

**The genome of *Aechmea fasciata* provides insights into the evolution of tank epiphytic habits  
and ethylene-induced flowering**

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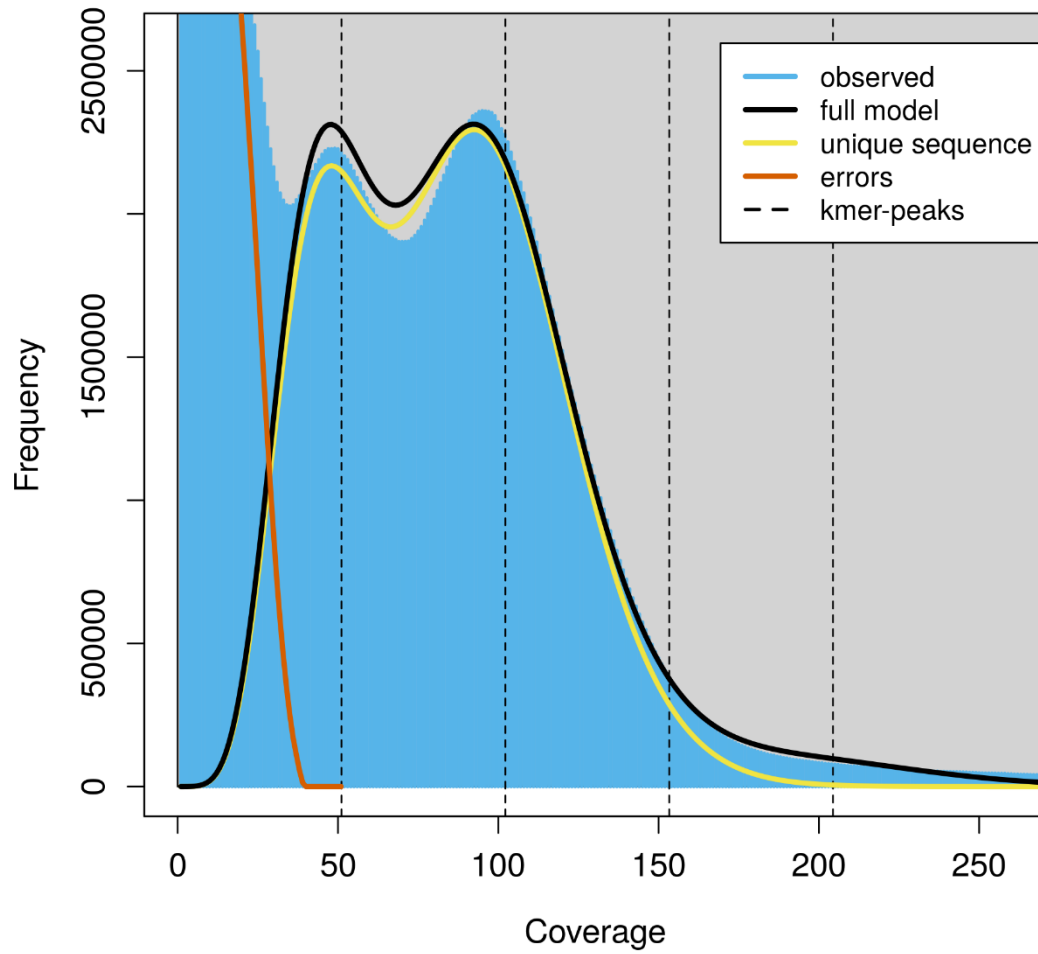
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4 National Gene Bank of Tropical Crops, Danzhou, 571700, Hainan, China

