Fig. 1 | Baboons in Amboseli experience shared environments at multiple scales. a, Our microbiota time series consisted of 17,265 16S rRNA gene sequencing gut microbial profiles. Each point represents a microbiota sample, plotted by the date it was collected (*x* axis). Each row (*y* axis) corresponds to a unique individual host. Samples were collected from 600 wild baboons living in five original social groups (indicated by dark colours marked with black dots in the legend) and seven groups that fissioned/fused from these original groups (no black dots). **b**, All baboon groups ranged over a shared ~60 km² area and the social groups had largely overlapping home ranges. Ranges are shown as 90% kernel densities over the sampling period specific to each group; five original social groups are shown with solid borders, fission and fusion products with dashed borders. **c**, Monthly rainfall amounts (blue bars, in mm) with yellow and green stripes along the *x* axis representing dry and wet seasons, respectively, with the width of the green stripes reflecting the number of months within the focal year that had at least 1 mm of rainfall. **d**, Temporal shifts in diet from the years 2000 to 2013, shown as the relative abundance of diet components in the five original social groups over 30-d sliding windows before each sample collection date. Colours correspond to the 13 most common food types, while the grey bars correspond to other or unknown food types. Coloured boxes around each panel in **d** reflect each of the five original, most extensively sampled social groups (colours as in **a** and **b**). The white bars indicate time periods where no diet data were collected. Credit for base map in **b**: Google, TerraMetrics.