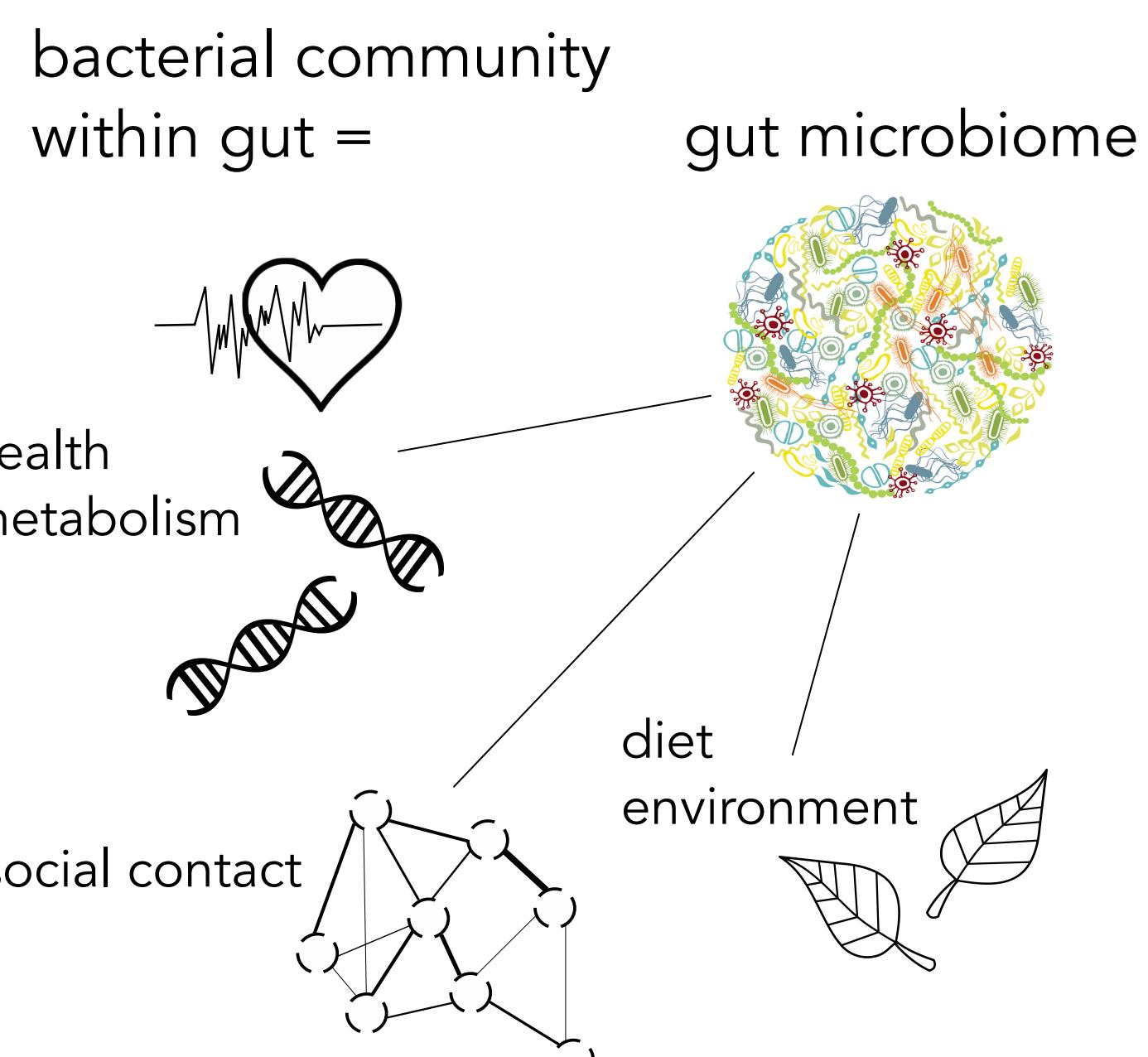


# Ecology and sociality shape the Grauer's gorilla gut microbiome

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## Background



## Questions

- What drives gut microbiome differentiation between individuals?
- Do populations and social groups harbour distinct gut microbial communities?
- Can these differences be attributed to relatedness, social contact, or diet?

## Approach

By sampling several social groups from two populations of the critically-endangered Grauer's gorilla, we compare the effects of diet, sociality, and environment on gut microbial diversity.