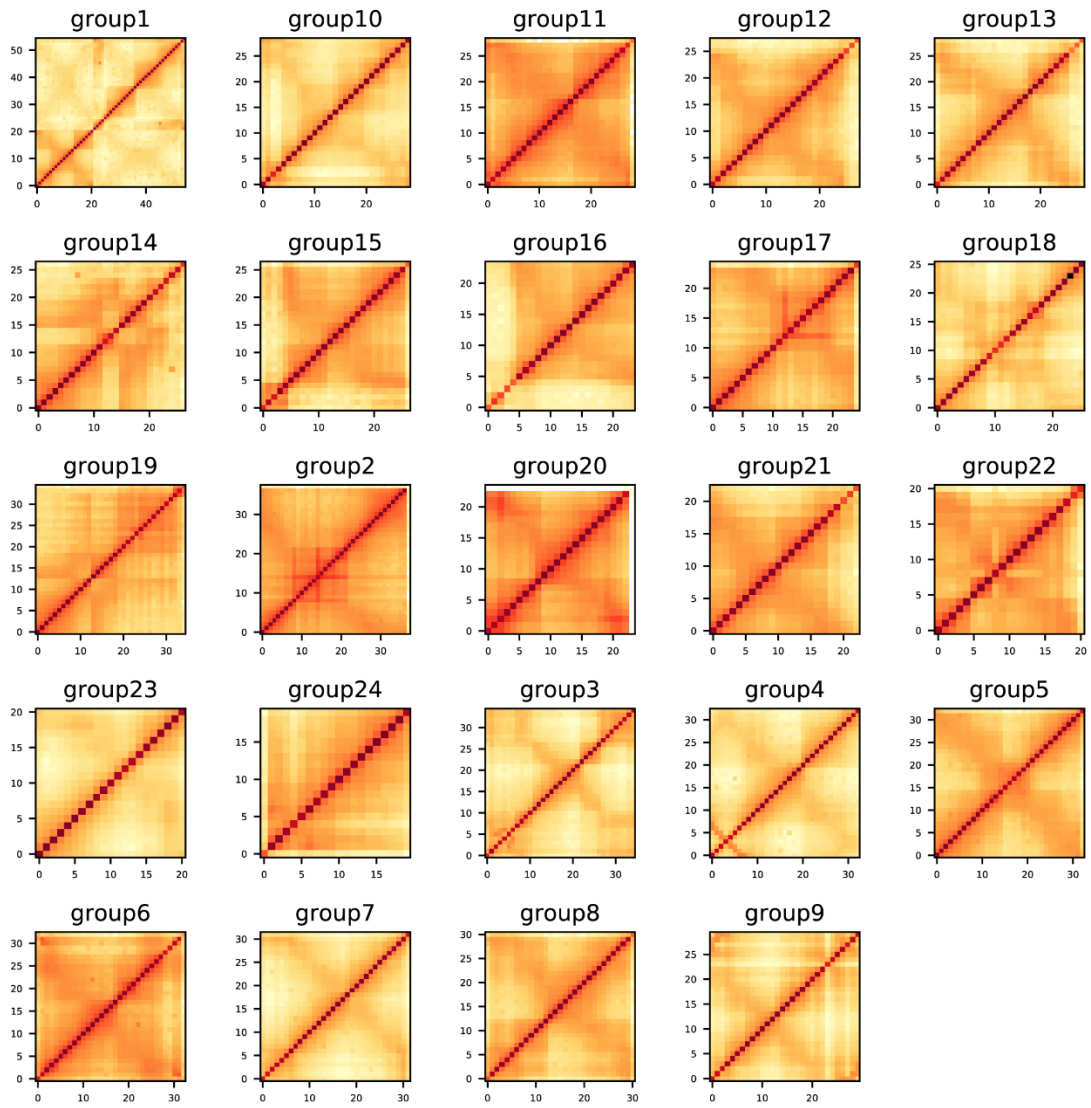
5 College of Horticulture and Landscape Architecture, Hainan University, Haikou, 570228, China

### GenomeScope Profile

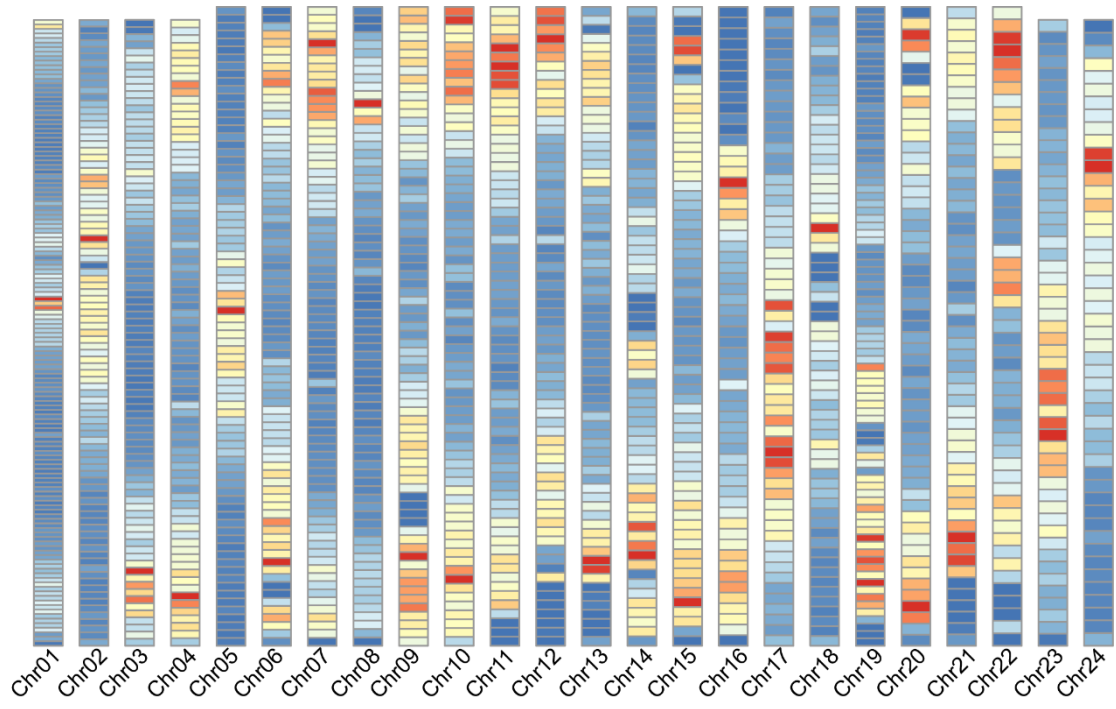
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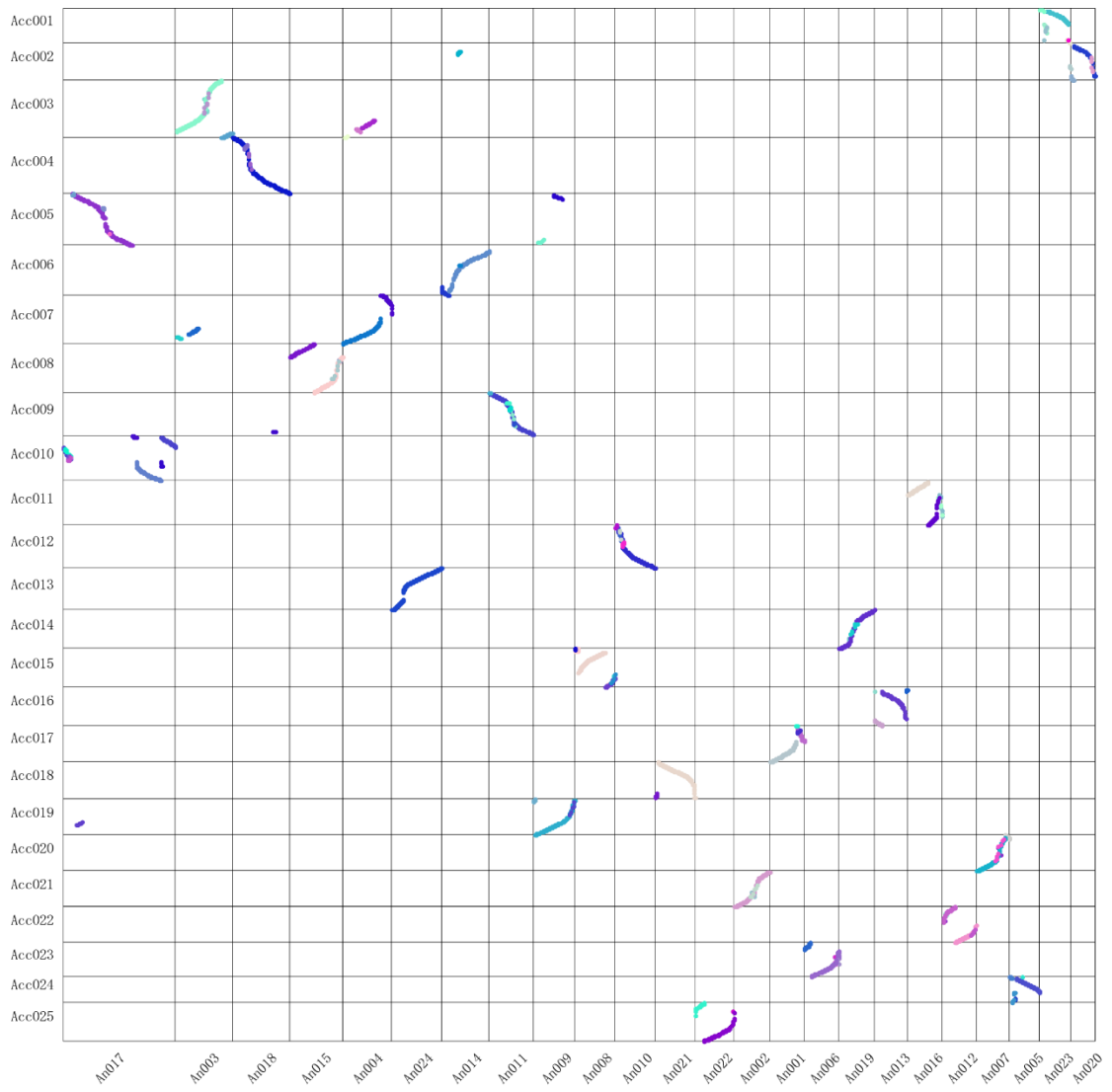
Supplementary Figure 1 Genome size estimation using GenomeScope.



