The *Journal of Experimental Botany* Supplementary Data

Article title: Fibre elongation requires normal redox homeostasis modulated by cytosolic ascorbate peroxidase (cAPX) in cotton (*Gossypium. hirsitum*)

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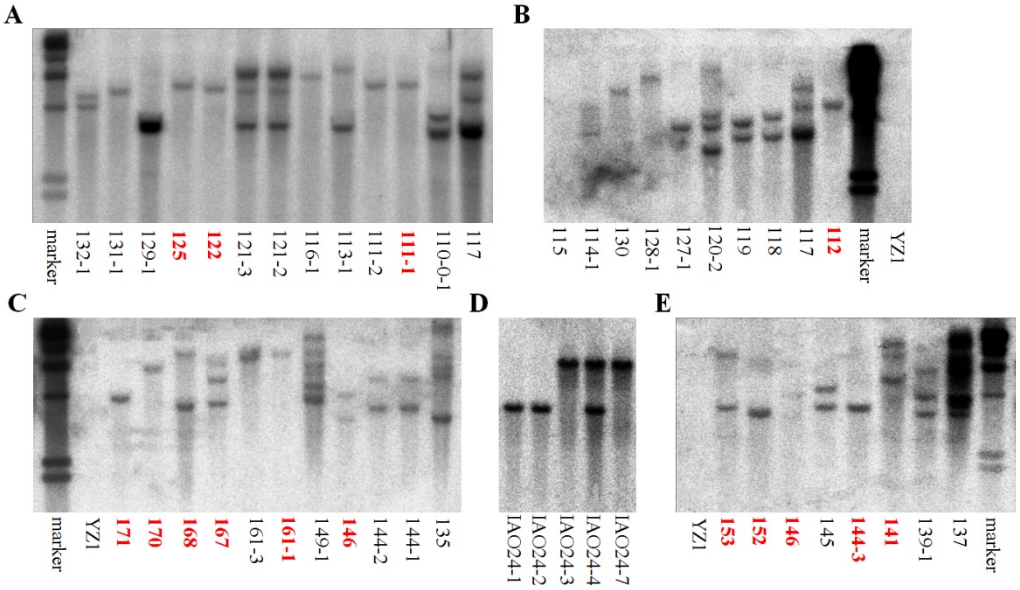
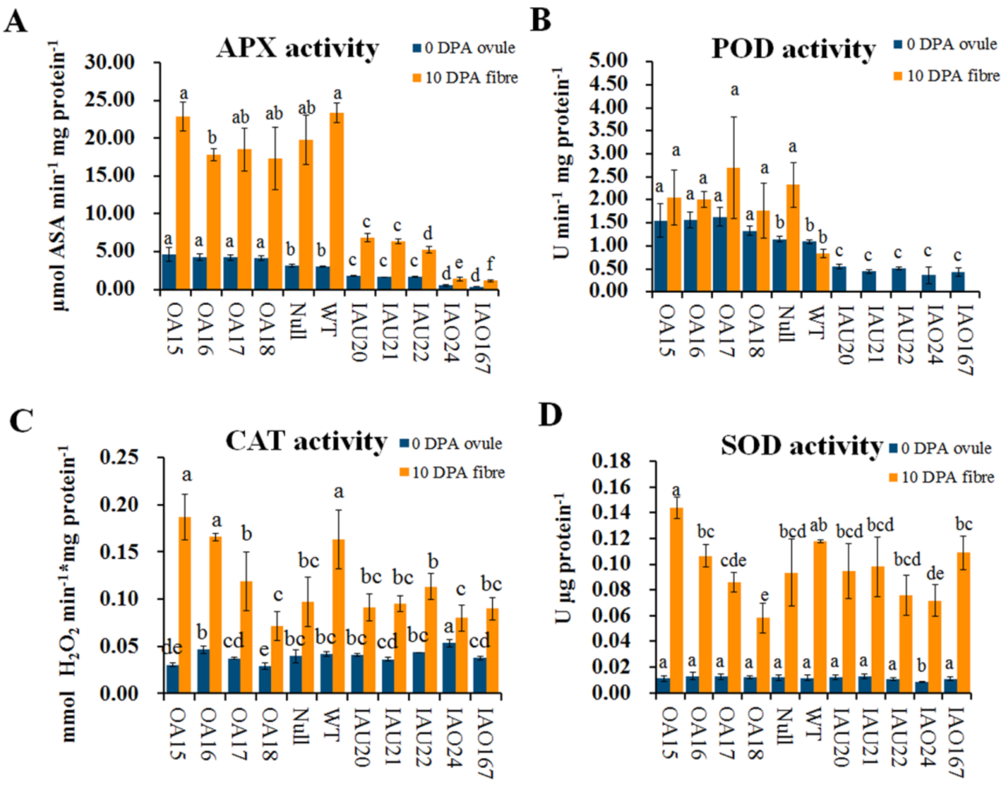
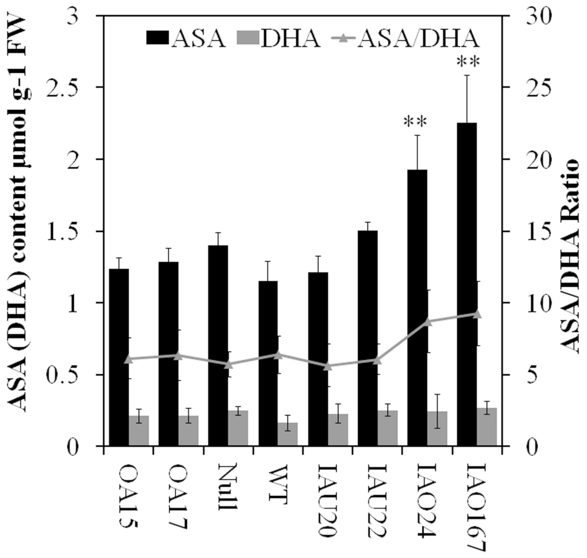


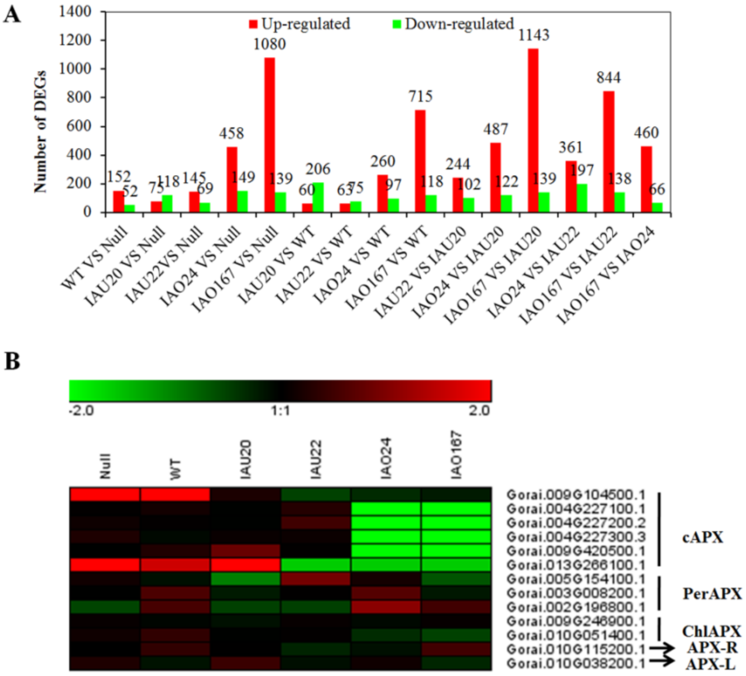
Supplementary Fig. S1. Southern blotting of transgenic plants. (A-B) Southern blotting of 35S over-expression lines. (C) Southern blotting of IAO lines. (D) A single plant from the IAO24 line was analysed by Southern blotting. IAO24-2 and IAO24-3 were different transformants that were separated from the same T0 plant (168/IAO24). (E) Southern blotting of IAU lines. *NPT II* was used as the probe. λ DNA digested with *Hind*III was used as the marker.



