

Expanded View Figures

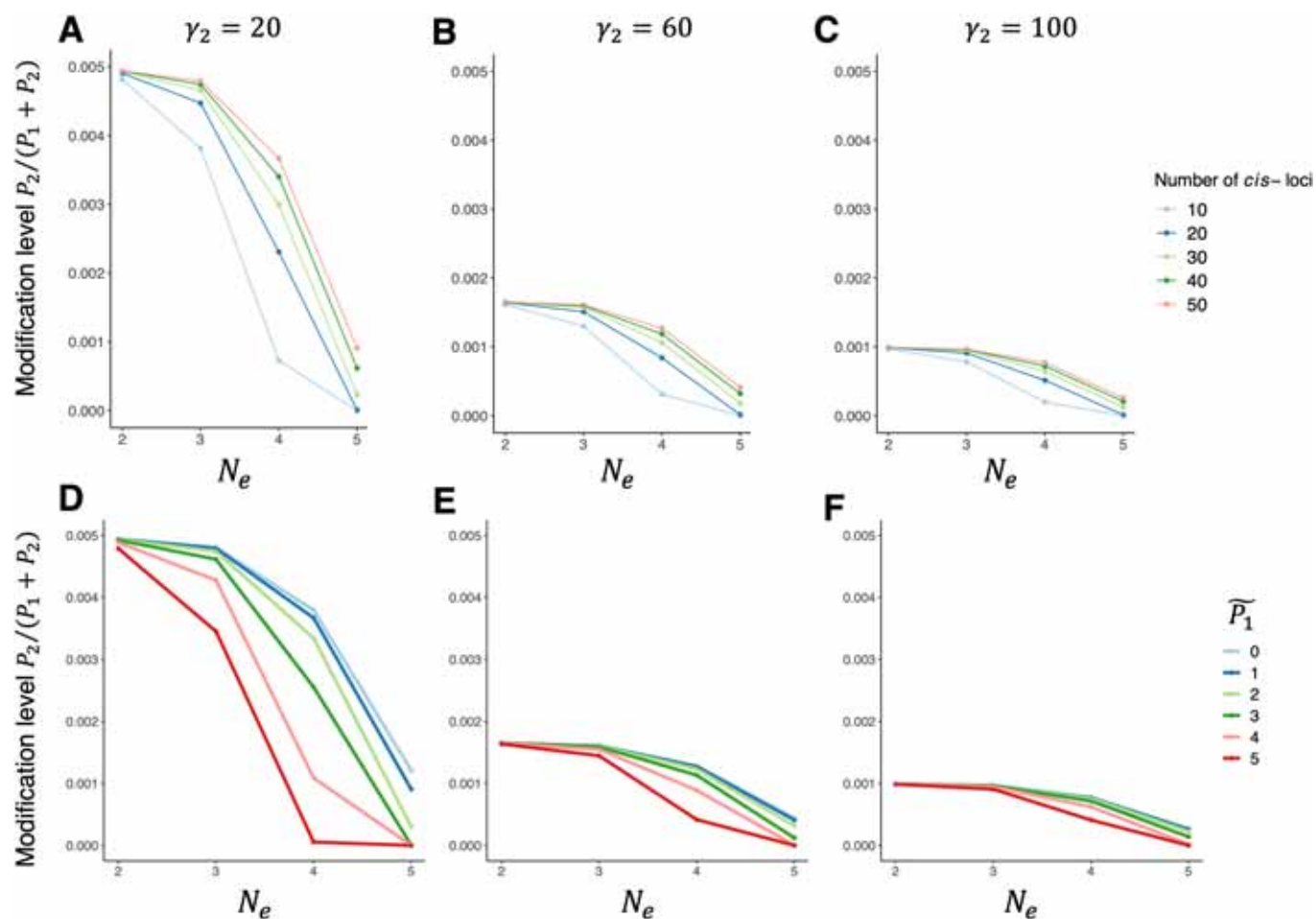


Figure EV1. Mean modification level varies with population genetic environment and genetic architecture.