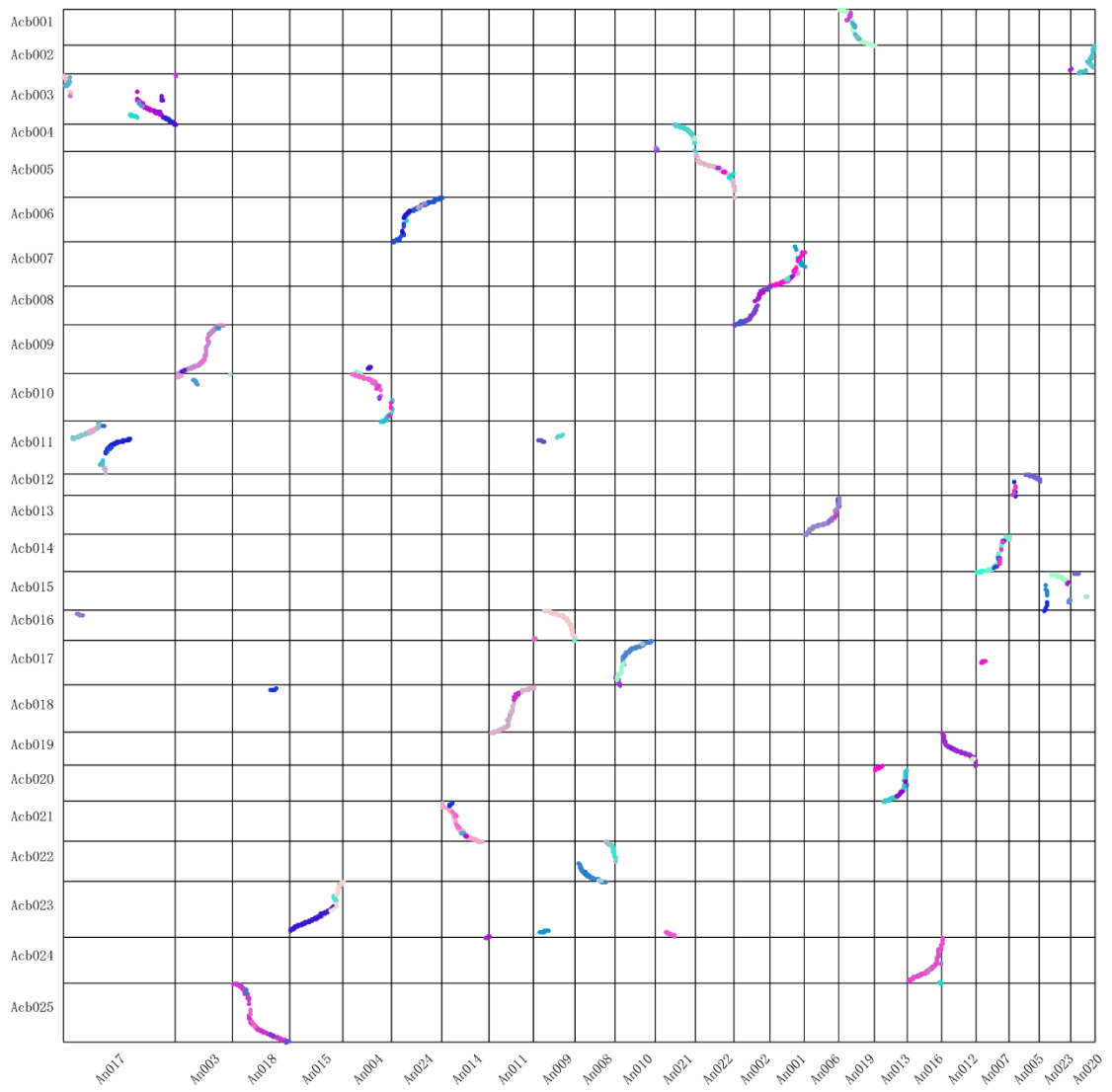
Supplementary Figure 2 Hi-C heatmap of each pseudo-chromosome.



