The wolf reference genome sequence (Canis lupus lupus) and its implications for Canis spp. population genomics - DTU Orbit (09/12/2018)

Background
An increasing number of studies are addressing the evolutionary genomics of dog domestication, principally through resequencing dog, wolf and related canid genomes. There is, however, only one de novo assembled canid genome currently available against which to map such data - that of a boxer dog (Canis lupus familiaris). We generated the first de novo wolf genome (Canis lupus lupus) as an additional choice of reference, and explored what implications may arise when previously published dog and wolf resequencing data are remapped to this reference.

Results
Reassuringly, we find that regardless of the reference genome choice, most evolutionary genomic analyses yield qualitatively similar results, including those exploring the structure between the wolves and dogs using admixture and principal component analysis. However, we do observe differences in the genomic coverage of re-mapped samples, the number of variants discovered, and heterozygosity estimates of the samples.

Conclusion
In conclusion, the choice of reference is dictated by the aims of the study being undertaken; if the study focuses on the differences between the different dog breeds or the fine structure among dogs, then using the boxer reference genome is appropriate, but if the aim of the study is to look at the variation within wolves and their relationships to dogs, then there are clear benefits to using the de novo assembled wolf reference genome.

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