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Corrigendum: Genome-wide identification of genes encoding cystathionine beta synthase domain-containing proteins in wheat and its relationship with anther male sterility under heat stress

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KEYWORDS

***Triticum aestivum* L., gene repetition events, cystathionine beta synthase, synteny analysis, gene expression**

A Corrigendum on

Genome-wide identification of genes encoding cystathionine beta synthase domain-containing proteins in wheat and its relationship with anther male sterility under heat stress

by Liu H, Wang Q, Xie L, Xu K, Zhang F, Ruan X, Li L and Tan G (2022) *Front. Plant Sci.* 13:1061472. doi: 10.3389/fpls.2022.1061472

In the published article, there was an error in the article title. Instead of "*Genome-wide identification of cystathionine beta synthase genes in wheat and its relationship with anther male sterility under heat stress*", it should be "*Genome-wide identification of genes encoding cystathionine beta synthase domain-containing proteins in wheat and its relationship with anther male sterility under heat stress*".

In the published article, there was an error in the legend for

Table 1, As requested by the reviewer, we have added an explanation of these genes in the footnotes of Table 1. The corrected legend and footnote appear below.

"Table 1. Information about the *TaCBS* members in wheat.

[a]Length of the amino acid sequence. [b]Molecular weight of the amino acid sequence. [c]Isoelectric point of the TaCBS proteins. [d]Number of transmembrane domains, as predicted by the TMHMM server. [e]Protein subcellular localization prediction by the BUSCA web server. The bold values indicate the selected transcript representing this gene. All *TaCBS* genes in the table indicate genes encoding cystathionine beta synthase domain-containing proteins."

In the published article, there was an error in the legend for Figure 3, As requested by the reviewer, we have modified the legend of Figure 3. The corrected legend appears below.

"Figure 3 Chromosomal localization of the genes encoding CDCPs in the wheat genome. The positions on the linkage map have been determined. 66 *TaCBS* members are mapped to 21 chromosomes (1A-7A, 1B-7B, and 1D-7D). Green colored lines represent the connections between duplication events. Megabase pairs (Mb) are used to measure the scale."

In the published article, there was an error in the legend for Figure 4. As requested by the reviewer, we have modified the legend of Figure 4. The corrected legend appears below.

"Figure 4 Genome-wide syntenic and localization analysis of the genes encoding CDCPs in wheat. The genes encoding CDCPs in wheat were mapped to different chromosomes with a cyan color. The red line indicates the synteny of gene pairs within the *TaCBS*. On the chromosome's outermost side are the *TaCBS* members names."

In the published article, there was an error in the legend for Figure 7. As requested by the reviewer, we have modified the first sentence of the legend of Figure 7. The corrected legend appears below.

"Figure 7 The differential expression of representative genes encoding CDCPs in different tissues by RNA-seq data reported in WheatOmics."

In the published article, there was an error in the legend for Figure 8. As requested by the reviewer, we have modified the first sentence of the legend of Figure 8.The corrected legend appears below.

"Figure 8 Enrichment analysis of GO and KEGG Pathway for the 66 TaCBS members considered in this study."

In the published article, there was an error in the legend for Figure 9. As requested by the reviewer, we have modified the first and second sentences of the legend of Figure 9. The corrected legend appears below.

"Figure 9 miRNAs targeting genes encoding CDCPs in wheat. (A) miRNA target network map for genes encoding CDCPs, with indigo boxes corresponding to *TaCBS* members and brownish yellow round shapes corresponding to predicted miRNAs."

In the published article, there was an error in the legend for Figure 11. As requested by the reviewer, we have modified the legend of Figure 11. The corrected legend appears below.

"Figure 11 The differential expression of 6 genes encoding CDCPs in Normal and HT-ms anther tissues by qRT-PCR (A, C, E, G, I, and K) and different tissues by RNA-seq data (B, D, F, H, J, and L). The x-axes and y-axes indicate the different stage in the Normal and HT-ms anthers and the relative gene expression levels, respectively. The electronic Fluorescent Pictograph (eFP) of wheat plant were visualized by Adobe Illustrator CS5 and TBtools. SPSS Statistics 23 software was used to analyze the data as means of three replicates ± standard error. Tukey's method was used to test significantly different means between parameters based on analysis of variance (ANOVA) at 95% confidence levels. Capped lines indicate standard error. $^{*}P < 0.05$; $^{**}P < 0.01$".

In the published article, there was an error in the **Supplementary Material**. As requested by the reviewer, we have modified **Figure S1** and the legend of **Figure S1** within Presentation 1. The correct figure and legend appears below.

"**Figure S1** Results of classification and conserved domains predicted using the SMART web site.

The CBS domain, the transmembrane region, the Phox and Bem1 (PB1) domain and the complexity region are represented by the pentagonal element, the blue column, the triangular element and the pink rectangular element, respectively. Other domains include DUF21, voltage chloride channel (Voltage CLC), and Carbohydrate binding domain (CBD). The classification according to one pair or two pairs of CBS domains (CBSX and CBSCBS). Other classifications are named by the other structural domains they contain for labeling, such as CBSCLC, CBSCBSCBD, CBSDUF1 and CBSCBSPB1. The 66 identified members corresponding to this protein are shown in parentheses."