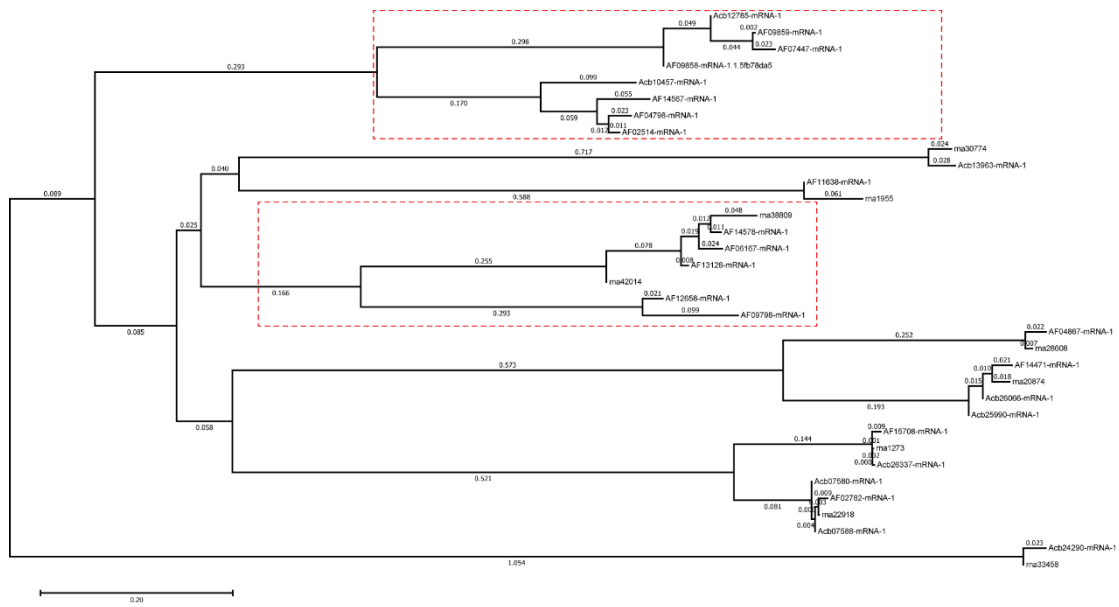
Supplementary Figure 3 Heat map of LTR distribution in each chromosome.



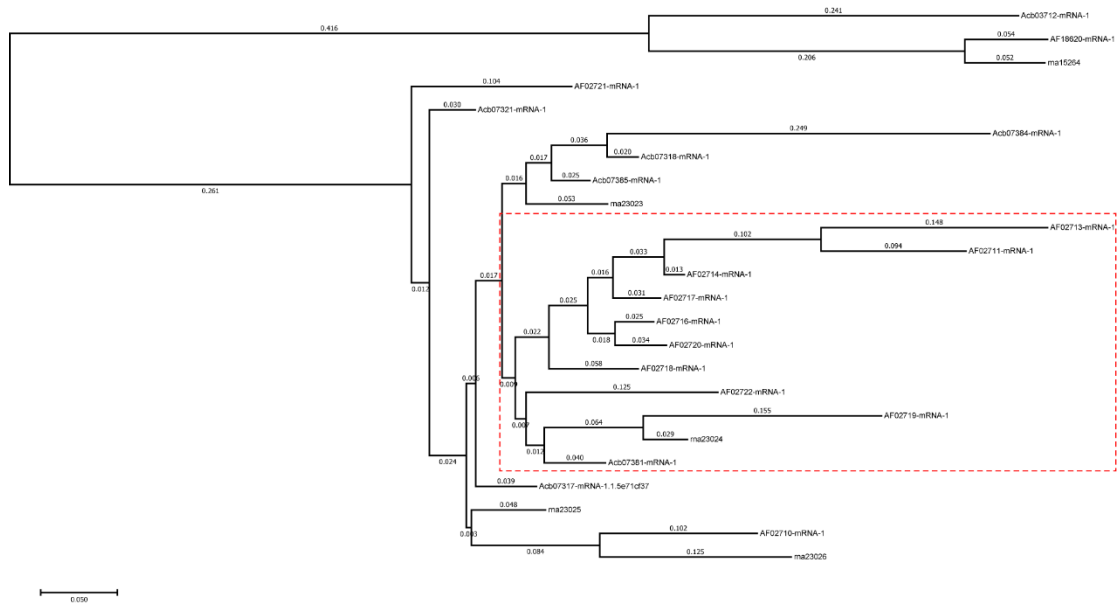
Supplementary Figure 4 Dot plot of synteny alignment between *A. comosus* and the ancestral genome.



