Gramene: A Resource for Comparative Grass Genomics

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Gramene (www.gramene.org) is a curated, open-source, data resource for comparative genome analysis in the plant kingdom, with emphasis on the grasses. GRAMENE Home Gramene is comprised of database modules that integrate publicly-available Resource for Compa information about genomic sequence, genes, proteins, biochemical pathways, maps and markers, QTL, and genetic and phenotypic diversity. Ontologies (controlled vocabularies) are used to associate the different types of data. Maize researchers and breeders can take advantage of known microsynteny between the different species of the grass family by using maps and genomic sequence as a reference point for gene and marker discovery in maize. Gramene releases data updates and feature improvements on a semi-annual basis. Online tutorials and help documents provide users with an overview of how to conduct a wide variety of operations on the database. Gramene is a collaborative effort between Cold Spring Gramene 29 Harbor Laboratory, the Department of Plant Breeding and Genetics at Cornell Gramene's release #29 includes many improvements to every section of our site, including our genome browser, Marts, University and various national and international projects dedicated to cereal genomics and genetics research. maps, markers, genes, proteins, and quick search. Visit http:// The database is updated 2 times a year, with the latest release (Build #29) on February 27, 2009. For help using Gramene, trowse through our help pages and FAQs jew one of our mail online tutorials or contact us A 16 **Biochemical Pathways** Comparative Map Viewer (CMAP) Search, view, and compare mapped genes, markers, QTL, and clones on various types of Gramene blog Stay informed about Gram **Gramene Maize** Data MySQL connectivity Genome Browser Gramene has implemented the ProServer lightweight DAS (Distributed Annotation System) Server from the Gramene Welcome to ProServer v457 10 rows as HTML Unique results only