Current Biology, Volume *35*

Supplemental Information

Early-life viability selection targets deleterious mutations in exons

Rebecca S. Chen, Carl D. Soulsbury, Kees van Oers, and Joseph I. Hoffman

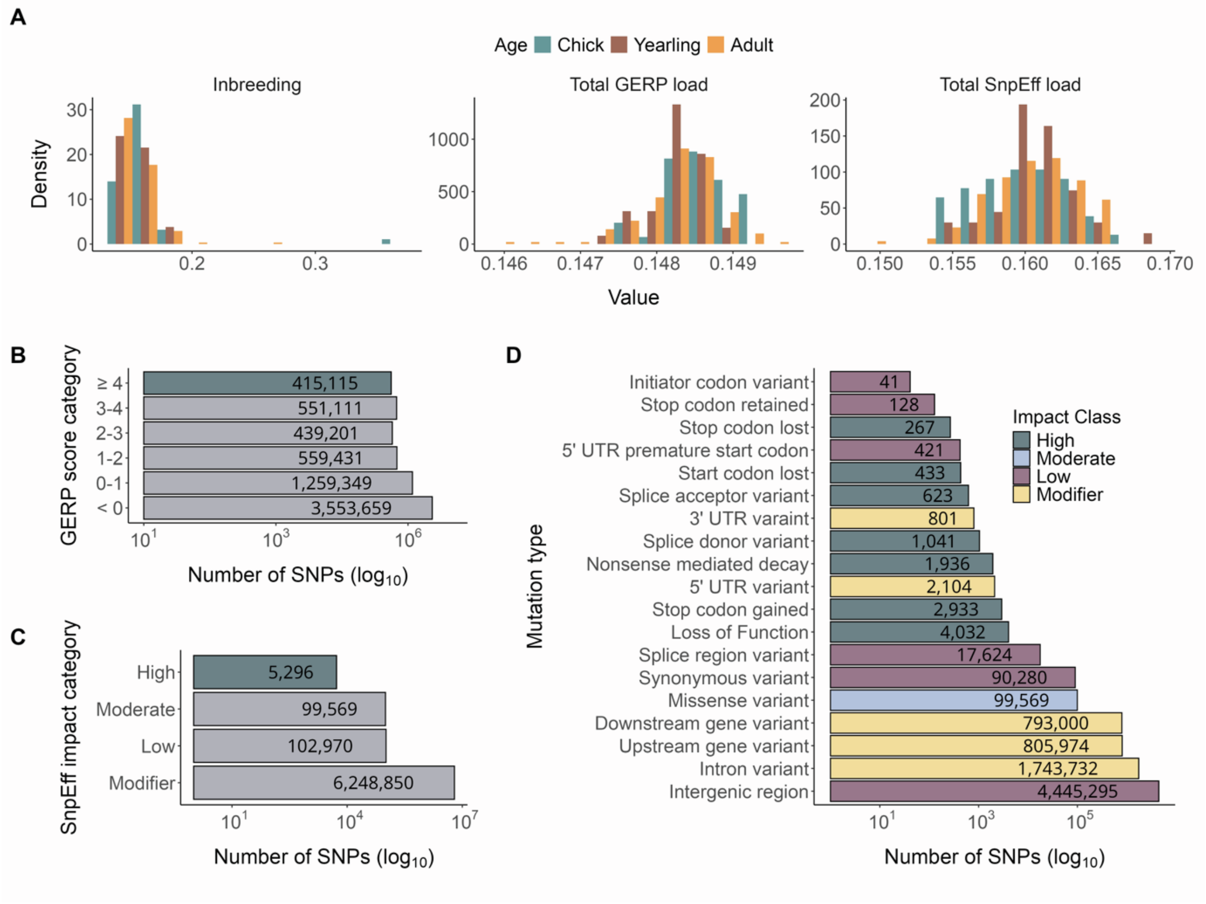

Figure S1. Summary of F_{ROH}, genomic mutation loads and predicted deleterious mutations, related to Figure 1. (A) Histograms of the density of genomic inbreeding (F_{ROH}), the total GERP load and the total SnpEff load, stratified by age (chicks, *n* = 45; yearlings, *n* = 39; and adults, *n* = 151); (B) Bar plot showing the number of SNPs assigned to each GERP score category. Mutations with the strongest predicted deleterious effects (i.e. SNPs with GERP scores ≥ 4) are highlighted in dark blue; (C) Bar plot showing the number of SNPs assigned to each SnpEff impact category. Mutations with the strongest predicted deleterious effects (i.e. SNPs classified as “high impact”) are highlighted in dark blue; (D) A detailed breakdown of the impact classes assigned to mutations annotated by SnpEff.

