

Score	Expect	Identities	Gaps	Strand	
902 bits(1000)	00	511/517(99%)	1/517(0%)	Plus/Plus	
Zv516 1		TAGACCCGTGGAACAAATTAAATTCGTCTAGTGAGGCACCACTGTATAGCAGTTCCTATT			60
Z.viv 67746986		TAGACCCGTGGAACGAATTAAATTTGTCTAGTGAGGCACCACTGTATAGCAGTTCCTATT			67747045
Zv516 61		TATCTACTTGCAATTTTGATGTGCTTTTCGAACTGCTA - GGTTGGCAGGAGCTGGGACCAAG			119
Z.vivt 67747046		TATCTACTTGCAATTTTGATGTGCTTTTCGAACTGCTAAGGTTGGCAGGAGCTGGGACCAAG			67747105
Zv516 120		CAACAGGAGCTCACCCCGTCACAGGGATTTCGAACCGCCAACCTTCTGATCAGCAAGCCCT			179
Z.viv 67747106		CAACAGGAGCTCACCCCGTCACAGGGATTTCGAACCGCCGACCTTCTGATCAGCAAGCCCT			67747165
Zv516 180		AGGCTCAGTGGTTTAGCCACAGCGCCACCTGGGTCCCTATCATAGGAATAAGTGTGTCC			239
Z.viv 67747166		AGGCTCAGTGGTTTAGCCACAGCGCCACCTGGGTCCCTATCATAGGAATAAGTGTGTCC			67747225
Zv516 240		TAAAAACAATTGCATGAAATGTGTGATTGCATGAGAATTTTAAAGACTGACCTACCCAAA			299
Z.viv 67747226		TAAAAACAATTGCATGAAATATGTGATTGCATGAGAATTTTAAAGACTGACCTACCCAAA			67747285
Zv516 300		TCTCTTGATGGTCATCCTGCTCATGTAACCCCTTGGCCTTACCACAAATGCTGTTAGTTAG			359
Z.vivt 67747286		TCTCTTGATGGTCATCCTGCTCATGTAACCCCTTGGCCTTACCACAAATGCTGTTAGTTAG			67747345
Zv516 360		GACTGCTTGAATTTTATTTCCACAGTTATCACATTCTTTTCAGACTCGAGGCGGCTTTCA			419
Z.viv 67747346		GACTGCTAGAATTTTATTTCCACAGTTATCACATTCTTTTCAGACTCGAGGCGGCTTTCA			67747405
Zv516 420		GCATAGTTAAAAACATTAAAAACAGCATAATGAAAGCATTTTATCATTTTTCCAGTCACA			479
Z.viv 67747406		GCATAGTTAAAAACATTAAAAACAGCATAATGAAAGCATTTTATCATTTTTCCAGTCACA			67747465
Zv516 480		AAATTTATGTTGAGCTTTTCTTGAAATGGACGGGTCT	516		
Z.viv 67747466		AAATTTATGTTGAGCTTTTCTTGAAATGGACGGGTCT	67747502		

Figure S1. Results of query in WGS archives of *Z. vivipara* with Zv516 sequence. Transitions A>G or C>T are highlighted in yellow.