119 faecal samples

Eastern part of DRC

2 populations

KBNP - 8 social groups

n = 80

NRCA - 1 social group

n = 11

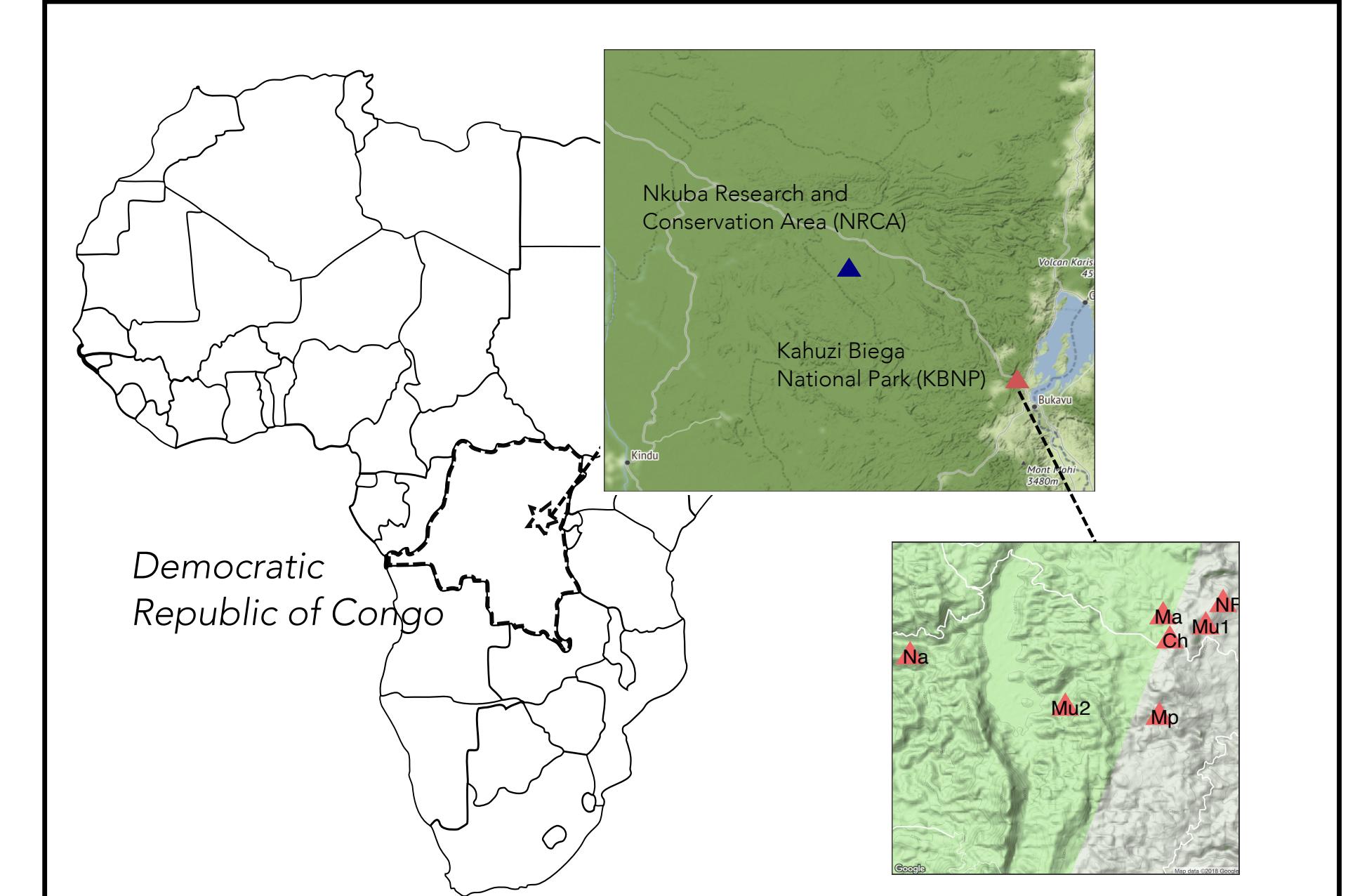


Figure 1: Location of sampled populations in Democratic Republic of Congo, separated by ~2500m altitude, ~165 km