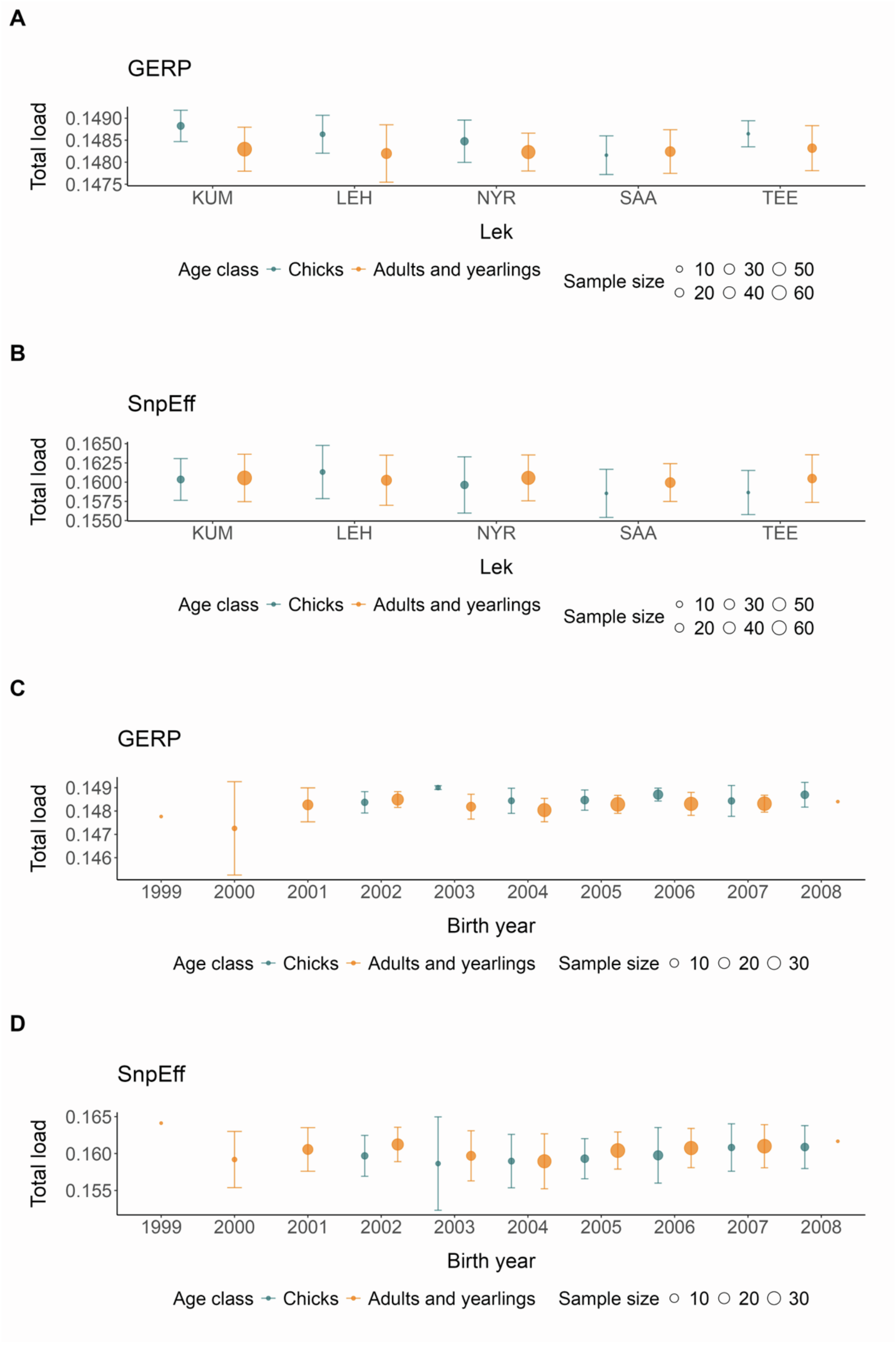

Figure S2. Spatial and temporal variation in genomic mutation load estimates, related to the STAR Methods. The total mutation load is plotted for each of the five lekking sites (KUM = Kummunsuo, LEH = Lehtosuo, NYR = Nyrölä, SAA = Saarisuo and TEE = Teerisuo) separately for (A) GERP; and (B) SnpEff mutations and against birth year separately for (C) GERP; and (D) SnpEff mutations. Points are colour-coded by age class as shown in the legend. Circles indicate means, with error bars showing standard deviations. Circle sizes are proportional to sample sizes as shown in the legend.

Response	**Parameter**	**Median beta coefficient**	**95% CI**
Total GERP load	Intercept	0.15	1.48 e^{-1}, 1.49 e^{-1}
	Site – LEH	-1.04 e^{-4}	-3.14 e^{-4}, 8.18 e^{-5}
	Site – NYR	-1.03 e^{-4}	-2.70 e^{-4}, 5.70 e^{-5}
	Site – SAA	-1.58 e^{-4}	-3.77 e^{-4}, 5.20 e^{-5}
	Site – TEE	-3.06 e^{-6}	-2.40 e^{-4}, 2.24 e^{-4}
Total SnpEff load	Intercept	0.16	1.60 e^{-1}, 1.61 e^{-1}
	Site – LEH	-3.85 e^{-5}	-1.29 e^{-3}, 1.22 e^{-3}
	Site – NYR	-1.61 e^{-4}	-1.19 e^{-3}, 8.17 e^{-4}