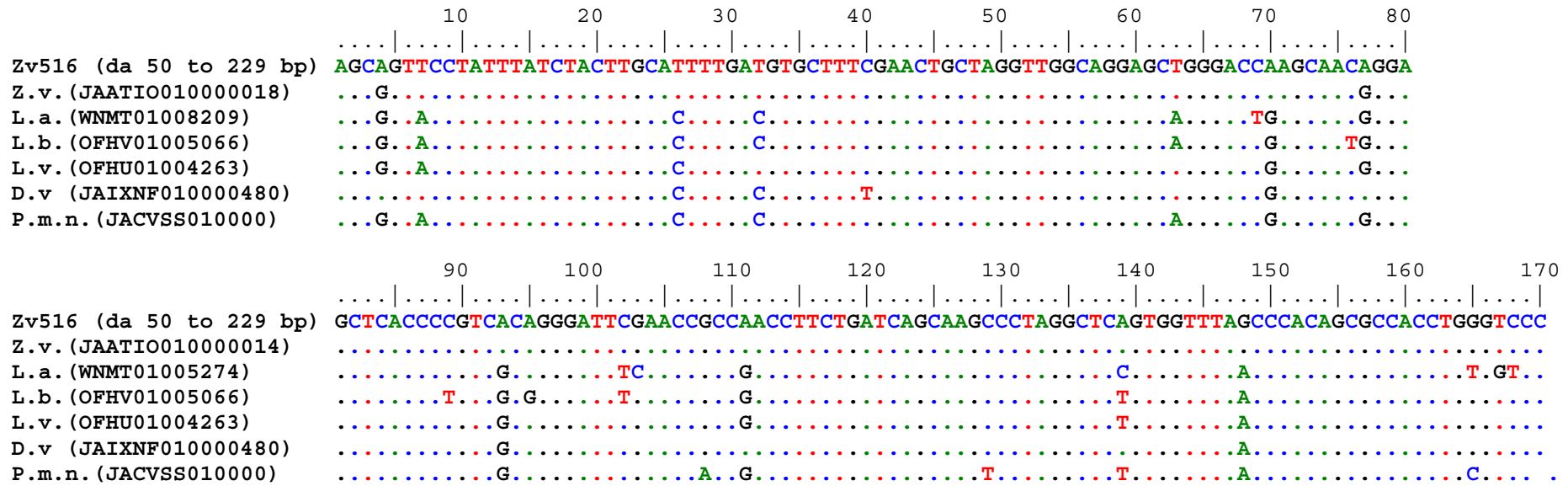
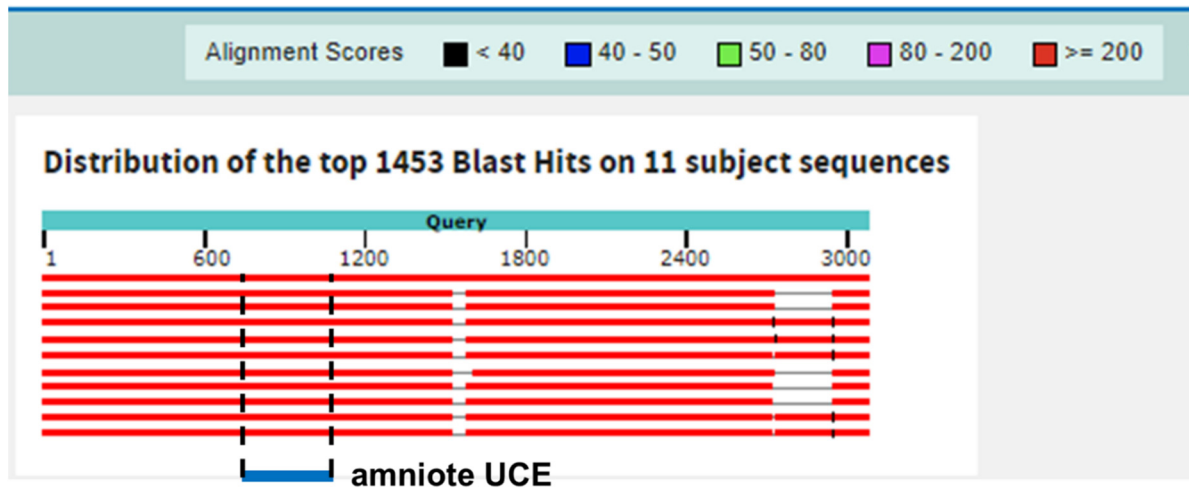


Figure S3. Alignments of the segment between 50 to 220 bp of ZV516 with homologous segments with highest identities of WGS of *Z. vivipara* (Z.v), *L. agilis* (L.a.), *L. bilineata* (L.b.), *L. viridis* (L.v.), and *P. m. nigriventris* (P.m.n.). In brackets, the relative accession numbers. References as in Figure S2.