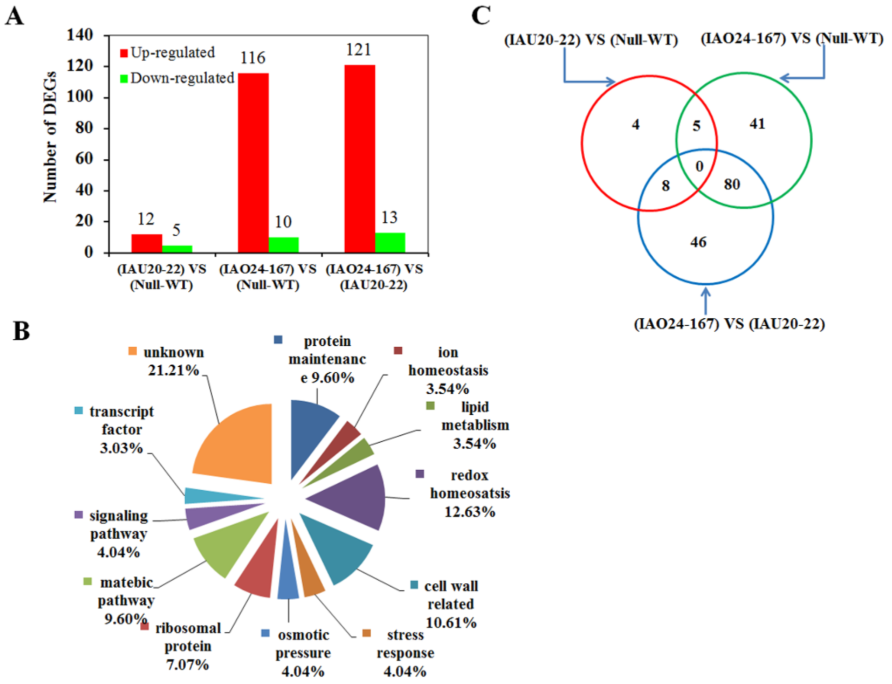
Supplementary Fig. S2. The activities of four types of enzymes were detected in 0 DPA ovules and 10 DPA fibres of the transgenic lines. (A), APX (ascorbate peroxidase) enzyme activity. (B), POD (type III peroxidase) enzyme activity. (C), CAT (catalase) enzyme activity. (D), SOD (superoxide dismutase) enzyme activity. Values with different letters (a, b, c d and e) above the bars in the histogram indicate significant differences at one development stage. (Mean ± se, n=3) (Duncan's multiple comparisons, *P* < 0.05).



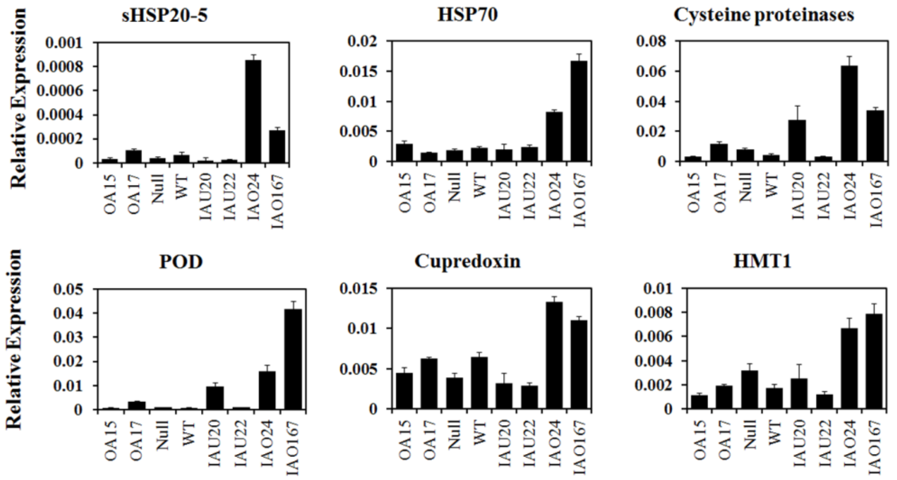
Supplementary Fig. S3. ASA (ascorbic acid) and DHA (dehydroascorbic acid) content in transgenic lines in 5 DPA fibres. *Indicates that the variance was very significant at *P* < 0.01 (**) compared with the null control. (mean ± sd, n=4), (Student's *t* test).



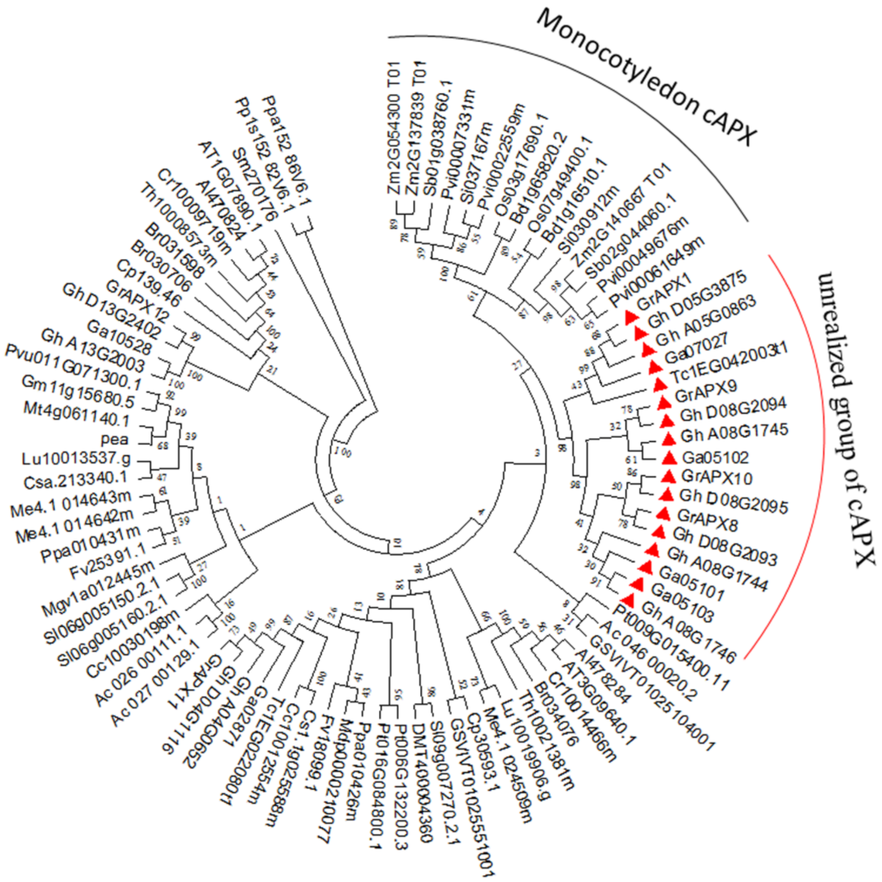
Supplementary Fig. S4. DEGs (Differentially Expressed Genes) between each two samples. (A) The number of DEG was compared between two samples. The filtering criteria were log2 ⩾ 1 and RPKM ⩾ 0.1. (B) Expression profiles of the APX family members in six samples.



Supplementary Fig. S5. DEGs (Differentially Expressed Genes) compared across groups. (A) Numbers of DEGs in the group comparison. (B) Gene cluster analysis. (C) The distribution of DEGs across three groups. Null and WT made up the Null-WT control group. IAU20 and IAU22 made up the IAU group. IAO24 and IAO167 made up the IAO group.



Supplementary Fig. S6. RT-qPCR of protein maintenance and oxidative stress-related DEGs (Differentially Expressed Genes) in 10 DPA fibres of transgenic lines. Relative expression levels were normalised against the expression of the cotton *GhUB7* gene.



Supplementary Fig. S7. Phylogenetic analysis of cytosolic APX from bryophytes, lichens, monocots and dicots. The tree was constructed using the neighbour-joining method with pairwise deletion. Amino acid sequences were used to calculate molecular distances. The red triangles indicate the unrealised group of the cytosolic APXs from dicots. All protein sequences were downloaded from Phytozome 9.1 (http://www.phytozome.net/cotton.php). A phylogenetic tree was constructed with MEGA 5.1. Molecular distances were calculated using the p-distance parameter. The phylogeny test employed the bootstrap method with 1000 replications.

