Construction, alignment and analysis of twelve framework physical maps that represent the ten genome types of the genus Oryza

2008

Posted by: webmaster
Posted on: 2008/2/28 0:00:00

Kim H, Hurwitz B, Yu Y, Collura K, Gill N, SanMiguel P, Mullikin JC, Maher C, Nelson W, Wissotski M, Braidotti M, Kudrna D, Goicoechea JL, Stein L, Ware D, Jackson SA, Soderlund C, Wing RA.

Genome Biol. 2008;9(2):R45. Epub 2008 Feb 28.

Abstract

We describe the establishment and analysis of a genus-wide comparative framework composed of 12 bacterial artificial chromosome fingerprint and end-sequenced physical maps representing the 10 genome types of Oryza aligned to the O. sativa ssp. japonica reference genome sequence. Over 932 Mb of end sequence was analyzed for repeats, simple sequence repeats, miRNA and single nucleotide variations, providing the most extensive analysis of Oryza sequence to date.