Acceleration of X-chromosome gene order evolution in the cattle lineage

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**Supplementary Figures**

**Supplementary Fig 1.** Rates of signed gene order rearrangements on the X chromosomes (A) and autosomes (B) of five mammals. The evolutionary tree is based on the estimation of divergence times provided by the TIMETREE database (http://www.timetree.org/). Gene order distances are based on 169 and 10,196 orthologous gene sets of the mammals on the X chromosome and autosomes, respectively. Rates are depicted as a color gradient from minimum to maximum, and the color scale is shown at bottom. The number on each lineage is the parsimony-inferred number of rearrangements, and the rates are indicated in parentheses. The rate is estimated only for external lineages. Internal lineages are striped.
Supplementary Fig 2. Gene order of 51 concordant markers orthologous genes on the cattle X chromosomes. Red lines indicate orthologous genes in the X-added region (XAR), and the blue line indicates orthologous genes in the X-conserved region (XCR) according to annotations of the human chromosome. The number to the right of each chromosome represents the chromosomal length.
Supplementary Fig 3. Rates of unsigned gene order rearrangements on the X chromosomes (A) and autosomes (B) of five mammals in 51 concordant markers. The evolutionary tree is based on the estimation of divergence times provided by the TIMETREE database (http://www.timetree.org). Gene order distances are based on 169 and 10,196 orthologous gene sets of the mammals on the X chromosome and autosomes, respectively. Rates are depicted as a color gradient from minimum to maximum, and the color scale is shown at bottom. The number on each lineage is the parsimony-inferred number of rearrangements, and the rates are indicated in parentheses. The rate is estimated only for external lineages. Internal lineages are striped.
Supplementary Fig 4. Rates of unsigned gene order rearrangements on the X chromosomes (A) and autosomes (B) of five mammals in Btau6.0. The evolutionary tree is based on the estimation of divergence times provided by the TIMETREE database (http://www.timetree.org/). Gene order distances are based on 372 and 11,740 orthologous gene sets of the mammals on the X chromosome and autosomes, respectively. Rates are depicted as a color gradient from minimum to maximum, and the color scale is shown at bottom. The number on each lineage is the parsimony-inferred number of rearrangements, and the rates are indicated in parentheses. The rate is estimated only for external lineages. Internal lineages are striped.
**Supplementary Fig5.** Rates of signed gene order rearrangements on the X chromosomes (A) and autosomes (B) of five mammals in Btau6.0. The evolutionary tree is based on the estimation of divergence times provided by the TIMETREE database (http://www.timetree.org/). Gene order distances are based on 372 and 11,740 orthologous gene sets of the mammals on the X chromosome and autosomes, respectively. Rates are depicted as a color gradient from minimum to maximum, and the color scale is shown at bottom. The number on each lineage is the parsimony-inferred number of rearrangements, and the rates are indicated in parentheses. The rate is estimated only for external lineages. Internal lineages are striped.