Scaling between mean modification level of splicing-type modification and effective population size N_e (shown in log10 scale). (A-C) Response of mean modification level to N_e under different combinations of *cis*-loci number (l) and decay rates of the dysfunctional isoform (γ_2), with optimal expression level $\bar{P}_1 = \exp(1)$ ($\ln \bar{P}_1 = 1$). (D-F) Response of mean modification level to N_e under different $\bar{P}_1 = \frac{\alpha}{\gamma_1}$ and γ_2 , with $l = 50$. All results are derived with initial *cis*-genotypic value $v_0 = l$, with $T = 10^8$ time steps, $\mu_{01} = \mu_{10} = 10^{-8}$, $Q = 100$, $\gamma_0 = 0$, $\gamma_1 = 1$, and $\bar{P}_1 = \alpha/\gamma_1$.

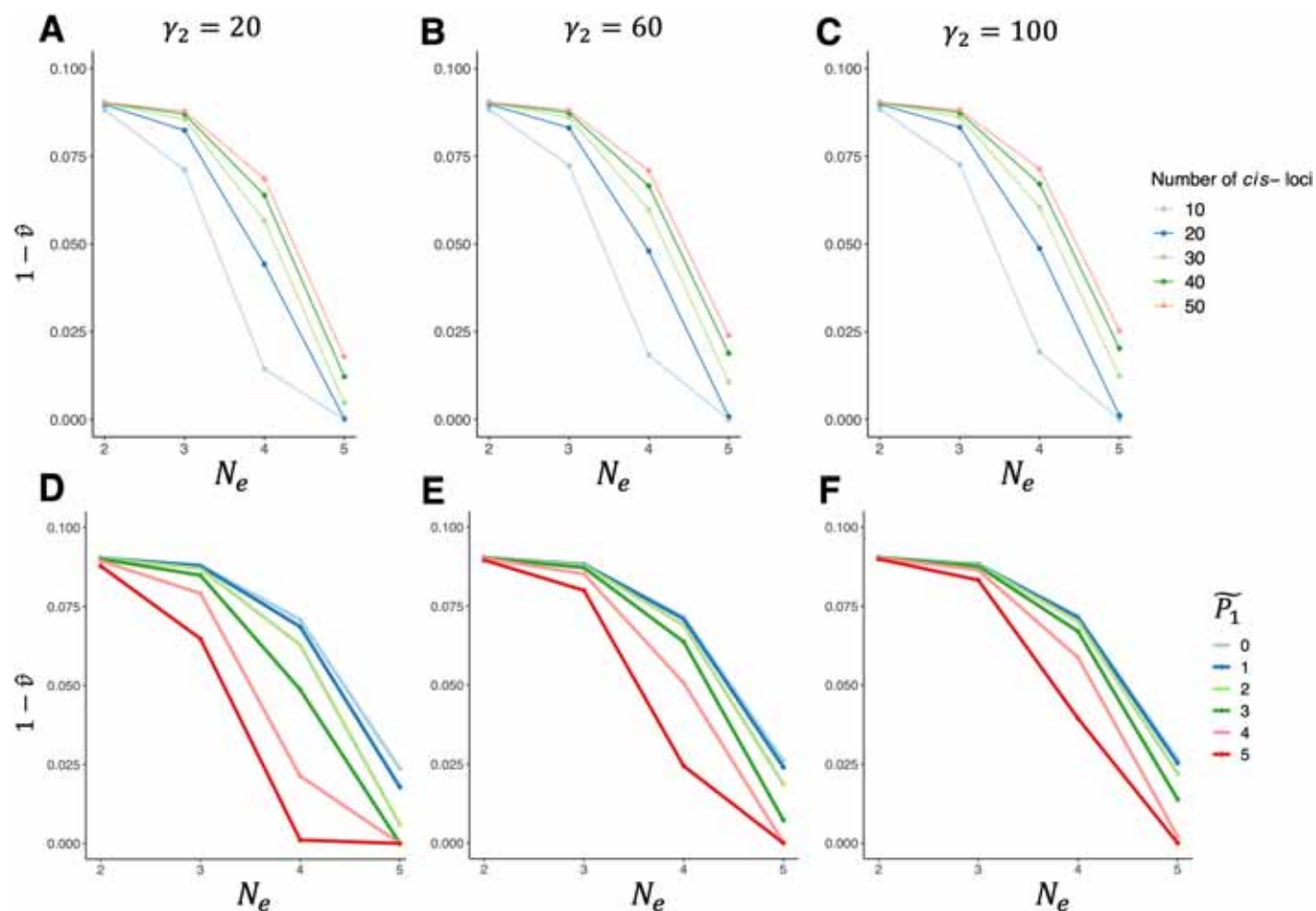


Figure EV2. Cis-genotypic value varies with population genetic environment and genetic architecture.

Scaling between normalized mean *cis*-genotypic value of splicing-type modification and N_e (shown in log10 scale). Represented by the Y-axes is $1 - \hat{v}$, which reflects the degree