Review of: "High-altitude adaptation and incipient speciation in geladas"

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The authors reported a chromosome-scale assembly of the gelada (*Theropithecus gelada*) and complemented it with population resequencing, hematological, and morphometric data. They tried to provide a comprehensive insight into the high-altitude adaptation and to elucidate potential basis underlying incipient speciation. The assembled reference genome and massive genetic data of various populations will be of value for research and genomics-assisted high-altitude adaptation work in the future. This is a very good study and the manuscript is written well to which I have only a few comments.

Main problems:

1. Assembly of the *Theropithecus gelada* genome sequences.

Only contig N50 and scaffold N50 were shown for comparison the assembled genome. The full use of Hi-C data will provide good suggestions to detect and improve the misjoins from the initially obtained contigs. They should provide detailed comparisons of assembly versions with the improvement using linkage map and Hi-C data, which should include how many links supported by linkage map and Hi-C, and the number of conflicts.

2. Conservation and population genomics

Authors should add a scatter plot and phylogenetic result to display the relationship between the samples, which were obtained from the t-Distributed Stochastic Neighbor Embedding (t-SNE) or other methods.

3. Genomic adaptations to high altitude

Only population structure and effective pop. Size analysis was based on whole-genome population resequencing data. Authors sequenced gelada populations at different altitudes, why not compare the population genetic difference among them to obtain genomic adaptations to high altitude?

4. Hi-C library generation and sequencing

The number of libraries and detailed Hi-C statistics (% unique-mapped reads, % self-circle, % dangling ends, % duplicates, etc…) should be provided.