This data contains conserved sites of cattle genome. These sites are firstly determined in humans and those sites that have the PhastCons score > 0.9 were lift-over to the cattle ARS-UCD 1.2 genome, following the previously described procedure1. In the zipped folder, there are \*.bed files labelled by the number of human chromosomes. Note that because there are more cattle chromosomes than humans, each bed file contains more cattle chromosomes than what is labelled on the file. For example, ‘cow.chrom-hg.chr1.100way.0.9.lift.bed’ contains sites on cattle chromosome from 1-29. In each bed file, the columns are:

1st column: cattle chromosome

2nd column: cattle position start

3rd column: cattle position end

4th column: id label in the original human PhastCons data

5th column: the PhastCons score of sites

Reference:

1 Xiang, R. *et al.* Quantifying the contribution of sequence variants with regulatory and evolutionary significance to 34 bovine complex traits. *Proceedings of the National Academy of Sciences* **116**, 19398-19408, doi:10.1073/pnas.1904159116 (2019).