Contents

FULL PAPERS

Molecular characteristics of early-stage female germ cells revealed by RNA sequencing of low-input cells and analysis of genome-wide DNA methylation

Identification of epistasis loci underlying rice flowering time by controlling population stratification and polygenic effect

131 D. SEN, K. PAUL, C. SAHA, G. MUNIHEREE, M. NAG, S. GHOSH, A. DAS, A. SEAL, AND S. TRIPATHY
A unique life-strategy of an endophytic yeast Rhodotorula mucilaginosa JCTA-51—a comparative genomics viewpoint

147 D. YADAV, A. DUTTA, AND S. S. MANDE
OTUX: V-region specific OTU database for improved 16S rRNA OTU picking and efficient cross-study taxonomic comparison of microbiomes

157 Y. M. SUVOROVA, M. A. KOROTKOVA, K. G. SKRYABIN, AND E. V. KOROTKOV
Search for potential reading frameshifts in cds from Arabidopsis thaliana and other genomes

171 Y. MIKI, K. YOSHIDA, N. MIZUNO, S. NASUDA, K. SATO, AND S. TAKUMI
Origin of wheat B-genome chromosomes inferred from RNA sequencing analysis of leaf transcripts from section Sitopsis species of Aegilops

183 A. ARIMOTO, K. NISHITSUJI, Y. HIGA, N. ARAKAKI, K. HISATA, C. SHINZATO, N. SATOH, AND E. SHOGUCHI
A siphonous macroalgal genome suggests convergent functions of homeobox genes in algae and land plants

CORRIGENDUM

Identification of epistasis loci underlying rice flowering time by controlling population stratification and polygenic effect