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Supplemental information

**CRISPR–Cas9-mediated construction of a cotton *CDPK* mutant library
for identification of insect-resistance genes**

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Figure S1

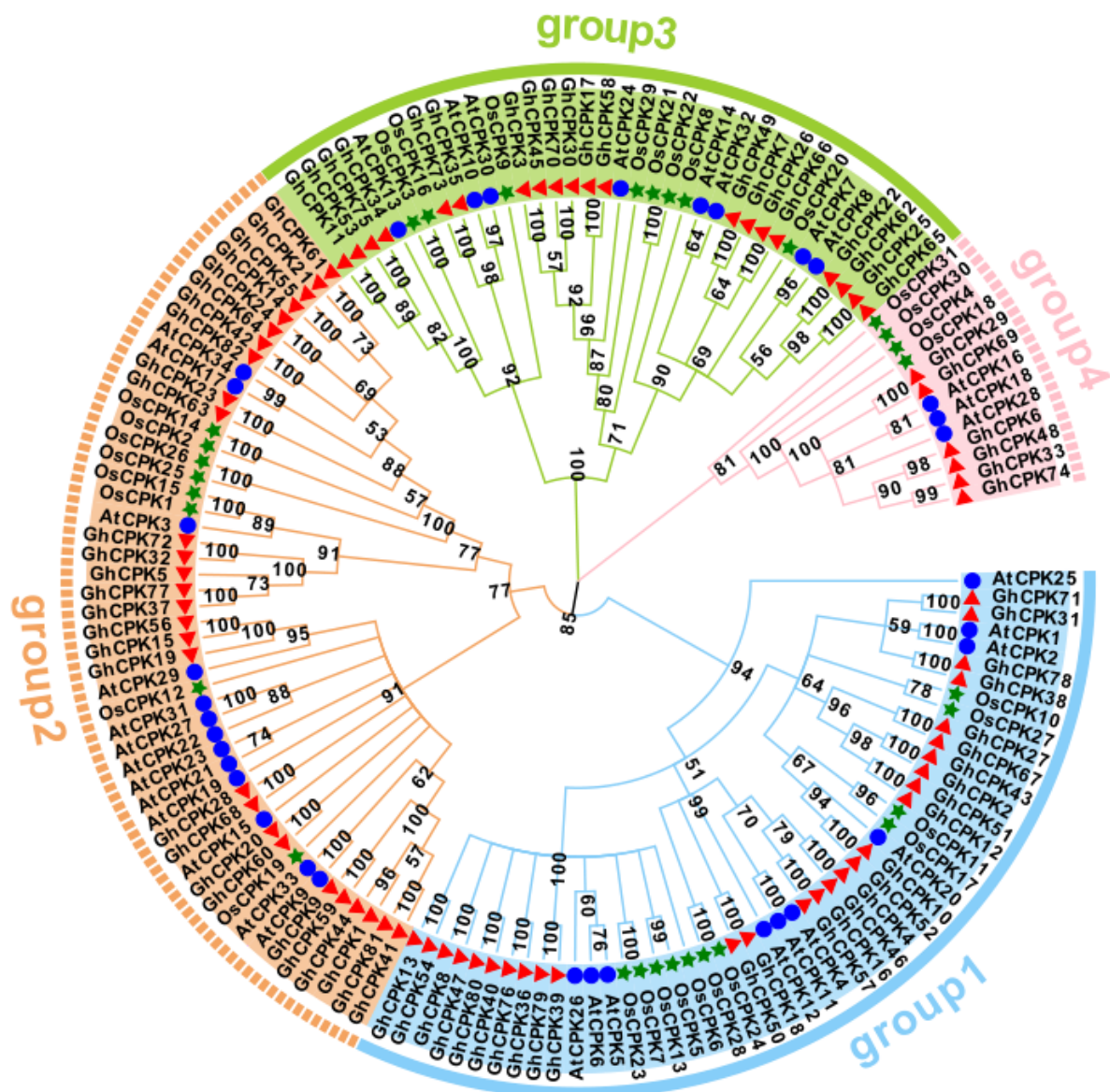


Figure S1 Phylogenetic analysis of CDPK gene families in *G. hirsutum*, *A. thaliana* and *O. sativa*. Groups 1, 2, 3, and 4 indicate different gene clusters. Different colors of symbols represent different species. Red triangles represent *G. hirsutum*, blue circles represent *A. thaliana* and green pentagrams represent *O. sativa*.

Figure S2

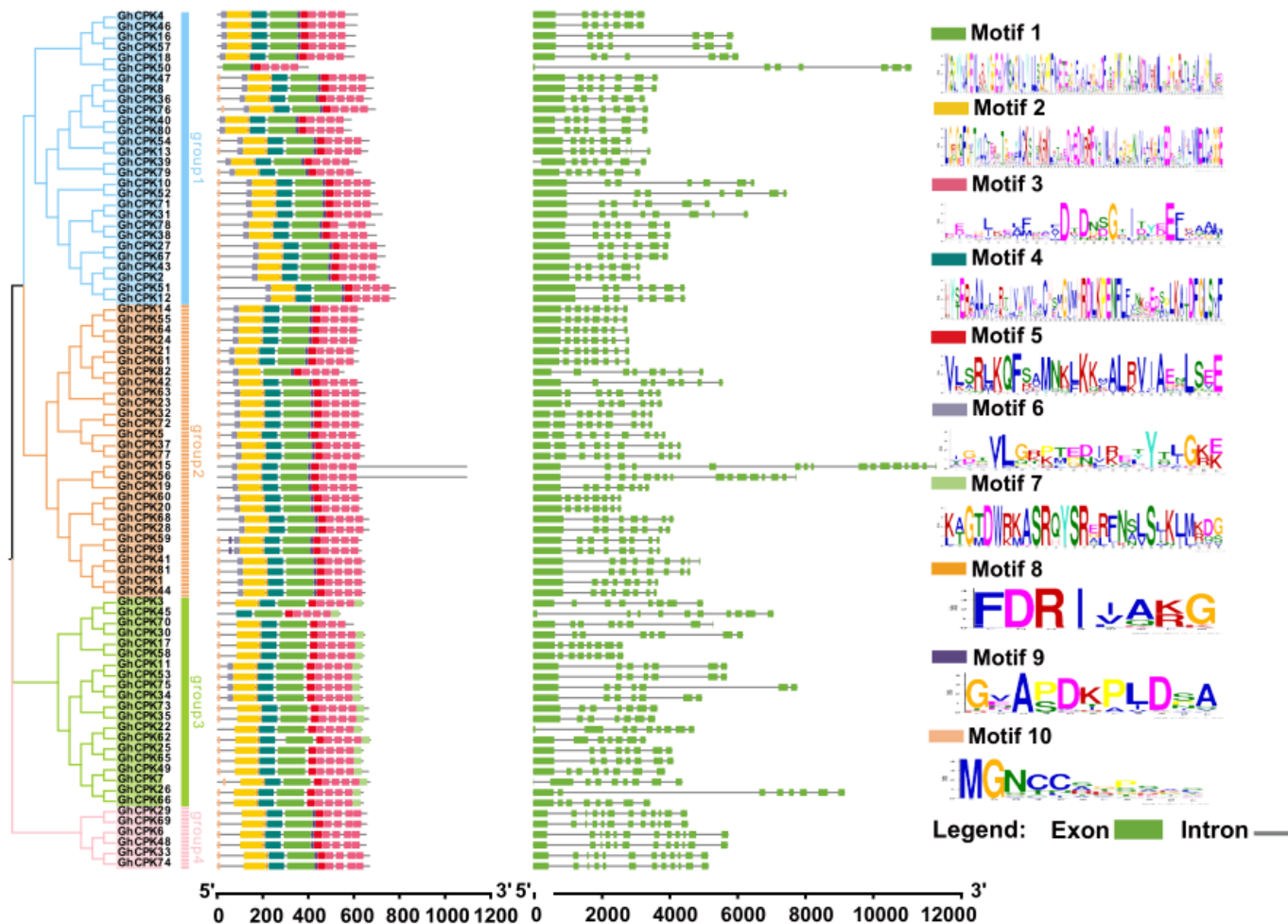


Figure S2 Phylogenetic tree, conserved protein motifs and gene structures of *GhCPKs* gene family. From left to right, it shows the phylogenetic tree, conserved protein motifs and gene structure of the *G. hirsutum* CDPK gene family. In the phylogenetic tree, different colors represent different subgroups. Within the protein conserved motifs, a total of 10 conserved motifs have been identified, distributed in different colored boxes. On the far right are the sequence logos of these protein motifs. In the exon-intron structure diagram, the green box represents exons and the black line represents introns.

Figure S4

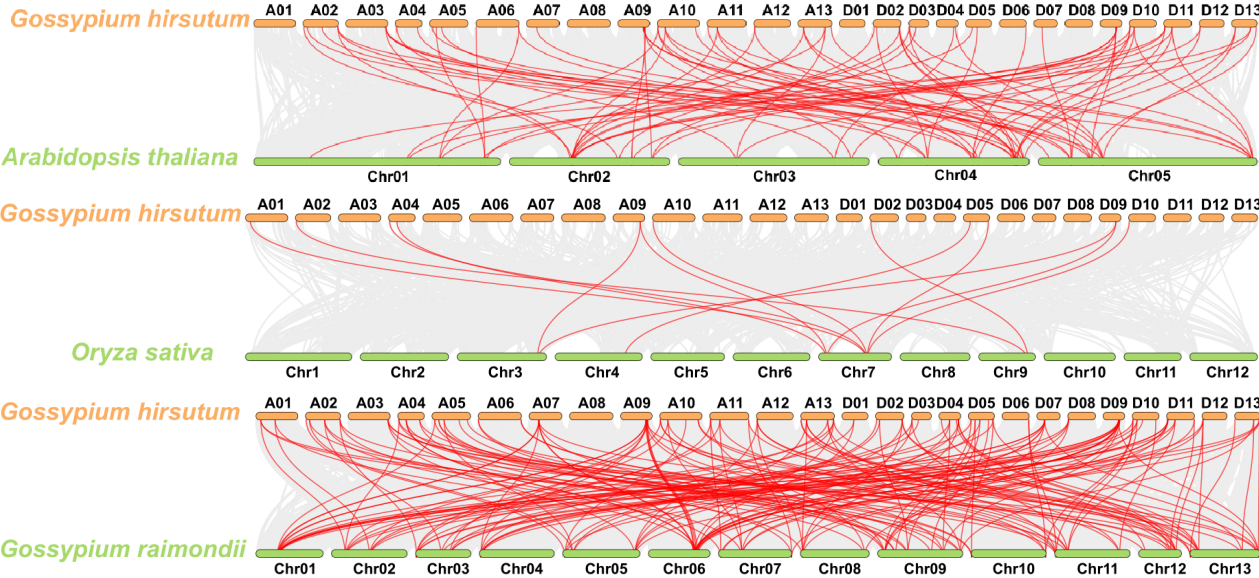


Figure S4 Collinearity analysis of CDPK genes between *G. hirsutum* with *A. thaliana*, *O. sativa* and *G. raimondii*. Grey lines indicate collinear blocks within the *G. hirsutum* genome and other plant genomes, and the red curve indicates CDPK genes with collinearity.

Figure S5

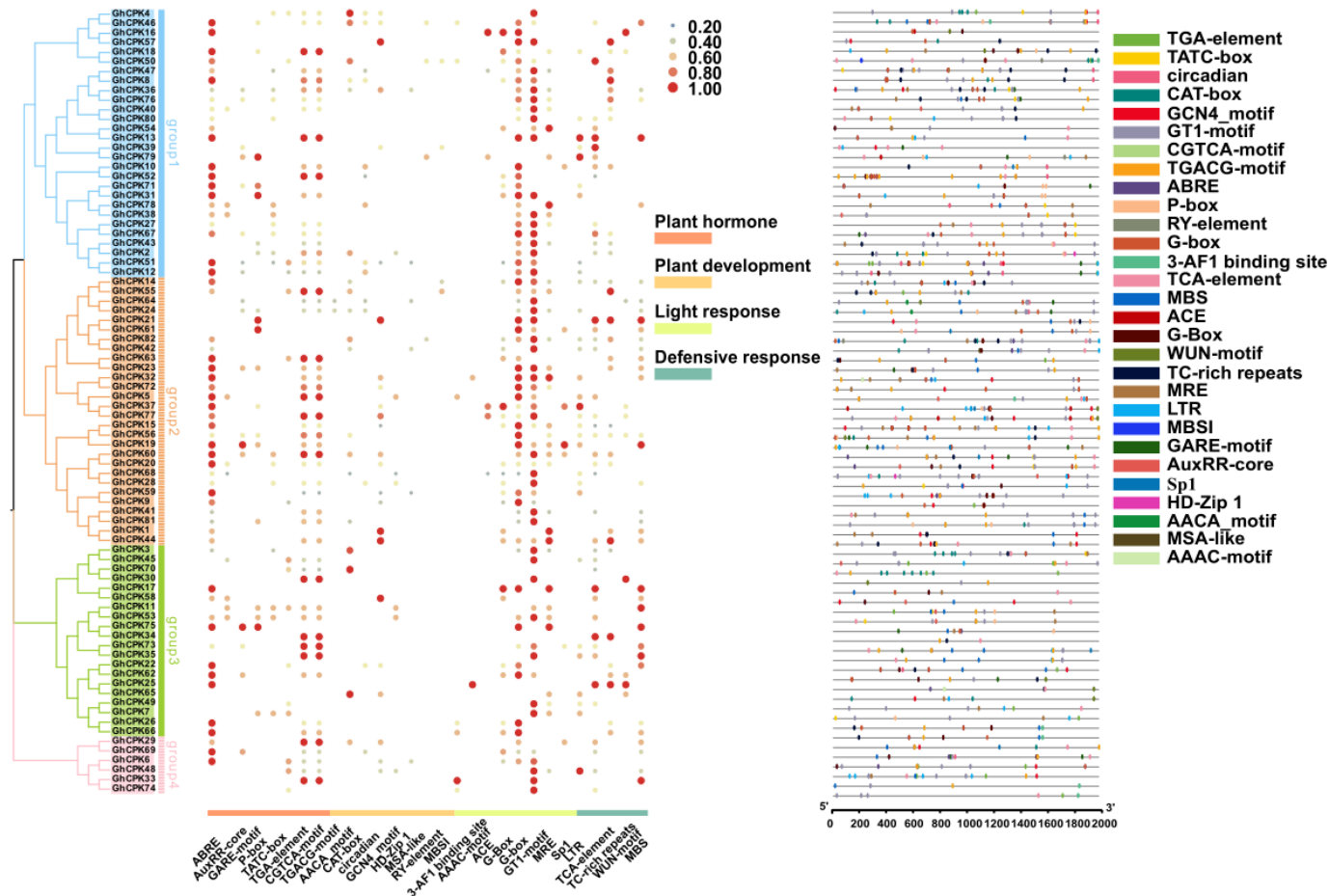


Figure S5 Cis-acting elements in the promoter regions of *GhCPKs*. On the left is the phylogenetic tree of the *GhCPKs* gene family. In the middle is a heat map of the number of all cis-acting elements. The larger and redder the circle, the greater the quantity represented. The diagram on the right shows the positional distribution of promoter cis-acting elements of the *GhCPK* genes. The black line indicates the promoter length of the *GhCPK* genes. The different colored boxes on the right represent cis-acting elements with different functions.