Supplementary Table S1. List of primers used in this study.

primer name	primer sequence	used for
GhAPX1$\mathrm{A_T}$ORFsens	ATGACCAAGTGTTACCCAACTGTG	RT-PCR/Northern
GhAPX1$\mathrm{A_T}$ORFanti	TTATGCATCAGCAAATCCTAGCTC	
GhAPX$\mathrm{A_T}$ORF-anti	GGGGACCACTTTGTACAAGAAAGCTGGGTcTTATGCATCAGCAAATCCTAGCTC	35s-GhAPX1/ORF-RNAi
GhAPX$\mathrm{A_T}$ORF-sens	GGGGACAAGTTTGTACAAAAAAGCAGGCTtgATGACCAAGTGTTACCCAACTGTG	35s-GhAPX1/ORF-RNAi
GhAPX1$\mathrm{A_T}$-3UTR-sens	GGGGACAAGTTTGTACAAAAAAGCAGGCTtgGCTGATGGTTGCGGAATAG	3'UTR-RNAi
GhAPX1$\mathrm{A_T}$-3UTR-anti	GGGGACCACTTTGTACAAGAAAGCTGGGTcCAAACTCAATTCAACATGTTCAAC	
GhAPX1$\mathrm{A_T}$3GSP1	ATGACCAAGTGTTACCCAACTGTGAGCG	5'RACE
GhAPX1$\mathrm{A_T}$3GSP2	GCTTGCTGGTGTCGTTGCCGTTGA	
GhAPX1$\mathrm{A_T}$5GSP1	AGAAGGCATCCTCATCGGCAGCATA	3'RACE
GhAPX1$\mathrm{A_T}$5GSP2	CTCCTTGTGGCACCTTCCCAGAGTG	
GhAPX1$\mathrm{A_T}$/$\mathrm{D_T}$-RT-S2	GCCGTTGAGATTACTGGTGGA	realtime PCR
GhAPX1$\mathrm{A_T}$/$\mathrm{D_T}$-RT-AS2	GACCCATTTGAGCACTAAACACC	
GhUB7S	GAAGGCATTCCACCTGACCAAC	realtime PCR
GhUB7AS	CTTGACCTTCTTCTTCTTGTGCTTG	
18S RNAS	GCTCGTAGTTGGACTTAGGGTGGGT	Northern
18S RNAAS	GGTCGGCATCGTTTATGGTTG	
Gorai.004G227100.1RTS1	CGTGGCTTTCCTATCTTCATTTC	realtime PCR
Gorai.004G227100.1RTAs2	TCCTCGCTAACGGTTGGGTAA	
Gorai.004G227300.3RTS2	GCCAACGACACACAGATGTTTTAG	realtime PCR
Gorai.004G227300.3RTAS2	AACGGATAACAAGTTTCAACACAA	
CTLS	CTTCTACACCAAGATTCCCCCTAT	realtime PCR
CTLAS	CCAATGGCTTCACTGATTCCTG	
CMLS	AACAAGGGAAGAACAACAACGAA	realtime PCR
CMLAS	TCTTCAAACTCTCGGCTGTTATCA	
PMEI-S	TTCAGAAACACCGCTGGTCCTAC	realtime PCR
PMEI-AS	CGGTCCCGTAGATGTCACATTCT	
FLA11-S	GATAAGGTGCTTTTGCCGTTGGA	realtime PCR
FLA11-AS	AATCAAAATCCCCCCAAAATAGCC	
TBL33-S	AAGCTCGACTCTCTCCTTACCTCT	realtime PCR
TBL33-AS	ATCCTTCTTCGCCCTTCCCTAT	
TBL-S	GCCGAGCTATCTCTAGACCAGTGA	realtime PCR
TBL-AS	GATTCTTCATACAGCGGACGACTC	
HMT1-S	TTTGAGACGAAAGATGGGAGTAGA	realtime PCR
HMT1-AS	ACCTTACGAGCACAACCTTCACA	
PHI9-S	CTACAACAATGGTGGTGAAGGTG	realtime PCR
PHI9-AS	TTTAAGCAAATCAACAGGGACAG	
FRO-S	TGACTCCTGATGGACCTCAAGAAT	realtime PCR
FRO-AS	AACACCAGCACAGGTAGAGCAAG	

Cupredoxin-S	TCACTGTGCGAATGGAATGAAAC	realtime PCR
Cupredoxin-AS	ACAACAGCCATAAATGGGGAGAG	
POD-S	GTTGGGTAATCCTAAAATGGGTTC	realtime PCR
POD-AS	ATAGCAGAGGTGACAGTGGATTTC	
SHSP1-S	ATTACCCAGACAAGCAAAGCAGA	realtime PCR
SHSP1-AS	ACGTCAAGAGAGAATGGATCAAAG	
SHSP2-S	GGCAACAGACGCAGCAACAAC	realtime PCR
SHSP2-AS	GTTTCCCTCCAGTCAATCCGA	
SHSP3-S	ACATTGTTCAGTCGGGTGGTATT	realtime PCR
SHSP3-AS	GCATCACCATTTCATCATACTTCA	
SHSP4-S	ATCATTGTTTCGGTTGGGTAAGC	realtime PCR
SHSP4-AS	TTTCTGGGGAGCCTGTCGTCA	
SHSP5-S	GCACTGGCTCGTTTGGTTTTG	realtime PCR
SHSP5-AS	CCATTCCACCTCTGCCTTTGC	
SHSP6S	ACCTGAACCTAAGAAGCCCAAGA	realtime PCR
SHSP6AS	AACTCACACAACCAGAATGAAACAC	
HSP70-S	TCCCGCAAATCACCGTGTGTT	realtime PCR
HSP70-AS	TTTCGCCTCAACTTTCTTCTTATGT	
Cysteine proteinases-S	AATGCCGTGTTATCAGTTGTGGT	realtime PCR
Cysteine proteinases-AS	AAGGCTTGTTGTCATTGTTGGTG	
DRL1-S	CTACTTTGATGACTGATGCCTTTG	realtime PCR
DRL1-AS	ATTACAGTCTCATACGGTGCTTCTT	
TP1-S	ATGCTCAGCCACCTGCTCTTACT	realtime PCR
TP1-AS	AAGGAGCGGTGGGTCAGTGTT	
LEA5-S	CGTCGGAGACAAGGGCTTATTC	realtime PCR
LEA5-AS	GCGGTGGCAAGTTTCTACTGTG	
MTN3-S	ACAACAAGGTCCAATTAGAGCAAT	realtime PCR
MTN3-AS	ACTTGTGAGTTGCTAATCATCCCT	
OS34-S	CAGTGCCCTAATCAGTTGAAAGC	realtime PCR
OS34-AS	AGAACCTGGACAAATCCGTTGG	
SAM-S	AGATTTCACTTGGGAGGTTGTCA	realtime PCR
SAM-AS	TTCTCATTGCTATTTCATTCATTACC	
ACO-S	CATTGCTTCCTTCTACAACCCG	realtime PCR
ACO-AS	GCCAGCATAGAGCTTCATGTAGTC	
BZIP44-S	ATCTTTCTCAGTTGTCTTCCTCCAC	realtime PCR
BZIP44-AS	TCTTCTTGCTGATTCCCTGTTTG	
PAR1-S	TGCGAAGATTTGCCCAACGAT	realtime PCR
PAR1-AS	AAGAAGGGAATCGGATGAAATGC	
YABBY-S	AGCAAGGAGTAGAGTTACGGGAATA	realtime PCR
YABBY-AS	GTTATAGCAACCATACCACAAGCG	
FLA7-S	ATCCGAAGAAACTGGTTCCTCAT	realtime PCR
FLA7-AS	CCATCCACCTAAGAATGCCAA	
HPRG1-S	TAGCATTCGTCACCCTTTCTTCC	realtime PCR
HPRG1-AS	GCATTTCAGGCTTCTCAAGTTTT	

Supplementary Table S2. Lists of total reads mapped to *Gossypium raimondii* genes and genome.

The list of total reads mapped to *G. raimondii* Gene

Sample ID	Null	WT	IAU20	IAU22	IAO24	IAO167
Total Reads	12434248(100%)	11719314(100%)	12329128(100%)	12200881(100%)	12435938(100%)	12377822(100%)
Total BasePairs	609278152(100%)	574246386(100%)	604127272(100%)	597843169(100%)	609360962(100%)	606513278(100%)
Total Mapped Reads	10419035(83.79%)	9722960(82.97%)	10209530(82.81%)	10142320(83.13%)	10196148(81.99%)	10099130(81.59%)
perfect match	6017861(48.4%)	5554469(47.4%)	5890185(47.77%)	5828836(47.77%)	5869132(47.19%)	5831075(47.11%)
<=2bp mismatch	4401174(35.4%)	4168491(35.57%)	4319345(35.03%)	4313484(35.35%)	4327016(34.79%)	4268055(34.48%)
unique match	10003362(80.45%)	9342655(79.72%)	9816695(79.62%)	9741754(79.84%)	9778887(78.63%)	9685212(78.25%)
multi-position match	415673(3.34%)	380305(3.25%)	392835(3.19%)	400566(3.28%)	417261(3.36%)	413918(3.34%)
Total Unmapped Reads	2015213(16.21%)	1996354(17.03%)	2119598(17.19%)	2058561(16.87%)	2239790(18.01%)	2278692(18.41%)

