**Supplementary material S2**

**Bayesian species distribution models integrate presence-only and presence-absence data to predict deer distribution and relative abundance.**

* **Additional figures**

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| Graphical user interface, chart, scatter chart  Description automatically generated |
| **Figure S1:** covariates entering the final models for red, sika and fallow deer. Tree cover density (in %), slope (in degrees), distance to forest edge (in m), elevation (in m), human footprint index (index value from 0 to 50) and density of small woody features (in %). |

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| Chart, scatter chart  Description automatically generated |
| **Figure S2:** spatial fields of the models for red deer (left), sika deer (centre), and fallow deer (right). The top row displays the mean of the shared spatial field, and the bottom row represents their standard deviation. |

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| A picture containing scatter chart  Description automatically generated |
| **Figure S3:** biplots representing the correlation between our predictions aggregated by county (*x* axes) and the county-level total culling returns (average values 2010 – 2018, *y* axes). The bottom right plot shows the values for sika deer removing County Wicklow, since the culling returns were much higher than what our model had predicted with respect to the rest of counties, which made the plot difficult to read. |

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| Chart, scatter chart  Description automatically generated |
| **Figure S4:** biplots representing the correlation between our prediction values extracted at the Coillte properties’ centroids (*x* axes) and the density values estimated from faecal pellet counts, *y* axes). |