Figure S6

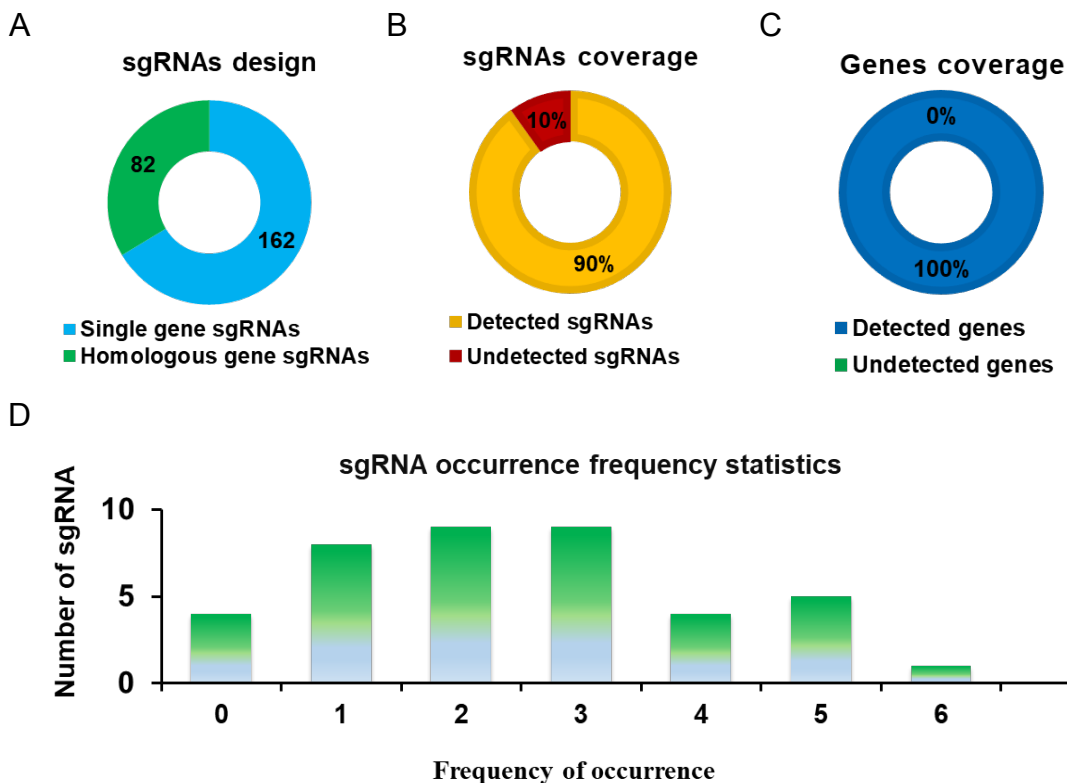
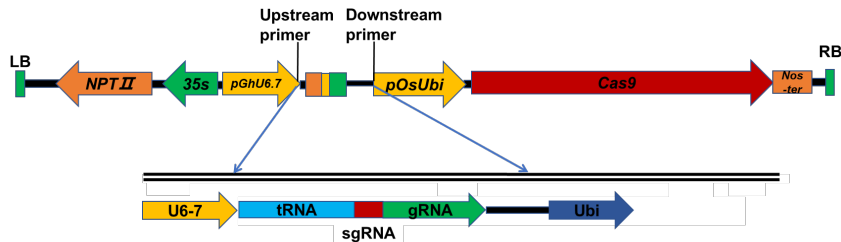


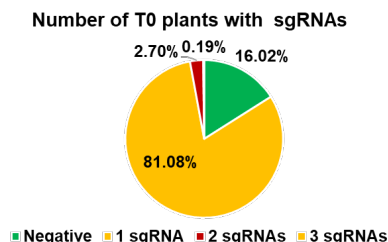
Figure S6 The number of sgRNAs in the *GhCPKs* gene family mutant library and the preliminary experimental results of mixed pool 1. (A) The quantity of different types of sgRNAs. Blue represents the quantity of sgRNAs targeting individual *GhCPKs*, green represents the quantity of sgRNAs targeting homologous *GhCPKs*. (B) Coverage of sgRNA in the preliminary experiment. Yellow color represents detected sgRNAs, red color represents undetected sgRNAs. (C) Coverage of gene in the preliminary experiment. Deep blue color represents detected genes, green color represents undetected genes. (D) Frequency statistics of sgRNA. The X-axis represents the frequency of occurrence of target sgRNAs, and the Y-axis represents the number of sgRNAs.

Figure S7

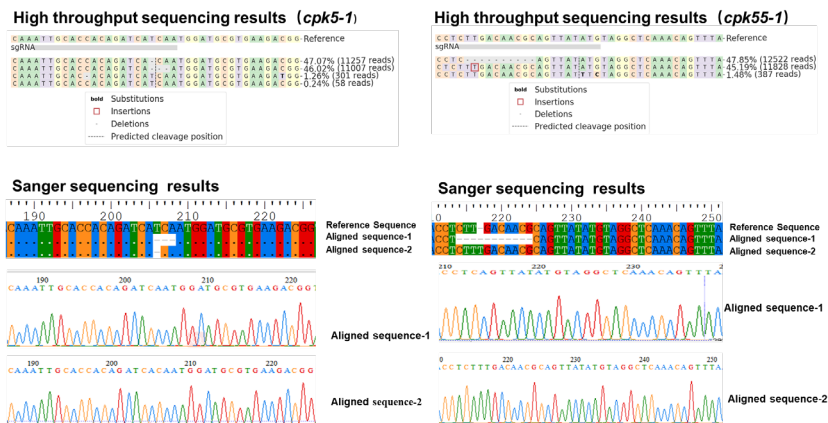
A



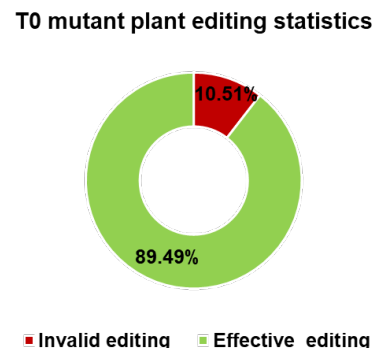
B



C



D



E



F

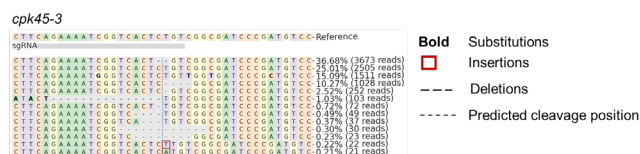
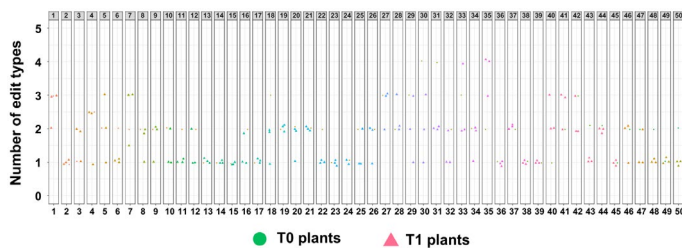


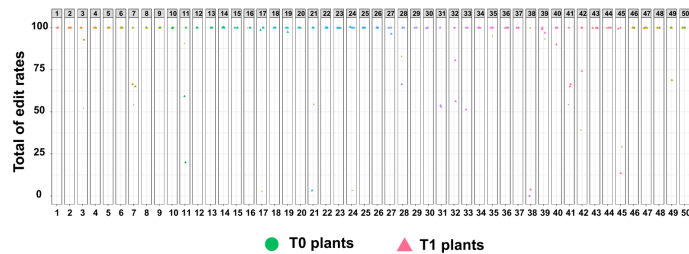
Figure S7 Molecular detection of T0 generation *GhCPKs* mutant library plants. (A) PCR amplification sgRNA vector sequence diagram. The different colored boxes represent different vector components. (B) Statistical analysis of the number of sgRNAs present in the T0 generation *GhCPKs* mutant library plants. Yellow means only one sgRNA, red means two sgRNA, and green means three sgRNA. (C) Comparison of high-throughput sequencing and Sanger sequencing results for gene editing plants. (D) Editing statistics of T0 generation *GhCPKs* mutant library plants. Green means that gene editing is detected, red means that gene editing is not detected. (E) Examples of one, two and multiple types of editing. Bold represents base substitutions, red boxes represent base insertions, dashes represent base deletions, and dashed lines represent predicted cleavage positions. (F) The most common editing types in the mutant library. Bold represents base substitutions, red boxes represent base insertions, dashes represent base deletions, and dashed lines represent predicted cleavage positions.

Figure S8

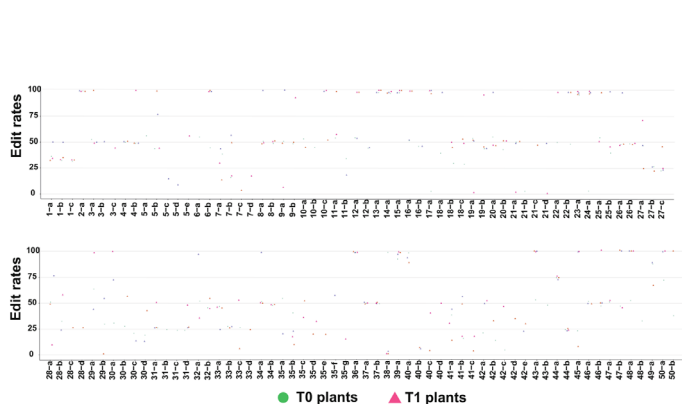
A



B



C



D

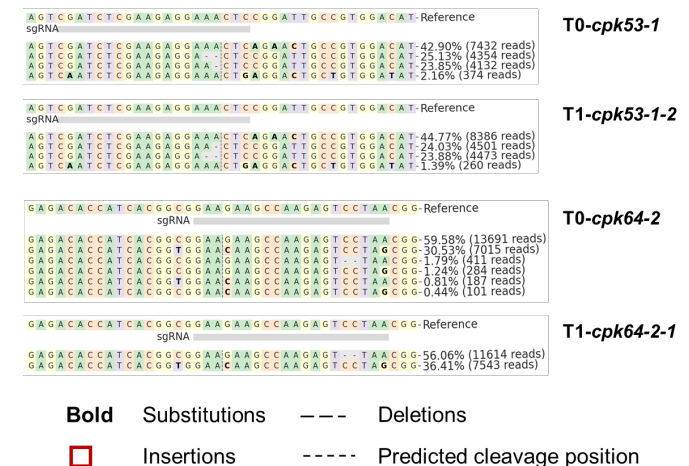


Figure S8 Genetic analysis of 50 *GhCPKs* gene-edited plants and their 150 progeny. (A) Editing type statistics of 50 *GhCPKs* gene-edited plants and their 150 progeny. The circle represents T0 generation plants, the triangle represents T1 generation plants. (B) Editing efficiency statistics of 50 *GhCPKs* gene-edited plants and their 150 progeny. (C) Statistical analysis of editing efficiency for each editing type in 50 *GhCPKs* gene-edited plants and their 150 progeny. (D) Examples of genetic states in different progenitor and progeny gene-edited plants. Bold represents base substitutions, red boxes represent base insertions, dashes represent base deletions, and dashed lines represent predicted cleavage positions.

Figure S9

A



B

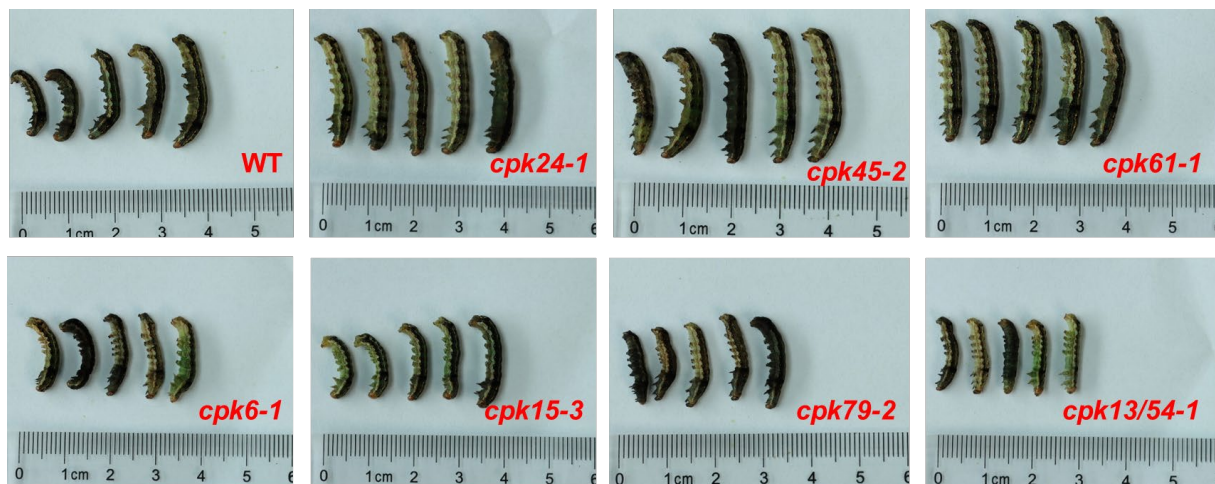


Figure S9 Example of insect resistance phenotypic screening in *GhCPKs* mutant library plants. (A) Field insect resistance phenotype of corresponding numbered plants. (B) Phenotype of *S. litura* larvae feeding on the corresponding numbered plants five days later.