The list of total reads mapped to *G. raimondii* Genome

Sample ID	Null	WT	IAU20	IAU22	IAO24	IAO167
Total Reads	12434248(100%)	11719314(100%)	12329128(100%)	12200881(100%)	12435938(100%)	12377822(100%)
Total BasePairs	609278152(100%)	574246386(100%)	604127272(100%)	597843169(100%)	609360962(100%)	606513278(100%)
Total Mapped Reads	10033456(80.69%)	9443822(80.58%)	9999095(81.1%)	9850187(80.73%)	10088288(81.12%)	9990549(80.71%)
perfect match	5557554(44.7%)	5193656(44.32%)	5578388(45.25%)	5462316(44.77%)	5660773(45.52%)	5620196(45.41%)
<=3bp mismatch	4475902(36%)	4250166(36.27%)	4420707(35.86%)	4387871(35.96%)	4427515(35.6%)	4370353(35.31%)
unique match	9254531(74.43%)	8700741(74.24%)	9192172(74.56%)	9081140(74.43%)	9075324(72.98%)	9043704(73.06%)
multi-position match	778925(6.26%)	743081(6.34%)	806923(6.54%)	769047(6.3%)	1012964(8.15%)	946845(7.65%)
Total Unmapped Reads	2400792(19.31%)	2275492(19.42%)	2330033(18.9%)	2350694(19.27%)	2347650(18.88%)	2387273(19.29%)

Supplementary Table S3. RPKM vaules of APXs in different fibre stages of *G. hirsutum* TM-1.

	GeneID	Root	Stem	Leaf	Petal	Anther	Stigma	Ovule 0 DPA	Fiber 10 DPA	Fiber 20 DPA	Ovule 10 DPA	Ovule 20 DPA
cAPX	Gh_A05G0863	224.13	404.83	261.51	94.50	86.86	279.83	119.64	833.48	66.35	214.00	165.58
	Gh_D05G3875	257.64	281.18	237.57	70.68	52.46	234.30	84.25	432.22	72.16	170.20	167.05
	Gh_A08G1744	40.03	57.03	47.38	7.32	5.38	63.03	55.21	40.38	13.35	51.99	56.49
	Gh_D08G2093	78.96	195.81	96.24	19.08	14.32	74.00	37.47	9.53	16.01	45.62	33.84
	Gh_A08G1745	2.32	1.51	2.60	0.00	0.20	1.62	4.39	0.42	1.42	2.99	1.81
	Gh_D08G2094	4.48	1.80	2.71	0.48	1.58	5.09	9.12	3.52	2.15	6.39	5.05
	Gh_A08G1746	81.40	88.66	79.05	22.48	69.58	93.89	83.60	111.66	32.54	126.08	56.72
	Gh_D08G2095	34.37	40.89	34.92	10.60	8.87	34.25	25.36	27.39	14.32	42.34	27.21
	Gh_A04G0652	0.93	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	Gh_D04G1116	0.12	0.00	0.17	0.00	0.40	0.00	0.00	0.00	0.26	0.00	0.09
	Gh_A13G2003	0.00	1.10	0.65	0.15	13.82	0.00	0.06	0.31	6.94	0.53	0.51
	Gh_D13G2402	0.00	0.16	0.33	0.00	11.59	0.00	0.13	0.00	0.00	0.54	0.00
perAPX	Gh_A02G1648	10.61	3.93	4.95	12.37	0.91	3.42	1.16	0.51	2.95	2.11	1.10
	Gh_D03G0074	4.63	2.02	2.73	6.83	0.61	2.07	0.60	0.44	1.08	1.40	0.20
	Gh_A01G1388	0.38	0.40	0.55	0.26	1.61	0.13	0.16	0.40	0.00	0.15	0.22
	Gh_D01G1632	1.34	0.13	0.55	0.91	2.42	1.04	2.56	0.07	0.00	1.79	0.00
	Gh_A03G1812	35.18	41.98	36.48	9.23	17.72	16.45	26.10	17.45	29.84	26.53	24.69
	Gh_D02G2245	25.52	17.44	29.85	7.54	13.85	11.53	25.09	12.62	17.36	16.69	20.04
tAPX	Gh_A06G0383	1.65	0.75	3.77	1.99	0.45	2.53	1.20	1.09	0.37	1.04	0.26
	Gh_D06G0413	0.60	0.88	1.88	2.59	0.10	2.29	1.46	0.84	0.50	1.41	0.43
sAPX	Gh_A05G3726	29.19	35.22	44.31	7.85	10.13	45.48	27.00	41.48	39.33	35.35	17.75
	Gh_D05G2244	23.01	25.59	30.28	6.63	4.73	29.88	22.40	50.03	24.32	37.02	14.28
APX-R	Gh_A06G2046	5.88	1.78	15.00	4.81	1.14	5.71	2.98	1.54	0.83	1.58	2.64
	Gh_D06G1049	0.80	1.01	2.07	0.54	0.27	0.65	1.34	5.49	0.35	0.37	0.55
APX-L	Gh_A06G0270	11.28	0.31	8.16	2.42	0.50	5.02	5.96	1.31	0.98	5.21	2.55
	Gh_D06G0293	9.30	0.21	9.69	2.83	0.63	3.83	6.10	1.10	0.98	3.60	5.23

cAPX, cytosolic APX; perAPX, peroxisomal APX; tAPX, thylakoid APX; sAPX, chloroplast stromal APX; APX-R, APX-R type of APX; APX-L, APX-L type of APX. GeneID indicated the gene ID number in the database *G. hirsutum* TM-1 (PRJNA248163)

Supplementary Table S4. List of all transgenic lines in different generations.

Construct [a]	T0 NO.	T0 leaf [b]	T0 10 DPA fibre [b]	Inserted copies	Seed (T0) [c]	T1/2/3 NO. [d]
35S::GhAPX1(OA) 19/24	110	0.107	0.015	2	Y	
	111-1	0.88	1.326	1	Y	OA15
	111-2	0.69		1	Y	
	111-3	0.553			Y	
	111-4					
	112	0.863	0.992	1	Y	OA16
	113-1	1.067	1.143	2	Y	
	113-2	0.847			Y	
	114-1			2		
	114-2	0.493				
	115					
	116-1	1.026				
	116-2			1		
	116-3	0.863	0.93		Y	
	117			3		
	118	0.676		2	Y	
	119	0.898		2	Y	
	120-2	0.867	0.728	3	Y	
	121-1	0.837			Y	
	121-2	0.163		3		
	121-3	0.648	0.398	3	Y	
	122	1.176	0.842	1	Y	OA17
	123	0.074	0.01		Y	
	124					
	125	0.738	0.916	1	Y	OA18
	126-1					
	126-2					
	127-1	0.575	1.077	1	Y	
	128-1	1.653	0.899	1	Y	
	128-3	2.034	0.782		Y	
	129-1	0.033		1	Y	
	129-2	2.191	1.024		Y	
	130		0.995	1	Y	
	131-1	0.832	0.871	1	Y	
	131-2				Y	
	132-1	1.836		2		
	132-2	1.437				
	133					
GhAPX1UTRi(IAU) 10/22	135			5	Y	
	136					
	137			6	Y	
	138					
	139-1		0.001	3 or 4	Y	
	139-4		0.002		Y	
	139-5		0.002		Y	
	140					
	141		0.611	2	Y	IAU19

	142				
	143				
	144-1	0.006	2	Y	
	144-2	0.002	2	Y	
	144-3	0.003	1?	Y	IAU20
	145	0.986	2	Y	
	146	0.01	2	Y	IAU21
	147-1				
	148-1				
	149-1	0.007	6	Y	
	150				
	151				
	152	0.003	1 or 2	Y	IAU22
	153	0.004	2	Y	IAU153
	154-1				
	155				
	156-1				
GhAPX1ORFi（IAO）5/13	160-1				
	161-1	1.062	1	Y	IAO23
	161-3	1.013	1	Y	
	162				
	163				
	164				
	165-1				
	166-1				
	167		3	Y	IAO167
	168		2	Y	IAO24
	169-1				
	170	0.012	1	Y	IAO25
	171	0.755	1	Y	IAO26
	172				

“a” 35S::GhAPX1 (OA) indicates overexpression of the *GhAPX1* construct; GhAPX1UTRi (IAU) indicates specific interference of the *GhAPX1* construct; GhAPX1ORFi（IAO）indicates suppression of the cytosolic APX construct. The ratio indicates the proportion of transgenic lines with setting seeds compared with all transgenic lines for one construct.