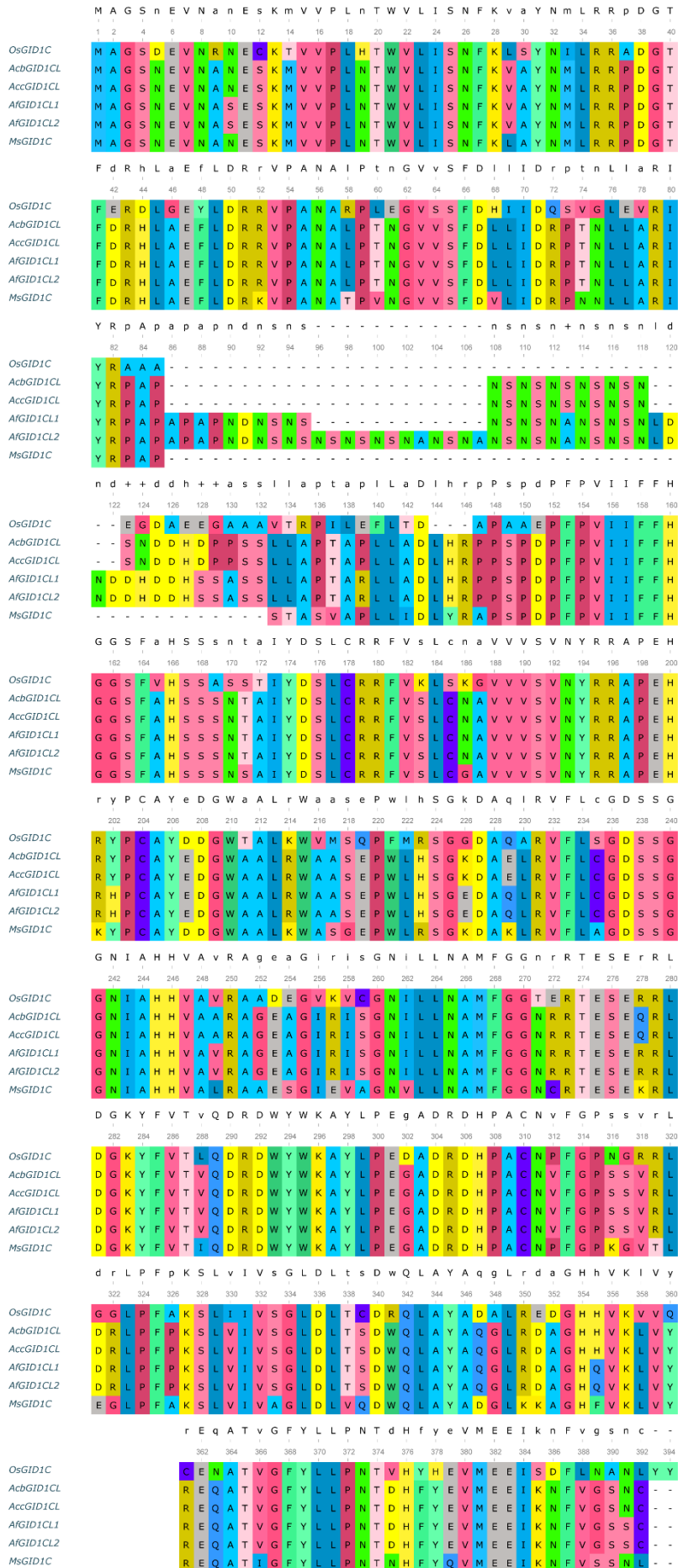
Supplementary Figure 5 Dot plot of synteny alignment between *A. bracteatus* and the ancestral genome.



Supplementary Figure 6 Phylogenetic analysis of *Ricesleeper2* gene families.

