

[Maize Genome](#)

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Zea mays L.
Image processed by Thomas Schoepke
www.plant-pictures.de

Maize Genome Sequencing Project

Corn (Maize) is a major crop in the U.S., a main source of global food supply, and an important model system for basic biological research. Knowledge gained from maize can also be used to improve its relatives such as sorghum, wheat, rice, switchgrass and Miscanthus. At AGI, we have been working on the maize genome since 1998. In the [Maize Mapping Project](#), we built a BAC-based maize agarose physical map and an integrated genetic and physical map. In the [maize sequencing pilot project](#), we constructed a maize high information content fingerprint (HICF) physical map and sequenced the ends of all BACs in the physical map. Extensive manual editing of the agarose map was performed. In July 2005, we released a sequencing-ready [maize physical map](#). In November, 2005, The Maize Sequencing Consortium was formed and awarded to sequence the maize genome. The [Maize Genome Sequencing Project](#) provided a maize reference genome sequence with finished high quality sequence in low copy regions. Co-PIs of the sequencing consortium are:

Richard Wilson, [Washington University at St. Louis](#)
Sandra Clifton, [Washington University at St. Louis](#)
Rod A. Wing, [Arizona Genomics Institute](#)
Doreen Ware, [Cold Spring Harbor Laboratory](#)
Lincoln Stein, [Cold Spring Harbor Laboratory](#)
Richard McCombie, [Cold Spring Harbor Laboratory](#)
Robert Martienssen, [Cold Spring Harbor Laboratory](#)
Patrick Schnable, [Iowa State University](#)
Srinivas Aluru, [Iowa State University](#)

In February, 2008 at the 50th Maize Genetic Meeting, the Maize Sequencing Consortium announced the draft sequence of the maize genome.



Since then, extensive work has been done to finish the remaining clones, improve the physical map, anchor the sequence to the genetic map, build an AGP (A Golden Path) to generate maize pseudomolecules, and to annotate the genome. Please visit the official project [website](#) for details. On March 20, 2009, AGI released an updated maize integrated genetic and physical map, consisting of 440 contigs. Please click here to check the quality of each contig, including order and orientation information. Please visit our [maize FPC ftp site](#) to download the file . The sequenced BACs are highlighted in red on the FPC map. The AGP and pseudomolecules for the 10 maize chromosomes and the unanchored contigs (chr0) are available for [download](#) We also released the maize [minimum tiling path \(MTP\)](#) for the sequencing project. This MTP will link the pseudomolecules to physical contigs. In the MTP website, when you click the clone name, it will show you the best hits of the clone to other clones in the sequencing project. The BES2BAC column indicates the sequence similarities of the BES of this clone to the sequenced BAC on its left or right end. A simple click will lead to the sequence alignment.

UPDATES ON THE MAIZE SEQUENCING PROJECTS! ([Click here for details at MaizeGDB](#))

[Maize Full Length cDNA Project](#) [The complete set of maize FLcDNA clones are available from the AGI Resource Center](#)

Maize Physical Map

[FPC](#) | [HICF FPC](#) | [BES](#)

[MSLL/HMPR](#)

Maize B73 RefGen_v2 Downloads

The complete list of maize FLcDNA clones

[FPC ftp site](#)

[Pseudomolecules](#)

[MTP, Clone list](#)

Sequences of Genetic Markers, the major genetic and physical changes, including the anchoring quality of each contig, are in [this table](#)

Maize B73 RefGen_v1 Downloads

[FPC ftp site](#)

[HICF FPC ftp site](#)

[Pseudomolecules](#)

[MTP](#)