**Table S1** Ranked set of candidate models predicting song sparrow song repertoire size, after excluding a potentially influential datapoint with low repertoire size and high MHC diversity (upper left corner of figure 1). Predictors were number of MHC superalleles and squared number of MHC superalleles.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Model** | **df** | **logLik** | **AICc** | **ΔAICc** | **Model Weight** |
| Null: intercept only | 2 | -55.7 | 115.8 | 0 | 0.50 |
| Quadratic: #MHC + (#MHC)2 | 4 | -53.5 | 116.5 | 0.69 | 0.35 |
| Linear: #MHC | 3 | -55.6 | 118.1 | 2.38 | 0.15 |

**Table S2** Model-averaged parameter estimates for predictors of song sparrow song repertoire size, after excluding a potentially influential datapoint with low repertoire size and high MHC diversity. Models were weighted as indicated in table S1 and conditionally averaged. Repertoire size increased with number of MHC superalleles and decreased with squared number of MHC superalleles.

|  |  |  |
| --- | --- | --- |
| **Parameter** | **ß ± SE** | **95% CI** |
| Intercept | 2.94 ± 7.03 | -11.02, 16.90 |
| #MHC | 1.92 ± 0.93 | 0.02, 3.82 |
| (#MHC)2 | -0.074 ± 0.036 | -0.15, -0.0001 |