**The Lithuanian reference genome LT1 - a human *de novo* genome assembly from the Baltic States**

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Chart, scatter chart

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Fig. S1. Comparison of chromosome X between LT1 and CHM13. Blue dots represent unique forward alignments and green dots unique reverse alignments, respectively. Orange dots denote repetitive alignments.

Chart, histogram

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Fig. S2. Complete size distribution of the consensus a) deletions, b) insertions, and c) inversions found in LT1. Number of bins: a) 54, b) 50, c) 21, respectively. Gaps on deletions Y axis are from 250 to 1,198 and from 1,550 to 4,000, aiming to reduce the overrepresentation of the first 2 bins.