Interest in the genetics of maize began in the early 1900s when geneticists began to document the many varieties and explore the implications of genetic crosses. Understanding the maize genome will enable geneticists to develop new and improved maize varieties that are more nutritious or can withstand harsher environments.

In this special poster, presented in conjunction with the first publication of the full maize genome sequence, we trace the history of modern maize from its beginnings as a wild grass called teosinte, to what is today one of the most productive and widespread crops in the world.

The Maize Genome Poster is available for download at: [www.sciencemag.org/products/posters/maize_poster.pdf](http://www.sciencemag.org/products/posters/maize_poster.pdf)
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Figure 1. Distribution of bases and their empirical quality values from SOLiD™ System Sequencing.
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Above: Treatment of C2C12 cells with H_2O_2 stimulates phosphorylation of AMPKα at Thr172, detected by the PathScan® Phospho-AMPKα (Thr172) Sandwich ELISA Kit #7658. The absorbance readings at 450 nm are shown in the top figure, while the corresponding western blots using Phospho-AMPKα (Thr172) (D79.5E) XP™ Rabbit mAb #4186 (left panel) or AMPKα (23A3) Rabbit mAb #3803 (right panel) are shown in the bottom figure.