A correction has been made to the **Abstract**. As requested by the reviewer, we have modified the text. This sentence previously stated:

"Together with anther phenotypes, paraffin sections, starch potassium iodide staining, and qRT-PCR data, we hypothesized that the *TaCBS* gene has a very important connection with the heat-stressed sterility process in wheat, and these data provide a basis for further insight into their relationship."

The corrected sentence appears below:

"Together with anther phenotypes, paraffin sections, starch potassium iodide staining, and qRT-PCR data, we hypothesized that the genes encoding CDCPs has a very important connection with the heat-stressed sterility process in wheat, and these data provide a basis for further insight into their relationship."

A correction has been made to **Introduction**, paragraph 4. As requested by the reviewer, we have modified the text.

These sentences previously stated:

"In addition, research on the CBS gene family has mainly concentrated on soybean, rice, cotton and Arabidopsis (Kushwaha et al., 2009; Ali et al., 2021; Hao et al., 2021), but there is no report on wheat. Therefore, considering the above studies, we speculate that CBS gene may play an important role in regulating fertility, especially in indehiscence of sterile anther in wheat, and these issues are worthy of further exploration. In this study, the genome-wide members of the wheat CBS gene family were identified by bioinformatics methods, and the physiological and biochemical properties, conserved motifs, cis-elements, gene collinearity and gene expression patterns of all family members were comprehensively analyzed. qRT-PCR was performed for the expression patterns of 6 TaCBS genes in wheat anther indehiscence under high-temperature stress conditions. These results provide a theoretical basis and technical reference for further analysis of the functional roles of the CBS gene family in wheat male sterility."

The corrected sentence appears below:

"In addition, research on the gene family encoding CDCPs has mainly concentrated on soybean, rice, cotton and *Arabidopsis* (Kushwaha et al., 2009; Ali et al., 2021; Hao et al., 2021), but there is no report on wheat. Therefore, considering the above studies, we speculate that genes encoding CDCPs may play an important role in regulating fertility, especially in indehiscence of sterile anther in wheat, and these issues are worthy of further exploration. In this study, the genome-wide members of the wheat gene family encoding CDCPs

TABLE 1 Information about the TaCBS members in wheat.

Gene Name	Gene Locus	CDS Length (bp)	AA[a]	MW[b] (kDa)	pI[c]	TMD[d]	SLP[e]
TaCBS1	TraesCS1A02G170000.1	1122	373	38.88	5.35	0	mitochondrion
TaCBS2	TraesCS1B02G187200.1	1122	373	38.95	5.47	0	mitochondrion
TaCBS3	TraesCS1D02G167600.1	1122	373	38.93	5.47	0	mitochondrion
TaCBS4	**TraesCS2A02G177000.1**	1362	453	48.06	4.82	0	cytoplasm
	TraesCS2A02G177000.2	1035	344	36.28	5.36	0	cytoplasm
TaCBS6	TraesCS2A02G281700.1	1278	425	46.95	5.45	0	nucleus
TaCBS6	TraesCS2A02G289200.1	1047	348	38.64	5.92	0	nucleus
	TraesCS2A02G289200.2	1371	456	50.92	5.56	0	nucleus
	TraesCS2A02G289200.3	1365	454	50.68	5.56	0	nucleus
	TraesCS2A02G289200.4	1314	437	48.82	5.58	0	nucleus
TaCBS7	TraesCS2A02G360600.1	1515	504	54.71	6.61	0	chloroplast
TaCBS8	TraesCS2B02G002100.1	666	221	23.38	7.87	0	chloroplast thylakoid membrane
TaCBS9	TraesCS2B02G203900.1	1260	419	44.39	4.97	0	cytoplasm
	TraesCS2B02G203900.2	1362	453	47.96	4.82	0	cytoplasm
	TraesCS2B02G203900.3	1149	382	40.74	5.00	0	nucleus
TaCBS10	TraesCS2B02G299000.1	1278	425	46.91	5.62	0	nucleus
TaCBS11	TraesCS2B02G305800.1	1050	349	38.69	6.00	0	nucleus
	TraesCS2B02G305800.2	1239	412	45.59	5.50	0	extracellular space
	TraesCS2B02G305800.3	1185	394	43.76	6.15	0	nucleus
	TraesCS2B02G305800.4	1371	456	50.89	5.74	0	nucleus
	TraesCS2B02G305800.5	1365	454	50.65	5.74	0	nucleus
	TraesCS2B02G305800.6	1395	464	51.83	5.74	0	nucleus
	TraesCS2B02G305800.7	1068	355	39.38	5.83	0	nucleus
	TraesCS2B02G305800.8	1164	387	43.34	6.76	0	nucleus
	TraesCS2B02G305800.9	1032	343	38.22	5.64	0	extracellular space
TaCBS12	TraesCS2D02G015500.1	666	221	23.52	8.73	0	chloroplast thylakoid membrane
	TraesCS2D02G015500.2	672	223	23.94	8.71	0	chloroplast thylakoid lumen
TaCBS13	**TraesCS2D02G185000.1**	1362	453	48.00	4.82	0	cytoplasm
	TraesCS2D02G185000.2	1035	344	36.33	5.23	0	cytoplasm
TaCBS14	TraesCS2D02G280600.1	1278	425	46.95	5.45	0	nucleus
TaCBS15	TraesCS2D02G287200.1	1047	348	38.70	5.65	0	nucleus
	TraesCS2D02G287200.2	1365	454	50.76	5.45	0	nucleus
	TraesCS2D02G287200.3	1068	355	39.48	5.42	0	nucleus
	TraesCS2D02G287200.4	1371	456	51.00	5.45	0	nucleus
	TraesCS2D02G287200.5	1164	387	43.45	6.51	0	nucleus
TaCBS16	TraesCS2D02G599900.1	1149	382	39.76	4.92	0	nucleus
TaCBS17	TraesCS3A02G226700.1	1206	401	44.09	5.67	0	nucleus
TaCBS18	TraesCS3A02G427100.1	1197	398	42.18	6.01	0	nucleus
TaCBS19	TraesCS3A02G429700.1	1290	429	46.99	5.14	0	nucleus