Figure S10

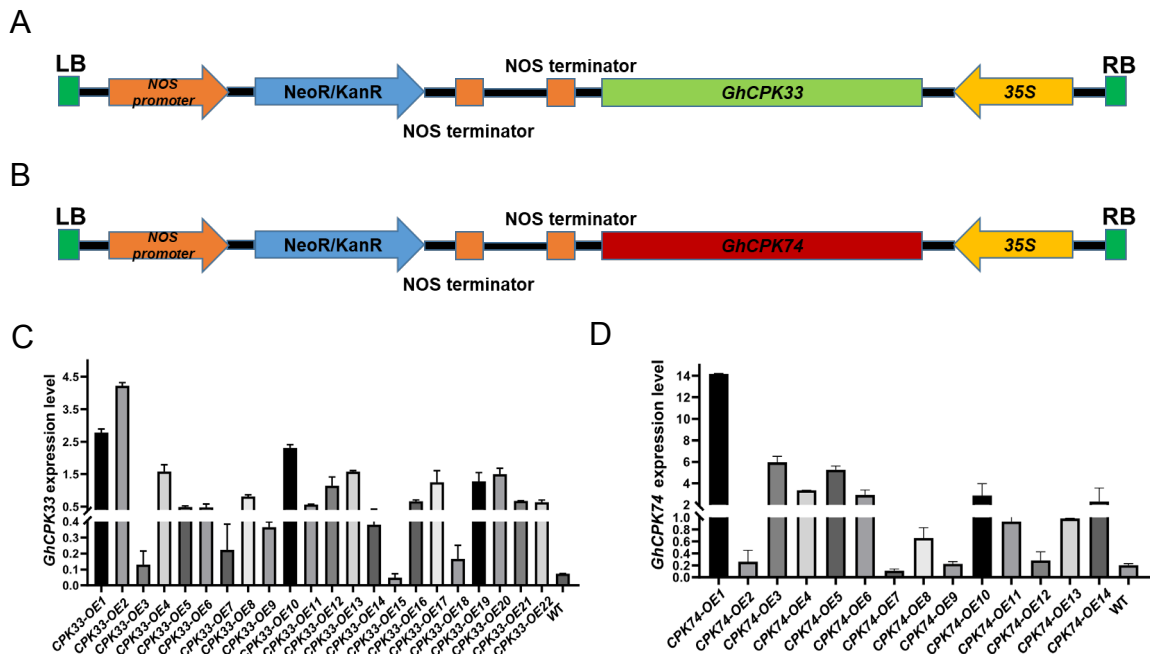
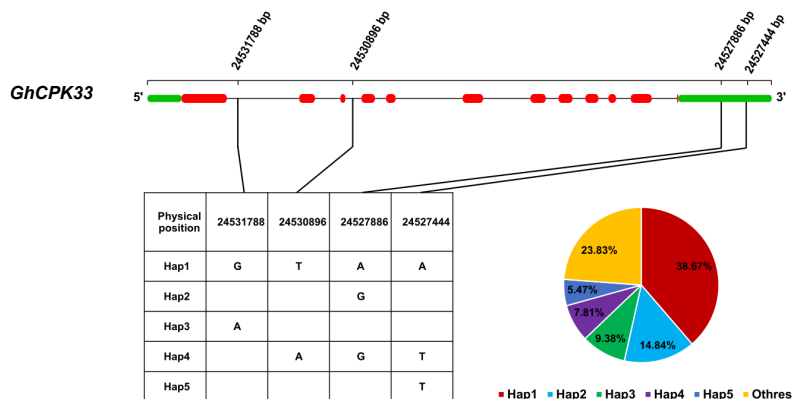


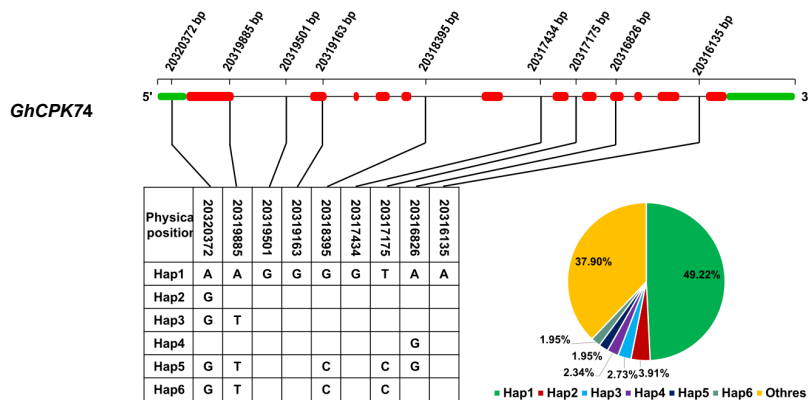
Figure S10 Construction of expression vectors and detection of expression levels for *GhCPK33* and *GhCPK74* overexpression materials. (A) Construction of *GhCPK33* overexpression vectors. (B) Construction of *GhCPK74* overexpression vectors. Different color boxes represent different carrier elements. (C) Detection of *GhCPK33* expression levels in T0-generation *CPK33-OE* overexpression materials. (D) Detection of *GhCPK74* expression levels in T0-generation *CPK74-OE* overexpression materials. The expression of *GhUB7* was used as internal control. Means \pm SE (n = 3).

Figure S11

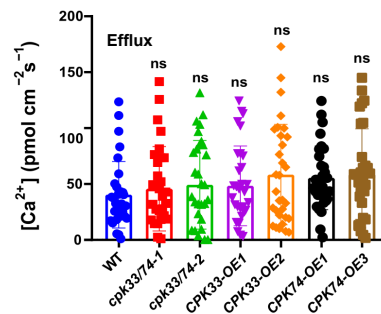
A



B



C



D

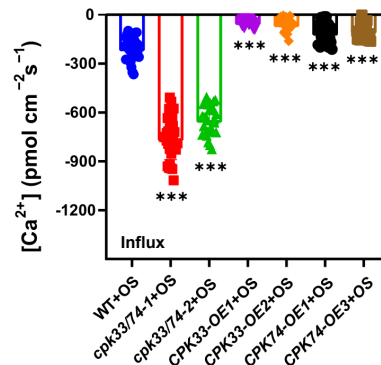


Figure S11 Haplotype analysis of *GhCPK33* and *GhCPK74* and the detection of average Ca^{2+} flow rate in leaf mesophyll cells.

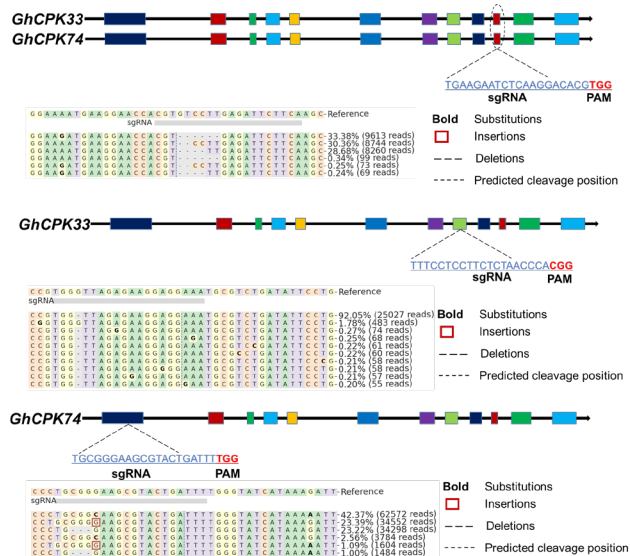
(A) The gene *GhCPK33* structure and single-nucleotide polymorphisms (SNPs) variants contained in the Ghlandraces population showed the five haplotypes with highest proportions, and the blank boxes were the same nucleotides as the reference genome (Hap1). The pie charts show the proportion of the five haplotypes. (B) The gene *GhCPK74* structure and single-nucleotide polymorphisms (SNPs) variants contained in the Ghlandraces population showed the six haplotypes with highest proportions, and the blank boxes were the same nucleotides as the reference genome (Hap1). The pie charts show the proportion of the six haplotypes. (C) In the untreated state, the average Ca^{2+} flow rate in leaf mesophyll cells of *cpk33/74*, *CPK33-OE*, *CPK74-OE* and WT over a 5-minute period. (D) After treatment with the OS of *S. litura*, the average Ca^{2+} flow rate in leaf mesophyll cells of *cpk33/74*, *CPK33-OE*, *CPK74-OE* and WT over a 5-minute period.

Figure S12

A



B



C

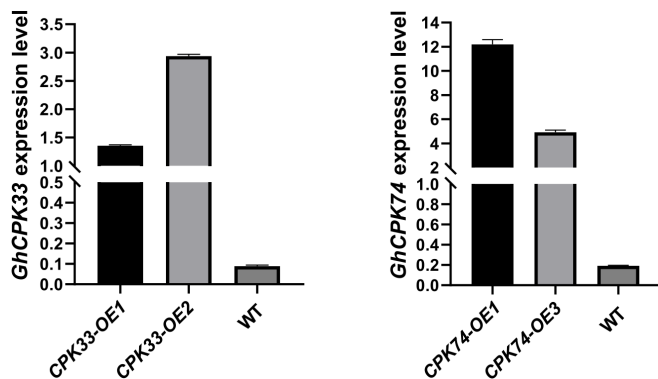


Figure S12 Cultivation, gene editing and expression level detection of T2 generation *cpk33/74*, *cpk33*, *cpk74*, *CPK33-OE*, *CPK74-OE* and WT plants. (A) Cultivation of T2 generation *cpk33/74*, *cpk33*, *cpk74*, *CPK33-OE*, *CPK74-OE* and WT plants. (B) Detection of editing in T2 generation *cpk33*, *cpk74* and *cpk74/33* plants. (C) Detection of *GhCPK33* and *GhCPK74* expression levels in T2 generation *CPK33-OE* and *CPK74-OE* overexpression materials. The expression of *GhUB7* was used as internal control. Means \pm SE (n = 3).

Figure S13

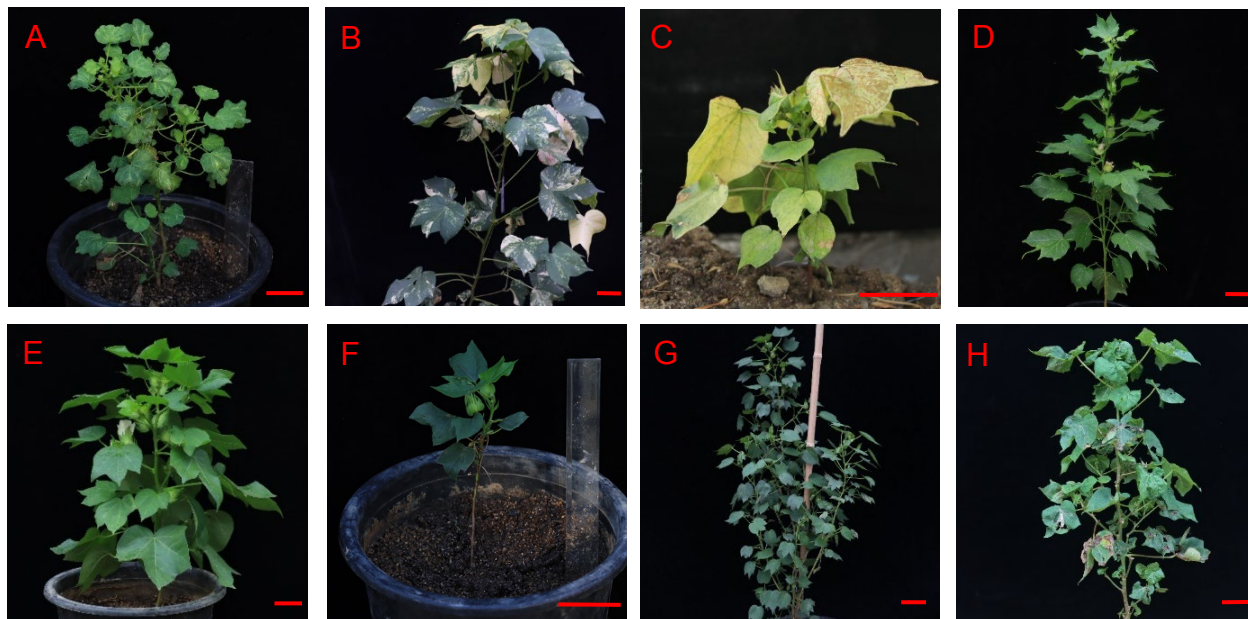


Figure S13 Identification of unique phenotypes in the T0 generation *GhCPKs* mutant library plants. (A) The leaf is round. (B) The leaves showed chimeric yellowing. (C) The plant type is dwarfed and the leaves turn yellow. (D) The fruit branches become shorter. (E) Dwarfing and compact plants. (F) Plant dwarfing and early maturing. (G) The leaves become smaller. (H) Necrotic spots appeared on the leaves. The red line represents 5 cm.

Figure S14

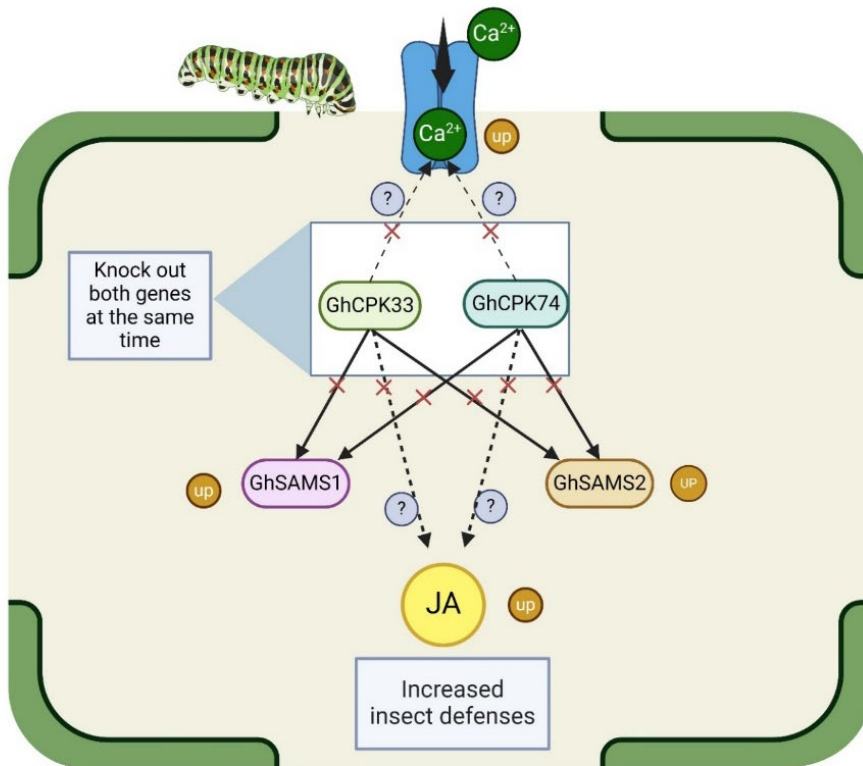


Figure S14 Models of *GhCPK33* and *GhCPK74* regulating pest defense in upland cotton. Under the induction of OS from the *S. litura*, simultaneously knocking out *GhCPK33* and *GhCPK74* can accelerate the influx of Ca^{2+} in cotton leaf mesophyll cells, enhance the synthesis of JA, and increase the expression of *GhSAMS1* and *GhSAMS2*, resulting in an increased defense capability of cotton against herbivorous insects.