A

<u>Description</u>	<u>Max Sc.</u>	<u>Cover</u>	<u>E value</u>	<u>Ident</u>	<u>Accession</u>
Vipera berus berus isolate VBER.BE-female contig_2421, whole genome shotgun sequence	5651	100%	0.0	100.00%	JTGP01002421.1
Crotalus horridus isolate 016-059-111 Sequence_11496_17634, whole genome shotgun sequence	2303	91%	0.0	94.28%	LVCR01011496.1
Protobothrops mucrosquamatus DNA, contig: contig_17432, isolate: PMUCROS, whole genome shotgun sequence	2283	91%	0.0	94.14%	BCNE02017432.1
Crotalus viridis viridis voucher SPM297 chromosome 3, whole genome shotgun sequence	2272	98%	0.0	94.01%	PDHV02000003.1
Protobothrops flavoviridis DNA, habu1_scaffold1518, whole genome shotgun sequence	2268	98%	0.0	93.95%	BFFQ01001082.1
Crotalus adamanteus isolate Cadam-KW1264 chromosome 3 Cadam-autosomal_3100_of_8908, whole genome shotgun sequence	2266	98%	0.0	93.94%	JADPQB010005561.1
Bothrops jararaca isolate BSP84406 BJARHA_0004115, whole genome shotgun sequence	2261	90%	0.0	93.93%	JAGTXL010004108.1
Crotalus pyrrhus voucher UTA:R-60292 CMI_contig_188929, whole genome shotgun sequence	2250	91%	0.0	93.75%	JPMF01187720.1
Crotalus tigris isolate CLP2741 scf7180000021597.42775, whole genome shotgun sequence	2242	91%	0.0	93.68%	VORL01001944.1
Crotalus tigris isolate CLP2741 scf7180000021553.44426, whole genome shotgun sequence	2242	98%	0.0	93.68%	VORL01001924.1
Crotalus tigris isolate CLP2741 scf7180000017866.186403, whole genome shotgun sequence	2242	98%	0.0	93.68%	VORL01000199.1

B

Figure S7. (A) Schematic representation of the hits obtained with the sequence flanking amniote UCE of *Vipera aspis* (in blue light in A) in WGS archive of Viperidae and **(B)** the relative description of the obtained hits (identity and coverage set > 90%).

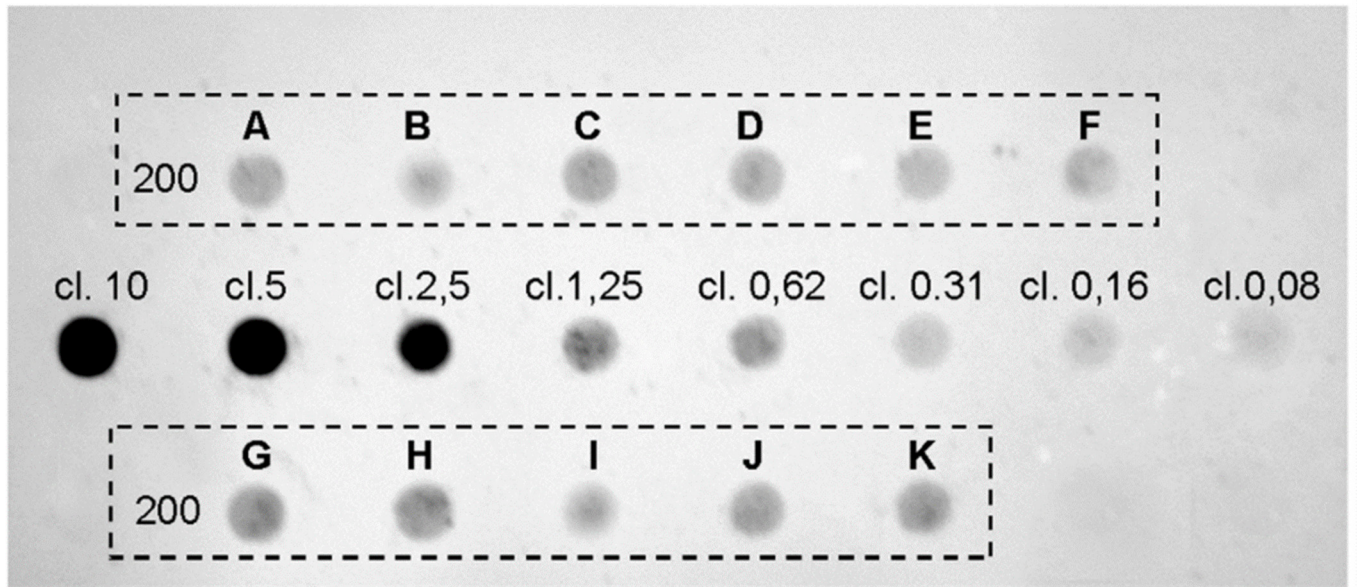


Figure S8. Quantitative dot blot with Zv516 probe to genomic DNA (200 ng) of a *Z. vivipara* samples (A-K) to scalar quantities (from 10 to 0.08 ng). Samples from: Osca (A=male, B=female); Oropa (C=male, D=female); Botany (E=male, F=female); Pourtalet (G=male, H=female); Pskov (I=male); Voloviz (J=female); Romania (K=female).