(Continued)

TABLE 1 Continued

Gene Name	Gene Locus	CDS Length (bp)	AA[a]	MW[b] (kDa)	pI[c]	TMD[d]	SLP[e]
TaCBS20	TraesCS3A02G433400.1	1125	374	40.66	6.23	1	endomembrane system
	TraesCS3A02G433400.2	1653	550	58.85	7.25	1	nucleus
TaCBS21	TraesCS3A02G445200.1	1632	543	58.45	6.10	1	chloroplast
TaCBS22	TraesCS3B02G257800.1	1209	402	44.21	5.70	0	nucleus
TaCBS23	TraesCS3B02G463800.1	1197	398	42.21	5.93	0	nucleus
TaCBS24	TraesCS3B02G467600.1	1323	440	47.71	5.22	0	nucleus
TaCBS25	TraesCS3B02G469200.1	1125	374	40.62	6.22	1	endomembrane system
	TraesCS3B02G469200.2	1650	549	58.75	7.24	1	nucleus
TaCBS26	TraesCS3B02G479900.1	1392	463	49.86	5.02	1	chloroplast
TaCBS27	TraesCS3B02G573900.1	1128	375	40.53	5.42	0	nucleus
TaCBS28	TraesCS3D02G224700.1	1218	405	44.19	5.45	0	nucleus
TaCBS29	TraesCS3D02G422700.1	1197	398	42.23	5.93	0	nucleus
TaCBS30	TraesCS3D02G425000.1	1293	430	47.07	5.20	0	nucleus
TaCBS31	TraesCS3D02G426800.1	1656	551	59.03	7.25	1	nucleus
TaCBS32	TraesCS3D02G438100.1	1632	543	58.54	6.23	1	chloroplast
TaCBS33	**TraesCS3D02G513700.1**	1578	525	56.14	6.77	1	chloroplast
TaCBS34	**TraesCS4A02G206600.1**	1635	544	58.23	6.40	1	chloroplast
TaCBS35	TraesCS4A02G247300.1	618	205	22.40	9.14	0	mitochondrion
TaCBS36	TraesCS4A02G320000.1	1494	497	54.40	6.25	0	nucleus
	TraesCS4A02G320000.2	1467	488	53.55	6.34	0	nucleus
TaCBS37	TraesCS4B02G022400.1	1464	487	54.21	6.42	4	endomembrane system
TaCBS38	TraesCS4B02G067600.1	642	213	23.39	9.10	0	mitochondrion
TaCBS39	TraesCS4B02G110100.1	1632	543	58.02	6.25	1	chloroplast
	TraesCS4B02G110100.2	1764	587	63.71	5.81	0	nucleus
TaCBS40	TraesCS4D02G066600.1	618	205	22.40	9.14	0	mitochondrion
TaCBS41	TraesCS4D02G107800.1	1635	544	58.17	6.58	1	chloroplast
TaCBS42	TraesCS5A02G053000.1	618	205	23.05	7.92	0	mitochondrion
TaCBS43	TraesCS5A02G118800.1	1635	544	58.79	6.78	1	chloroplast
TaCBS44	TraesCS5A02G209500.1	1623	540	58.71	6.59	1	mitochondrion
TaCBS45	TraesCS5B02G063400.1	618	205	23.10	8.65	0	mitochondrion
TaCBS46	TraesCS5B02G117400.1	1464	487	52.77	6.30	0	chloroplast
	TraesCS5B02G117400.2	1641	546	59.02	7.70	1	chloroplast
TaCBS47	TraesCS5B02G207600.1	1626	541	58.75	6.40	1	mitochondrion
TaCBS48	**TraesCS5B02G559100.1**	1494	497	54.31	6.05	0	nucleus
	TraesCS5B02G559100.2	1467	488	53.49	6.14	0	nucleus
TaCBS49	TraesCS5D02G064300.1	618	205	23.05	7.92	0	mitochondrion
TaCBS50	**TraesCS5D02G130200.1**	1629	542	58.49	6.82	1	chloroplast
	TraesCS5D02G130200.2	1452	483	52.28	6.13	0	chloroplast
TaCBS51	TraesCS5D02G215700.1	1626	541	58.81	8.40	1	mitochondrion