GhCPK66	Gh_D09G1163	Ghir_D09G012710.1	D09	38278169	38281037	-	531	60227.3	6.76	MGNCCVTS	N	Y	4	III	M	0	N
GhCPK67	Gh_D09G1249	Ghir_D09G013620.1	D09	39552322	39555623	-	610	68213.9	4.96	MGNNCFKT	N	Y	4	I	C M	0	N
GhCPK68	Gh_D10G0130	Ghir_D10G001600.1	D10	1030951	1034394	-	551	62014.3	6.17	MGCFSSKH	Y	Y	4	II	M	0	N
GhCPK69	Gh_D10G0863	Ghir_D10G009490.1	D10	10909734	10913532	-	544	61950.2	8.81	MGICLSTT	Y	Y	4	IV	M	0	N
GhCPK70	Gh_D10G1303	Ghir_D10G013990.1	D10	24177574	24181997	-	495	56317.6	5.41	MGSCISTQ	Y	Y	3	III	M	0	N
GhCPK71	Gh_D10G2029	Ghir_D10G021750.1	D10	56010875	56015207	-	584	64984.3	5.14	MGNTCVGP	N	Y	4	I	M	0	N
GhCPK72	Gh_D11G0227	Ghir_D11G002390.1	D11	1905499	1908419	-	530	60355.2	6.56	MGNENRPP	N	Y	4	II	M	0	N
GhCPK73	Gh_D11G0314	Ghir_D11G003360.1	D11	2722348	2725395	+	550	62311.9	6.53	MGNENACV	N	Y	4	III	C M	0	N
GhCPK74	Gh_D11G1774	Ghir_D11G018640.1	D11	19767240	19771544	-	554	62788.1	9.48	MGACLSTT	Y	Y	4	IV	M	0	N
GhCPK75	Gh_D11G3329	Ghir_D11G036410.1	D11	66059614	66066098	+	527	59284.3	6.39	MGNENRSP	N	Y	4	III	M	0	N
GhCPK76	Gh_D12G0121	Ghir_D12G001340.1	D12	1591928	1594742	-	575	64573.8	6.07	MRLHYCMR	N	Y	4	I	N	0	Y
GhCPK77	Gh_D12G2743	Ghir_D12G024580.1	scaffold4587_D12	20270	23886	-	534	60242.7	6.39	MGNENSQP	Y	Y	4	II	C M	0	N
GhCPK78	Gh_D13G0033	Ghir_D13G000300.1	D13	246690	250046	-	573	64084.6	6.22	MGNENCVGP	N	Y	3	I	M	0	N
GhCPK79	Gh_D13G0560	Ghir_D13G005790.1	D13	7586741	7589365	-	523	58400.4	6.41	MGNENCLGS	N	Y	4	I	M	0	N
GhCPK80	Gh_D13G0561	Ghir_D13G005800.1	D13	7614829	7617628	-	487	54631	4.86	MRRRAIDHQ	N	N	4	I	C	0	N
GhCPK81	Gh_D13G1455	Ghir_D13G015090.1	D13	45574159	45578015	+	536	60415.3	6.37	MGNENCLTKN	Y	Y	4	II	M	0	N
GhCPK82	Gh_D13G2278	Ghir_D13G023730.1	D13	58814168	58818344	+	461	51476	6.4	MGNENCTRG	N	Y	4	II	M	0	N

MW molecular weight, pI isoelectric points, M Cell membrane, C Cytoplasm, N nucleus

The myristoylation sites were predicted by the Myristoylator program (<http://web.expasy.org/myristoylator/>).

The palmitoylation sites were predicted by CPS-Palm (<http://lipid.biocuckoo.org/index.php>)

Number of EF-hands were predicted by SMART database (<http://smart.embl-heidelberg.de/>)

The subcellular localizatio were predicted by DeepLoc-2.0 (<https://services.healthtech.dtu.dk/services/DeepLoc-2.0/>)

The transmembrane domains were predicted by DeepTMHMM (<https://dtu.biolib.com/DeepTMHMM/>)

The signal peptides were predicted by SignalP-6 (<https://biolib.com/DTU/SignalP-6/>)

Table S2 sgRNA of CDPK gene family mutant library in the *Gossypium hirsutum*

sgRNA sequence	Targeted gene ID	Targeted gene name	sgRNA sequence	Targeted gene ID	Targeted gene name
TCCTCTTCTCCGTTTCTGTG TGGTGGAATTGGGGTTGAAC	Gh_A01G0621	GhCPK1	ATCAAAGCTCACAGAGGCAG CTCTCTGAAATAGAAGGCCA	Gh_A01G0621 and Gh_D01G2360	GhCPK1 and GhCPK44
AATGAAGCAGACCATCTAGT ACAAGGAAGGGTCCAAGACA	Gh_A01G1119	GhCPK2	CTTTGCATCGAGAAAGGTAC TGCTCGACAGAGATACGAAG	Gh_A01G1119 and Gh_D01G1194	GhCPK2 and GhCPK43
GCAAGTTGTCCGCAACCACC CCTTCCCTAAGTGTGTTGAAT	Gh_A02G0144	GhCPK3	CGACAAGTATCCATTCTCGT AGAGACGGACTTCAGAAAAT	Gh_A02G0144 and Gh_D02G0183	GhCPK3 and GhCPK45
GACAGCAGCAACCAAAGGAT CGACAGCAGCAACCAAAGGA	Gh_A02G0609	GhCPK4	CTTCAAGCGTGATAGCACGG TGGAACATCAGGTTGTGCCT	Gh_A02G0609 and Gh_D02G0663	GhCPK4 and GhCPK46
CAGTGGAAACAATTAGCTTCG ATTGCACCACAGATCATCAA	Gh_A02G1029	GhCPK5	TGCAATGGTCTTCCGTCCAC GGAAAGCAGCTAACTTGTGT	Gh_A02G1029 and Gh_D03G0701	GhCPK5 and Gh_D03G0701
TCTTAGGGTAAAAGCACCAA AGTGCACCGTGACATGAAAC	Gh_A02G1635	GhCPK6	TGAGTATTCCGATTACCGGA AACTCCGGAGGAACACTACGAA	Gh_A02G1635 and Gh_D03G0087	GhCPK6 and GhCPK48
GCAAGCTTAGGTAGAACTTA TCACACCCAAGTTCATATCT	Gh_A02G1796	GhCPK7	GTTCTAAATGATCCAACCTGG AACAGCTTCTCATGAGAAGA	Gh_A02G1796 and Gh_D03G0609	GhCPK7 and GhCPK49
GCAAATATGGAGAGATCCGT CAGTCCATATTACGTTGCTC	Gh_A03G1505	GhCPK8	ATAAGCATGAGAGATGCCCC AGGCCAAGTTTTTACCGACG	Gh_A03G1505 and Gh_D02G1973	GhCPK8 and GhCPK47
GTTGGACACAAGTATGTGAA ATTCACAATTGCCCTGCACA	Gh_A04G0148	GhCPK9	TGAGAAGTGAACCCAACAA TGTCGAAAAGATGTTAACGC	Gh_A04G0148 and Gh_D05G3567	GhCPK9 and GhCPK59
GAACAATGCCAATAAAGGCTT GGTTGGAAGTCCATATTATG	Gh_A04G0467	GhCPK10	AAAGGCAGCTGCGCTTGCTA GTAGCTATGATGCAAGACAC	Gh_A04G0467 and Gh_D04G0900	GhCPK10 and GhCPK52
GTAGTAATGAACCAACCCGT GAGGAAACTCAGAACTGCCG	Gh_A04G0780	GhCPK11	TGGCTCTGAGGTTCTCAA TGGAACCAGACCCAAAGCTC	Gh_A04G0780 and Gh_D04G1271	GhCPK11 and GhCPK53
GGTCCTAAACCAGCCGAAGA TTGCAGAAAAGTCTTCATG	Gh_A04G1372	GhCPK12	GATCTTGTAAGAAGACCCT GTTCCCTTCAGGCCATCCTT	Gh_A04G1372 and Gh_D04G0895	GhCPK12 and GhCPK51
GTCGATATCGAAGACGAAGT GCTAAGAAGAAGATGGTTGG	Gh_A04G1429	GhCPK13	CTTTCTGCCTTATTTTCAGGA GACGATTAAGGCACGTACG	Gh_A04G1429 and Gh_D04G1486	GhCPK13 and GhCPK54
CGCTGCTTCTTTGCTTCGCA GTCTAATATTGTCGAGCTCA	Gh_A05G0617	GhCPK14	CTTACTTAGAACCTGCACTG CTGAAGCACATAACCAAGAAG	Gh_A05G0617 and Gh_D05G0748	GhCPK14 and GhCPK55
CTAACCACTGACAAGGACGT GTTATTTGAATCACGGCCAA	Gh_A05G1571	GhCPK15	GCTGATGCCTTGAATTCGAG AGAGGAAAACATGAGCCGCG	Gh_A05G1571 and Gh_D05G1749	GhCPK15 and GhCPK56
TTCAGCATAGCCGATGCCTT TGTTGGGTCTTTCATTCCAA	Gh_A05G2355	GhCPK16	CATAGCAGAGAGACTCTCTG GATAATACAGCGGAATCCAG	Gh_A05G2355 and Gh_D05G2622	GhCPK16 and GhCPK57
TAACATAAGACAACGTACCG ATCCAAAGCCAAGCTGCGGA	Gh_A05G2859	GhCPK17	TCGTTGGAGGAGCTTAAAGA TTTGTCCAGGATGGTAATACG	Gh_A05G2859 and Gh_D05G3156	GhCPK17 and GhCPK58
GGGTTCTGAACTTATGGAAT GTTCCGAGTGACGGCAAATG	Gh_A05G3246	GhCPK18	CAGTTTATTCAAGTGCACCG GAAAGGGAAGAGAATCTGGT	Gh_A05G3246 and Gh_D04G0366	GhCPK18 and GhCPK50
GATTTGTTGGACAGGATGGG ACAGAAGCAAGCCCGATTGA	Gh_A06G0013	GhCPK19	CATCAAGCAAATAATCTCCG ACATAGCACCCGAAGTTCTT	Gh_A06G1772 and Gh_D06G2206	GhCPK20 and GhCPK60

AGTGAGGAAGATGTTGACAA CTTGTTTTGTTGGCTAATGG	Gh_A06G1772	GhCPK20	GATGCGCCAAAGCAAGCAGA GATTACTAACCTGCCAGAA	Gh_A07G1099 and Gh_D07G1198	GhCPK21 and GhCPK61
GCAGAAGGTTCCACCACGAG GATGAACTCATCGTAGTCTA	Gh_A07G1099	GhCPK21	TTGTGTACTGATCCCAACTC GAAGGAAGCTTCCCCCTGA	Gh_A07G1123 and Gh_D07G1228	GhCPK22 and GhCPK62
GCTAACATTGGCCAGACGAG GCAAACAAGAACATCCACAA	Gh_A07G1123	GhCPK22	ACCATAGATTCCGATAACAG GGTCATTGCAGGATGTTTAT	Gh_A08G2530 and Gh_D08G0142	GhCPK23 and GhCPK63
CACTTCGACAAAGACAATAG GTATGGCACGTTTCATGATGT	Gh_A08G2530	GhCPK23	GAAAAGGAAACCCAAAGAGG TGAGAAAAGGAAACCCAAAG	Gh_A09G1033 and Gh_D09G1054	GhCPK24 and GhCPK64
CTTCACCTGTAAGAGATCCA GGGGAGGCTGTATTATTCCT	Gh_A09G1033	GhCPK24	GCTGAAGAAGAGAGACTAA TTGTCAGTTGAGGAAGTAGC	Gh_A09G1067 and Gh_D09G1074	GhCPK25 and GhCPK65
CAAGGGGACACTACACTGAA TGGAGATGTTTTGGTTCAAG	Gh_A09G1067	GhCPK25	AGTGGATGTTTGGAGTGCTG TGATTGTTGAACGTGCAGGA	Gh_A09G1157 and Gh_D09G1163	GhCPK26 and GhCPK66
TGAGGAACTAAGAGATGAGT AGATGAGTTGGCTGATGAGC	Gh_A09G1157	GhCPK26	CATCAGCCTGAACCCAACTG CCTAGGACTAAAGAATCAAG	Gh_A09G1248 and Gh_D09G1249	GhCPK27 and GhCPK67
TGGTGAACCTGACTTCACAT CATCAGCCTGAACCCAACTG	Gh_A09G1248	GhCPK27	AGACAAGCCAATAGGTAGCG GGACGGGAGAATTAACTACG	Gh_A10G0124 and Gh_D10G0130	GhCPK28 and GhCPK68
GGTGGATGAAGCCAGCATCA TAGCAGCAAGCATAAATTGC	Gh_A10G0124	GhCPK28	GCAGCAGTCAGTCTAGCCCCG CTGTCACTAATTGTTGGCCA	Gh_A10G0886 and Gh_D10G0863	GhCPK29 and GhCPK69
CCATTCATGACGTGAACCAT TTAGAGGCCCTGAAAGGCCA	Gh_A10G0886	GhCPK29	GCTCTACTACAAGACGACCC ATGATAGATCCGGTACCAAA	Gh_A10G1195 and Gh_D10G1303	GhCPK30 and GhCPK70
TCGAAGATATTCTTCCCCGA AAGTGGAACTAAGCTACG	Gh_A10G1195	GhCPK30	AGGAGCTTATGAGGATGCAG GGAAGCTTGCCATTCTTTGG	Gh_A10G1756 and Gh_D10G2029	GhCPK31 and GhCPK71
TAAACCAGAGACCAAACAAG CGGTGCGTATGTGCATTAGC	Gh_A10G1756	GhCPK31	GATGCTACGACAAGATCCCA TACGACAAGATCCCAAGGAA	Gh_A11G0213 and Gh_D11G0227	GhCPK32 and GhCPK72
TTCCGACCAGAATCGGACAC TATCTTTCAGGTCTGCAGGA	Gh_A11G0213	GhCPK32	TGAAGAATCTCAAGGACACG TTGCAGTTCGTAGAAGTCGG	Gh_A11G1615 and Gh_D11G1774	GhCPK33 and GhCPK74
TTTCCTCCTTCTCTAACCCA AGCTTCTCCAGCACACCCCGT	Gh_A11G1615	GhCPK33	TTTCACGTCTTCTCTTGCAA TTACACTGAAAGAGCTGCCG	Gh_A11G2941 and Gh_D11G3329	GhCPK34 and GhCPK75
GTAAACATCCTGTCAGCGTC TACCTCGTGGATCGCAAGCT	Gh_A11G2941	GhCPK34	ACATTATAGCAACCTCGCGT TGTTCGGCAGATGTTAGAAC	Gh_A11G3011 and Gh_D11G0314	GhCPK35 and GhCPK73
AGGTAATGCCAAACTCACCT GAGTCACCGAACACGAATAG	Gh_A11G3011	GhCPK35	TCCATGGATTTCCCAAAACG GAATCGAAGACGAACCATG	Gh_A12G0109 and Gh_D12G0121	GhCPK36 and GhCPK76
CAAGCATTACGGACCAGAAG ATAGTGGGAGCATCGATTAT	Gh_A12G0109	GhCPK36	ATGTAGTCCAGAAGTATTG TTTGTGCCGGCAGATCGTGA	Gh_A12G2686 and Gh_D12G2743	GhCPK37 and GhCPK77
ACCGTGTTCCTTACAGGA TCCATCCTGTAGGAAGAACA	Gh_A12G2686	GhCPK37	CTAAGCCTCCTCATGTGAAG ATATTGACCAAGTCTTGCA	Gh_A13G0017 and Gh_D13G0033	GhCPK38 and GhCPK78
TAGCGGCACAATTGATTATG TCTTGCCTAGTCTCCGATTT	Gh_A13G0017	GhCPK38	GAGCTGTCAACCGTTCTGAA AGGAACTGTAACAGCGGGA	Gh_A13G0563 and Gh_D13G0560	GhCPK39 and GhCPK79
TGTGCATTCACCCTTCAGAA TTGACTTCAGCTCTTACCCA	Gh_A13G0563	GhCPK39	CCTCAATAAACTAGAACGCG TGGCTTGCAGAAATGTTTA	Gh_A13G0566 and Gh_D13G0561	GhCPK40 and GhCPK80