Table S1. Samples of *Z. vivipara*, with their relative clade (Surget-Groba et al., 2006), origin, sex, sex chromosome system, shape of the W chromosome and reproductive modality.

Clade (Surget-Groba et al., 2006)	Origin	Sex	Sex chromosome system	W shape	Reproductive modality
A	Oropa (Italy)	1 ♂, 1 ♀	ZZ/ZW	microchromosome	oviparous
A	Camporosso (Italy)	1 ♀	ZZ/ZW	microchromosome	oviparous
A	Fusine (Italy)	1 ♂, 1 ♀	ZZ/ZW	microchromosome	oviparous
B	Pourtalet (France)	1 ♂, 1 ♀	Z ₁ Z ₁ Z ₂ Z ₂ /Z ₁ Z ₂ W	Telocentric macrochromosome	viviparous
D	Pskov (Russia)	1 ♂, 1 ♀	Z ₁ Z ₁ Z ₂ Z ₂ /Z ₁ Z ₂ W	Telocentric macrochromosome	viviparous
D	Romany	1 ♀	Z ₁ Z ₁ Z ₂ Z ₂ /Z ₁ Z ₂ W	Submetacentric macrochromosome	viviparous
E	Voloviz (Ukraine)	1 ♂, 1 ♀	Z ₁ Z ₁ Z ₂ Z ₂ /Z ₁ Z ₂ W	Metacentric macrochromosome	viviparous
E	Botany (Slovakia)	1 ♂, 1 ♀	Z ₁ Z ₁ Z ₂ Z ₂ /Z ₁ Z ₂ W	Metacentric macrochromosome	viviparous
F	Oscs (Hungary)	1 ♂, 1 ♀	ZZ/ZW	microchromosome	viviparous

Table S2. Complete list of samples used in the phylogenetic analysis.