(Continued)

TABLE 1 Continued

Gene Name	Gene Locus	CDS Length (bp)	AA[a]	MW[b] (kDa)	pI[c]	TMD[d]	SLP[e]
TaCBS52	TraesCS5D02G565200.1	1125	374	41.04	6.60	0	extracellular space
	TraesCS5D02G565200.2	1467	488	53.59	6.31	0	nucleus
	TraesCS5D02G565200.3	1494	497	54.42	6.22	0	nucleus
TaCBS53	TraesCS6A02G132700.1	1317	438	46.55	5.17	0	nucleus
TaCBS54	TraesCS6A02G235600.1	1176	391	40.70	5.41	0	mitochondrion
TaCBS55	TraesCS6A02G283600.1	1791	596	63.61	6.06	7	endomembrane system
	TraesCS6A02G283600.3	2346	781	83.05	6.77	9	organelle membrane
TaCBS56	TraesCS6A02G392100.1	651	216	23.59	8.64	0	chloroplast
	TraesCS6A02G392100.2	654	217	23.72	8.64	0	chloroplast
	TraesCS6A02G392100.3	636	211	23.11	8.30	0	chloroplast
TaCBS57	TraesCS6B02G160900.1	1311	436	46.51	5.11	0	nucleus
TaCBS58	TraesCS6B02G264200.1	1167	388	40.53	5.35	0	nucleus
TaCBS59	TraesCS6B02G432300.1	654	217	23. 41	7.62	0	nucleus
	TraesCS6B02G432300.2	657	218	23.54	7.62	0	nucleus
	TraesCS6B02G432300.3	606	201	21.57	6.89	0	chloroplast
TaCBS60	TraesCS6D02G122400.1	1323	440	46.85	5.37	0	nucleus
TaCBS61	TraesCS6D02G218300.1	1158	385	40.07	5.43	0	nucleus
TaCBS62	TraesCS6D02G264100.1	2358	785	83.62	6.59	9	organelle membrane
TaCBS63	TraesCS6D02G378000.1	651	216	23.49	8.31	0	chloroplast
	TraesCS6D02G378000.2	636	211	23.01	7.64	0	chloroplast
	TraesCS6D02G378000.3	747	248	26.92	6.22	0	nucleus
	TraesCS6D02G378000.4	606	201	21.77	7.66	0	chloroplast
TaCBS64	TraesCS7A02G240700.2	2232	743	79.25	6.19	8	endomembrane system
TaCBS65	TraesCS7B02G136300.1	2232	743	79.11	6.19	8	endomembrane system
TaCBS66	TraesCS7D02G239700.2	2232	743	79.23	6.10	8	endomembrane system
	TraesCS7D02G239700.3	2241	746	79.55	6.49	8	endomembrane system

[a]Length of the amino acid sequence. [b]Molecular weight of the amino acid sequence. [c]Isoelectric point of the TaCBS proteins. [d]Number of transmembrane domains, as predicted by the TMHMM server. [e]Protein subcellular localization prediction by the BUSCA web server. The bold values indicate the selected transcript representing this gene. All *TaCBS* genes in the table indicate genes encoding cystathionine beta synthase domain-containing proteins.

were identified by bioinformatics methods, and the physiological and biochemical properties, conserved motifs, cis-elements, gene collinearity and gene expression patterns of all family members were comprehensively analyzed. qRT-PCR was performed for the expression patterns of 6 *TaCBS* genes in wheat anther indehiscence under high-temperature stress conditions. These results provide a theoretical basis and technical reference for further analysis of the functional roles of the gene family encoding CDCPs in wheat male sterility.”

A correction has been made to **Materials and Methods**, **Phylogenetic tree analysis of wheat CBS gene family** heading. The heading has been corrected to **Phylogenetic tree analysis of wheat gene family encoding CDCPs**.

A correction has been made in **Materials and methods, Phylogenetic tree analysis of wheat gene family encoding CDCPs**. As requested by the reviewer, we have modified the text.

This sentence previously stated:

“MEGA-X software was used to construct a phylogenetic tree of the CBS gene family from the above plant species and wheat.”

“The corrected sentence appears below:

“MEGA-X software was used to construct a phylogenetic tree of the gene family encoding CDCPs from the above plant species and wheat.”