CAGCCAAATGGTGCATAATT TATGTACCGAGATTTGCGACT GTGTTAACATCCTGCAGACT AACATCGATACTGACAACAG ATAGGGCAAGCAATGAACAG TTGGTGATGGAATTGTGCGG CTTGCAAGTCGATCGCGAAA CGTGCTCTAATGCAGGCCGT AGATCAACTACGAGGAGTTC CCTGATTAAGATGGAAGGTA CAGAAAATCGGTCACTCTGT CAGAAAATCGGTCACTCTGT TCAACCGTAAAATGAGCGGA CCGACGACAACAGCAACCAA AGCTGAAAGTCTTTCCGAGG ACTTCGGGAGCAACGTAATA CACTTACGTTGCAATAGACA TAGCAGTTCGTAAAAGCCGT GGTCAACATCACCATGGCAA GGATGACAATGCAGTCCATT GCGTTCGGGGTGAAGTCAA TCAATTTGGGAGACGCGTTC TGGCTTAGGGTCTCTTCTCC CCTGTCTGTGCAATAAGCAA GGAAGGGAACAATGCCAAAA AAGGGCAGCTGCACTTGCTA ACAAAAACCATGTCATTGGG CGATCTCGAAGAGGAAACTC TGTGTACAGAGCTTTCCACG GTCGATATCGAAGAGGAAGT CATATAACTGCGTTGTCAAG CAGAGCTTGCTCTAGTTCTT GGTTTCTTCAAGTTGAACAC GATAAACCTGAATGAAAGCG GTCTTTCATTCCAAACGCAT TGGTTGTTGCTGAATTGTGG TCCCAATCCTCAATCCCGGA TGAGGTTCAAATGTTGATGC TGAAAGAGCAGCTGCTTCCA GAAAGAGCAGCTGCTTCCAT	Gh_A13G0566 Gh_A13G1164 Gh_A13G1891 Gh_D01G1194 Gh_D01G2360 Gh_D02G0183 Gh_D02G0663 Gh_D02G1973 Gh_D03G0087 Gh_D03G0609 Gh_D04G0366 Gh_D04G0895 Gh_D04G0900 Gh_D04G1271 Gh_D04G1486 Gh_D05G0748 Gh_D05G1749 Gh_D05G2622 Gh_D05G3156 Gh_D05G3567	GhCPK40 GhCPK41 GhCPK42 GhCPK43 GhCPK44 GhCPK45 GhCPK46 GhCPK47 GhCPK48 GhCPK49 GhCPK50 GhCPK51 GhCPK52 GhCPK53 GhCPK54 GhCPK55 GhCPK56 GhCPK57 GhCPK58 GhCPK59	CAGCCTGCAAAAATAAAACCG CTATCTGATAACAAGCCCGG AAGGAGGTTAACAGCTGCC ACACTTGAAGAACTCAGGCA	Gh_A13G1164 and Gh_D13G1455 Gh_A13G1891 and Gh_D13G2278	GhCPK41 and GhCPK81 GhCPK42 and GhCPK82
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TTAGTTTCGAAAACGACCCA	Gh_D06G2206	GhCPK60
TGACGATGGACCCGAATGAG		
GTGTTGTGTAGGTGATTGCG	Gh_D07G1198	GhCPK61
ATCACCAACCCACTGAATAG		
TGCTCTTTGTAACAGGTGAA	Gh_D07G1228	GhCPK62
GCACTTCACCCATATTATGT		
AATGTTCTTCCCGATCCATT	Gh_D08G0142	GhCPK63
TGATGTAATGTTGACAATT		
GAAGAAGCCAAGAGTCCTAA	Gh_D09G1054	GhCPK64
TAGTGCTTGCTCTAGTTCTT		
TATGCAAGAGAATGAACGAG	Gh_D09G1074	GhCPK65
AGGTTGATGTCTGGAGTGCT		
GTCACATTACTCAGAACCAG	Gh_D09G1163	GhCPK66
AGATGAGTTGGCTGATGAGC		
ACAGACTGCTATAAAGAACG	Gh_D09G1249	GhCPK67
AATCCTGAAGTTGGTAAGAG		
TAGCAGCAAACATAAACCGT	Gh_D10G0130	GhCPK68
GCTATGAAGGAGTATGGAAT		
GTTGCCATAGGCAATGAAAA	Gh_D10G0863	GhCPK69
GGATACACCTACGTTGCCAT		
TTTCCCCCAGATTAACGTTG	Gh_D10G1303	GhCPK70
CTACGACGAGTTCACAACAA		
GAAGTCGGACTGAAAAGAGT	Gh_D10G2029	GhCPK71
CTTGCAAATCGATTGCAAAG		
TCATTATGATGGGTACCGCC	Gh_D11G0227	GhCPK72
CATTATGATGGGTACCGCCT		
AAAGAGTCCCACAGAAACAG	Gh_D11G0314	GhCPK73
AGCTCGGCCGAGGTGAATTT		
AAATCAGTACGCTTCCCGCA	Gh_D11G1774	GhCPK74
CGTGGTTCCTTCATCTTCCA		
GACGTGAAATCGAATTTCTC	Gh_D11G3329	GhCPK75
CGTGCTTGCAGGAGTTCCAA		
CAAGCATTACGGACCGGAGG	Gh_D12G0121	GhCPK76
TAGCGGGAGCATCGATTACG		
TTGATTTTCGCATCAGATCCA	Gh_D12G2743	GhCPK77
TAAGTGTTCTTCTACAGGA		
AATCTGTTTCAGCCGTAATG	Gh_D13G0033	GhCPK78
ATAGCGGCACAATGATTATG		
GGCGAATGCACAACATCTTT	Gh_D13G0560	GhCPK79
GGATGTGGAGGATGCTAGGA		

GGCCTAAAGTGTAAGCTCA	Gh_D13G0561	GhCPK80
TATGTACCGAGATTTGACC		
GTGCCAAGGATCTAGTCTGC	Gh_D13G1455	GhCPK81
ATTGTTGGCCAGAAACATGC		
ATCGGAAAAGAACTAGGTCG	Gh_D13G2278	GhCPK82
AACTAGGTCGTGGTCAATTT		

Table S3 Primers for constructing the vector mixing pool

Downstream primer	Primer name	Upstream primer	Primer name
ttctagctctaaaacCACAGAAACGGAGAAGAGGAtgcaccagccgggaat	GhCPK1	AAGCATCAGATGggcaAACAAAGCACCAGTGGTCTAG	pRGEB32-7S
ttctagctctaaaacGTTCAACCCCAATTCCACCAAtgcaccagccgggaat	GhCPK2		
ttctagctctaaaacACTAGATGGTCTGCTTCATtgcaccagccgggaat	GhCPK3		
ttctagctctaaaacTGTCTTGGACCCTTCCTTGTtgcaccagccgggaat	GhCPK4		
ttctagctctaaaacGGTGGTTGCCGACAACCTTGtgcaccagccgggaat	GhCPK5		
ttctagctctaaaacATTCAAACACTTAGGGAAGGtgcaccagccgggaat	GhCPK6		
ttctagctctaaaacATCCTTTGGTTGCTGCTGTtgcaccagccgggaat	GhCPK7		
ttctagctctaaaacTCCTTTGGTTGCTGCTGTCGtgcaccagccgggaat	GhCPK8		
ttctagctctaaaacCGAAGCTAATTGTTCCACTGtgcaccagccgggaat	GhCPK9		
ttctagctctaaaacTTGATGATCTGTGGTGCAAtgcaccagccgggaat	GhCPK10		
ttctagctctaaaacTTGGTGCTTTTACCCTAAGAtgcaccagccgggaat	GhCPK11		
ttctagctctaaaacGTTTCATGTACGGTGCACtgcaccagccgggaat	GhCPK12		
ttctagctctaaaacTAAGTTCTACCTAAGCTTGtgcaccagccgggaat	GhCPK13		
ttctagctctaaaacAGATATGAACTTGGGTGTGAtgcaccagccgggaat	GhCPK14		
ttctagctctaaaacACGGATCTCTCCATATTTGtgcaccagccgggaat	GhCPK15		
ttctagctctaaaacGAGCAACGTAATATGGACTGtgcaccagccgggaat	GhCPK16		
ttctagctctaaaacTTCACATACTTGTGTCCAACtgcaccagccgggaat	GhCPK17		
ttctagctctaaaacTGTGCAGGGCAATTGTGAAtgcaccagccgggaat	GhCPK18		
ttctagctctaaaacATAATCGATGCTCCACTAtgcaccagccgggaat	GhCPK19		
ttctagctctaaaacCATAATATGGACTTCCAACtgcaccagccgggaat	GhCPK20		
ttctagctctaaaacACGGGTTGGTTCATTACTAtgcaccagccgggaat			
ttctagctctaaaacCGGCAGTTCTGAGTTTCTCtgcaccagccgggaat			
ttctagctctaaaacTCTTCGGCTGGTTTAGGACCtgcaccagccgggaat			
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ttctagctctaaaacACTTCGTCTTCGATATCGACtgcaccagccgggaat			
ttctagctctaaaacCCAACCATCTTCTTAGCtgcaccagccgggaat			
ttctagctctaaaacTGCGAAGCAAAGAAGCAGCGtgcaccagccgggaat			
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ttctagctctaaaacACGTCCTTGTGAGTGGTTAGtgcaccagccgggaat			
ttctagctctaaaacTTGGCCGTGATTCAAATAACtgcaccagccgggaat			
ttctagctctaaaacAAGGCATCGGCTATGCTGAAtgcaccagccgggaat			
ttctagctctaaaacTTGGAATGAAAGACCCAACAtgcaccagccgggaat			
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ttctagctctaaaacTCCGCAGCTTGGCTTTGGATtgcaccagccgggaat			
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ttctagctctaaaacCCCATCCTGTCCAACAAATCtgcaccagccgggaat			

ttctagctctaaaacTCAATCGGGCTTGCTTCTGTgcaccagccgggaat	GhCPK17
ttctagctctaaaacTTGTCAACATCTTCCCTCACTgcaccagccgggaat	GhCPK20
ttctagctctaaaacCCATTAGCCAACAAAACAAGTgcaccagccgggaat	GhCPK21
ttctagctctaaaacGCTGGTGGTGAACCTTCTGCTgcaccagccgggaat	GhCPK22
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ttctagctctaaaacCTCGTCTGGCCAATGTTAGCgcaccagccgggaat	GhCPK24
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ttctagctctaaaacACATCATGAACGTGCCATACgcaccagccgggaat	GhCPK27
ttctagctctaaaacTGGATCTCTTACAGGTGAAGTgcaccagccgggaat	GhCPK28
ttctagctctaaaacAGGAATAATACAGCCTCCCCgcaccagccgggaat	GhCPK29
ttctagctctaaaacTTCAGTGTAGTGTCCCCTTgcaccagccgggaat	GhCPK30
ttctagctctaaaacCTTGAACCAAAACATCTCCATgcaccagccgggaat	GhCPK31
ttctagctctaaaacACTCATCTCTTAGTTCCTCAgcaccagccgggaat	GhCPK32
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ttctagctctaaaacATGTGAAGTCAGGTTACCAgcaccagccgggaat	GhCPK34
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ttctagctctaaaacATGGTTCACGTCATGAATGGgcaccagccgggaat	GhCPK38
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ttctagctctaaaacTTCTGGGCAGGTTAGTAATCtgcaccagccgggaat
ttctagctctaaaacGAGTTGGGATCAGTACACAAtgcaccagccgggaat
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ttctagctctaaaacCTGTTATCGGAATCTATGGTtgcaccagccgggaat
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ttctagctctaaaacCCTCTTTGGGTTTTCTTTTtgcaccagccgggaat
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ttctagctctaaaacCAGTTGGGTTTCAGGCTGATGtgcaccagccgggaat
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ttctagctctaaaacTTTGGTACCGGATCTATCATtgcaccagccgggaat
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ttctagctctaaaacCCAAAGAATGGCAAGCTTCCtgcaccagccgggaat
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ttctagctctaaaacTTCCTTGGGATCCTGTCGTAtgcaccagccgggaat
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ttctagctctaaaacCGGCAGCTCTTTCAGTGTAAtgcaccagccgggaat
ttctagctctaaaacACGCGAGGTTGCTATAATGTtgcaccagccgggaat
ttctagctctaaaacGTTCTAACATCTGCCGAACAtgcaccagccgggaat

