

**Supplementary Table 2.** Population genetic parameters for 4 putatively neutral nuclear loci unlinked to *Brevinin1.1* (1246 bp) in 3 frog species (*Arcadlin*, *Myosin*, *FIBI7*, and *Tyrosinase*). Population sites are numbered as in Figure 1. For all statistical tests, \* =  $p < 0.05$  and \*\* =  $p < 0.01$ .

Site	Species	2N <sup>a</sup>	Locus	Length <sup>b</sup>	HW <sup>c</sup>	S <sup>d</sup>	H <sup>e</sup>	Hd <sup>f</sup>	$\pi$ <sup>g</sup>	$\pi_s$ <sup>h</sup>	ZnS <sup>i</sup>	$\pi_n/\pi_s$ <sup>j</sup>	Tajima's D <sup>k</sup>
1	<i>R. pipiens</i>	74	<i>Arcadlin</i>	265	y	4	6	0.69	0.005	0.011	0.24	0.05**	1.60
			<i>Myosin</i>	150	y	6	6	0.61	0.011	0.016	0.22	0.00*	0.69
			<i>FIBI7</i>	258	y	10	5	0.33	0.004	0.005	0.30	0.00	-1.28
			<i>Tyrosinase</i>	573	y	9	8	0.78	0.005	0.017	0.21	0.07**	1.11
			Mean $\pm$	312 $\pm$	y	7.3 $\pm$	6.3 $\pm$	0.60 $\pm$	0.005 $\pm$	0.012 $\pm$	0.24 $\pm$	0.03**	0.53 $\pm$
			St. Dev.	182		2.8	1.3	0.19	0.003	0.006	0.04	-	1.26
2	<i>R. pipiens</i>	44	<i>Arcadlin</i>	265	y	4	5	0.68	0.005	0.009	0.19	0.04**	0.80
			<i>Myosin</i>	150	y	6	5	0.67	0.012	0.019	0.23	0.05*	0.84
			<i>FIBI7</i>	258	y	4	3	0.32	0.004	0.005	0.61*	0.00	0.21
			<i>Tyrosinase</i>	573	y	9	7	0.73	0.004	0.013	0.21	0.00**	0.32

			Mean $\pm$	312 $\pm$	y	5.8 $\pm$	5.0 $\pm$	0.60 $\pm$	0.005 $\pm$	0.011 $\pm$	0.31 $\pm$	0.04**	0.54 $\pm$
			St. Dev.	182		2.4	1.6	0.19	0.004	0.006	0.20	-	0.32
14	<i>R. blairi</i>	54	<i>Arcadlin</i>	265	y	2	3	0.50	0.002	0.004	0.03	0.00*	0.33
			<i>Myosin</i>	150	y	2	3	0.46	0.003	0.005	0.03	0.00	0.25
			<i>FIBI7</i>	258	y	1	2	0.04	0.000	0.000	-	0.00	-1.10
			<i>Tyrosinase</i>	573	y	2	3	0.51	0.001	0.000	0.01	>4.1	0.33
			Mean $\pm$	312 $\pm$	y	1.8 $\pm$	2.8 $\pm$	0.38 $\pm$	0.001 $\pm$	0.002 $\pm$	0.02 $\pm$	0.13	-0.05 $\pm$
			St. Dev.	182		0.5	0.5	0.23	0.001	0.003	0.01	-	0.70
15	<i>R. blairi</i>	46	<i>Arcadlin</i>	265	y	1	2	0.41	0.002	0.003	-	0.00	1.13
			<i>Myosin</i>	150	y	2	3	0.55	0.004	0.006	0.05	0.00	0.64
			<i>FIBI7</i>	258	y	2	3	0.17	0.001	0.001	0.00	0.00	-1.15
			<i>Tyrosinase</i>	573	y	3	4	0.54	0.001	0.000	0.05	>4.4	-0.08
			Mean $\pm$	312 $\pm$	y	2 $\pm$	3.0 $\pm$	0.42 $\pm$	0.001 $\pm$	0.003 $\pm$	0.03 $\pm$	0.14	0.13 $\pm$
			St. Dev.	182		0.8	0.8	0.18	0.002	0.003	0.03	-	0.99
16	<i>R. palustris</i>	40	<i>Arcadlin</i>	265	y	4	4	0.67	0.006	0.012	0.32	0.00**	1.55

			<i>Myosin</i>	150	y	4	2*	0.51	0.014*	0.016*	1.00*	0.64	2.77**
			<i>FIBI7</i>	258	y	13	6	0.53*	0.015	0.017	0.36	0.00*	0.71
			<i>Tyrosinase</i>	573	y	5	3	0.57	0.002	0.007	0.66*	0.12**	0.14
			Mean $\pm$	312 $\pm$	y	6.5 $\pm$	3.8 $\pm$	0.57 $\pm$	0.007 $\pm$	0.013 $\pm$	0.58 $\pm$	0.21**	1.29 $\pm$
			St. Dev.	182		4.4	1.7*	0.07	0.006	0.005	0.32*	-	1.14**
17	<i>R. palustris</i>	46	<i>Arcadlin</i>	265	y	1	2	0.20	0.001	0.002	-	0.00	-0.18
			<i>Myosin</i>	150	y	0	0	0.00	0.000	0.000	-	0.00	-
			<i>FIBI7</i>	258	y	13	3**	0.48*	0.018*	0.021*	0.56*	0.00*	1.62
			<i>Tyrosinase</i>	573	y	7	4	0.67	0.003	0.010	0.54*	0.08**	-0.04
			Mean $\pm$	312 $\pm$	y	5.3 $\pm$	2.3 $\pm$	0.34 $\pm$	0.005 $\pm$	0.008 $\pm$	0.55 $\pm$	0.02**	0.47 $\pm$
			St. Dev.	182		6.0	1.7**	0.30	0.008	0.010	0.02*	-	1.00

<sup>a</sup>2N = number of alleles = twice the number of individuals

<sup>b</sup>Length = locus length in base pairs

<sup>c</sup>HW = in Hardy-Weinberg equilibrium; y = yes

<sup>d</sup>S = total number of segregating sites among the 4 loci

<sup>e</sup>h = mean number of haplotypes per locus; tested whether h is significantly low given S

<sup>f</sup>Hd = mean haplotype diversity per locus, equivalent to expected heterozygosity; tested whether Hd is significantly low given S

<sup>g</sup> $\pi$  = mean number of pairwise differences among sequences; tested whether  $\pi$  is significantly extreme given S

<sup>h</sup> $\pi_s$  = mean number of pairwise differences among sequences at silent sites; tested whether  $\pi_s$  is significantly extreme given silent S

<sup>i</sup>ZnS = mean linkage disequilibrium statistic of Kelly (1997) per locus; tested whether ZnS is significantly high given S

<sup>j</sup> $\pi_n/\pi_s$  = ratio of nonsynonymous nucleotide variation to synonymous nucleotide variation; tested whether significantly different than 1

<sup>k</sup>Tajima's D = statistic of Tajima (1989); tested whether significantly different than 0.