Sample	Accession Number	Reference
<i>Lacerta bilineata</i>	OFHV01000637	Kolora et al., 2019
<i>Lacerta viridis</i>	OFHU01002950	Kolora et al., 2019
<i>Lacerta agilis</i>	WNMS01000006	Gemmell et al., 2019 (unpublished)
<i>Podarcis muralis nigroventris</i>	JACVSS010000004	Feiner et al., 2020 (unpublished)
<i>Pogona vitticeps</i>	CEMB01545297	Georges et al., 2015
<i>Zootoca vivipara</i>	JAATIO010000004	Yurchenko et al., 2020 (unpublished)
<i>Darevskia valentin</i>	JAIXNF010000039	Ochkalova et al. 2022
<i>Anolis carolinensis</i>	AAWZ02007580	Alföldi et al., 2011
<i>Pogona vitticeps</i>	CEMB01545297	Georges et al., 2015
<i>Gekko japonicus</i>	LNDG01040291	Liu et al., 2015
<i>Crotalus viridis</i>	PDHV02000003	Pasquesi et al., 2018
<i>Hydrophis cyanocinctus</i>	RSAE01483536	Lu and Li, 2018 (unpublished)
<i>Laticauda colubrina</i>	BHFR01000097	Kishida et al., 2019
<i>Laticauda laticaudata</i>	BHFT01057486	Kishida et al., 2019
<i>Ophiophagus hannah</i>	AZIM01002741	Vonk et al., 2013
<i>Python bivittatus</i>	AEQU02037777	Castoe et al., 2011
<i>Protobothrops flavoviridis</i>	BFFQ01001082	Shibata et al., 2018
<i>Protobothrops mucrosquamatus</i>	BCNE02017432	Aird et al., 2017
<i>Pseudonaja textilis</i>	ULFR01000035	Edwards, 2018 (unpublished)
<i>Thamnophis sirtalis</i>	LFLD01011979	Warren & Wilson, 2015 (unpublished)
<i>Thermophis baileyi</i>	QLTV01002530	Li et al., 2018
<i>Vipera berus</i>	JTGP01002421	Liu et al., 2014 (unpublished)
<i>Sphenodon punctatus</i>	QEPC01012035	Rutherford & Gemmell, 2018 (unpublished)
<i>Apalone spinifera</i>	APJP01387532	Minx et al., (unpublished)
<i>Terrapene mexicana</i>	PRFB02000111	Deem & Warren, 2018 (Unpublished)
<i>Chrysemys bellii</i>	NC_024225	Shaffer et al., 2013
<i>Platysternon megacephalum</i>	QXTE01000205	Gong, 2019 (Unpublished)
<i>Malaclemys terrapin</i>	MDXI01003495	Pop et al., 2016 (Unpublished)
<i>Malaclemys terrapin</i>	MDXI01003563	Pop et al., 2016 (Unpublished)
<i>Pelodiscus sinensis</i>	AGCU01030334	Wang et al., 2013
<i>Pelodiscus sinensis</i>	AGCU01030335	Wang et al., 2013
<i>Cuora amboinensis</i>	SCPV01025202	Minx & Bermingham, 2019 (Unpublished)
<i>Cuora mccordi</i>	RQSS01010584	Minx & Bermingham, 2019 (Unpublished)
<i>Chelonia mydas</i>	AJIM01254912	Wang et al., 2013
<i>Chelonoidis abingdonii</i>	PKMU01007745	Quesada et al., 2018 (Unpublished)
<i>Crocodylus porosus</i>	MDVP01000029	Pham et al., 2016 (Unpublished)
<i>Crocodylus porosus</i>	JRXG02001380	Green et al., 2014
<i>Alligator sinensis</i>	AVPB01056796	Wan et al., 2013 ((Unpublished)
<i>Alligator mississippiensis</i>	LPUV01000502	Putnam et al., 2015 ((Unpublished)
<i>Alligator mississippiensis</i>	LPUU01002723	Putnam et al., 2015 (Unpublished)
<i>Gavialis gangeticus</i>	MDVQ01000044	Pham et al., 2016 (Unpublished)
<i>Gavialis gangeticus</i>	JRWT01216621	Green et al., 2014
<i>Gallus gallus</i>	PDMY01000296	Sohn et al., 2017 (unpublished)
<i>Apteryx haastii</i>	PTFD01000561	Sackton et al., 2019
<i>Falco peregrinus</i>	MLQY01000053	Damas et al., 2016 (unpublished)
<i>Ornithorhynchus anatinus</i>	NW_001783474	Warren et al., 2008
<i>Vombatus ursinus</i>	NW_020954603	Yazar, 2018 (unpublished)
<i>Sarcophilus harrisii</i>	AFEY01099549	Miller et al., 2011
<i>Phascolarctos cinereus</i>	NW_018343981	Johnson et al., 2018
<i>Monodelphis domestica</i>	NC_008802	Mikkelsen et al., 2007

<i>Homo sapiens</i>	NC_000001	Gregory et al., 2006
<i>Rattus norvegicus</i>	NC_005104	Gregory et al., 2006
<i>Eulemur fulvus</i>	PVJU010000509	Johnson et al., 2018 (unpunished)
<i>Microgale talazaci</i>	PVJH01030361	Johnson et al., 2018 (unpunished)
<i>Pipistrellus pipistrellus</i>	PVIQ01002874	Johnson et al., 2018 (unpunished)

Table S3. Results of Search in WGS archives of BLAST Taxid Lacertidae with Zv516. Nr.H. = number of hits; e-v = value; Id = identity; * = value of the highest hit.

Sequence		<i>Z. viv.(a)*</i>	<i>L. agi.(b)*</i>	<i>L. bil(c)*</i>	<i>L. vir.(c)*</i>	<i>D. val.(d)*</i>	<i>P. m. nig.(e)*</i>
Zv516 (whole sequence)	Nr. H	1	---	---	---	---	---
	e-v	0.0	---	---	---	---	---
	id	99%	---	---	---	---	---
Zv516 (from 50 to 220 bp)	Nr. H	4854	>5000	>5000	4188	>5000	1810
	e-v	2e-80*	7e-70*	4e-57*	5e-56*	2e-124	2e-68*
	id	995	95%	89%	90%	93%	91%
Zv516 (from 220 bp to 3') 3'3'end	Nr. H	1	1	1	1	1	1
	e-v	8e-150	4e-128	82-130	4e-128	2e-124	1e-182
	id	99%	95%	95%	95%	93%	86%

a = JAATIO010000004 (Yurchenko et al., 2020) [40]; b = WNMS01000006 (Gemmell et al., 2019, unpublished); c = OFHV01006883 (Kolara et al., 2019) [41]; d = JAIXNF010000029 (Ochkalova et al. 2022) [42] e = JACVSS010000004 (Feiner et al., 2020, unpublished).