GhCPK15 and GhCPK56

GhCPK16 and GhCPK57

GhCPK17 and GhCPK58

GhCPK18 and GhCPK59

GhCPK20 and GhCPK60

GhCPK21 and GhCPK61

GhCPK22 and GhCPK62

GhCPK23 and GhCPK63

GhCPK24 and GhCPK64

GhCPK25 and GhCPK65

GhCPK26 and GhCPK66

GhCPK27 and GhCPK67

GhCPK28 and GhCPK68

GhCPK29 and GhCPK69

GhCPK30 and GhCPK70

GhCPK31 and GhCPK71

GhCPK32 and GhCPK72

GhCPK33 and GhCPK74

GhCPK34 and GhCPK75

GhCPK35 and GhCPK73

ttctagctctaaaacCGTTTTGGGAAATCCATGGAAtgcaccagccgggaat
ttctagctctaaaacCATGGTTCGTCTTCCGATTCtgcaccagccgggaat
ttctagctctaaaacCAATACTTCTGGAGCTACATtgcaccagccgggaat
ttctagctctaaaacTCACGATCTGCCGGCACAAAtgcaccagccgggaat
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ttctagctctaaaacTTCAGAACGGTTGACAGCTCtgcaccagccgggaat
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ttctagctctaaaacCGGTTTTATTTTGCAGGCTGtgcaccagccgggaat
ttctagctctaaaacCCGGGCTTGTTATCAGATAGtgcaccagccgggaat
ttctagctctaaaacGGGCAGCTGTAAACCTCCTTtgcaccagccgggaat
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GhCPK36 amd GhCPK76

GhCPK37 and GhCPK77

GhCPK38 and GhCPK78

GhCPK39 and GhCPK79

GhCPK40 and GhCPK80

GhCPK41 and GhCPK81

GhCPK42 and GhCPK82

Table S4 Validation of vector library construction for pool 1

Targeted gene ID	Targeted gene name	sgRNA sequence	Count	Gene covered
Gh_A01G0621	GhCPK1	TCCTCTTCTCCGTTTCTGTG TGGTGAATTGGGGTTGAAC	4 6	Yes
Gh_A01G1119	GhCPK2	AATGAAGCAGACCATCTAGT ACAAGGAAGGGTCCAAGACA	2 0	Yes
Gh_A02G0144	GhCPK3	GCAAGTTGTCGGCAACCACC CCTTCCCTAAGTGTGTTGAAT	5 4	Yes
Gh_A02G0609	GhCPK4	GACAGCAGCAACCAAAGGAT CGACAGCAGCAACCAAAGGA	2 1	Yes
Gh_A02G1029	GhCPK5	CAGTGAACAATTAGCTTCG ATTGCACCACAGATCATCAA	2 5	Yes
Gh_A02G1635	GhCPK6	TCTTAGGGTAAAAGCACCAA AGTGCACCGTGACATGAAAC	1 4	Yes
Gh_A02G1796	GhCPK7	GCAAGCTTAGGTAGAACTTA TCACACCCAAGTTCATATCT	0 1	Yes
Gh_A03G1505	GhCPK8	GCAAATATGGAGAGATCCGT CAGTCCATATTACGTTGCTC	1 3	Yes
Gh_A04G0148	GhCPK9	GTTGGACACAAGTATGTGAA ATTCACAATTGCCCTGCACA	3 3	Yes
Gh_A04G0467	GhCPK10	GAACAATGCCAATAAGGCTT GGTTGGAAGTCCATATTATG	3 4	Yes
Gh_A04G0780	GhCPK11	GTAGTAATGAACCAACCCGT GAGGAACTCAGAACTGCCG	1 1	Yes
Gh_A04G1372	GhCPK12	GGTCCTAAACCAGCCGAAGA TTGCAGAAAAGTCTTCATG	2 1	Yes
Gh_A04G1429	GhCPK13	GTCGATATCGAAGACGAAGT GCTAAGAAGAAGATGGTTGG	0 3	Yes
Gh_A05G0617	GhCPK14	CGCTGCTTCTTTGCTTCGCA GTCTAATATTGTCGAGCTCA	2 2	Yes
Gh_A05G1571	GhCPK15	CTAACCACTGACAAGGACGT GTTATTTGAATCAGGCCAA	3 3	Yes
Gh_A05G2355	GhCPK16	TTCAGCATAGCCGATGCCTT TGTTGGTCTTTCATTCCAA	1 2	Yes
Gh_A05G2859	GhCPK17	TAACATAAGACAACGTACCG ATCCAAAGCCAAGCTGCGGA	3 2	Yes
Gh_A05G3246	GhCPK18	GGGTTCTGAAGTATGGAAT GTTCGGAGTGACGGCAAATG	5 5	Yes
Gh_A06G0013	GhCPK19	GATTTGTTGGACAGGATGGG ACAGAAGCAAGCCCGATTGA	2 5	Yes
Gh_A06G1772	GhCPK20	AGTGAGGAAGATGTTGACAA CTTGTTTTGTTGGCTAATGG	0 3	Yes

Table S5 Primers for sgRNA high throughput detection

Primer name	Primer sequence
GTL-1-F	GACgcctagAGAAGCATCAGATGGGCAAA
GTL-2-F	GACgcgctaAGAAGCATCAGATGGGCAAA
GTL-3-F	GACgcggatAGAAGCATCAGATGGGCAAA
GTL-4-F	GACgcgtaAGAAGCATCAGATGGGCAAA
GTL-5-F	GACgctacgAGAAGCATCAGATGGGCAAA
GTL-6-F	GACgtacgaAGAAGCATCAGATGGGCAAA
GTL-7-F	GACgtcacgAGAAGCATCAGATGGGCAAA
GTL-8-F	GACgtcgctAGAAGCATCAGATGGGCAAA
GTL-9-F	GACgtcgtaAGAAGCATCAGATGGGCAAA
GTL-10-F	GACgtggacAGAAGCATCAGATGGGCAAA
GTL-11-F	GACgacatgAGAAGCATCAGATGGGCAAA
GTL-12-F	GACgacgtaAGAAGCATCAGATGGGCAAA
GTL-13-F	GACgactgtAGAAGCATCAGATGGGCAAA
GTL-14-F	GACgagtcaAGAAGCATCAGATGGGCAAA
GTL-15-F	GACgatcgaAGAAGCATCAGATGGGCAAA
GTL-16-F	GACgcaccgAGAAGCATCAGATGGGCAAA
GTL-1-R	GACacgtcaGACCCGAATTTGTGGACCTG
GTL-2-R	GACaccatgGACCCGAATTTGTGGACCTG
GTL-3-R	GACacgagcGACCCGAATTTGTGGACCTG
GTL-4-R	GACacagcgGACCCGAATTTGTGGACCTG
GTL-5-R	GACatgatgGACCCGAATTTGTGGACCTG
GTL-6-R	GACatcateGACCCGAATTTGTGGACCTG
GTL-7-R	GACatggtcGACCCGAATTTGTGGACCTG
GTL-8-R	GACatgctgGACCCGAATTTGTGGACCTG
GTL-9-R	GACagcacgGACCCGAATTTGTGGACCTG
GTL-10-R	GACagctcaGACCCGAATTTGTGGACCTG
GTL-11-R	GACagatgtGACCCGAATTTGTGGACCTG
GTL-12-R	GACagacgaGACCCGAATTTGTGGACCTG

Table S6 Primers for gene editing detection of *GhCPKs* mutant library materials

Primer sequence	sgRNA	Gene ID	Gene name
TCCATTTTGGGCAGGTAA AGGTCCTTGGCACTCTCTG	TCCTCTTCTCCGTTTCTGTG	Gh_A01G0621	GhCPK1
AATGACCCAAAGACAACAATC GTGGTCCCGAACTGTCCT	ACAAGGAAGGGTCCAAGACA	Gh_A01G1119	GhCPK2
TAATCAATCATCATCAATACCGA TCGTAATCTTCACGGCATAA	GACAGCAGCAACCAAAGGAT	Gh_A02G0609	GhCPK4
TAATCAATCATCATCAATACCGA TCGTAATCTTCACGGCATAA	CGACAGCAGCAACCAAAGGA	Gh_A02G0609	GhCPK4
AGAAGAAATTATTGGTTTGAAGG GTAAATTGTTTAAAAGCACAGTGA	CAGTGGAAACAATTAGCTTCG	Gh_A02G1029	GhCPK5
AATCTTAGTTTTCTTCAAGTTTC GAGCACTTTACCTTTAGAGCAA	ATTGCACCACAGATCATCAA	Gh_A02G1029	GhCPK5
AAAGTTGCGGCTGAGTGTC AGTCTGGACGTGTTGACTTAAA	AGTGCACCGTGACATGAAAC	Gh_A02G1635	GhCPK6
GATGGATACTGCCAATAGAGG GTCTGTGCCGCCAAATATC	GCAAGCTTAGGTAGAACTTA	Gh_A02G1796	GhCPK7
GAAAAAAGAAGCAAAATCCATT CAATGTCAACGTCAGTCCTTAG	TCACACCCAAGTTCATATCT	Gh_A02G1796	GhCPK7
ATAATGAAACCGATGTCGTCTG ATACATCTGCTTCTGGTCCATAAT	CAGTCCATATTACGTTGCTC	Gh_A03G1505	GhCPK8
TCAACTCAAGCCCTAGGTA CATAAACCGCATAATTTCAATC	GTTGGACACAAGTATGTGAA	Gh_A04G0148	GhCPK9
ATGTGCTGGTGGTGAGTTGT CGAAATCAGTAGCCTTCAAAA	ATTCACAATTGCCCTGCACA	Gh_A04G0148	GhCPK9
TGAGAACACTGCCCTGTAC CGAATTGTCCTTGACCTAACTT	GAACAATGCCAATAAGGCTT	Gh_A04G0467	GhCPK10
GAGAGTTCGGCGTTACTTATCT AACCGCATTGTCGTCTC	GAGGAAACTCAGAACTGCCG	Gh_A04G0780	GhCPK11
ATGGGAAATGTTTGTGCTACA GCCTTTGGCTTAGGGTCT	GGTCCTAAACCAGCCGAAGA	Gh_A04G1372	GhCPK12
CCAGCGAACAAGAAAGCA TCCCTCCTAACATCATCCAC	GTCGATATCGAAGACGAAGT	Gh_A04G1429	GhCPK13
AAGCATTCCGTTTCAATTGG	CGCTGCTTCTTTGCTTCGCA	Gh_A05G0617	GhCPK14

AGGGGAATCTTCATCCTTATT	CGCTGCTTCTTTGCTTCCCA	Gh_A05G0617	GhCPK14
CAAGGAGGATATTGAGGATGTT	GTCTAATATTGTCTGAGCTCA	Gh_A05G0617	GhCPK14
CGTGCGAAGCAAAGAAGC			
ATTGAAAAGGCTACGAAACG	CTAACCACTGACAAGGACGT	Gh_A05G1571	GhCPK15
CATAAGCACCTTTGAACTCCA			
TTGTGGAGTGCCTTCAGC	GTTATTTGAATCACGGCCAA	Gh_A05G1571	GhCPK15
TATCTGGTAAAAGGGAACGAC			
ATTTCTTATTCGGAGGTGTTCT	TGTTGGGTCTTTTCATTCCAA	Gh_A05G2355	GhCPK16
TCATTTAATATCCTGTGTTGGG			
GTTTCGACATAAGAACGGGA	ATCCAAAGCCAAGCTGCGGA	Gh_A05G2859	GhCPK17
ATGACCTTTAGCGACGATTC			
AGAAATCGGTGGTCTGAAAG	GGGTTCTGAACTTATGGAAT	Gh_A05G3246	GhCPK18
TAGCAAAGGATCAAAAAGTAAGTG			
AGAAATCGGTGGTCTGAAAG	GTTCCGAGTGACGGCAAATG	Gh_A05G3246	GhCPK18
TAGCAAAGGATCAAAAAGTAAGTG			
ATGGATCGGGAAGAACATCT	CACTTCGACAAAGACAATAG	Gh_A08G2530	GhCPK23
GCATACCATACTCACGGAGAG			
GCGCATATTATATTGCACCAG	GTATGGCACGTTTCATGATGT	Gh_A08G2530	GhCPK23
CCTTTTAGTTTTCGCCATGAAT			
TTTTACAAGCCAGGTTGAGAT	CTTCACCTGTAAGAGATCCA	Gh_A09G1033	GhCPK24
TTCAGGTCCATATTTCTCTTT			
CCATCACGGTGGAAACAAG	GGGGAGGCTGTATTATTCCT	Gh_A09G1033	GhCPK24
ATGTTGTAGGTGGCTGTAATGT			
GAAGCATTGCGCCAAGC	CAAGGGGACACTACACTGAA	Gh_A09G1067	GhCPK25
AACCTGAACAACCTTCGACAAT			
TCTGCGAGATTCCTTAAACG	TGGAGATGTTTTGGTTCAAG	Gh_A09G1067	GhCPK25
TGCAACAAACTCCTCGTAACT			
TTTACTGCCATCTCCATTCAC	AGATGAGTTGGCTGATGAGC	Gh_A09G1157	GhCPK26
ACCAGTCTAACCTTGCTGTGTC			
CATTTTGGGGTGGTAAGACT	TGGTGAACCTGACTTCACAT	Gh_A09G1248	GhCPK27
TTGGGGTTTCTAACAAGCAT			
TGCCGCTTGTTTGATGTTA	GGTGGATGAAGCCAGCATCA	Gh_A10G0124	GhCPK28
TGTTCCAAAAGTTTGATTTGC			
ATGGGTTGTTTTAGCAGCA	TAGCAGCAAGCATAAATTGC	Gh_A10G0124	GhCPK28
AAGGCTTCAAAGGGACAGA			

