Supplementary Material

Population-specific association of *Clock* gene polymorphism with annual cycle timing in stonechats

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Table S1. Breeding latitude, migration distance [km], *Clk* poly-Q repeat length frequencies (Q_{8-15}) and gene diversity (GD) of nine stonechat (*Saxicola spp.*) populations listed by increasing latitude. Gene diversity was calculated with a subset of the data including 518 birds captured in the wild (i.e. excluding captive-bred individuals).

| Populations	n	Latitude	Distance	Q8	Q9	Q10	Q11	Q12	Q13	Q14	Q15	GD
Kenya	95	0°14'S	0	0	0.005	0	0.089	0.032	0.858	0.016	0	0.256
Tanzania	44	3°5'S	0	0	0.011	0.023	0.045	0.023	0.864	0.034	0	0.253
Canary	61	28°46'N	0	0	0	0	0.008	0	0.008	0.984	0	0.033
Spain	93	37°39'N	0	0.089	0	0	0.258	0	0.21	0.511	0	0.631
Japan	11	43.6°N	4900	0.032	0	0	0.273	0	0.546	0.182	0	0.609
Austria	64	48°14'N	1700	0.023	0	0	0.164	0.016	0.156	0.641	0	0.541
Germany	47	51°47'N	1700	0.011	0.021	0	0.160	0.021	0.213	0.564	0.011	0.617
Kazakhstan	60	51.5°N	2600	0	0	0.017	0.208	0	0.583	0.050	0.142	0.597
Ireland	106	52°N	1200	0	0.005	0	0.104	0.038	0.462	0.392	0	0.623
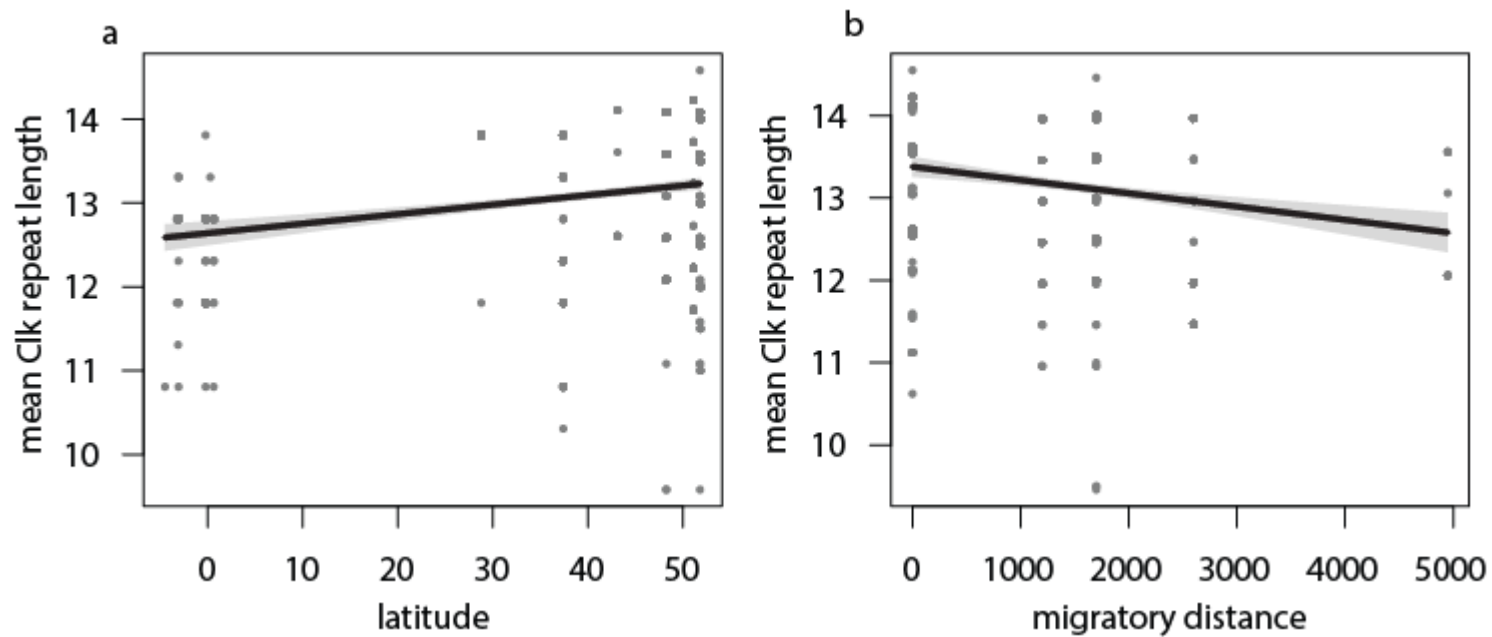
Figure S1. Results from linear model investigating breeding latitude (a) and migratory distance (b) of nine stonechat populations in relationship to *Clk* gene mean repeat length (including origin as a random effect). The model shows that mean repeat length of individuals increases at higher latitudes and decreases with longer migratory distance ($p < 0.05$).