“b” Relative expression level of $GhAPX1A_{T}/D_{T}$ in the transgenic lines compared with WT by RT-qPCR.

“c” “Y” indicates the line used to collect seeds.

“d” Lines selected for further analysis of the T1/2/3 generation.

Supplementary Table S5. Fibre quality analysis with a HVI (High Volume Instrument) harvested from T3 plants grown in fields (2013).

2013 (T3)	UHML (mm)	UI (%)	Mic	Str (g/tex)	Elg (%)	MR	SFI
OA15	27.18±0.29bc	85.93±0.64a	5.81±0.09b	27.03±0.91a	6.65±0.06a	0.86±0.006ab	7.03±0.26c
OA16	26.41±0.22de	84.65±0.35abc	5.96±0.06b	25.40±0.28bc	6.60±0.00ab	0.86±0.007ab	7.65±0.21bc
OA17	26.77±0.22cd	84.45±0.76abc	6.31±0.10a	26.08±1.00ab	6.65±0.06a	0.86±0.005a	7.80±0.50bc
OA18	25.94±0.47ef	84.45±1.17abc	5.00±0.13d	23.93±1.60de	6.35±0.06c	0.83±0.006d	7.88±0.84abc
NG	27.91±0.54b	85.30±0.77ab	5.33±0.01c	25.65±0.76abc	6.60±0.00ab	0.84±0.005c	7.23±0.34c
WT	27.59±0.48b	85.00±1.01ab	5.37±0.10c	25.05±0.6bcd	6.53±0.05ab	0.84±0.000c	7.43±0.43bc
IAU20	28.52±0.16a	85.18±0.64ab	5.36±0.23c	26.40±0.74ab	6.60±0.00ab	0.85±0.005bc	7.25±0.26c
IAU21	26.16±0.21def	84.65±0.92abc	5.03±0.04d	22.00±0.28f	6.35±0.07c	0.82±0.000d	7.75±0.64bc
IAU22	28.42±0.37a	84.80±1.07abc	5.54±0.03c	25.68±0.55abc	6.63±0.05ab	0.85±0.005bc	7.40±0.43bc
IAO24	**25.63±0.99f**	**83.27±0.93bc**	**4.94±0.40d**	**23.57±0.25e**	**6.27±0.23c**	**0.82±0.012d**	**8.80±0.89a**
IAO167	**27.17±0.08bc**	**83.65±2.05c**	**4.70±0.04e**	**24.20±0.28cde**	**6.50±0.14b**	**0.82±0.000d**	**8.35±1.34ab**

Mature fibres were harvested from experimental fields at Huazhong Agricultural University, Wuhan, Hubei province on one experiment plot in 2013 (mean ± sd, n=3). Three samples were collected from each line for the fibre quality measurements. UHML, Upper Half Mean Length refers to the mean length of the top half of the fibres; UI, uniformity index; Mic, Micronaire; Str, Strength; Elg, Elongation; MR, maturity ratio; SFI, short fibre index. Values with different letters (a, b, c, d, e and f) indicate significant differences (Duncan's multiple comparisons. $P < 0.05$) in one fibre quality index.

Supplementary Table S6. List of DEGs (Differentially Expressed Genes) screened by group comparison of the transgenic lines.

Gene ID	log2Ratio((IAU20-22)/(Null-WT))	Probability	log2Ratio((IAO24-167)/(Null-WT))	Probability	log2Ratio((IA024-167)/(IAU20-22))	Probability	Transcript Annotation
HSP							
Gorai.011G254900	-1.37	0.64	1.75	0.81	3.12	0.88	Kunitz family trypsin and protease inhibitor protein
Gorai.011G254400	-1.56	0.54	1.71	0.75	3.27	0.83	Kunitz family trypsin and protease inhibitor protein
Gorai.006G036600	-4.07	0.33	4.86	0.91	8.93	0.92	HSP20-like chaperones superfamily protein
Gorai.001G110000	0.22	0.12	3.42	0.82	3.21	0.80	HSP20-like chaperones superfamily protein
Gorai.009G131100	0.22	0.27	1.81	0.83	1.59	0.81	HSP20-like chaperones superfamily protein
Gorai.001G114100	0.26	0.48	1.64	0.87	1.38	0.85	HSP20-like chaperones superfamily protein
Gorai.005G043700	-0.16	0.39	1.47	0.86	1.63	0.87	HSP20-like chaperones superfamily protein
Gorai.013G139100	-0.28	0.50	1.33	0.84	1.61	0.87	HSP20-like chaperones superfamily protein
Gorai.004G006500	0.20	0.43	1.31	0.85	1.10	0.83	HSP20-like chaperones superfamily protein
Gorai.009G095100	0.13	0.32	1.20	0.83	1.07	0.82	HSP20-like chaperones superfamily protein
Gorai.001G114300	0.15	0.32	1.05	0.80	0.90	0.76	HSP20-like chaperones superfamily protein
Gorai.005G070000	-0.30	0.49	1.04	0.80	1.34	0.83	HSP20-like chaperones superfamily protein
Gorai.011G256600	-0.45	0.44	1.35	0.79	1.81	0.82	heat shock cognate protein 70-1
Gorai.003G073700	-0.38	0.47	1.01	0.77	1.39	0.81	F-box family protein
Gorai.009G064800	5.17	0.95	0.89	0.28	-4.29	0.93	Eukaryotic aspartyl protease family protein
Gorai.008G203800	-0.24	0.38	1.58	0.85	1.81	0.86	Cysteine proteinases superfamily protein
Gorai.009G453600	0.04	0.10	1.72	0.81	1.68	0.80	Chaperone DnaJ-domain superfamily protein
Gorai.009G042000	-0.09	0.23	1.54	0.86	1.64	0.87	17.6 kDa class II heat shock protein
Gorai.010G097900	-0.23	0.46	1.33	0.85	1.56	0.85	17.6 kDa class II heat shock protein
ion homeostasis							
Gorai.002G026400	0.20	0.34	1.36	0.82	1.16	0.80	proton gradient regulation 5
Gorai.013G258500	-0.63	0.66	1.00	0.78	1.62	0.85	histidine-containing phosphotransmitter 3
Gorai.012G001300	-0.11	0.16	2.56	0.87	2.66	0.88	Heavy metal transport/detoxification superfamily protein

Gorai.010G249000	0.12	0.25	1.19	0.81	1.07	0.79	Heavy metal transport/detoxification superfamily protein
Gorai.002G219600	-0.79	0.68	1.17	0.81	1.96	0.86	Heavy metal transport/detoxification superfamily protein
Gorai.007G372700	-0.54	0.55	1.55	0.83	2.10	0.86	gamma tonoplast intrinsic protein
Gorai.008G082300	2.02	0.69	2.83	0.81	0.82	0.58	electron carriers
lipid metablism							
Gorai.003G093900	0.83	0.64	1.99	0.85	1.15	0.78	Plant stearoyl-acyl-carrier-protein desaturase family protein
Gorai.005G038900	-0.28	0.54	0.86	0.78	1.15	0.83	lipid transfer protein 1
Gorai.002G183100	0.64	0.61	1.81	0.85	1.17	0.79	glycosylphosphatidylinositol-anchored lipid protein transfer 1
Gorai.010G240200	1.05	0.80	1.36	0.84	0.31	0.53	GDSL-like Lipase/Acylhydrolase superfamily protein
Gorai.010G002300	-0.73	0.54	4.03	0.96	4.76	0.97	GDSL-like Lipase/Acylhydrolase superfamily protein
Gorai.002G090200	-0.33	0.32	1.68	0.81	2.01	0.83	GDSL-like Lipase/Acylhydrolase superfamily protein
Gorai.010G202800	1.52	0.79	2.07	0.85	0.55	0.60	3-ketoacyl-CoA synthase 19
Redox homeostasis							
Gorai.002G064200	1.48	0.77	2.20	0.85	0.72	0.67	Ycf1 protein
Gorai.004G219800	0.43	0.52	1.55	0.83	1.12	0.79	Ycf1 protein
Gorai.011G078900	0.41	0.48	1.40	0.81	1.00	0.75	Ycf1 protein
Gorai.010G119900	0.65	0.67	1.36	0.83	0.70	0.70	Ycf1 protein
Gorai.008G073700	0.72	0.70	1.14	0.80	0.42	0.58	Ycf1 protein
Gorai.012G032000	0.42	0.62	1.44	0.85	1.02	0.82	0
Gorai.012G162900	0.49	0.48	1.61	0.81	1.12	0.76	squalene epoxidase 2
Gorai.011G020200	-0.01	0.08	2.00	0.86	2.01	0.86	Quinone reductase family protein
Gorai.004G150600	0.36	0.49	1.25	0.81	0.89	0.74	photosynthetic electron transfer D
Gorai.012G016200	1.45	0.67	3.76	0.93	2.32	0.86	Peroxidase superfamily protein
Gorai.010G001900	-1.27	0.35	2.62	0.78	3.89	0.83	Peroxidase superfamily protein
Gorai.009G192200	-1.00	0.53	1.49	0.76	2.49	0.82	Peroxidase superfamily protein
Gorai.001G163400	-0.21	0.43	0.84	0.77	1.04	0.82	NADH dehydrogenase 5B
Gorai.007G322600	-0.38	0.54	0.90	0.77	1.28	0.82	metallothionein 3
Gorai.007G175100	0.03	0.12	1.19	0.83	1.16	0.82	glutathione S-transferase PHI 9
Gorai.009G087600	-0.22	0.32	1.29	0.80	1.51	0.81	cytochrome-c oxidases;electron carriers

