-183	12.43	0.51	0.64	2.77	0.10 n.s.	
126-128	2.97	0.96	0.51	2.05	-0.88 *	0.00	126-131	3.86	0.08	0.24	1.32	0.67 *	0.17

257-272	6.78	0.52	0.75	3.92	0.20 *	0.11	263-272	7.70	0.52	0.63	2.70	0.18 *	0.09
236-278	18.90	0.52	0.72	3.56	0.28 *	0.11	230-274	17.60	0.72	0.86	7.35	0.17 *	0.07
140-160	8.98	0.55	0.77	4.42	0.29 *	0.11	140-162	9.76	0.70	0.75	4.03	0.07 n.s.	0.00
252-269	5.78	0.41	0.47	1.87	0.12 n.s.		253-269	5.76	0.74	0.73	3.65	-0.02 n.s.	
143-178	11.86	0.58	0.70	3.36	0.06 n.s.	0.01	149-183	18.00	0.78	0.91	11.24	0.14 *	0.07
221-239	5.95	0.65	0.62	2.63	-0.05 n.s.		221-239	8.00	0.84	0.80	4.88	-0.05 n.s.	
109-144	12.60	0.60	0.88	8.20	0.31 *	0.14	110-145	15.16	0.85	0.84	6.33	-0.01 n.s.	0.02
213-236	7.74	0.82	0.77	4.37	-0.06 n.s.		213-235	6.52	0.58	0.66	2.92	0.12 n.s.	
95-118	9.87	0.72	0.73	3.68	0.01 n.s.		103-112	5.62	0.50	0.52	2.10	0.05 n.s.	
112-140	8.72	0.78	0.80	5.10	0.03 n.s.		112-137	8.75	0.72	0.78	4.52	0.08 n.s.	
190-257	24.07	0.86	0.93	13.89	0.08 *	0.03	190-262	25.53	0.75	0.93	15.15	0.20 *	0.10
136-167	4.78	0.76	0.68	3.12	-0.12 n.s.		147-167	5.00	0.34	0.34	1.52	0.00 n.s.	
	12.40	0.64	0.73	5.89				12.85	0.65	0.74	6.23		