A correction has been made to the **Materials and methods**, **Analysis of protein domain, exon and intron structure, and**

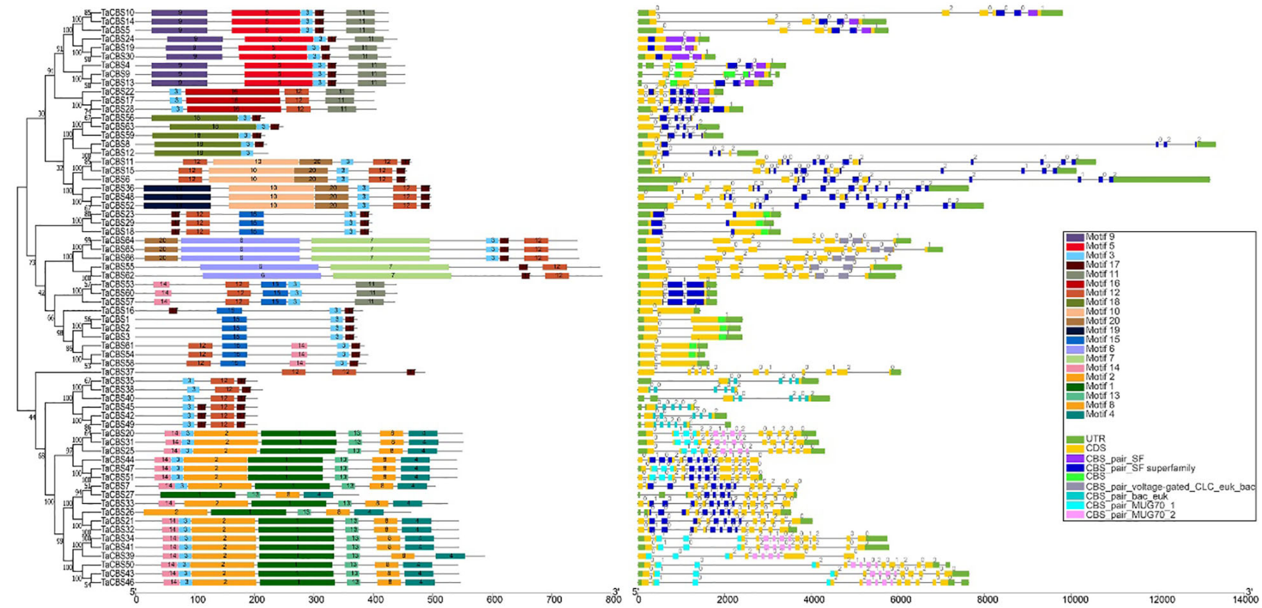

FIGURE 2
Phylogenetic relationship, conserved motifs, gene structure, and conserved domain of TaCBS proteins. Different colors are used to represent different motifs in the figure and in the upper right corner. Black lines represent non-conserved sequences in MEME results and introns in the exon-intron structure, respectively. The phylogenetic tree is constructed similarly to Figure 1.