Gorai.008G030000	-0.07	0.15	-2.22	0.82	-2.15	0.81	cytochrome BC1 synthesis
Gorai.008G125300	-0.83	0.61	1.03	0.74	1.86	0.82	Cytochrome b561/ferric reductase transmembrane with
Gorai.009G233600	0.27	0.22	3.14	0.89	2.87	0.88	Cupredoxin superfamily protein
Gorai.009G280000	-0.32	0.25	1.87	0.79	2.20	0.80	Cupredoxin superfamily protein
Gorai.004G227300	-0.01	0.09	-5.58	0.98	-5.57	0.98	ascorbate peroxidase 2
Gorai.009G104500	-7.97	1.00	-8.15	1.00	-0.17	0.19	ascorbate peroxidase 1
Gorai.004G227200	0.19	0.30	-3.95	0.89	-4.14	0.91	ascorbate peroxidase 1
Gorai.004G227100	0.05	0.16	-4.87	0.97	-4.92	0.97	ascorbate peroxidase 1
Gorai.008G027600	0.06	0.09	2.72	0.85	2.66	0.85	2Fe-2S ferredoxin-like superfamily protein
cell wall related							
Gorai.005G025000	-0.09	0.23	0.94	0.79	1.03	0.82	xyloglucan endotransglucosylase/hydrolase 16
Gorai.013G016700	-0.34	0.28	1.91	0.81	2.25	0.82	TRICHOME BIREFRINGENCE-LIKE 33
Gorai.010G194900	-0.74	0.61	0.98	0.73	1.72	0.82	TRICHOME BIREFRINGENCE-LIKE 33
Gorai.010G171400	0.27	0.47	1.31	0.84	1.04	0.81	Tetratricopeptide repeat (TPR)-like superfamily protein
Gorai.011G148900	-0.20	0.38	0.84	0.76	1.04	0.80	Tetratricopeptide repeat (TPR)-like superfamily protein
Gorai.005G194900	-0.16	0.29	1.07	0.78	1.23	0.80	Pollen Ole e 1 allergen and extensin family protein
Gorai.006G061200	0.31	0.35	1.72	0.82	1.41	0.79	LOB domain-containing protein 42
Gorai.008G056000	0.38	0.56	1.41	0.84	1.03	0.81	LOB domain-containing protein 41
Gorai.005G225000	-0.21	0.22	1.64	0.79	1.85	0.80	hydroxyproline-rich glycoprotein family protein
Gorai.011G137200	4.45	0.81	-0.90	0.13	-5.35	0.82	homolog of carrot EP3-3 chitinase
Gorai.006G083000	-0.27	0.24	1.88	0.80	2.15	0.81	Glycine-rich protein family
Gorai.005G187500	-1.13	0.80	0.27	0.47	1.39	0.83	germin-like protein 7
Gorai.004G061700	-0.88	0.78	0.74	0.76	1.61	0.87	FASCICLIN-like arabinoogalactan 7
Gorai.001G131200	0.12	0.10	3.07	0.81	2.96	0.80	FASCICLIN-like arabinogalactan-protein 11
Gorai.007G374100	-0.36	0.61	0.90	0.79	1.27	0.84	FASCICLIN-like arabinogalactan-protein 11
Gorai.006G078900	-0.18	0.29	1.37	0.82	1.56	0.82	chitinase-like protein 2
Gorai.008G272000	5.82	0.87	0.03	0.06	-5.79	0.87	chitinase A
Gorai.008G272100	4.51	0.80	0.63	0.13	-3.88	0.77	chitinase A
Gorai.007G027100	-0.66	0.22	3.39	0.86	4.05	0.88	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S

Gorai.008G237600	0.33	0.44	1.87	0.86	1.53	0.83	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S
Gorai.007G090100	-0.41	0.53	1.55	0.85	1.96	0.87	Plant invertase/pectin methylesterase inhibitor superfamily
stress response							
Gorai.011G023600	3.00	0.50	4.96	0.82	1.97	0.67	Wound-responsive family protein
Gorai.005G206100	0.43	0.33	2.66	0.86	2.23	0.84	Wound-responsive family protein
Gorai.009G174200	0.89	0.58	2.55	0.87	1.66	0.82	Wound-responsive family protein
Gorai.005G206000	0.20	0.32	2.24	0.88	2.05	0.87	Wound-responsive family protein
Gorai.005G205900	0.20	0.38	1.41	0.84	1.21	0.82	Wound-responsive family protein
Gorai.003G134300	0.45	0.55	2.54	0.90	2.09	0.88	Pathogenesis-related thaumatin superfamily protein
Gorai.008G044000	5.50	0.89	-2.96	0.18	-8.46	0.90	pathogenesis-related gene 1
Gorai.003G083600	-0.21	0.19	2.07	0.81	2.28	0.81	Disease resistance-responsive (dirigent-like protein) family
osmotic pressure							
Gorai.001G228900	-1.09	0.54	2.32	0.85	3.40	0.89	stomagen
Gorai.003G160400	5.49	0.87	1.44	0.20	-4.05	0.83	osmotin 34
Gorai.007G338600	-0.68	0.49	1.44	0.78	2.12	0.82	osmotin 34
Gorai.009G041800	0.77	0.48	2.31	0.82	1.54	0.76	Mitochondrial substrate carrier family protein
Gorai.013G220800	-0.28	0.42	0.96	0.76	1.25	0.80	Mitochondrial substrate carrier family protein
Gorai.004G086000	-0.14	0.28	2.05	0.88	2.19	0.89	homolog of Medicago truncatula MTN3
Gorai.011G202100	0.21	0.40	1.01	0.80	0.80	0.75	cell wall / vacuolar inhibitor of fructosidase 1
Gorai.011G202200	-0.30	0.48	1.00	0.79	1.30	0.83	cell wall / vacuolar inhibitor of fructosidase 1
ribosomal protein							
Gorai.011G034100	0.48	0.65	1.25	0.84	0.77	0.75	structural constituent of ribosome
Gorai.004G205100	0.44	0.58	1.10	0.81	0.66	0.70	RNA polymerase subunit alpha
Gorai.013G136400	0.39	0.61	1.18	0.83	0.78	0.76	ribosomal protein S8
Gorai.005G167500	0.37	0.58	1.33	0.84	0.95	0.78	ribosomal protein S19
Gorai.009G350300	0.59	0.66	1.61	0.86	1.03	0.81	Ribosomal protein L36
Gorai.009G325200	0.26	0.51	1.20	0.84	0.94	0.78	ribosomal protein L22
Gorai.007G372600	0.13	0.33	1.13	0.83	1.01	0.82	ribosomal protein L2
Gorai.002G152200	-0.34	0.32	1.83	0.82	2.16	0.84	ribosomal protein L16