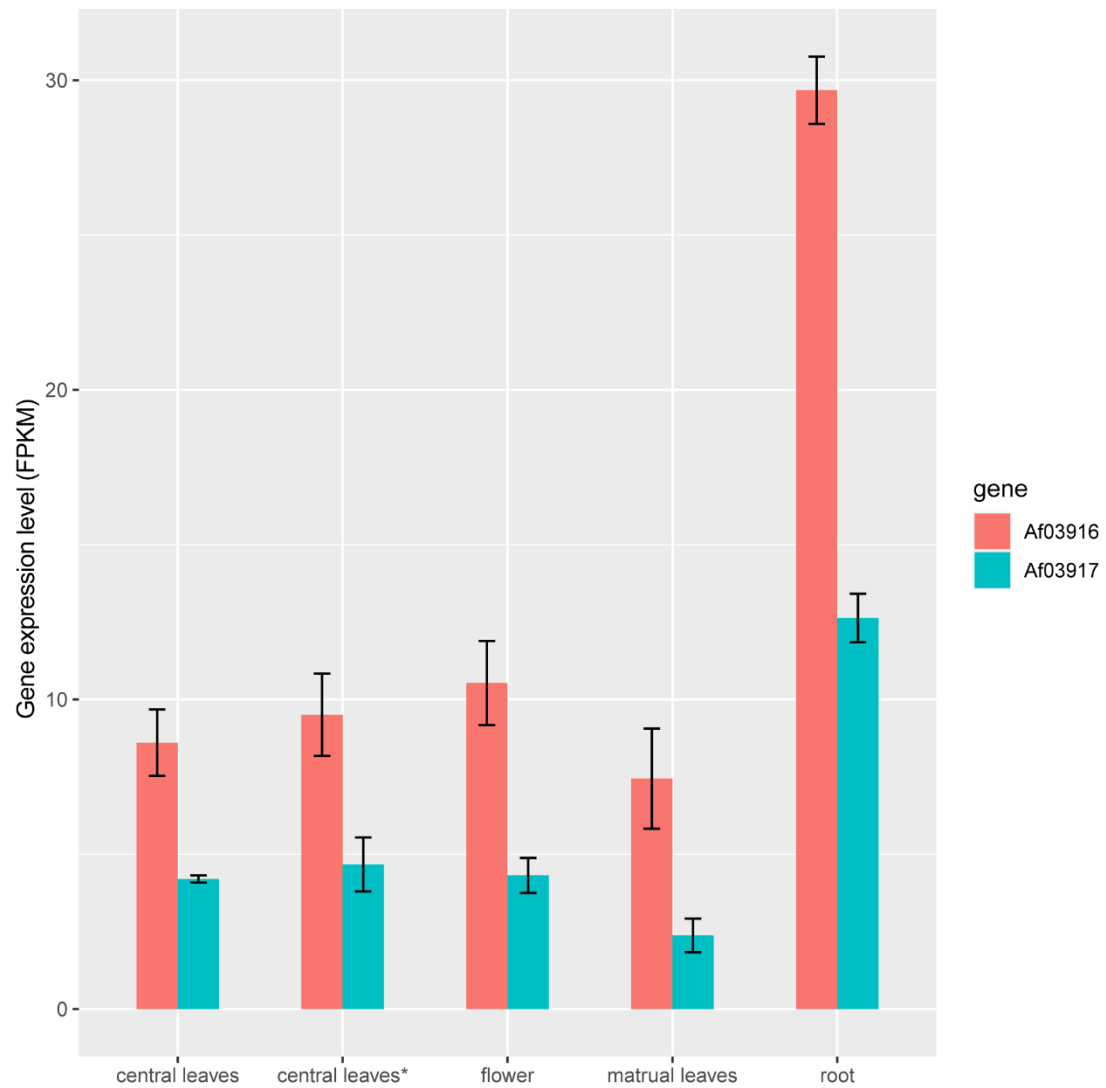


Supplementary Figure 7 Phylogenetic analysis of *TPS10* gene families.





Supplementary Figure 8 Multiple alignment of *GID1C* proteins. Os, *Oryza sativa subsp. Japonica*;  
Ms, *Musa acuminata subsp. malaccensis*; Acb, *A. bracteatus*; Acc, *A. comosus*; Af, *A. fasciata*.



Supplementary Figure 9 Gene expression analysis of two *GID1C*-like genes in *A. fasciata*. Af03916, *AfGID1C-like1*; Af03917, *AfGDI1C-like2*.

**a** GRAS pfam03514 Pssm-ID: 397536 Cd Length: 374 Bit Score: 442.88 E-value: 5.43e-152

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      10      20      30      40      50      60      70      80
gi 1147553370 245 LVHALLACAEAVQRENLAADALLKEISVLAASQGGAMRKVAAYFAEALARRIYN-----LRPPRPDASLFYDLYA 316
Cdd:pfam03514 1 LVHLLLACAEAVSSGDLSLAQATLARLNQLASPAQDPMQRLAAVFTALAAARLARsgssiysaLPPRPTSPDSIERISA 80

      90     100     110     120     130     140     150     160
gi 1147553370 317 H--FYEASPLKFAHFTANQAILEAFACRRVHVVDLGVRRQLWPALLQALALRPGGAPSFRLTAVGPP--ASGDALRE 392
Cdd:pfam03514 81 Yk1FYEVSPYKFGHFTANQAILEAFEGEERVHIIIDFDIGQGLQWPSLIQALASRPGGPHLRITGTIGDPqfSSAEEL 160

      170     180     190     200     210     220     230     240
gi 1147553370 393 VGWKLARFADAVRVDFRYRPLVAASLADLDAYTLQ-RPSaaaaaaaaaeveeeeeeaaeEAVAVNAVLELHQVLAQGA 471
Cdd:pfam03514 161 TGDRLAQFADSLGVVPEFNPLVAKRLEDLDLEMLDvRPG-----EALAVNCVFAHRLHLDSEVSLE 221

      250     260     270     280     290     300     310     320
gi 1147553370 472 K---VLGTVRALRPRVFTVVEQEAHNAGSFRDRFTEALHYYSTVFDLSLEGCSAGSSDR-VMAEAYVGREIANVVGCE 546
Cdd:pfam03514 222 SprdtFLRLVRSLNPKVVTLVEQEAHNHNSAPFLNRFVEALHYYSALFDSLEATLPRDSEERrKVERELLGREIVNVVACE 301