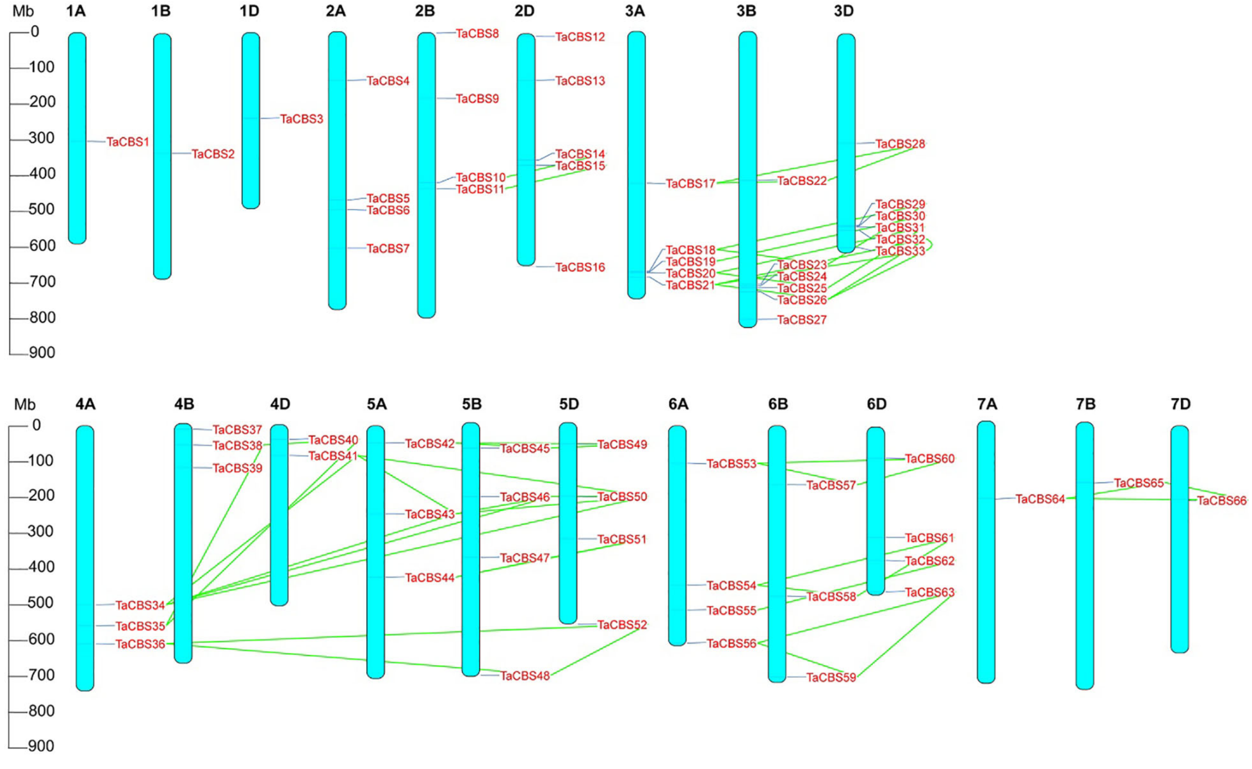

FIGURE 3
Chromosomal localization of the genes encoding CDCPs in the wheat genome. The positions on the linkage map have been determined. 66 TaCBS members are mapped to 21 chromosomes (1A-7A, 1B-7B, and 1D-7D). Green colored lines represent the connections between duplication events. Megabase pairs (Mb) are used to measure the scale.

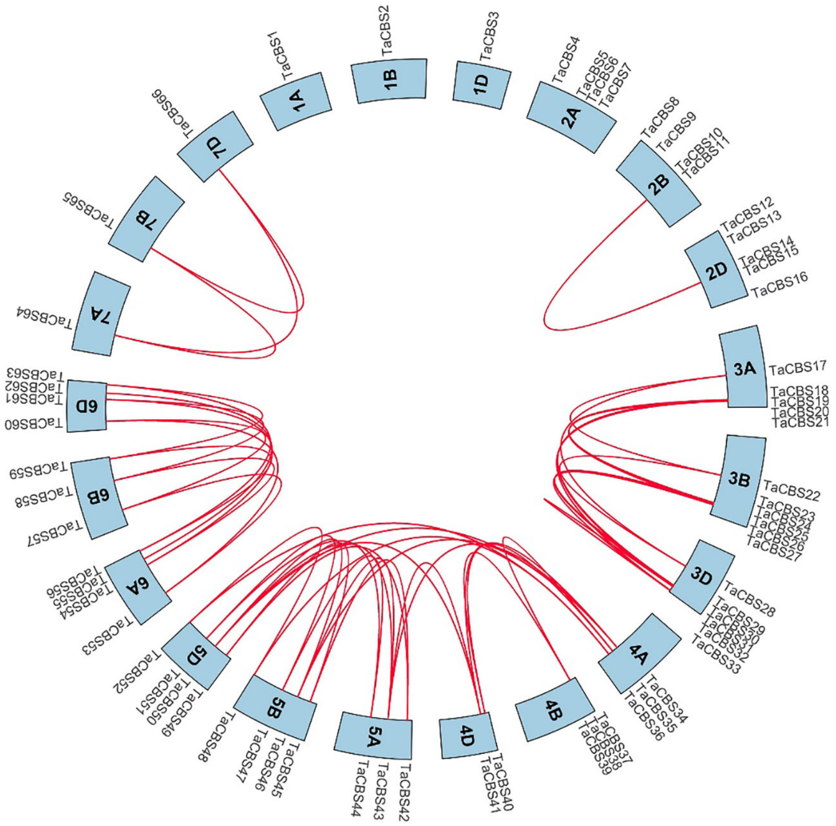

FIGURE 4
Genome-wide syntenic and localization analysis of the genes encoding CDCPs in wheat. The genes encoding CDCPs in wheat were mapped to different chromosomes with a cyan color. The red line indicates the synteny of gene pairs within the *TaCBS*. On the chromosome's outermost side are the *TaCBS* members names.