Table S4. Search with the sequence SINE Squam 1 clone 22 of *D. raddei* (AN DQ393692) in Whole Genome Sequence archives (WGS) of therein lacertid species. *, values referred to max and minus score of filtered hits.

Species	Nr Hits		Score*	Coverage*	e-value*	Similarity*	Accession Nr.*
	total	filtered					
<i>Z. vivipara</i>	>5000	23	Max 498	98%	1e-138	94.15%	JAATIO010000001
			Min 435	95%	3e-120	90.15%	JAATIO010000434
<i>L. agilis</i>	> 5000	69	Max 520	98%	2e-145	94.33%	WNMS01000008
			Min 439	96%	5e-121	90.31%	WNMT01012604
<i>L. viridis</i>	4211	94	Max 511	97%	5e-143	95.12%	OFHU01004678
			Min 446	95%	3e-128	91.51%	OFHU01004492
<i>L. bilineata</i>	> 5000	58	Max 534	100%	1e-149	92.68%	OFHV01006015
			Min 427	97%	1e-117	90.12%	OFHV01003655
<i>D. valentini</i>	> 5000	217	Max 628	100%	3e-178	94,78%	JAIXNF010000011
			Min 484	95%	7e-135	91,30%	JAIXNF010030895
<i>P. muralis. nigroventris</i>	1807	63	Max 500	100%	1e-139	93.41%	JACVSS010000004
			Min 438	97%	1e-120	91,46%	JACVSS010000094

Table S5. Results of WGS Blast search with SINE Squam 1 of *D. raddei* in different families of Sauria.

Family	Species	Nr Hits	Score*	Coverage* (>30%)	e-value*	Identity > 70%	Accession Nr.*
Agamidae	<i>Pogona vitticeps</i>	16	Max 135	50%	8e-30	80.32%	CEMB01030769
			Min 115	50%	1e-23	78.68%	CEMB01025910
Dactyloidae	<i>Anolis carolinensis</i>	57	Max 141	50%	2e-31	79.71%	AAWZ02025084
			Min 97	51%	4e-18	80.30%	AAWZ02017996
Phrynosomatidae	<i>Phrynosoma platyrhinos</i>	44	Max 145	30%	6e-32	89.08%	JAIPUX010000439J
			Min 115	30%	4e-23	84.75%	AIPUX010003289
Gekkonidae	<i>Gekko japonicus</i>	2	Max 134	43%	4e-29	81.52%	LNDG01099016
			Min 132	42%	1e-28	81.87%	LNDG01099339
Varanidae	<i>Varanus komodoensis</i>	45	Max 134	48%	5e-29	79.80%	VEXN01001127
			Min 104	43%	4e-20	78.09%	SJPD01000048

Table S6. Results of query in Blast Search Refseq_rna with SINE Squam 1 sequence of *Z. vivipara* (sequence 351 bp).

Description	Score	Cover	Evalue	Ident	Accession
Thiamine pyrophosphokinase1 (TPK1), transcript variant X7, mRNA	348	64%	2e-91	94.27%	XM_035101363.1
Pleckstrin homology domain containingA5 (PLEKHA5), transcript variantX12, mRNA	342	93%	1e-89	85.67%	XM_035127630.1
Plpha tubulin acetyltransferase 1(ATAT1), transcript variant X1, misc_RNA	342	68%	1e-89	92.18%	XR_004692038.1
Putative methyltransferase DDB_G0268948 (LOC118097380), transcript variant X1, mRNA	311	60%	e-80	93,36	XM_035140166.1
Katanin regulatory subunit B1 like 1 (KATNBL1), transcript variant X1, mRNA	279	62%	9e-71	89.95%	XM_035110838.1
Phosphatidylinositol glycan anchor biosynthesis class Z(PIGZ), transcript variant X3, mRNA Range 1	104	68%	6e-18	88.51%	XM_035133894.1
Phosphatidylinositol glycan anchor biosynthesis class Z(PIGZ), transcript variant X3, mRNA Range 2	95	68%	6e-18	78.30%	XM_035133894.1

Table S7. Results of BLAST search in Transcriptoma sequence archives (TSA) of deposited sequences of lacertid species with whole SINE Squam 1 of *Z. vivipara* (hits filtered with Identity > 70% and coverage > 60%; here reported data of sequences with maximum and minimum score for each species).

