**Extended Data Fig. 1 | high-quality genomes of *I. verum* and *A. gramineus*.**

**a**,Chromosome-level assembly of the *I. verum* genome using Hi-C technology. **b**, **c**, Chromosome-level assembly of the *A. gramineus* genome using Hi-C technology. **d**, Morphological characteristics of *A. gramineus*: schematic representations of (a) aerial parts; (b) cross section of spadix; spadices; (d) spadices with pseudo-spathe; (e) leaves.

图表, 旭日形

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**Extended Data Fig. 2 | WGD in *I. verum* and *A. gramineus*.**

**a**,Synteny blocks of the *I. verum* genome. **b**,Synteny blocks of the *A. gramineus* genome. **c**, The Ks distributions of intragenomic synteny blocks. **d**, Synteny patterns between genomic regions from *I. verum*, *Am. trichopoda*, and *A. gramineus*.

图示

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**Extended Data Fig. 3 | The identified ancestral angiosperm karyotype (AAK) comprising 16 protochromosomes, each of which was retained as the chromosome-like ‘synteny blocks’ or chromosomes cross multiple species (shaded orange)**

图表, 树状图

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**Extended Data Fig. 4 | A single shared fusion between Amborellales and Nymphaeales.**

**a**, The evolutionary trajectory of this shared fusion and a further inversion event in Amborellales. **b**, The local syntenic blocks related to AAK1 and AAK2 with *Am. trichopoda* as a reference.

图示

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**Extended Data Fig. 5 | A single shared fusion between Austrobaileyales and Mesangiospermae.**

**a**, The evolutionary trajectory of the shared fusion. **b**, An inversion event of the fused chromosome in Mesangiospermae. **c**, The local syntenic blocks related to AAK16 and AAK7 with *I. verum* as a reference.

图示

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**Extended Data Fig. 6 | Evolutionary differences between ancestral monocot karyotype and the other four clades of Mesangiospermae.**

**a**, Representative species of five Mesangiospermae clades (*A. gramineus*, monocots; *L. chinense*, magnoliids; *C. sessilifolius*, Chloranthus; *C. demersum*, Ceratophyllum; *V. vinifera*, eudicots) and out group (*Am. trichopoda*, Amborella). The ancestral chromosomes are distinguished by different colors, and the chromosomes produced by the fusion include different colors. **b**, The local syntenic blocks related to AAK16 and AAK7. **c**, The local syntenic blocks related to AAK1 and AAK9.

图形用户界面, 日历

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**Extended Data Fig. 7 | Inconsistent structural variation for monocots and magnolias** **with *Aristolochia* as a reference.**

**a**, The evolutionary trajectory of evolutionary events related to AAK7, AAK16 and AAK14. The primitive AMAK13 was still retained in *A. gramineus*, but in the common ancestor of the other monocots, it further fused with AAK14 to produce the protochromosome 5. AMAK 13 was obviously fragmented into two parts in magnolias and a part of AAK 16 in this primitive chromosome was connected again with a part of AAK 14 in one chromosome of *Ar. fimbriata*. Moreover, the structural variation of Piperales is not consistent in Magnoliales and Laurales and is not representative of magnoliids. **b**, The local syntenic blocks related to AAK3 with *Am. trichopoda* as a reference.

文本, 日历, 白板

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**Extended Data Fig. 8 | Inconsistent structural variation for monocots and magnolias with Aristolochia as a reference.**

**a**, The evolutionary trajectory of evolutionary events related to AAK3 (Chromosome 10 of *Am. trichopoda*). The primitive AMK3 was still retained in *A. gramineus*, but these fission positions in other monocots and magnoliids are inconsistent, indicating that these structural variations in monocots and magnolias are independent. **b**, The local syntenic blocks related to AAK3 with *Am. trichopoda* as a reference.

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**Extended Data Fig. 9 | the τ event and the following two shared fusion events.**

**a**, The evolutionary relationship between major clades of monocots with *A. gramineus* as a reference. **b**, the two shared fusions after the σ event. **c**, The local syntenic blocks related to AMKA1, AMKA6 and AMKA8.

图示

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**Extended Data Fig. 10 | The ancestral chromosome karyotype accurately identified the polyploidy levels and corrected the assembly.**

**a**, The marked questions indicate that the current branch's polyploidy levels are in disputes. **b**, The syntenic depth ratio of AMKA2 and AMKA6 identified to be 8 in *Dendrobium chrysotoxum*, which indicates three WGDs. **c**, Using chromosomes 4, 11, 12, and 16 of *Elaeis guineensis* as a reference, which were produced by AMKA5 after two WGDs, the syntenic depth ratio identified to be 31 in *Musa acuminata*, which indicates five WGDs. **d**, the two shared fusions in *Oryza sativa* and *A. comosus* indicate that the σ event in Poales was a hexaploidization event. **e**, Chromosome 8 of *S. polyrhiza* has a fragment of AMKA6, while this structural variation did not occur in *Spirodela intermedia*. Similarly, chromosomes 24 and 25 of *A. comosus* may be broken from the AMKA5, and they are the complete AMKA5 in *Ananas bracteatus*.

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