to which *cis*-genotype favors production of the dysfunction and toxic isoform I_2 . (A-C) Response of $1 - \hat{v}$ to N_e under different combinations of l and γ_2 , with optimal expression level $\tilde{P}_1 = \exp(1)$ ($\ln \tilde{P}_1 = 1$). (D-F) Response of $1 - \hat{v}$ to N_e under different $\tilde{P}_1$ and γ_2 , with $l = 50$. All results are derived with initial *cis*-genotypic value $v_0 = l$, time of evolution $T = 10^8$ time steps, and $\mu_{01} = \mu_{10} = 10^{-8}$, $Q = 100$, $\gamma_0 = 0$, $\gamma_1 = 1$, and $\tilde{P}_1 = \alpha/\gamma_1$.

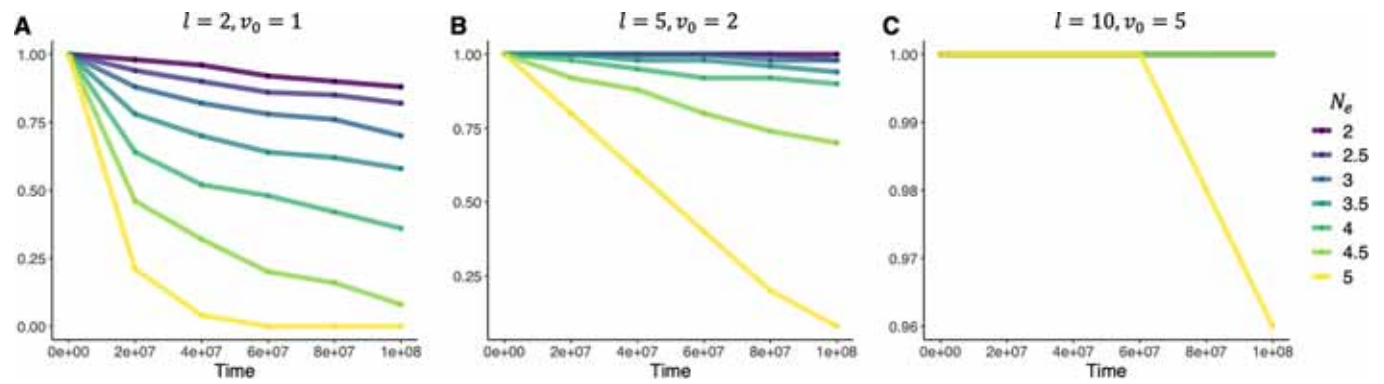


Figure EV3. Conservation of modification events as a function of time since divergence.

(A) $l = 2, v_0 = 1$. (B) $l = 5, v_0 = 2$. (C) $l = 10, v_0 = 5$. Y-axes represent among-gene median of proportion of lineages (species) that share a modification event when selection on Q is weak ($\sigma_Q = 20$). When two curves in the same panel completely overlap, the one with the largest corresponding N_e is shown.