CGGTATAAGCATAGTGGGACTT	TTAGAGGCCCTGAAAGGCCA	Gh_A10G0886	GhCPK29
GAACTGAATGAACAGCCATAAT			
TGTACCGATTCCAAAACATTAT	AAGTGGAACACTAAGCTACG	Gh_A10G1195	GhCPK30
AAGTTCTTCGACTTCGATGTAA			
CCCGAATGCCTGATGACT	TAAACCAGAGACCAAACAAG	Gh_A10G1756	GhCPK31
CTGCACTGGACACCCTTTT			
AAATGCAGAGTGAGGTCAACAT	TATCTTTCAGGTCTGCAGGA	Gh_A11G0213	GhCPK32
CGATATTCATCACCTTTTCTT			
ACGCTAAGGAAAAGGATGGA	TTTCCTCCTTCTCTAACCCA	Gh_A11G1615	GhCPK33
CGGGAAGACAACTAGATTACC			
TGTGACGGGATAGACCTTGT	GTAAACATCCTGTCAGCGTC	Gh_A11G2941	GhCPK34
TGGTCTTACTGTGCCTGCTA			
TGGTTGGAAGCCCGTATT	CAAGCATTACGGACCAGAAG	Gh_A12G0109	GhCPK36
ACACATAGAAGTGCCTTGAAAATC			
TATTTCAATTTGTTCTCAGGCTG	ATAGTGGGAGCATCGATTAT	Gh_A12G0109	GhCPK36
GATGTAGCCACTGTTGTCCCTA			
CATTTTCGGATGTGATTCTTTC	ACCGTGTTCTTCCTACAGGA	Gh_A12G2686	GhCPK37
TGCGTCTTCGGTTATTGG			
CATTTTCGGATGTGATTCTTTC	TCCATCCTGTAGGAAGAACA	Gh_A12G2686	GhCPK37
TGCGTCTTCGGTTATTGG			
AAGGAATCTTCGCTGCTGT	TGTGCATTACCCCTTCAGAA	Gh_A13G0563	GhCPK39
CATGACCATCAAACAGATAATAAT			
GGACAGGGACAGTTTGGG	CAGCCAAATGGTGCATAATT	Gh_A13G0566	GhCPK40
CTATCAAACAGTTCGCCTCC			
GGACAGGGACAGTTTGGG	TATGTACCGAGATTTGACT	Gh_A13G0566	GhCPK40
CTATCAAACAGTTCGCCTCC			
AATGCTAATGTGTGACCTGACT	AACATCGATACTGACAACAG	Gh_A13G1164	GhCPK41
TAGATCCCAGTCGAGCTAATC			
GGGACAACCTAATATCGTGG	TTGGTGATGGAATTGTGCGG	Gh_A13G1891	GhCPK42
GCATAATCGTCCGAAGCA			
TGGTGCTAATCTTGCTGAATC	CGTGCTCTAATGCAGGCCGT	Gh_D01G1194	GhCPK43
ATCTGCCTGTGATTCCCAA			
TTGATCTTATCCTTAACCCCTAA	CCTGATTAAGATGGAAGGTA	Gh_D01G2360	GhCPK44
AAACTTCAAATGCCATAGTCA			
TGATGGACACCGACGAGA	CAGAAAATCGGCTCACTCTGT	Gh_D02G0183	GhCPK45

GATTATGTCCGCAACCGTA	CAGAAAACGGTACCTCTGT	Gh_D02G0163	GhCPK45
CTTTACCTGAATACCCCGAC	TCAACCGTAAAATGAGCGGA	Gh_D02G0663	GhCPK46
CCTTCATACAAGCAAGAAAAAT	CCGACGACAACAGCAACCAA	Gh_D02G0663	GhCPK46
TAATCAATCATCATCAATACCGA	AGCTGAAAGTCTTTCCGAGG	Gh_D02G1973	GhCPK47
TCGTAATCTTCACGGCATAA	ACTTCGGGAGCAACGTAATA	Gh_D02G1973	GhCPK47
AGCTGTTTCTCATTAACATGCT	CACTTACGTTGCAATAGACA	Gh_D03G0087	GhCPK48
TTCAAGGTAGAGCCGTATCTTC	TAGCAGTTCGTAAAAGCCGT	Gh_D03G0087	GhCPK48
TGTGTGGTTTACAATGTTAGGC	GGTCAACATCACCATGGCAA	Gh_D03G0609	GhCPK49
ATCAATACCTGCCCAAATG	GCGTTCGGGGTGAAGTCAAA	Gh_D04G0366	GhCPK50
ACCGAAGAAACAAAGTGGG	TGGCTTAGGGTCTCTTCTCC	Gh_D04G0895	GhCPK51
ATCCAGAAGCACAAATCAA	CCTGTCTGTGCAATAAGCAA	Gh_D04G0895	GhCPK51
TTGCCCGTTTTATTAGTAGGA	AAGGGCAGCTGCACTTGCTA	Gh_D04G0900	GhCPK52
CTACAACCTTCTGAGTATTCCGATT	CGATCTCGAAGAGGAAACTC	Gh_D04G1271	GhCPK53
AGAAAGGAAAAAGAAGCAGAA	TGTGTACAGAGCTTTCCACG	Gh_D04G1486	GhCPK54
CAATGTCAACGGCAGTCC	CATATAACTGCGTTGTCAAG	Gh_D05G0748	GhCPK55
TGTAATAAACAGGATGGACAAAT	CAGAGCTTGCTCTAGTTCTT	Gh_D05G0748	GhCPK55
TCAAACCTGAACTATTCAATTCCTT	GGTTTCTTCAAGTTGAACAC	Gh_D05G1749	GhCPK56
CCGACAACGAAGGTGAGA	GTCTTTCATTCCAAACGCAT	Gh_D05G2622	GhCPK57
ATAGGCGTGGACATTGACAT			
GCGTCCGACATGGATATATTA			
GGGCTTCCAACCACATCA			
CTTACGAAGATGCTGTGGCTAT			
ATTTTCGGGCTTGAGGTC			
GAGTTCGGCGTTACTTATCTTT			
GAACCGCATTGTCGTCCT			
ATAAGACTCCCAACATTCGTG			
ATCTCCCTCCTAACATCATCC			
TGGCTCATTGTTTTGTTTCG			
CGCAAAGCAACTTTCTTGAA			
AAAGACAACAGCGGGTAATG			
CAACTTCAGAAACGATTCCTT			
AAAGCCCTTCAAATCTCCC			
ACTGGACTGCACACGAGCT			
ATTTCTTATTCGGAGGTGTTCT			
TCATTTAATATCCTGTGTTGGG			

GGCAGAGGCATTTATGTTGT AAGAAGAATGTCCGCTACACA CAATTATCGTTGGAGGAGCT	TGGTTGTTGCTGAATTGTGG	Gh_D05G2622	GhCPK57
ACGTACACCATTTTCATGTAAAT AGGATTATTGCCAAAGGACA CCGATAACCCGAAATCAGTA	TGAGGTTCAAATGTTGATGC	Gh_D05G3156	GhCPK58
AGGATTATTGCCAAAGGACA CCGATAACCCGAAATCAGTA AGGATTATTGCCAAAGGACA	TGAAAGAGCAGCTGCTTCCA	Gh_D05G3567	GhCPK59
CCGATAACCCGAAATCAGTA AGATGTTCTGTTCCGATTGTATT CTCATTCGGGTCCATCGT	GAAAGAGCAGCTGCTTCCAT	Gh_D05G3567	GhCPK59
AATCAATAATTTCTGAAAATTGT CGCTGTTATCGGTGTCCA	TTAGTTTCGAAAACGACCCA	Gh_D06G2206	GhCPK60
TTCTGAAGTTGACATCGATAATG TTTCCTCATCATTGCCACA	GTGTTGTGTAGGTGATTGCG	Gh_D07G1198	GhCPK61
CAGATTTGCAGATCCTAGTGG TGTAAGTGTTTCATCATTCCGCC	ATCACCAACCCACTGAATAG	Gh_D07G1198	GhCPK61
TAACAAAAGGCGGATGCG ACTATCGTTACCCGCTGTTG	GCACTTCACCCATATTATGT	Gh_D07G1228	GhCPK62
CATTGAAAACACACCCCAT GTTATCGTGCCGCTGTTAT	AATGTTCTTCCCGATCCATT	Gh_D08G0142	GhCPK63
TGCCAATGAAAAGGGAGAC CCAATGTTGTAGGTGGCTTTA	CAACAACAAGAACAATTTCA	Gh_D08G0142	GhCPK63
ACAATAGCGGGTAATCATAGTTT TATCAATATCAACTTCGGAATG	GAAGAAGCCAAGAGTCCTAA	Gh_D09G1054	GhCPK64
CGGTTCCGTTGGATTCTT AATTCAGAGTTCCATCACCATC	TAGTGCTTGCTCTAGTTCTT	Gh_D09G1054	GhCPK64
TCAATGAGATTGTGGGAAGC CTGGATGCACACATTGTCTCT	TATGCAAGAGAATGAACGAG	Gh_D09G1074	GhCPK65
GAAGAAGTCATTACTIONGCCATCA TTGCTTCCCATTCTTCTTATT	AGGTTGATGTCTGGAGTGCT	Gh_D09G1074	GhCPK65
TTTACTGCCATCTCCATTAC ACCAGTCTAACCTTGTCTGTGTC	GTCACATTACTIONCAGAACCAG	Gh_D09G1163	GhCPK66
AGGGAACAAGAAGGGAAATC TGCTCTTAACATTATGGGG	AGATGAGTTGGCTGATGAGC	Gh_D09G1163	GhCPK66
TGTAAGCCAAACGAGAAGGA	ACAGACTGCTATAAAGAACG	Gh_D09G1249	GhCPK67
	AATGCTGAACTTGCTAAGAG	Gh_D09G1249	GhCPK67

CAATGCCTCCCTAAATCCA	AAATCTGAAATTCGTAAGAA	Gh_D10G1247	GhCPK67
CAGTTCAAAGCCAAGCCTA	GTTGCCATAGGCAATGAAAA	Gh_D10G0863	GhCPK69
AAAGAATACCTTCATTTTCTCAAT	GGATACACCTACGTTGCCAT	Gh_D10G0863	GhCPK69
CAGTTCAAAGCCAAGCCTA	CTTGCAAATCGATTGCAAAG	Gh_D10G2029	GhCPK71
AAAGAATACCTTCATTTTCTCAAT	TCATTATGATGGGTACCGCC	Gh_D11G0227	GhCPK72
TTGGGACGACTTTCTTTG	CATTATGATGGGTACCGCCT	Gh_D11G0227	GhCPK72
ACAACATGAACTGCCACTGC	AAAGAGTCCCACAGAAACAG	Gh_D11G0314	GhCPK73
ATGGGTAACGTGAACCGTCC	AGCTCGGCCGAGGTGAATTT	Gh_D11G0314	GhCPK73
CGATGGGTGGAGTGTTGG	AAATCAGTACGCTTCCCCGA	Gh_D11G1774	GhCPK74
ATGGGTAACGTGAACCGTCC	CGTGCTTGCAGGAGTTCCAA	Gh_D11G3329	GhCPK75
CGATGGGTGGAGTGTTGG	CAAGCATTACGGACCGGAGG	Gh_D12G0121	GhCPK76
TGTGTGGGTTTTGGCTTG	TAGCGGGAGCATCGATTACG	Gh_D12G0121	GhCPK76
AAATATCAAGCTGAAATCCATG	TTGATTTTCGCATCAGATCCA	Gh_D12G2743	GhCPK77
TCCGAGTTCTGAAAGATGTGA	TAAGTGTTCTTCCTACAGGA	Gh_D12G2743	GhCPK77
CTTCCGCTTGGAGATTGAC	AATCTGTTTCAGCCGTAATG	Gh_D13G0033	GhCPK78
AACCCTCTGCCACCACTG	GGCGAATGCACAACATCTTT	Gh_D13G0560	GhCPK79
TTCCCAATGGTGTATCGCT	GGATGTGGAGGATGCTAGGA	Gh_D13G0560	GhCPK79
TCACGCCCGTAAAGATTCT	GGCCTAAAGTGTAAGCTCA	Gh_D13G0561	GhCPK80
GCGGTTCGATGCAAAGATA			
GGTTGGAAGCCCCTATTA			
AGAACCAAAGAAAAGAAACATC			
GCTATTTTCATTTGTTCTCAGGC			
GTTATGCTCGGCACAGGC			
TTAAGCACGCCTATGGAATA			
ATCTTTGGCACTGTTGGAAA			
GACACAGACAGGGTATGCTTC			
CTTGCGTCGTCGGTTATT			
ATGGGTAATACTTGTGTAGGACC			
TCTTTAGATGCTACTTCATTCCC			
CGCTGCTGTGCTAAAAGG			
ATTGCTTTGTATCAAGGTTTCAG			
GACAAGGACAGTTTGGGATTA			
CGTATAAAGTATCCTCATAAGCG			
GAAGAGCCATTGATCACCAA			
AATCTGAATCTCCCTCCTAACA			

GCAGAACTGAGAAGGGAATAT AAATAAAGGCTGCTGTAAAGAA	GTGCCAAGGATCTAGTCTGC	Gh_D13G1455	GhCPK81
TCCCACCGTTACTTCACAT CCGTTTCGCTATCGTCTTA	ATCGGAAAAGAACTAGGTCG	Gh_D13G2278	GhCPK82
TCCCACCGTTACTTCACAT CCGTTTCGCTATCGTCTTA	AACTAGGTCGTGGTCAATTT	Gh_D13G2278	GhCPK82
ATGTGCAGGGTTGCAGGT TCAGTCGTCGTGAGCTTCC	CTTTGCATCGAGAAAGGTAC	Gh_A01G1119 and Gh_D01G1194	GhCPK2 and GhCPK43
TGACTTCTCATCTGATCCCTG ATTCGATGGTTTTGATTAGT	TGCTCGACAGAGATACGAAG	Gh_A01G1119 and Gh_D01G1194	GhCPK2 and GhCPK43
ATTTGATTATGGAAGTGTGTGC GAGCCCGAAATCAGTAGGTT	GGAAAGCAGCTAACTTGTGT	Gh_A02G1029 and Gh_D03G0701	GhCPK5 and Gh_D03G0701
GACCCTTTACTTGAGGAGGC GATACCAGGCAAGCACAAA	TGAGTATTCCGATTACCGGA	Gh_A02G1635 and Gh_D03G0087	GhCPK6 and GhCPK48
TGTTGATTTACCGAGTTTGT ATTGTCACAAGAGTGCCAAAT	AACTCCGGAGGAACTACGAA	Gh_A02G1635 and Gh_D03G0087	GhCPK6 and GhCPK48
AGAAAGGAAAAAAGAAGCAGAA CAATGTCAACGGCAGTCC	GTTCTAAATGATCCAAGTGG	Gh_A02G1796 and Gh_D03G0609	GhCPK7 and GhCPK49
GCATTTGTTTTTACAGGATGGT AGAAAACCTGGAACATCTCTGT	TGAGAAGTGGAACCCAACAA	Gh_A04G0148 and Gh_D05G3567	GhCPK9 and GhCPK59
CTTACGAAGATGCTGTGGCTAT GGCTTGAGGTCACGATGC	AAAGGCAGCTGCGCTTGCTA	Gh_A04G0467 and Gh_D04G0900	GhCPK10 and GhCPK52
TCTTGCTGGTTGTAGATTTTATTC AAAGACACTTACCAGCCCAA	TGGCTCCTGAGGTTCTCAA	Gh_A04G0780 and Gh_D04G1271	GhCPK11 and GhCPK53
TCGTGGGTAAATAGATTTCAAA ATCCACCTCCCTTCCCTG	TGGAACCAGACCCAAAGCTC	Gh_A04G0780 and Gh_D04G1271	GhCPK11 and GhCPK53
GATTCTTTGGTGTAGACTATGGA GTCTCAGCGGCAGAACTTA	GTTCCTTTCAGGCCATCCTT	Gh_A04G1372 and Gh_D04G0895	GhCPK12 and GhCPK51
CAAAGAGGATGTGGATGATGTT GTAATGCCCCCTCTGGATAA	GACGATTAAAGGCACGTACG	Gh_A04G1429 and Gh_D04G1486	GhCPK13 and GhCPK54
GGGTCACTCTGGCAAATACTA ATCGTCCACTGTTGTCTGT	CATAGCAGAGACTCTCTG	Gh_A05G2355 and Gh_D05G2622	GhCPK16 and GhCPK57
ATACAAAGCGAAAGGGAAGG GCCTCTGCCAACTCTTTT	TTTGTCAGGATGGTAATACG	Gh_A05G2859 and Gh_D05G3156	GhCPK17 and GhCPK58
CATTGACAACAACGGGACA	GAAAGGGAAGAGAATCTGGT	Gh_A05G3246 and Gh_D04G0366	GhCPK18 and GhCPK50