Species	Nr Hits	Score*	Coverage* (> 60%)	e-value*	Similarity* (>70%)	Accession Nr.
<i>Zootoca vivipara</i>	18	Max 409 Min 283	89% 60%	3e-111 2e-73	90.19% 90.65%	GEHX01034844 GEHX01153091
<i>Podarcis cretensis</i>	26	Max 398 Min 276	79% 60%	6e-108 3e-71	92.50% 90.14%	GEHS01066897 GEHS01072124
<i>Darevskia unisexualis</i>	100	Max 370 Min 279	72% 60%	1e-99 2e-72	92.94% 90.23%	GEHW01278948 GEHW01278703
<i>Parvilacerta parva</i>	4	Max 364 Min 279	73% 60%	6e-98 2e-72	92.25% 90.23%	GEHM01098890 GEHM01098903
<i>Phoenicocerta troodoca</i>	1	Max 324	70%	1e-85	90.32%	GEHR01069599
<i>Dinarolacerta mosorensis</i>	7	Max 303 Min 281	55% 52%	1e-79 2e-73	94.77% 94.12%	GEHQ01010225 GEHQ01010227

Table S8. (A) Results of BLASTX search in deposited Squamata sequences with whole SINE Squam 1 (351 bp) of *Z. vivipara* (*, data refer to max score alignment); **(B)** alignment with the predicted protein EYD10_12493 of *Varanus komodoensis*.

A

Specie - Description	Score	Cover*	E value*	Identity*	Accession*
<i>Varanus komodoensis</i> – Hypoth. protein EYD10_12493	54.7	34%	2e-06	67.50%	KAF7240913
<i>Varanus komodoensis</i> - Glut. receptor-interacting prot. 2	55.8	43%	5e-06	56.86%	KAF7249872
<i>Varanus komodoensis</i> - Growth fact. Recep.-bound prot.	52.4	28%	5e-05	78.79%	KAF7247830
<i>Zootoca vivipara</i> - Transmembrane protein 42 isoformX1	43.9	23%	0.022	70.37%	XP_034985869
<i>Zootoca vivipara</i> - cx9C motif-containing protein 4 isof.	44.3	20%	0.027	83.33%	XP_034969199
<i>Varanus komodoensis</i> - Phosphatase and actin regulator	44.3	23%	0.041	74.07%	KAF7248857

B

Hypothetical protein EYD10_12493 [*Varanus komodoensis*]

```

Query  313  GLADQKVGGSNSCDGVSSRCLVPAPANLAVRKHVKVQVDK 194
          GL D+KV GSN  +GVSSRC VPAPANLAVRKH      +K
Sbjct  55   GLVDRKVAGSNLHNGVSSRCSVPAPANLAVRKHADASREK 94

```

Table S9. Results of BLAST Search in WGS archives of deposited lacertid sequences with Zv817 (Hits filtered with identity >80% and coverage > 90%).Nr.H = number of hits; E-v = value; Id = identity; * = value of the highest hit.

sequence		<i>Z. viv.</i> (a)*	<i>L. agi</i> (b)*	<i>L. bil.</i> (c)*	<i>L. vir</i> (d)*	<i>D. val.</i> (e)*	<i>P. m. nig.</i> (f)*
Zv817 (whole sequence)	Nr.	1	---	---	---	---	---
	e-v	0.0	---	---	---	---	---
	id	98%	---	---	---	---	---
Zv817 (from 5' to 685 bp)	Nr.	1	2	1	1	1	1
	e-v	0.0	0.0	0.0	0.0	0.0	0.0
	id	99%	99%	97%%	97%	97	97%
Zv817 (from 686 bp to 3')	Nr.	504	25	13	15	536	35
	e-v	2e-56	3e-48	1e-49	3e-51	1e-48	1e-51
	id	98%	95%	95%	96%	94%	96%

a = JAATIO010000004 (Yurchenko et al., 2020) [40]; b = WNMS01000006 (Gemmell et al., 2019, unpublished);c = OFHV01006883 (Kolara et al., 2019) [41]; d = OFHU01004521 (Kolara et al., 2019) [41]; e = JAIXNF010025682 (Ochkalova et al., 2022) [42]; f = JACVSS010000004 (Feiner et al., 2020, unpublished).

Table S10. Results of search with the trait of TC1-Mariner of *P. marinus* in Whole Genome Sequence archives (WGS) of therein reptile species. *, values refer to maximum and minimum score of filtered hits.

