Table S1. Percentage of genetic variability (*up*) based on *gidA*–nucleotide and amino acids sequences within and among different *Rickettsiella* populations infecting *Ixodes ricinus*.

	***up* (%) [min. – max.]**							
	Nucleotides				**Amino acids**			
Clades	**I**	**II**	**III**	**IV**	**I**	**II**	**III**	**IV**
I	0.4 [0-1.7]	13.2 [12.5–13.7]	13.7 [11.3–14.8]	14.3 [13.9–15.0]	0.5 [0–2.8]	7.4 [6.0–9.1]	7.5[6.5–9.1]	7.3 [6.6–9.1]
II		0.07 [0–0.3]	11.7 [11.3–12.6]	13.0 [12.2–13.5]		0.2 [0–0.8]	7.5 [6.6–8.3]	7.8 [7.1–8.7]
III			0.58 [0–3.9]	15.5 [14.5–16.0]			0.5 [0–3.3]	8.2 [6.8–9. 5]
IV				2.0 [0–4.8]				1.5 [0-3.3]

Table S2. Protein sequence motifs of a fragment of *gidA* gene of *Rickettsiella* spp. obtained from questing *Ixodes ricinus* populations collected from different European regions.

	12	13	26	33	35	38	41	49	52	72	80	82	84	94	111	114	115	116	122	124	135	136	140	148	152	174	236	239
Clade I	N	A	S	Q	N	V	M	Y	T	A	P	S	S	F	T	C	E	I	S	N	V	V	A	Y	K	V	A	T
	N	A	S	Q	N	V	M	Y	T	A	P	S	S	F	T	C	E	I	S	N	V	V	T	Y	K	V	A	T
Clade II	Y	A	S	Q	N	A	I	Y	A	A	P	A	S	L	T	Y	S	V	S	Y	R	D	A	Y	K	I	T	L
	Y	A	S	Q	N	A	I	Y	T	A	P	A	S	L	T	Y	S	V	S	Y	R	D	A	Y	K	I	T	L
Clade III	Y	A	S	E	D	V	V	C	T	A	P	A	S	L	T	Y	S	I	S	K	I	E	K	Y	K	V	A	I
	Y	T	S	E	D	V	V	C	T	A	S	A	S	L	T	Y	S	I	S	D	I	E	K	H	K	V	A	I
	Y	A	S	E	D	V	V	C	T	A	S	A	S	L	T	Y	S	I	S	E	I	E	K	H	K	V	A	I
Clade IV	K	T	G	Q	N	V	V	Y	A	A	P	A	F	L	S	F	E	V	S	N	I	E	T	Y	K	I	A	T
	K	T	G	Q	N	V	V	Y	A	A	P	A	F	L	S	F	K	V	S	N	I	E	T	Y	R	I	A	T
	K	T	G	Q	N	V	V	Y	A	S	P	A	F	L	S	F	K	V	S	N	I	E	T	Y	R	I	A	T

NOTE:

A = Alanine
C = Cysteine
D = Aspartic acid
E = Glutamic acid
F = Phenylalanine
G = Glycine
H = Histidine

I = Isoleucine
K = Lysine
L = Leucine
M = Methionine
N = Asparagine
P = Proline
Q = Glutamine

R = Arginine
S = Serine
T = Threonine
V = Valine
Y = Tyrosine