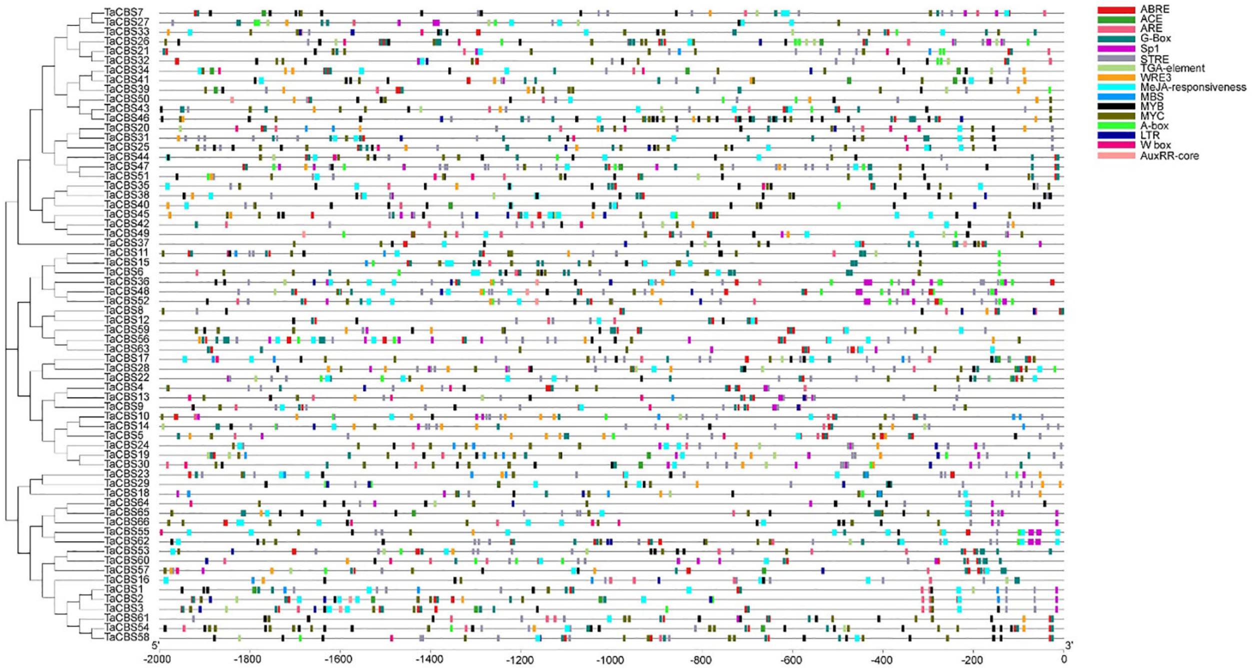

FIGURE 6
Kind, quantity and position of cis-acting elements in TaCBSs. 2000 bp nucleotide length of the gene promoter is indicated on the horizontal axis; color codes indicate different cis-acting elements. The phylogenetic tree is drawn in the same way as Figure 2.

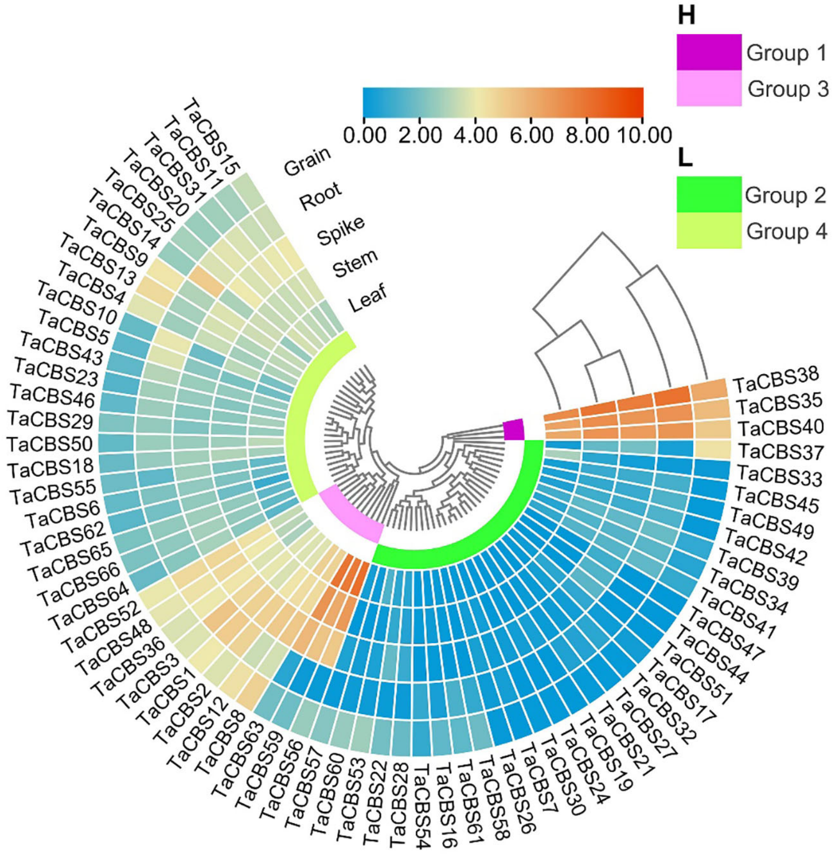

FIGURE 7
The differential expression of representative genes encoding CDCPs in different tissues by RNA-seq data reported in WheatOmics. The legend represents the log transcripts per kilobase million (TPM) values. The transcriptome expression results are shown as a heat map in blue/yellow/brownish red colors. The clusters of low and high expression are represented by different colors.

