**Supplementary statistical tables**

For all analyses, sample size corrected Akaike Information Criterion (AICc) model comparisons were used to determine best fit. Distribution codes are as follows: LNB-ZI = zero-inflated linear negative binomial, QNB-ZI = zero-inflated quadratic negative binomial, LNB = linear negative binomial, QNB = quadratic negative binomial, N= normal (Gaussian), B = Beta, and G-P = generalized Poisson (log link).

**Table S2. Top models, dAICc values, and weights for effects of host taxa on tongueworm infection abundance per host.**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Model** | **Distribution** | **Rank** | **dAICc** | **Df** | **Weight** |
| Infection abundance ~ Host taxa Infection abundance ~ Host taxaInfection abundance ~ Host taxaInfection abundance ~ 1 | LNBLNB-ZIQNB-ZILNB | 1234 | 0.01.813.430.0 | 3442 | 0.7100.290<0.001<0.001 |

**Table S3. Top models, dAICc values, and weights for effects of host taxa on lungworm infection abundance per host.**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Model** | **Distribution** | **Rank** | **dAICc** | **Df** | **Weight** |
| Infection abundance ~ Host taxa \* SiteInfection abundance ~ Host taxa \* Site Infection abundance ~ Host taxa + SiteInfection abundance ~ Host taxa + Site  | QNBQNB-ZIQNBQNB-ZI | 1234 | 0.02.010.812.8 | 5645 | 0.72770.26770.00330.0012 |

**Table S4. Top models, dAICc values, and weights for impacts of host taxa and parasite species on within-host nucleotide diversity π.**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Model** | **Distribution** | **Rank** | **dAICc** | **Df** | **Weight** |
| log(π) ~ Host taxa \* Parasite species log(π) ~ Host taxa + Parasite species log(π) ~ Parasite species log(π) ~ Host taxa | NNNN | 1234 | 0.03.05.217.7 | 5433 | 0.7700.1710.059<0.001 |

**Table S5 Top models, dAICc values, and weights for impacts of host taxa and parasite species on within-host Shannon-Weiner diversity H’.**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Model** | **Distribution** | **Rank** | **dAICc** | **Df** | **Weight** |
| sqrt(H’) ~ Host taxa \* Parasite speciessqrt(H’) ~ Host taxa + Parasite species sqrt(H’) ~ Parasite species sqrt(H’) ~ Host taxa  | NNNN | 1234 | 0.00.81.93.1 | 5433 | 0.4420.2950.1690.094 |

**Table S6. Top models, dAICc values, and weights for impacts of host taxa and parasite species on within-host haplotype diversity *h*.**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Model** | **Distribution** | **Rank** | **dAICc** | **Df** | **Weight** |
| *h* ~ Host taxa \* Parasite species *h* ~ Parasite species *h* ~ Host taxa + Parasite species *h* ~ Host taxa | BBBB | 1234 | 0.04.74.96.0 | 5343 | 0.81030.07680.06960.0412 |

**Table S7. Top models, dAICc values, and weights for impacts of host taxa and parasite species on within-host haplotype richness *hrich*.**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Model** | **Distribution** | **Rank** | **dAICc** | **Df** | **Weight** |
| *hrich* ~ Parasite species*hrich* ~ Host taxa + Parasite species*hrich* ~ Host taxa \* Parasite species*hrich* ~ Host taxa  | G-PG-PG-PG-P | 1234 | 0.01.42.53.4 | 3453 | 0.50830.25290.14410.0914 |