

THE COMPLETE SEQUENCE OF A HUMAN GENOME

In two earlier posts we have reported the sequencing of entire chromosomes (X and 8) from telomere-to-telomere (T2T). The T2T consortium has now finished the end-to-end sequencing of an entire haplogenome. There are no gaps; the centromeres as well as the short arms of the acrocentric chromosomes are included. The results have been deposited on [bioRxiv](#) and the paper will, most likely, appear soon in a high-level journal. This version was called T2T-CHM13. The CHM13 cell line is haploid, and was chosen because the absence of a second haploid set could greatly facilitate the task.

This version will surely be the starting point of a new human reference genome. Some of the authors belong to the UCSC genome centre. And, in fact, this version is already on UCSC ([t2t-chm13-v1.0](#)).