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Genomic insights into early and mid-late maturity of Korean *Oryza sativa* cultivars

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Rice (*Oryza sativa L.*) is staple food cultivated across numerous regions worldwide, playing a crucial role in global food security. Improving rice yield and quality is a primary goal in agriculture. Central to this is the genetic regulation of maturity timing and heading date, critical traits for optimizing harvest and productivity. However, genomic analysis in Oryza sativa has been limited by its reliance on the single reference genome of the *japonica* cultivar "*Nipponbare*", which fails to capture the vast genetic diversity among cultivars. In this study, we address this gap by performing *de novo* assembly of reference-level genomes for major Korean rice cultivars with distinct maturation times (early and mid-late) using both Nanopore and MGI sequencing data. By constructing a comprehensive pan-genome, we aim to identify the key genetic determinants controlling crop maturity. This work establishes a foundational genetic resource for developing tailored cultivars with enhanced yield and environmental adaptability, thereby deepening our understanding of major agronomic traits and advancing precision breeding technologies in rice.