	Site – SAA	-8.12 e^{-4}	-2.01 e^{-3}, 4.53 e^{-4}
	Site – TEE	-4.33 e^{-4}	-1.85 e^{-3}, 1.06 e^{-3}
Total GERP load	Intercept	0.15	1.47e^{-1}, 1.49e^{-1}
	Year – 2000	-5.20 e^{-4}	-1.71e^{-3}, 6.93e-^{4}
	Year – 2001	4.95 e^{-4}	-4.94e^{-4}, 1.49e^{-3}
	Year – 2002	7.08 e^{-4}	-2.91e^{-4}, 1.67e^{-3}
	Year – 2003	5.35 e^{-4}	-4.32 e^{-4}, 1.55 e^{-3}
	Year – 2004	3.14 e^{-4}	-6.83 e^{-4}, 1.30 e^{-3}
	Year – 2005	5.63 e^{-4}	-4.10 e^{-4}, 1.53 e^{-3}
	Year – 2006	6.53 e^{-4}	-3.00 e^{-4}, 1.61 e^{-3}
	Year – 2007	5.60 e^{-4}	-4.01 e^{-4}, 1.53 e^{-3}
	Year – 2008	8.84 e^{-4}	-1.18 e^{-4}, 1.89 e^{-3}
Total SnpEff load	Intercept	0.16	0.16, 0.17
	Year – 2000	-4.80 e^{-3}	-1.23 e^{-2}, 1.70 e^{-3}
	Year – 2001	-3.52 e^{-3}	-9.32 e^{-3}, 2.46 e^{-3}
	Year – 2002	-3.19 e^{-3}	-8.95 e^{-3}, 2.67 e^{-3}
	Year – 2003	-4.48 e^{-3}	-1.04 e^{-2}, 1.49 e^{-3}
	Year – 2004	-5.13 e^{-3}	-1.08 e^{-2}, 7.64 e^{-4}
	Year – 2005	-3.94 e^{-3}	-9.57 e^{-3}, 1.97 e^{-3}
	Year – 2006	-3.63 e^{-3}	-9.25 e^{-3}, 2.18 e^{-3}
	Year – 2007	-3.11 e^{-3}	-8.92 e$^{-3,}$ 2.70 e^{-3}
	Year – 2008	-3.11 e^{-3}	-9.13 e^{-3}, 3.03 e^{-3}

