**Supplementary Figure 1.** Cytochrome b haplotype network produced using the TCS algorithm in PopART of the 34 haemosporidian lineages detected in this study. *Leucocytozoon* lineages are denoted in blue, *Plasmodium* lineages are denoted in red, and *Haemoproteus* lineages are denoted in yellow. Shown in red text and with larger blue circles are *Leucocytozoon* lineages that were particularly abundant in our sample (detected 12 or more times).

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**Supplementary Table 2.** Model output of five generalized linear mixed effects models predicting prevalence and coinfections of haemosporidian lineages in parapatric host thrushes excluding west coast sampling (n=274). Three predictive variables were included in the models (host species, latitude, and sampling year centered by site) to evaluate their predictive capacity. All models included a random intercept of sampling site and the coinfection models include site-centered year as a random slope.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Dependent Variable** | **Independent variable** | **Estimate** | **P-value** | **Standard error** |
| *Leucocytozoon* Prevalence | HostSpecies | -3.04310 (relative to *C. bicknelli*) | **2.39e-08** | 0.54523  |
| Latitude | 0.34699  | **2.90e-05**  | 0.08299  |
| Year (site-centered) | -0.02805  | 0.309657 | 0.02761  |
| *Plasmodium* Prevalence | HostSpecies | -0.05731 (relative to *C. bicknelli*) | 0.917 | 0.55249  |
| Latitude | 0.04740  | 0.574 | 0.08428  |
| Year (site-centered) | 0.05677  | 0.065 | 0.03077  |
| *(Para) Haemoproteus* Prevalence | HostSpecies | 1.66474 (relative to *C. bicknelli*) | 0.232 | 1.39224  |
| Latitude | 0.07199  | 0.727 | 0.20592  |
| Year (site-centered) | 0.04816  | 0.361 | 0.05276  |
| Haemosporidian coinfection rate(all genera) | HostSpecies | -1.14506 (relative to *C. bicknelli*) | 0.0825 | 0.65940  |
| Latitude | 0.43272  | **2.70e-06 \*\*** | 0.09222  |
| Year | 0.08265  | 0.2676 | 0.07454 |
| *Leucocytozoon* coinfection rate | HostSpecies | -2.6943 (relative to *C. bicknelli*) | **0.018018 \*** | 1.1391  |
| Latitude | 0.5363  | **0.001634 \*\*** | 0.1703 |
| Year (site-centered) | 0.1299  | 0.173842 | 0.0955  |

**Supplementary Table 3.** CRF regression coefficients of haemosporidian lineage infection probability produced by MRFcov. Note that only the ten most abundant lineages were included in this analysis.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Parasite lineage** | **Variable**  | **Rel\_importance**  | **Standardised\_coef**  | **Raw\_coef** |
| H\_COLL2 | Species1 | 1 | 0.497527  | 0.497527 |
| H\_POEATR01 | L\_CATUST11  | 0.9731689  | -0.7190642 | -0.7190642 |
|  | L\_CATMIN01  | 0.0268311  | -0.1193968 | -0.1193968 |
| L\_CATGUT02 | L\_CATMIN07  | 1 | -0.4595424 | -0.4595424 |
| L\_CATMIN01 | L\_CATUST11  | 0.5644376  | -2.627631 | -2.627631 |
|  | L\_CATMIN07  | 0.4270797  | -2.285656 | -2.285656 |
| L\_CATMIN07 | L\_CATUST11  | 0.45324400  | -2.4272869 | -2.4272869 |
|  | L\_CATMIN01  | 0.40189419  | -2.2856564 | -2.2856564 |
|  | L\_CATUST09  | 0.11814765  | -1.2392748 | -1.2392748 |
|  | L\_CATGUT02  | 0.01624579  | -0.4595424 | -0.4595424 |
| L\_CATMIN08 | L\_CATUST11  | 0.90623394  | -1.4548368 | -1.4548368 |
|  | PC1\_L\_CATUST11  | 0.08004731  | -0.4323819 | -0.4323819 |
|  | L\_CATUST09  | 0.01371876  | -0.1789994 | -0.1789994 |
| L\_CATUST09 | L\_CATMIN07  | 0.56725094  | -1.2392748 | -1.2392748 |
|  | L\_CATUST11  | 0.24067416  | -0.8072252 | -0.8072252 |
|  | Abiesbalsamea\_L\_CATUST11  | 0.15075462  | 0.6388741 | 0.6388741 |
|  | PC1 | 0.02225526  | 0.2454688 | 0.2454688 |
|  | L\_CATMIN08  | 0.01183431  | -0.1789994 | -0.1789994 |
| L\_CATUST11 | L\_CATMIN01  | 0.39111914  | -2.6276314 | -2.6276314 |
|  | L\_CATMIN07  | 0.33375086  | -2.4272869 | -2.4272869 |
|  | L\_CATMIN08  | 0.11989711  | -1.4548368 | -1.4548368 |
|  | L\_POEHUD01  | 0.04595379  | -0.9006801 | -0.9006801 |
|  | L\_CATUST09  | 0.03691217  | -0.8072252 | -0.8072252 |
|  | H\_POEATR01  | 0.02928974  | -0.7190642 | -0.7190642 |
|  | Abiesbalsamea\_L\_CATUST09  | 0.02312122  | 0.6388741 | 0.6388741 |
|  | PC1\_L\_CATMIN08  | 0.01059047  | -0.4323819 | -0.4323819 |
| L\_POEHUD01 | L\_CATUST11  | 0.92986436  | -0.9006801 | -0.9006801 |
|  | L\_CATMIN07  | 0.03774676  | -0.1814682 | -0.1814682 |
|  | L\_CATUST09  | 0.01950420  | -0.1304442 | -0.1304442 |
|  | Betulapapyrifera\_L\_CATMIN07  | 0.01288468  | 0.1060224 | 0.1060224 |
| P\_BT7 | L\_CATMIN07  | 0.91889723  | -0.071144407 | -0.071144407 |
|  | Abiesbalsamea | 0.04209880  | 0.015227975 | 0.015227975 |
|  | PC2\_L\_CATMIN07  | 0.02142594  | 0.010863687 | 0.010863687 |
|  | Piceaglauca\_L\_CATMIN07  | 0.01757803  | -0.009839937 | -0.009839937 |