Gorai.004G166700	0.20	0.42	1.11	0.83	0.91	0.78	ribosomal protein L16
Gorai.007G246200	0.19	0.24	1.75	0.82	1.56	0.79	ribosomal protein L14
Gorai.008G180700	-0.46	0.28	2.50	0.84	2.96	0.85	ribonuclease 3
Gorai.001G025700	0.07	0.18	1.16	0.82	1.09	0.81	nuclear poly(a) polymerase
Gorai.013G128500	0.16	0.21	1.73	0.81	1.57	0.79	chloroplast ribosomal protein S15
Gorai.007G083900	-0.02	0.11	1.17	0.83	1.18	0.83	
matebic pathway							
Gorai.013G053000	-1.31	0.71	1.09	0.75	2.40	0.85	unknown seed protein like 1
Gorai.011G215100	0.29	0.53	-0.83	0.76	-1.12	0.82	unknown seed protein like 1
Gorai.011G033300	0.43	0.59	1.24	0.83	0.81	0.75	SGNH hydrolase-type esterase superfamily protein
Gorai.007G129000	0.82	0.74	1.25	0.82	0.43	0.61	ralf-like 33
Gorai.009G410600	-0.08	0.22	-1.12	0.82	-1.03	0.81	poly(A) binding protein 7
Gorai.004G103600	7.69	0.84	#N/A	#N/A	-7.69	0.83	plant natriuretic peptide A
Gorai.011G282700	1.14	0.80	0.63	0.67	-0.50	0.62	HXXXD-type acyl-transferase family
Gorai.004G085500	-0.28	0.22	2.00	0.79	2.28	0.80	Flavin-containing monooxygenase family protein
Gorai.009G019500	0.21	0.20	2.05	0.81	1.84	0.79	early nodulin-related
Gorai.002G069500	-5.83	0.83	-5.82	0.83	0.01	0.08	Dynamin related protein 5A
Gorai.013G006700	-5.14	0.85	-5.24	0.85	-0.09	0.08	Dynamin related protein 4C
Gorai.004G213300	-0.51	0.57	0.94	0.75	1.45	0.82	cytochrome P450, family 86, subfamily A, polypeptide 8
Gorai.009G071700	-2.62	0.55	3.28	0.88	5.89	0.94	cytochrome P450, family 706, subfamily A, polypeptide 6
Gorai.006G224400	0.54	0.23	3.00	0.81	2.46	0.77	Cytochrome P450 superfamily protein
Gorai.001G177300	0.63	0.57	1.68	0.83	1.05	0.76	ATP synthase subunit beta
Gorai.005G109000	0.25	0.40	1.35	0.83	1.10	0.80	ATP synthase subunit beta
Gorai.005G217500	0.48	0.62	1.32	0.83	0.84	0.75	ATP synthase epsilon chain
Gorai.007G054600	-0.33	0.37	1.35	0.79	1.69	0.82	alpha/beta-Hydrolases superfamily protein
Gorai.007G304400	0.62	0.62	1.57	0.83	0.96	0.74	Adenine nucleotide alpha hydrolases-like superfamily protein
signaling transduction							
Gorai.004G123800	-0.41	0.38	1.40	0.78	1.81	0.81	SAUR-like auxin-responsive protein family
Gorai.005G071300	-0.53	0.62	0.95	0.77	1.48	0.83	S-adenosylmethionine synthetase family protein

Gorai.006G066200	0.49	0.50	1.49	0.81	1.01	0.75	Protein kinase superfamily protein
Gorai.007G220200	-0.73	0.62	1.13	0.78	1.85	0.84	Gibberellin-regulated family protein
Gorai.009G182300	-1.72	0.78	1.02	0.75	2.73	0.87	ethylene-forming enzyme
Gorai.005G016900	-0.56	0.61	0.88	0.74	1.44	0.82	EF hand calcium-binding protein family
Gorai.011G257500	3.19	0.86	1.28	0.55	-1.91	0.79	Cysteine/Histidine-rich C1 domain family protein
Gorai.008G127100	-0.57	0.68	0.64	0.72	1.21	0.83	Calcium-binding EF-hand family protein
transcript factor							
Gorai.006G159000	0.47	0.58	1.75	0.86	1.28	0.82	sequence-specific DNA binding transcription factors
Gorai.009G016700	-0.16	0.34	-2.88	0.90	-2.72	0.89	plant-specific transcription factor YABBY family protein
Gorai.002G148300	-0.43	0.25	2.38	0.82	2.80	0.83	PAR1 protein
Gorai.001G025500	-0.02	0.12	0.99	0.81	1.01	0.82	Mitochondrial transcription termination factor family protein
Gorai.009G323600	-2.84	0.36	3.11	0.78	5.95	0.85	Homeobox-leucine zipper protein family
Gorai.002G126500	-0.33	0.51	1.22	0.83	1.56	0.84	basic leucine-zipper 44
unknown							
Gorai.003G017000	4.87	0.95	4.25	0.91	-0.61	0.64	Protein of unknown function (DUF677)
Gorai.003G120500	-0.10	0.19	1.50	0.82	1.60	0.83	Protein of unknown function (DUF579)
Gorai.007G055100	-0.54	0.20	2.87	0.80	3.41	0.82	Protein of unknown function (DUF579)
Gorai.002G163200	-1.12	0.54	1.53	0.75	2.64	0.82	Protein of unknown function (DUF579)
Gorai.013G137000	-0.64	0.73	0.74	0.76	1.38	0.85	Protein of unknown function (DUF579)
Gorai.007G256700	0.61	0.41	2.22	0.81	1.60	0.77	Protein of unknown function (DUF1637)
Gorai.001G247300	-0.58	0.42	1.51	0.77	2.09	0.81	Plant protein of unknown function (DUF828)
Gorai.002G075100	7.80	0.85	4.70	0.41	-3.10	0.75	
Gorai.007G320400	-4.26	0.89	0.15	0.25	4.42	0.90	
Gorai.008G264100	6.90	0.75	7.39	0.81	0.49	0.34	
Gorai.009G330800	1.56	0.37	4.97	0.91	3.40	0.86	
Gorai.003G045900	1.79	0.42	4.83	0.90	3.04	0.83	
Gorai.002G267200	-0.04	0.07	3.58	0.81	3.63	0.80	
Gorai.009G438000	-2.56	0.57	2.83	0.85	5.39	0.93	
Gorai.003G046000	0.34	0.35	2.83	0.90	2.49	0.88	

Gorai.009G041900	-2.54	0.54	2.55	0.81	5.09	0.90
Gorai.009G272400	0.19	0.16	2.51	0.82	2.33	0.81
Gorai.013G053100	-1.23	0.64	2.28	0.86	3.51	0.91
Gorai.002G214400	1.37	0.68	2.27	0.82	0.90	0.65
Gorai.011G293400	0.79	0.70	2.04	0.87	1.25	0.82
Gorai.002G152800	-0.42	0.34	1.96	0.83	2.38	0.85
Gorai.005G262100	-0.02	0.09	1.86	0.84	1.88	0.84
Gorai.007G052300	0.61	0.70	1.75	0.87	1.15	0.82
Gorai.011G014600	-0.46	0.54	1.69	0.86	2.15	0.88
Gorai.007G252600	0.25	0.44	1.58	0.86	1.33	0.84
Gorai.006G093200	0.22	0.33	1.57	0.83	1.35	0.81
Gorai.007G322200	0.42	0.63	1.57	0.86	1.15	0.83
Gorai.003G182700	0.20	0.37	1.33	0.83	1.13	0.81
Gorai.002G090500	-0.56	0.61	1.33	0.83	1.89	0.86
Gorai.007G303200	-0.15	0.29	1.26	0.82	1.42	0.83
Gorai.007G322100	0.37	0.61	1.26	0.84	0.90	0.78
Gorai.012G100900	0.08	0.21	1.24	0.83	1.16	0.82
Gorai.001G035600	0.25	0.42	1.15	0.81	0.90	0.75
Gorai.007G116800	-0.33	0.54	-1.11	0.81	-0.78	0.72
Gorai.002G211000	-0.87	0.40	2.16	0.80	3.03	0.84
Gorai.013G079000	-0.45	0.41	1.38	0.78	1.83	0.82
Gorai.007G326100	-0.69	0.64	0.82	0.71	1.52	0.81
Gorai.007G235900	-0.83	0.75	0.61	0.71	1.44	0.84
Gorai.007G320800	-1.07	0.77	0.29	0.47	1.36	0.81
Gorai.001G276700	-0.38	0.62	0.74	0.76	1.12	0.83
Gorai.002G117600	-0.02	0.10	0.99	0.79	1.01	0.80

The log2Ratio ((IAU20-22)/(Null-WT)) indicates the log2 value of the gene expression levels in the IAU20 and IAU22 groups compared with the control group; the log2Ratio ((IAO24-167)/(Null-WT)) indicates the log2 value of the gene expression levels in the IAU24 and IAU167 groups compared with the control group; the log2Ratio ((IA024-167)/(IAU20-22)) indicates the log2 value of the gene expression levels in the IAU24 and IAU167 groups compared with the IAU20 and IAU22 groups.

The probability indicates the probability of one gene being differentially expressed between two groups.