Table S1. Outputs of Bayesian linear models testing for differences in the total GERP and SnpEff loads among leks and birds born in different years, related to the STAR Methods. In the top two models, lekking site was used as a predictor, where Kummunsuo was the reference lek. In the bottom two models, birth year was used as a predictor, where 1999 was the reference year. LEH = Lehtosuo, NYR = Nyrölä, SAA = Saarisuo and TEE = Teerisuo. Shown are the median beta coefficients and 95% credible intervals (CIs).

Model	Response	Median	95% CI (lower, upper)	Conditional R^2 [95% CI]	Marginal R^2 [95% CI]
Early-life	F_{ROH}	**0.36**	**0.05, 0.68**	0.04 [1.00 e^{-3}, 0.09]	0.02 [1.39 e^{-7}, 0.06]
	Total GERP load	**0.63**	**0.32, 0.94**	0.07 [0.02, 0.13]	0.06 [0.01, 0.12]
	Total SnpEff load	-0.17	-0.49, 0.15	0.01 [7.64 e^{-6}, 0.04]	5.0 e^{-3} [1.12 e^{-9}, 0.03]
	Total GERP load in exons	**0.99**	**0.69, 1.29**	0.18 [0.11, 0.26]	0.15 [0.09, 0.24]
	Total GERP load in promoters	0.15	-0.18, 0.47	0.01 [3.78 e^{-6}, 0.05]	4.0 e^{-3} [8.01 e^{-10}, 0.03]
	Total GERP load in introns	-0.01	-0.33, 0.31	0.01 [9.21 e^{-7}, 0.04]	2.0 e^{-3} [2.45 e^{-10}, 0.02]
Late -life	F_{ROH}	-0.02	-0.38, 0.31	0.02 [1.03 e^{-5}, 0.08]	2.0 e^{-3} [4.84 e^{-10}, 0.02]
	Total GERP load	0.04	-0.32, 0.37	0.01 [2.45 e^{-6}, 0.04]	3.0 e^{-3} [2.73 e^{-10}, 0.02]
	Total SnpEff load	0.15	-0.20, 0.50	0.01 [1.61 e^{-5}, 0.04]	4.0 e^{-3} [3.67 e^{-10}, 0.03]
	Total GERP load in exons	-0.18	-0.53, 0.17	0.06 [1.0 e^{-3}, 0.13]	0.01 [7.60 e^{-9}, 0.04]
	Total GERP load in promoters	-0.29	-0.65, 0.04	0.02 [2.73 e^{-5}, 0.07]	0.01 [2.18 e^{-8}, 0.05]
	Total GERP load in introns	0.19	-0.15, 0.54	0.01 [2.90 e^{-5}, 0.05]	0.01 [5.39 e^{-10}, 0.04]

Table S2. Outputs of Bayesian GLMMs of genomic inbreeding and mutation load estimates comparing chicks with yearlings and adults combined, and yearlings with adults, related to Figures 1 and 2. Shown are point estimates and 95% credible intervals (CIs) of the standardised β estimates of age, where chicks were compared to yearlings and adults combined in the early-life models and where yearlings were compared to adults in the late-life models. CIs that do not overlap zero are highlighted in bold. The conditional R^2 refers to the variance explained by the fixed and random effects, whereas the marginal R^2 refers to the variance explained only by the fixed effects.