      330     340     350     360     370     380     390
gi 1147553370 547 GPERTERHETLAQWRGRMGAGFHPVPIGSDAFKQASTLLALFsgggGGGFRVEEREGCLTLCWHTRPLIATSAR 622
Cdd:pfam03514 302 GAERVERHETFGKWRERMRRAGFRPVPLSEFAVKAKLLRLYY---VDGYTVEEDNGSLVLGWKGRPLVAASAWR 374

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**b** DELLA pfam12041 Pssm-ID: 403308 Cd Length: 68 Bit Score: 118.26 E-value: 3.76e-32

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      10      20      30      40      50      60      70
gi 1147553370 46 DELLATLGKYVRSSDMADVAQKLEQLDMAMmgsCAAPDDGFLLSq1h1ppSDVHHYVNSDLSSWLDMSISELN 119
Cdd:pfam12041 1 DELLAVLGYKVRSSDMADVAQKLEQLEMVMG--NAQEDGISHLA-----SDTVHHYVNSDLSSWVWESMISELN 65

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**c** GRAS pfam03514 Pssm-ID: 397536 Cd Length: 374 Bit Score: 448.65 E-value: 2.46e-154

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      10      20      30      40      50      60      70      80
Query_9724 239 LVHLLLACAEAVQRENLAADALLKEISVLAASQGGAMRKVAAYFAEALARRIYN-----LHPPRPDASLFYDLYA 310
Cdd:pfam03514 1 LVHLLLACAEAVSSGDLSLAQATLARLNQLASPAQDPMQRLAAVFTALAAARLARsgssiysaLPPRPTSPDSIERISA 80

      90     100     110     120     130     140     150     160
Query_9724 311 H--FYEASPLKFAHFTANQAILEAFACRRVHVVDLGVRRQLWPALLQALALRPGGAPSFRLTAVGPP--ASGDALRE 386
Cdd:pfam03514 81 Yk1FYEVSPYKFGHFTANQAILEAFEGEERVHIIIDFDIGQGLQWPSLIQALASRPGGPHLRITGTIGDPqfSSAEEL 160

      170     180     190     200     210     220     230     240
Query_9724 387 VGWKLARFADAVRVDFRYRPLVAASLADLDAYTLQ-RPSaaaaaeveeeeeeaaeEAVAVNAVLELHQVLAQPGA 462
Cdd:pfam03514 161 TGDRLAQFADSLGVVPEFNPLVAKRLEDLDLEMLDvRPG-----EALAVNCVFAHRLHLDSEVSLEsprd 225

      250     260     270     280     290     300     310     320
Query_9724 463 -VLGTVRALRPRVFTVVEQEAHNAGSFRDRFTEALHYYSTVFDLSLEGCSAGSSDR-VMAEAYVGREIANVVGWEGPER 540
Cdd:pfam03514 226 tFLRLVRSLNPKVVTLVEQEAHNHNSAPFLNRFVEALHYYSALFDSLEATLPRDSEERrKVERELLGREIVNVVACEGAER 305

      330     340     350     360     370     380     390
Query_9724 541 TERHETLAQWRGRMGAGFHPVPIGSDAFKQASTLLALFsgGGGFRVEEREGCLTLCWHTRPLIATSAR 611
Cdd:pfam03514 306 VERHETFGKWRERMRRAGFRPVPLSEFAVKAKLLRLYY---YVDGYTVEEDNGSLVLGWKGRPLVAASAWR 374

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**d** DELLA pfam12041 Pssm-ID: 403308 Cd Length: 68 Bit Score: 118.64 E-value: 3.13e-32