Supplementary Table S7. RPKM vaules of APX family members in 10 DPA and 20 DPA fibres of demosticated and wild *G. hirsutum*.

Abbr.	GeneID	TM1_10	Maxxa_10	CRB252_10	Coker315_10	CascotL7_10	yucTX2090_10	yucTX2094_10	yucTX2095_10	palmeriTX665_10	TM1_20	Maxxa_20	CRB252_20	Coker315_20	CascotL7_20	yucTX2090_20	yucTX2094_20	yucTX2095_20	palmeriTX665_20
cAPX	Gorai.004G227100.1	10.2	16.7	32.7	26.1	27.8	66.6	40.1	38.6	23.6	25.2	22.9	0.0	9.1	16.8	89.2	39.5	0.0	66.5
	Gorai.004G227200.2	2.8	5.0	16.7	11.8	18.0	20.5	3.2	15.8	6.0	3.4	1.2	0.0	2.4	4.1	13.2	3.2	0.0	12.5
	Gorai.004G227300.3	11.7	14.5	53.8	51.4	56.1	55.4	14.7	42.9	16.7	11.2	7.6	0.0	13.1	15.8	53.1	9.3	0.0	56.0
	Gorai.009G104500.1	198.2	246.5	531.9	530.8	373.8	342.0	203.2	313.6	194.5	150.0	169.3	86.1	115.2	153.5	314.0	145.5	220.0	317.7
	Gorai.009G420500.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.4	0.0	0.0	0.0	0.0	0.0	0.0	0.2
	Gorai.013G266100.1	0.3	0.1	0.1	0.2	0.0	0.1	0.2	0.3	0.3	0.2	0.0	0.0	0.0	0.6	0.5	0.0	0.4	0.3
perAPX	Gorai.002G196800.1	0.1	0.2	0.1	0.0	0.0	0.0	0.0	0.1	0.1	0.1	0.0	0.0	0.2	0.0	0.1	0.2	0.0	0.1
	Gorai.005G254100.1	4.8	6.0	7.9	8.6	6.4	12.5	6.2	11.1	5.8	4.3	5.6	2.0	3.9	2.4	14.0	9.0	8.4	10.8
	Gorai.003G008200.1	0.5	0.6	0.6	0.4	0.3	0.3	0.6	0.5	0.4	0.7	0.2	0.3	0.4	0.0	1.4	0.9	0.8	0.5
chlAPX	Gorai.009G246900.1	64.6	70.2	72.8	73.8	70.1	27.6	36.3	35.6	48.9	23.1	36.7	12.0	13.1	16.8	23.5	14.0	19.2	34.0
	Gorai.010G051400.1	0.5	0.9	0.9	0.6	0.6	0.9	0.7	0.8	0.4	0.5	0.5	0.7	0.5	0.4	0.7	0.7	0.7	0.3

APX-R	Gorai.010G115200.1	0.4	2.5	1.2	0.5	0.6	1.1	1.0	1.0	0.5	0.3	0.7	0.0	0.0	0.2	1.8	0.5	0.5	0.8
APX-L	Gorai.010G038200.1	0.3	2.9	0.8	0.7	0.5	2.4	1.1	2.1	0.7	0.7	0.7	0.6	0.0	0.7	2.9	1.4	1.4	1.3

cAPX, cytosolic APX; perAPX, peroxisomal APX; tAPX, thylakoid APX; sAPX, chloroplast stromal APX; APX-R, APX-R type of APX; APX-L, APX-L type of APX. Data of Expression levels for wild cottons (yucTX2090, yucTX2094, yucTX2095 and palmeriTX665) and domestication cottons (TM1, Maxxa, CRB252, Coker315 and CascotL7) were downloaded from NCBI (SRA061240). “_10”or “_20” indicates the gene expression levels in 10 DPA or 20 DPA fibers.

Supplementary Table S8. RPKM vaules of APXs in different fibre stages of *G. raimondii*.

	GeneID	0 DPA	3 DPA	10 DPA	20 DPA
cAPX	Gorai.004G227200.2	35.5101	10.4998	75.2364	45.0922
	Gorai.004G227100.1	31.2071	9.75488	25.5556	22.6662
	Gorai.004G227300.3	62.8232	21.8755	70.7763	77.6137
	Gorai.009G104500.1	86.8625	26.3403	230.473	230.854
	Gorai.009G420500.1	0	0	0	0
	Gorai.013G266100.1	0.34089	0	3.02774	1.40049
perAPX	Gorai.003G008200.1	0.375829	0.571451	1.82586	1.58229
	Gorai.002G196800.1	0.720512	0.304589	0.580874	0.705325
	Gorai.005G254100.1	31.7938	8.36749	15.1295	27.444
chlAPX	Gorai.009G246900.1	20.4657	8.90649	33.7845	18.1002
	Gorai.010G051400.1	8.43791	1.42891	3.03986	2.3913
APX-R	Gorai.010G115200.1	0.619905	0.156482	6.9611	1.01954
APX-L	Gorai.010G038200.1	2.2117	2.20223	6.40041	1.61945

cAPX, cytosolic APX; perAPX, peroxisomal APX; tAPX, thylakoid APX; sAPX, chloroplast stromal APX; APX-R, APX-R type of APX; APX-L, APX-L type of APX.

Supplementary Table S9. Classification of APX genes in different species according to the amino acid sequences.

Species	Abbreviation	Total	Ⅰ	Ⅱ	Ⅲ	Ⅳ	Ⅴ
Manihot esculenta	Me	12	3	3	5	1	-
Ricinus communis	Rc	7	2	2	1	1	1
Linum usitatissimum	Lu	10	3	4	2	1	-
Populus trichocarpa	Pt	11	4	3	2	1	1
Medicago truncatula	Mt	7	2	2	1	1	1
Phaseolus vulgaris	Pvu	7	1	3	1	1	1
Glycine max	Gm	10	1	6	2	1	-
Cucumis sativus	Csa	7	2	2	1	1	1
Prunus persica	Ppe	7	2	2	1	1	1
Malus domestica	Mdp	11	4	4	2	1	-
Fragaria vesca	Fv	7	2	3	1	1	-
Arabidopsis thaliana	At	8	2	2	2	1	1
Arabidopsis lyrata	Al	10	3	5	2	1	-
Capsella rubella	Cr	8	2	4	1	1	-
Brassica rapa Chiifu-401 v1.2	Br	10	4	2	2	1	1
Thellungiella halophila	Th	9	2	4	2	1	-
Carica papaya	Cp	6	2	2	1	-	1
Gossypium raimondii	Gr	13	6	3	2	1	1
Gossypium arboreum	Ga	13	6	3	2	1	1
Gossypium hirsutum	Gh	26	12	6	4	2	2
Theobroma cacao	Tc	6	1	2	1	1	1
Citrus sinensis	Csi	6	2	2	1	1	-
Citrus clementina	Cc	8	2	2	1	1	1
Eucalyptus grandis	Eg	8	3	2	1	1	1
Vitis vinifera	GSVIVT	7	2	3	1	1	-
Solanum tuberosum	DMT	6	1	2	1	1	1
Solanum lycopersicum	Sl	9	3	2	2	1	1
Mimulus guttatus v1.1	Mg	5	2	1	1	1	-
Aquilegia coerulea	Ac	7	3	1	1	1	1
Sorghum bicolor v1.4	Sb	8	2	2	3	1	-
Zea mays	Zm	8	3	2	3	-	-
Setaria italica	Si	8	2	2	3	1	-
Panicum virgatum v0.0	Pvi	18	4	5	7	2	-
Oryza sativa	Os	10	2	2	4	1	1
Brachypodium distachyon	Bd	9	2	2	3	1	1
Selaginella moellendorffii	Sm	6	1	2	2	1	-
Physcomitrella patens v1.6	Ppa	5	2	1	1	1	-
Chlamydomonas reinhardtii	Cr	3	-	-	2	1	-
Volvox carteri	Vc	3	-	-	2	1	-
Coccomyxa subellipsoidea C-169	Csu	5	-	2	2	1	-
Micromonas pusilla CCMP1545	Mp1545	3	-	-	1	1	1
Micromonas pusilla RCC299	Mp299	4	-	-	3	1	-
Ostreococcus lucimarinus	Ol	3	-	-	2	1	-

Ⅰ, cytosolic APX; Ⅱ, peroxisome APX; Ⅲ, chloroplast APX; Ⅳ, APX-R; Ⅴ, APX-L. “-” indicates that it doesn’t find the type of APX in the species.