Amplified ~390 bp V4 region of 16S rRNA gene with primers 515F/806R

Computed measures of inter-individual diversity of gut microbiome composition, based on presence-absence and abundance of bacterial taxa

## Results

1. Geographically separate populations of gorillas harbour distinct gut microbiome communities

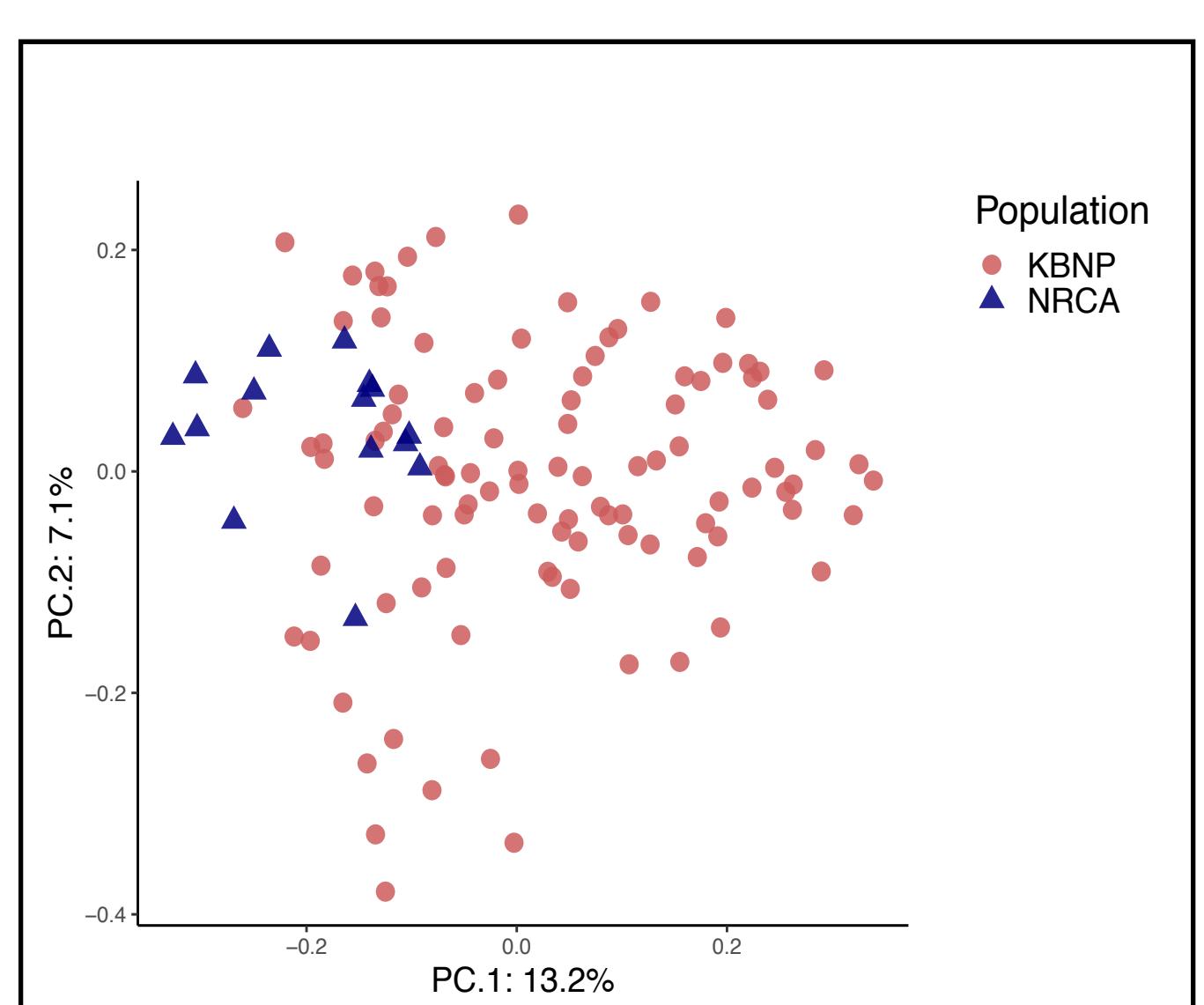


Figure 2: Principle coordinates plot of Bray-Curtis dissimilarity, separating samples by population