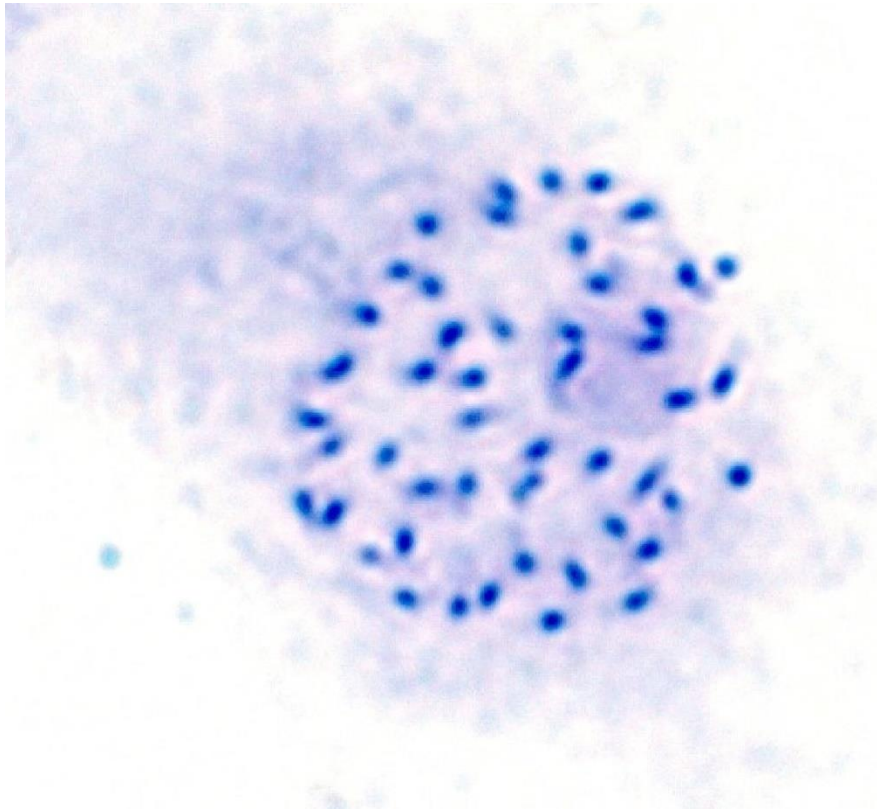
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      10      20      30      40      50      60      70
Query_9724 49 DELLATLGKYVRSSDMADVAQKLEQLDMAMmgsCAAPDDGFLLSq1h1ppSDVHHYVNSDLSSWLDMSISELN 122
Cdd:pfam12041 1 DELLAVLGYKVRSSDMADVAQKLEQLEMVMG--NAQEDGISHLA-----SDTVHHYVNSDLSSWVWESMISELN 65

```

Supplementary Figure 10 Domain analysis of *AcSLR1-like* and *AfSLR1-like* based on searches of the NCBI Conserved Domain Database. a, alignment of *AcSLR1-like* at the GRAS domain; b, alignment of *AcSLR1-like* at the DELLA domain; c, alignment of *AfSLR1-like* at the GRAS domain; d, alignment

of *AfSLR1-like* at the DELLA domain.



Supplementary Figure 11 Root tip chromosome karyotype analysis of *A. fasciata*.

Supplementary Table 1 Summary of genome assembly.

Type	Length (bp)	Count
N10	9050129	6
N20	7538727	12
N30	6962080	19
N40	5533891	28
N50	4689950	38
N60	2670604	53
N70	967756	86
N80	509414	166
N90	213451	329
Min.	45520	–
Max.	11307573	–
Ave.	792203	–
Total	529983447	669

Supplementary Table 2 Summary of protein-coding genes in *A. fasciata*.

Protein coding gene number	26,216
Total length of protein coding gene (bp)	108,991,579
Average length of protein coding gene (bp)	4157
Total exon length (bp)	28,099,890
Average length of exon (bp)	198
Total intron length (bp)	80891689
Average length of intron (bp)	712

Supplementary Table 3 Summary of BUSCO analysis of protein-coding genes from *A. fasciata* geome (93.4%).

397	Complete BUSCOs (C)
348	Complete and single-copy BUSCOs (S)
49	Complete and duplicated BUSCOs (D)
19	Fragmented BUSCOs (F)
9	Missing BUSCOs (M)
425	Total BUSCO groups searched

Supplementary Table 4 Summary of BUSCO analysis of *A. fasciata* geome (98.4%).

418	Complete BUSCOs (C)
410	Complete and single-copy BUSCOs (S)
8	Complete and duplicated BUSCOs (D)
5	Fragmented BUSCOs (F)
2	Missing BUSCOs (M)
425	Total BUSCO groups searched

Supplementary Table 5 Summary of repeat sequences in the *A. fasciata* genome.

		Number	Length (bp)	% of repeats	% of genome
	<b>Repeats total</b>	499787	214719703	100	61.72471
LTR Retrotransposon	Gypsy	18790	83223889	38.75932	23.92408
	Copia	5445	13830252	6.441073	3.975734
	unknown	14837	18093919	8.426762	5.201395
Retrotransposon	LINE	5398	3349713	1.56004	0.9629301
	SINE	4	236	1.099107e-04	6.784208e-05
Unclassified	Unknown	143904	83787245	39.02168	24.08602

retroelement					
DNA transposon	Helitron	174	199246	0.09279353	0.05727654
	Academ-1	1	60	2.794341e-05	1.724799e-05
	MuLE-MuDR	921	1586369	0.7388092	0.4560279
	PIF-Harbinger'	123	100598	0.04685085	0.02891855
	hAT-Tip100	39	49081	0.02285817	0.01410914
	hAT-Tag1	114	249706	0.01162939	0.0717821
<b>TE total</b>		189750	204470314	95.22662	58.77836
	Simple_repeat	310037	10249389	4.773381	2.946356

Supplementary Table 6 ChIP-qPCR analysis of the binding of *AfEIL1-like* to *AfFTL2*.

Primer: 448-1: F, TAACGCACTCTCCCCTCAA; R, TCATTTATTCACGCCCTCTG.										
		CT	AVE.	VOL(ul)	IDF	$\Delta$ CT	$\Delta$ CT (DNA normalized )	%INPUT	$\Delta\Delta$ Ct [ChIP/NIS]	Fold Enrichment
EXP	IN 448-1	22.45	22.33	2	101	7.166666667	13.82487815	0.006891234	-2.05754719	4.16
		22.38								
		22.16								
	IP 448-1 EIN3	29.45	29.49666667	200	51	10.21	15.88242534	0.00165544		
		28.41								
		30.63								
	IgG 448-1		32.54	100	51	10.21	15.88242534	0.00165544		
		32.54								
	IN 448-1	22.45	22.33	2	101	7.166666667	13.82487815	0.006891234		
		22.38								
22.16										

Primer: 448-2:F, TCAAACAAAGAAATACCCCG; R, CCAACGAATCTGACGGCAT.										
		CT	AVE.	VOL(ul)	IDF	$\Delta$ CT	$\Delta$ CT (DNA normalized )	%INPUT	$\Delta\Delta$ Ct [ChIP/NIS]	Fold Enrichment
EXP	IN 448-1	21.96	22.03666667	2	101	6.57	13.22821148	0.010421052	-2.07754719	4.22
		21.99								
		22.16								

IP 448-1 EIN3	28.69	28.60666667	200					
	28.7							
	28.43							
IgG 448-1	32.05	31.67	100	51	9.633333333	15.30575868	0.002468923	
	31.55							
	31.41							
IN 448-1	21.96	22.03666667	2					
	21.99							
	22.16							