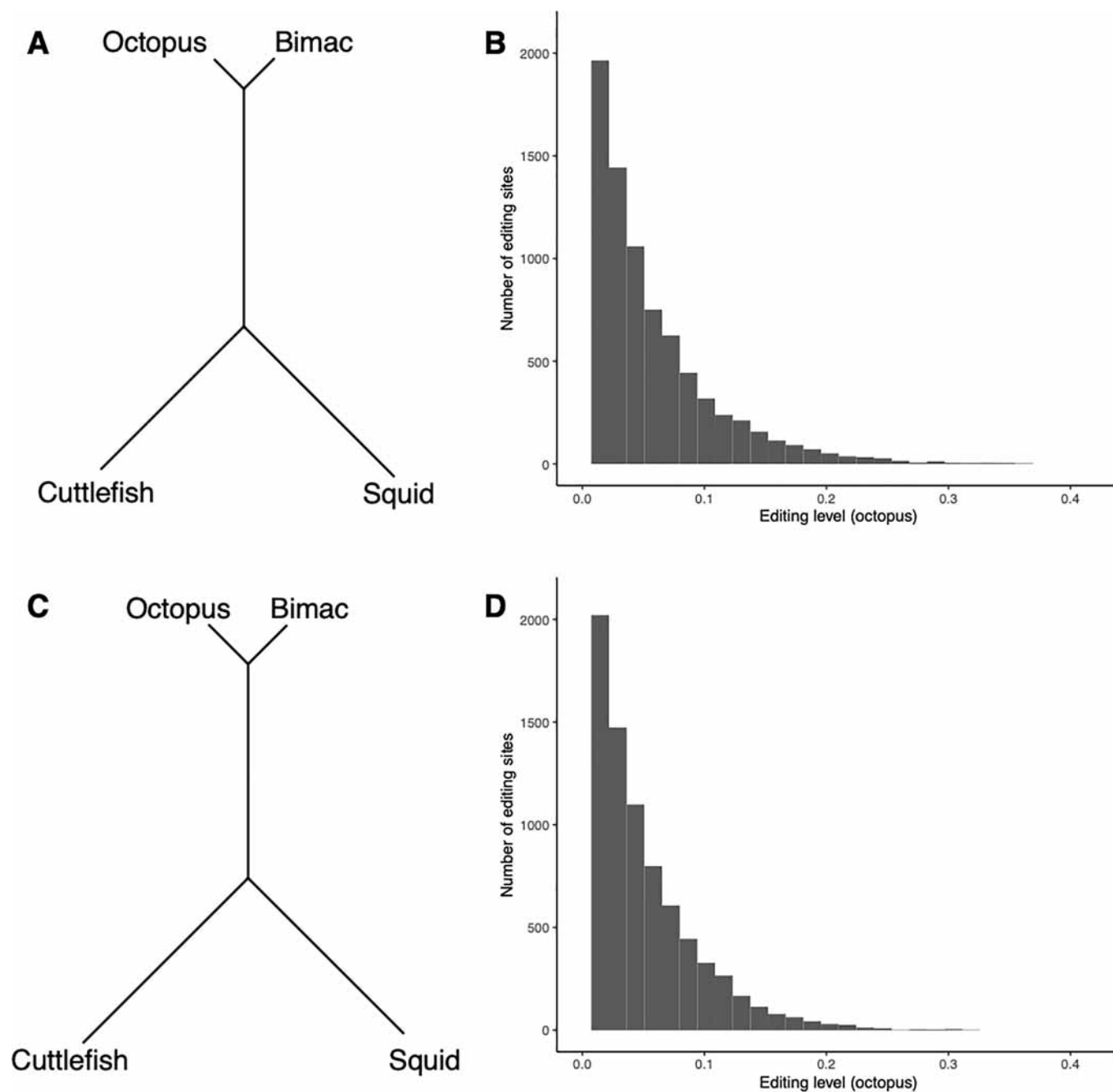


Figure EV4. Simulations of A-to-I RNA editing along the coleoid phylogeny.

(A) Neighbor-joining tree of four coleoid species based on simulated neutral editing levels. (B) Distribution of neutral editing levels in the octopus. (C) Neighbor-joining tree of four coleoid species based on simulated deleterious editing levels. (D) Distribution of deleterious editing levels in the octopus.