Dear Editors,

We submit our manuscript describing the role gene regulation has played during the evolution of a domesticated animal species (sheep). We explore the impact that sequence elements controlling gene expression have had during the twin evolutionary processes of animal domestication and subsequent artificial selection. To address this question, we report the first functional annotation of any livestock genome. This was derived from our experimental ChIP-seq data and comparative genomics, and should be of interest to researchers for the interpretation of GWAS and optimization of genomic predictions.

Our major findings describe the clear role proximal gene regulatory features have played in the evolution of modern sheep. We base these conclusions on whole-genome sequence data collected from over 40 globally distributed sheep breeds and comparison against genome sequences from descendants of their wild ancestors, namely Asiatic mouflon. We apply a series of population sequence diversity analyses to identify genomic regions under positive selection, before intersecting them with the functional annotation described above.

This work addresses an emerging field concerned with the identification and interpretation of sequence elements responsible for controlling gene expression in livestock species. Large-scale efforts are underway within at least two major animal international consortium that follow the footsteps of ENCODE (FAANG, FAASG). We therefore anticipate our work will be of broad interest to the readership of *Nature Communications*, and represents a significant advance in our understanding of animal domestication and selection.

On behalf of the authors

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