Species	Nr. Hits	Score*	Coverage* (50% - 100%)	e-value*	Similarity* (70% -100%)	Accession Nr.*
<i>Z. vivipara</i>	96	Max 68	100%	3e-09	75.00%	JAATIO010000003
		Min 44	80%	0.038	71.70%	JAATIO010000145
<i>L. agilis</i>	68	Max 60.8	61%	1e-07	79,22%	WNMS01000016
		Min 44.6	55%	0.038	74.29%	WNMT01000297
<i>L. viridis</i>	37	Max 58.1	58.1%	6e-08	78.56%	OFHU01000839
		Min 44.6	55.0%	0,038	74.29%	OFHU01000030
<i>L. bilineata</i>	45	Max 59.3	59.9%	2e-06	72.44%	OFHV01006511
		Min 44.6	55%	0.038	74.29%	OFHV01000090
<i>D. valentini</i>	76	Max 56.3	59.9%	3e-06	70,63%	OFHV01006511
		Min 42.8	55%	0.019	84.21%	OFHV01000090
<i>P. muralis.</i>	23	Max 56.3	100%	2e-05	71.43%	SIRZ01000013
		Min 47.3	65%	0.011	86.84%	JACVSS010000075
Anguimorpha	5	Max 54.5	68%	4e-05	85.11%	SJPD01000010
		Min 45.5	69%	0.019	81.63%	SJPD01000003
Iguania	57	Max 55.4	99%	2e-05	70.40%	CEMB01028658
		Min 44.6	96%	0.038	69.92%	CEMB01006489
Gekkota	7	Max 50	99%	2e-04	70.40%	JAHVXK010001622
		Min 46.5	76%	0.007	72,45%	JAHVXK010000809
Pythonidae	7	Max 52.7	74%	3e-05	73.40%	AEQU02240766
		Min 44.6	96%	0.038	69.92%	CEMB01006489
Elapidae	1037	Max 90.6	81%	2e-15	81.00%	SOZL01001309
		Min 42.9	74%	0.018	71.58%	AEQU02101608
Colubridae	1706	Max 98.7	80%	3e-18	83.25%	WNWU01000035
		Min 42.9	82%	0.017	71.43%	JAHWGE010095033
Viperidae	3568	Max 98.7	91.5%	4e-16	81.63%	JAGTXL010000638
		Min 44.6	79%	0.047	71.57%	BCNE02002671
Turtles	4	Max 54.5	81%	2e-04	75.00%	VOGN01020891
		Min 49.1	81%	0.010	73.53%	QXTE01000131
Crocodylia	0	-	-	-	-	-
<i>Spheonodon</i>	0	-	-	-	-	-

Table S11. Results of BLAST Search in Refseq_rna of deposited sequence of Lacertide with the TC1-Mariner-like segment found in *Z. vivipara*. (hits filtered with Identity > 80% and coverage >50%). *Refers to sequences with maximum score.

Organism	<i>Zootoca vivipara</i>	<i>Podarcis muralis</i>
Hits	286	75
Score*	203	107
Cover*	100%	618
E-value*	6e-49	3e-20
Identity.*	96.72%	96.72%
Accession Number*	XM_035131993	XM_028706021
Description*	Glycerophosphodiester phosphodiesterase 1(GDE1), transcript variantX2, mRNA	IQ motif containing E (IQCE), mRNA

Table S12. Results of BLAST Search in Transcriptoma (TSA) of deposited sequence of Lacertidae with the TC1-Mariner-like segment found in *Z. vivipara* (filter: Identity > 80%; cover >50%). * Refers to sequences with maximum score.

Organism	<i>Zootoca vivipara</i>	<i>Parvilacerta parva</i>	<i>Dinarolacerta mosorensis</i>
Hits	32	3	1
Score*	176	99.6	89.7
Cover*	100%	61%	61%
E-value.*	1e-41	3e-18	1e-15
Identity*	91.80	90.70	86.84
Accession Nr,	GEHX01281806	GEHM01028735	GEHQ01046318
Description*	<i>Zootoca vivipara</i> breed wildtype contig281929, transcribed RNA sequence	<i>Parvilacerta parva</i> breed wildtype contig28751, transcribed RNA sequence	<i>Dinarolacerta mosorensis</i> breed wildtype contig46328, transcribed RNA sequence

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