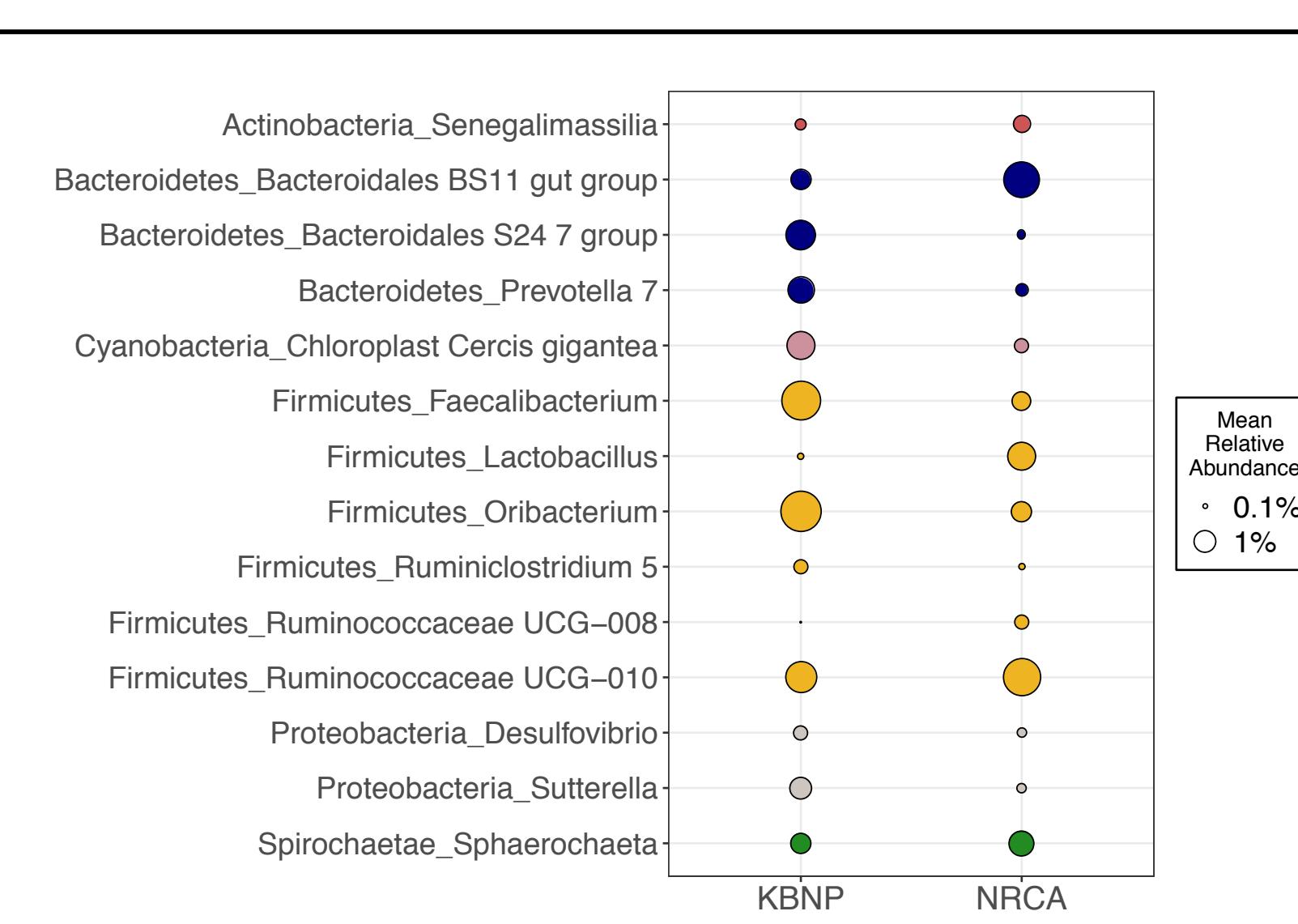


Figure 3: Specific genera are differentially abundant between populations

3. Kinship does not influence gut microbiome composition [KBNP population, Mantel test:  $r = -0.007$ ,  $p = 0.623$ ]

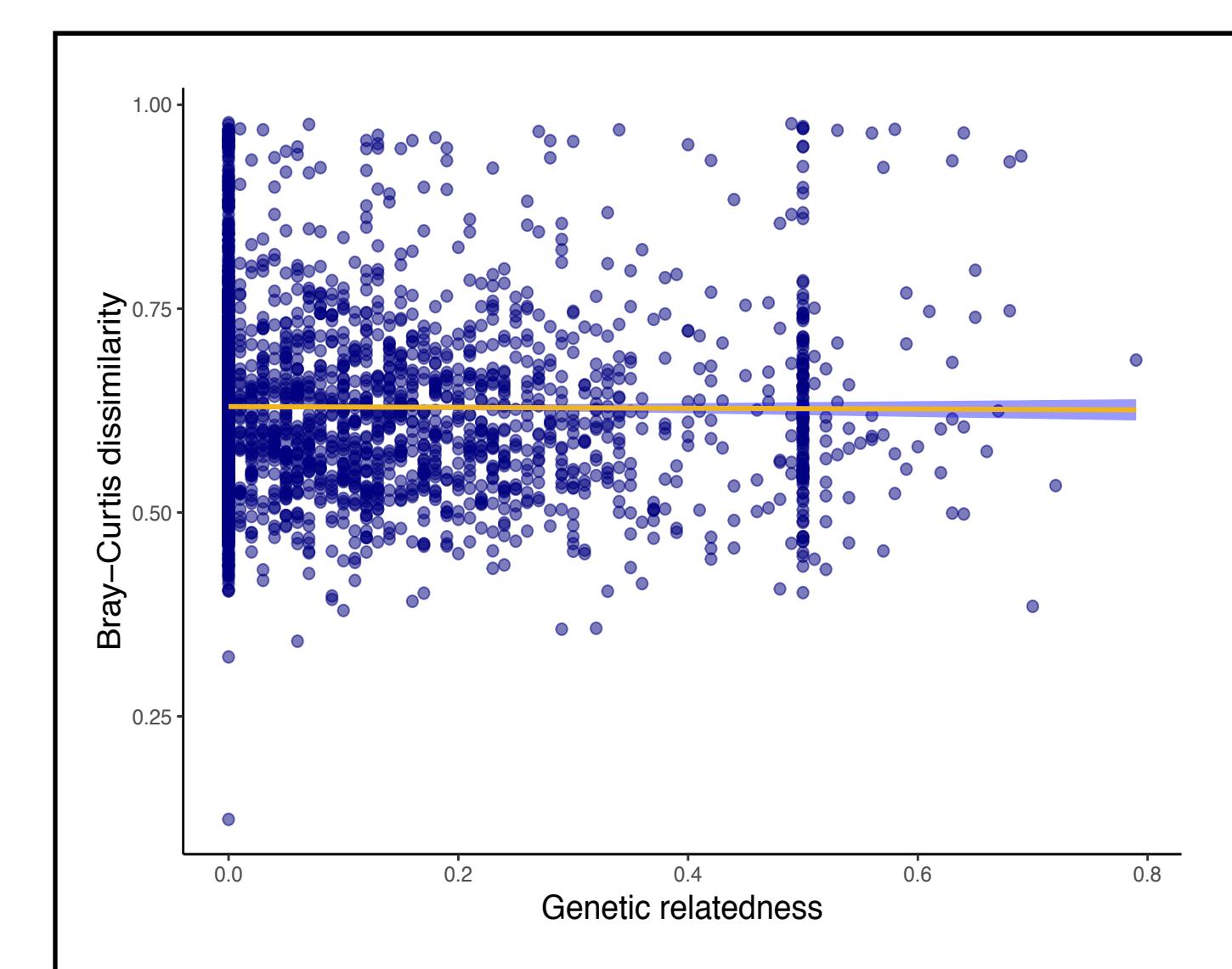


Figure 5: Genetic relatedness, inferred through genotyping at 13 microsatellite loci, does not predict gut microbiome dissimilarity across the KBNP sample

2. Within a single population (KBNP) comprised of 8 social groups, members of the same social group have more similar gut microbiota to one another, than to members of different social groups