ACGTCGCTTAATCCAAACTC	CAAAAGGAAATGAGACTGGCAA	Gh_A06G1772 and Gh_D06G2206	GhCPK18 and GhCPK59
AGTGGGTGAGTTCCGAAATA	CATCAAGCAAATAATCTCCG	Gh_A06G1772 and Gh_D06G2206	GhCPK20 and GhCPK60
ATAGAAGAAGTTTCCGAGTTTG	ACATAGCACCCGAAGTTCTT	Gh_A06G1772 and Gh_D06G2206	GhCPK20 and GhCPK60
TTTCGGTTTGTCTGTCTTTATC	GATTACTAACCTGCCAGAA	Gh_A07G1099 and Gh_D07G1198	GhCPK21 and GhCPK61
TACAAGATAACACCAGCACTCC	GGTCATTGCAGGATGTTTAT	Gh_A08G2530 and Gh_D08G0142	GhCPK23 and GhCPK63
CCAACAGGTGAAGAATTCAAAG	GGTCAATTGCAGGATGTTTAT	Gh_A08G2530 and Gh_D08G0142	GhCPK23 and GhCPK63
AAAAGGAAATGAGACTGGCAA	GGTCAATTGCAGGATGTTTAT	Gh_A08G2530 and Gh_D08G0142	GhCPK23 and GhCPK63
CATTGAAAACACACCCCAT	GGTCAATTGCAGGATGTTTAT	Gh_A08G2530 and Gh_D08G0142	GhCPK23 and GhCPK63
GTTATCGTGCCGCTGTTAT	GGTCAATTGCAGGATGTTTAT	Gh_A08G2530 and Gh_D08G0142	GhCPK23 and GhCPK63
TATATCACTCACGGTATATCAAAAA	GGTCAATTGCAGGATGTTTAT	Gh_A08G2530 and Gh_D08G0142	GhCPK23 and GhCPK63
TCATAAAATATAATCAACATCACGC	GGTCAATTGCAGGATGTTTAT	Gh_A08G2530 and Gh_D08G0142	GhCPK23 and GhCPK63
GCTACAAAATGCCAAGAAAAG	GGTCAATTGCAGGATGTTTAT	Gh_A08G2530 and Gh_D08G0142	GhCPK23 and GhCPK63
CTCAGCAATCACCTGGAAAT	GGTCAATTGCAGGATGTTTAT	Gh_A08G2530 and Gh_D08G0142	GhCPK23 and GhCPK63
AGGTGAAAGGTTTACGGAGAT	GGTCAATTGCAGGATGTTTAT	Gh_A08G2530 and Gh_D08G0142	GhCPK23 and GhCPK63
GCCCTTGTGCGGTAGAAT	GGTCAATTGCAGGATGTTTAT	Gh_A08G2530 and Gh_D08G0142	GhCPK23 and GhCPK63
CTGATTATTAGGGTTAGGTTGC	GGTCAATTGCAGGATGTTTAT	Gh_A08G2530 and Gh_D08G0142	GhCPK23 and GhCPK63
TCACGGGTAGAACTTACTCTTA	GGTCAATTGCAGGATGTTTAT	Gh_A08G2530 and Gh_D08G0142	GhCPK23 and GhCPK63
GGCTGTAATCTCTGAAGTGGA	GGTCAATTGCAGGATGTTTAT	Gh_A08G2530 and Gh_D08G0142	GhCPK23 and GhCPK63
CTTTTTCAGTTTGTGTGTTCC	GGTCAATTGCAGGATGTTTAT	Gh_A08G2530 and Gh_D08G0142	GhCPK23 and GhCPK63
ATTTTGTTCACCTTCCAAGTTAC	GGTCAATTGCAGGATGTTTAT	Gh_A08G2530 and Gh_D08G0142	GhCPK23 and GhCPK63
GAGCAGCAGTCAGTCTAGCC	GGTCAATTGCAGGATGTTTAT	Gh_A08G2530 and Gh_D08G0142	GhCPK23 and GhCPK63
CAGCGACGACCAACTCTCT	GGTCAATTGCAGGATGTTTAT	Gh_A08G2530 and Gh_D08G0142	GhCPK23 and GhCPK63
CATGAAACATAAGATCAAAAACCT	GGTCAATTGCAGGATGTTTAT	Gh_A08G2530 and Gh_D08G0142	GhCPK23 and GhCPK63
CACAAGCGAACTAATAGATTCA	GGTCAATTGCAGGATGTTTAT	Gh_A08G2530 and Gh_D08G0142	GhCPK23 and GhCPK63
CGCCTATCCCCAATTCT	GGTCAATTGCAGGATGTTTAT	Gh_A08G2530 and Gh_D08G0142	GhCPK23 and GhCPK63
TGTGCTGGTGGAGAACTTTT	GGTCAATTGCAGGATGTTTAT	Gh_A08G2530 and Gh_D08G0142	GhCPK23 and GhCPK63
TCCTCCTGCTGATTCACAAA	GGTCAATTGCAGGATGTTTAT	Gh_A08G2530 and Gh_D08G0142	GhCPK23 and GhCPK63
TTCCGACAGTGCCAAAGAT	GGTCAATTGCAGGATGTTTAT	Gh_A08G2530 and Gh_D08G0142	GhCPK23 and GhCPK63
CAGATGATCTGCAGTTTATTTCTT	GGTCAATTGCAGGATGTTTAT	Gh_A08G2530 and Gh_D08G0142	GhCPK23 and GhCPK63
GCTTCTTTGTATTCGTCCTGAT	GGTCAATTGCAGGATGTTTAT	Gh_A08G2530 and Gh_D08G0142	GhCPK23 and GhCPK63
CTCCACAACAATCAAAACCAC	GGTCAATTGCAGGATGTTTAT	Gh_A08G2530 and Gh_D08G0142	GhCPK23 and GhCPK63
AGGTTCCATTGACCCTTTG	GGTCAATTGCAGGATGTTTAT	Gh_A08G2530 and Gh_D08G0142	GhCPK23 and GhCPK63
ATCAGATGAACAAGGTACATTCC	GGTCAATTGCAGGATGTTTAT	Gh_A08G2530 and Gh_D08G0142	GhCPK23 and GhCPK63
ATGGGGAATTGTTGTAGATCTC	GGTCAATTGCAGGATGTTTAT	Gh_A08G2530 and Gh_D08G0142	GhCPK23 and GhCPK63
TAAGTAACTCCGAACTCACCTC	GGTCAATTGCAGGATGTTTAT	Gh_A08G2530 and Gh_D08G0142	GhCPK23 and GhCPK63

CGTGCAAGTCAATCTCCAA TTCACAAAGCTCCATAACCA TGTTGTTTAAAAATGTATCCCA TAGTTTGTTTCATTGCCGAGA AGGTAAAGACAGATACTTTTCGC CAAATATCAGCTTCATGTCCAT TAGGGAAACTGGGAATGAAG AAAGGAAAGTTGTCCCGAAT TTTGATCTTCACATTTTTTTCTC ACCGTTTCTTGGGGTCTC GCCCTAATATCCGATAGC ATGATTCAAAAAGAAATGGAGA GCCTGATCCTTTTGTGTTTTC TCCCGTATCTCTGTATCCTTCA AAGAAATAAGGGGATTGAAAGA	ACATTATAGCAACCTCGCGT TCCATGGATTTCCCAAACG ATGTAGCTCCAGAAGTATTG CTAAGCCTCCTCATGTGAAG ATATTCGACCAAGTCTTGCA GAGCTGTCAACCGTTCTGAA TGGCTTGCGAGAAATGTTTA ACACTTGAAGAACTCAGGCA	Gh_A11G3011 and Gh_D11G0314 Gh_A12G0109 and Gh_D12G0121 Gh_A12G2686 and Gh_D12G2743 Gh_A13G0017 and Gh_D13G0033 Gh_A13G0017 and Gh_D13G0033 Gh_A13G0563 and Gh_D13G0560 Gh_A13G0566 and Gh_D13G0561 Gh_A13G1891 and Gh_D13G2278	GhCPK35 and GhCPK73 GhCPK36 and GhCPK76 GhCPK37 and GhCPK77 GhCPK38 and GhCPK78 GhCPK38 and GhCPK78 GhCPK39 and GhCPK79 GhCPK40 and GhCPK80 GhCPK42 and GhCPK82
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Table S7 The other primers used in this study

Primer	Sequence	Note
GhCPK33-OE-S	ATGGGAGCCTGTCTCTCC	Overexpression
GhCPK33-OE-A	CTATAACTTCCGAGAATTCCG	Overexpression
GhCPK74-OE-S	ATGGGAGCCTGTCTCTCC	Overexpression
GhCPK74-OE-A	CTATAACTTCCGAGAATTCCG	Overexpression
GhCPK33-QRT-S	CACCGCAAACATCAACCCT	qRT-PCR
GhCPK33-QRT-A	GTAGAACTTGGCTTCCCTTTGA	qRT-PCR
GhCPK74-QRT-S	CACCGCAAACATCAACCCT	qRT-PCR
GhCPK74-QRT-A	CGAACTTGGCTTCCCTTTGA	qRT-PCR
GhCPK33-104-S	CAGGTACCCGGGGATCC ATGGGAGCCTGTCTCTCC	BiFC
GhCPK33-104-A	CTGCCACCGCCGTCGAC CTATAACTTCCGAGAATTCCG	BiFC
GhCPK74-104-S	CAGGTACCCGGGGATCC ATGGGAGCCTGTCTCTCC	BiFC
GhCPK74-104-A	CTGCCACCGCCGTCGAC CTATAACTTCCGAGAATTCCG	BiFC
GhCPK33-BD-S	ATGGAGGCCGAATTC ATGGGAGCCTGTCTCTCC	Y2H
GhCPK33-BD-A	GCAGGTGACGGATCC CTATAACTTCCGAGAATTCCG	Y2H
GhCPK74-BD-S	ATGGAGGCCGAATTC ATGGGAGCCTGTCTCTCC	Y2H
GhCPK74-BD-A	GCAGGTGACGGATCC CTATAACTTCCGAGAATTCCG	Y2H
GhCPK33-771-S	CTCGGTACCCGGGGATCC ATGGGAGCCTGTCTCTCC	LCI
GhCPK33-771-A	TACGAGATCTGGTTCGAC CTATAACTTCCGAGAATTCCG	LCI
GhCPK74-771-S	CTCGGTACCCGGGGATCC ATGGGAGCCTGTCTCTCC	LCI
GhCPK74-771-A	TACGAGATCTGGTTCGAC CTATAACTTCCGAGAATTCCG	LCI
GhCPK33-BP-S	GGGGACAAGTTTGTACAAAAAAGCAGGCTCA ATGGGAGCCTGTCTCTCC	Subcellular Localization
GhCPK33-BP-A	GGGGACCACTTTGTACAAGAAAGCTGGGTA CTATAACTTCCGAGAATTCCG	Subcellular Localization
GhCPK74-BP-S	GGGGACAAGTTTGTACAAAAAAGCAGGCTCA ATGGGAGCCTGTCTCTCC	Subcellular Localization
GhCPK74-BP-A	GGGGACCACTTTGTACAAGAAAGCTGGGTA CTATAACTTCCGAGAATTCCG	Subcellular Localization
GhSAMS1-AD-S	CAGATTACGCTCATATG ATGGAGACCTTTCTATTACATC	Y2H
GhSAMS1-AD-A	TGCTTGGGTGGAATTC TTAAGATTGGGGCTTGTC	Y2H
GhSAMS2-AD-S	CAGATTACGCTCATATG ATGGAGACCTTTCTATTACATCT	Y2H

GhSAMS2-AD-A	TGCTTGGGTGGAATTC TTAAGACTGAGGCTTCTCCCA	Y2H
GhSAMS1-106-S	AGGACGCCGGCGGATCC ATGGAGACCTTTCTATTACATC	BiFC
GhSAMS1-106-A	AAGCTCTGCAGGTCGAC TTAAGATTGGGGCTTGTCC	BiFC
GhSAMS2-106-S	AGGACGCCGGCGGATCC ATGGAGACCTTTCTATTACATCT	BiFC
GhSAMS2-106-A	AAGCTCTGCAGGTCGAC TTAAGACTGAGGCTTCTCCCA	BiFC
GhSAMS1-772-S	GGCGGTACCCGGGATCCA ATGGAGACCTTTCTATTACATC	LCI
GhSAMS1-772-A	AAGCTCTGCAGGTCGAC TTAAGATTGGGGCTTGTCC	LCI
GhSAMS2-772-S	GGCGGTACCCGGGATCCA ATGGAGACCTTTCTATTACATCT	LCI
GhSAMS2-772-A	AAGCTCTGCAGGTCGAC TTAAGACTGAGGCTTCTCCCA	LCI
GhSAMS1-QRT-S	CATCAAGCCTGTCATCCCT	qRT-PCR
GhSAMS1-QRT-A	CCAGCCACCATAAGTGTCAA	qRT-PCR
GhSAMS2-QRT-S	AAACATGCACCAAGACCAAC	qRT-PCR
GhSAMS2-QRT-A	TCAAGACCCACATCATCAGAA	qRT-PCR
GhSAMS1-VIGS-S	CAAAATGGCATGCCTGCAGACTAGT TATGCCACTGATGAAACCC	VIGS
GhSAMS1-VIGS-A	GAATTCACTAGACCTAGGGGCGCGCC TTGATGACATGCTCCTTGAGG	VIGS
GhSAMS2-VIGS-S	CAAAATGGCATGCCTGCAGACTAGT GCCGCTCTATCGGATTTGT	VIGS
GhSAMS2-VIGS-A	GAATTCACTAGACCTAGGGGCGCGCC GTGCCATTCTTCCTAACCTCA	VIGS