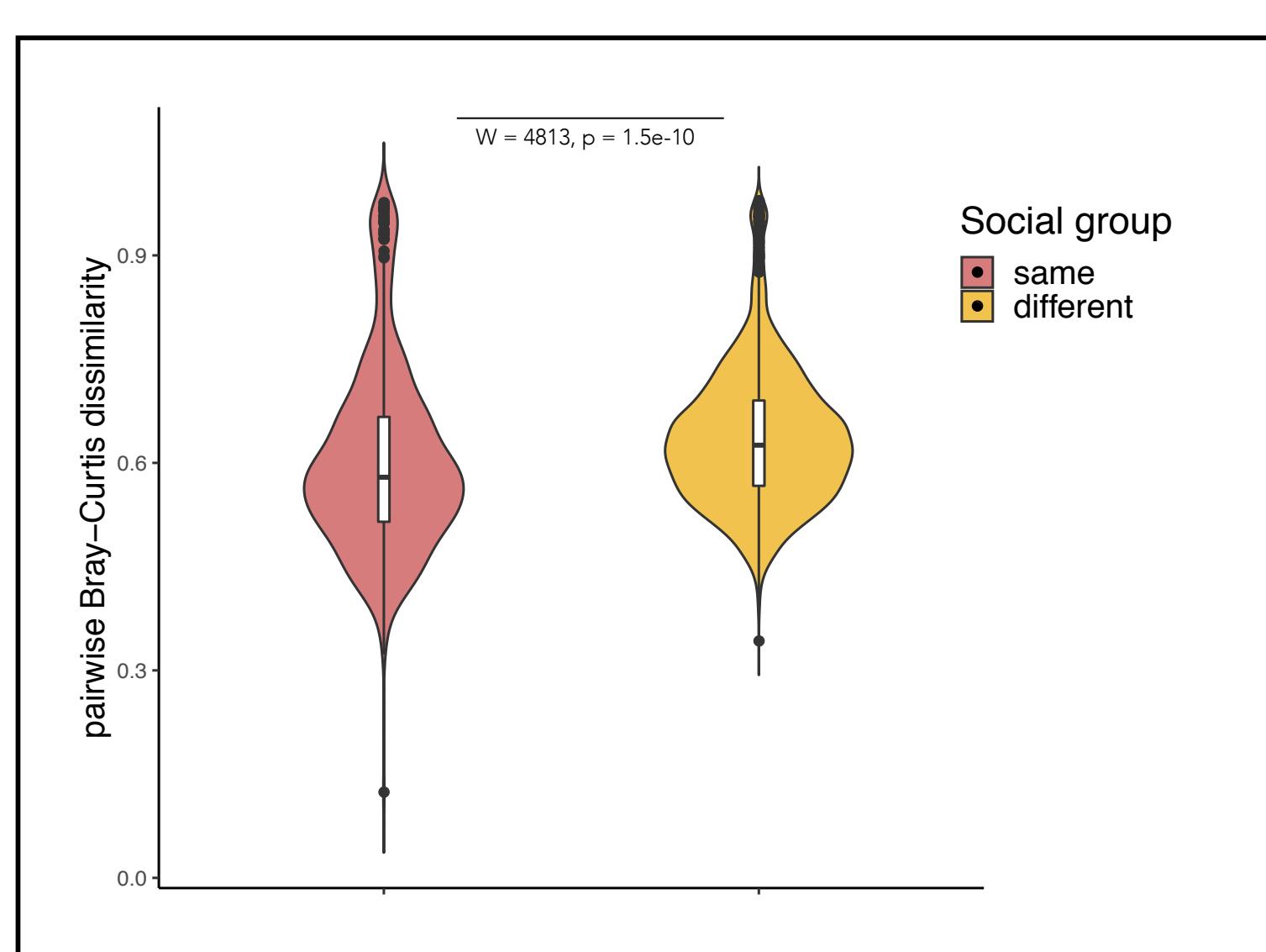


Figure 4: Dissimilarity between members of the same group is lower than dissimilarity between members of different groups

Social group membership explains 22% of variation across the KBNP sample (PERMANOVA, Bray-Curtis metric:  $p < 0.001$ ), controlling for age and sex

## Conclusions and future steps

Gut microbial composition reflects host environment

Differentially abundant genera between populations linked to digestion of dietary substrates

Within-group similarity likely influenced more by contact than diet, given range overlap and gorilla diet pattern

To disentangle the effects of association and diet:

- integrate information on feeding proximity networks within a single (habituated) social group
- investigate functional differences in bacterial taxa between populations

Acknowledgements: Peter Niehoff genotyped samples and provided estimates of relatedness