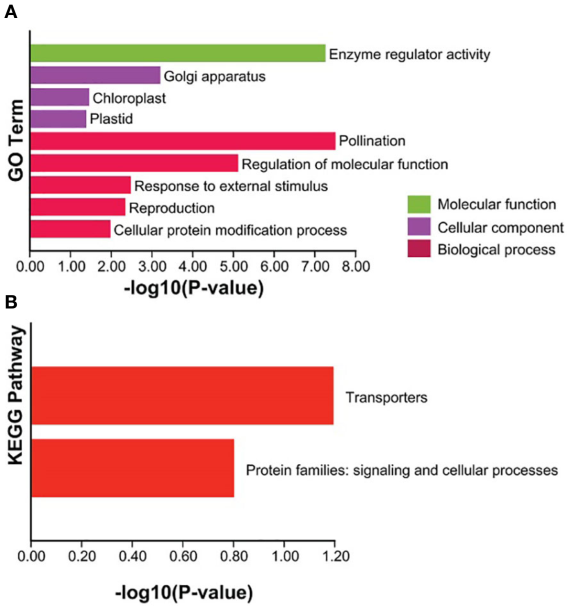

FIGURE 8
Enrichment analysis of GO and KEGG Pathway for the 66 TaCBS members considered in this study. **(A)** GO enrichment. Three main categories of GO enrichment are shown in green terms, purple terms, and dark red terms, respectively. **(B)** KEGG enrichment. KEGG enrichment are shown in red terms.

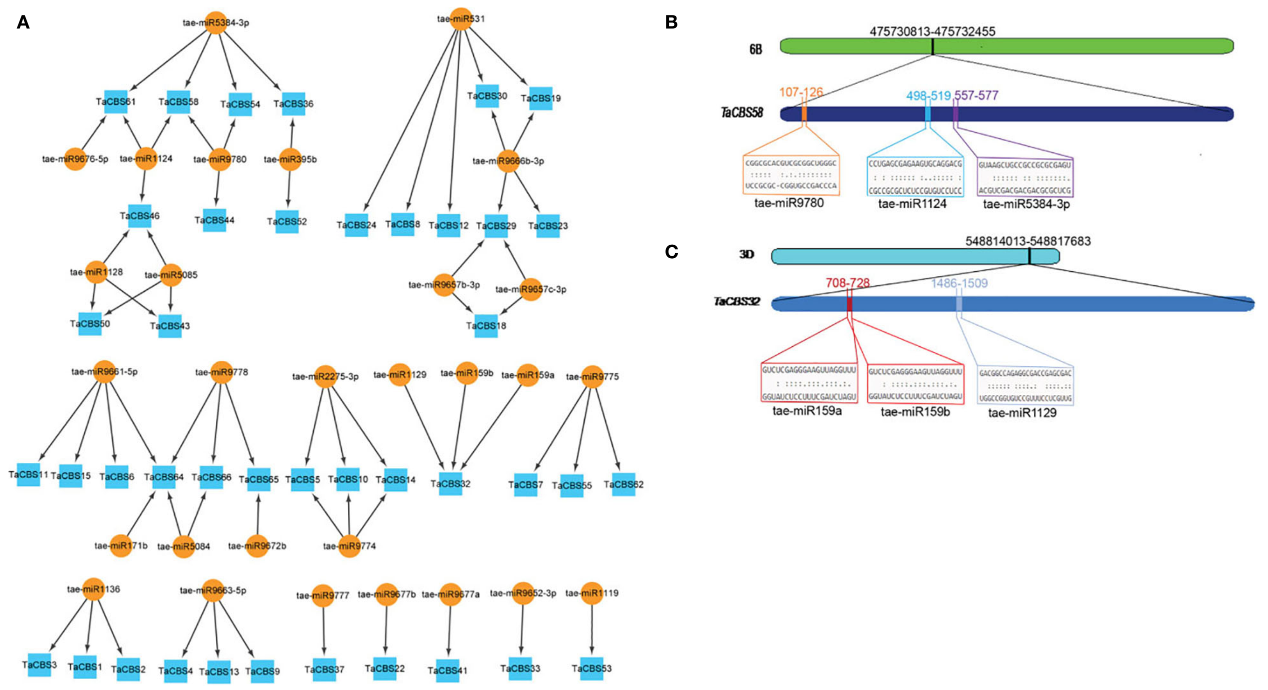

FIGURE 9
miRNAs targeting genes encoding CDCPs in wheat. **(A)** miRNA target network map for genes encoding CDCPs, with indigo boxes corresponding to *TaCBS* members and brownish yellow round shapes corresponding to predicted miRNAs. **(B)** It is evident from the graphic illustration that the *TaCBS58* gene is targeted by miRNAs (tae-miR9780, tae-miR1124, and tae-miR5384-3p). **(C)** There are three miRNAs that target the *TaCBS32* gene (tae-miR159a, tae-miR159b, and tae-miR1129) illustrated in this graphic. 6B and 3D represent chromosomes. *TaCBS58* and *TaCBS32* represent the location of miRNAs on gene sequence. Color boxes indicate the RNA sequences of the complementary sites 5′ to 3′ and the predicted miRNA sequences 3′ to 5′ in Figures 9B, C. The complete dataset of predicted miRNAs is presented in **Supplementary Table 10**.

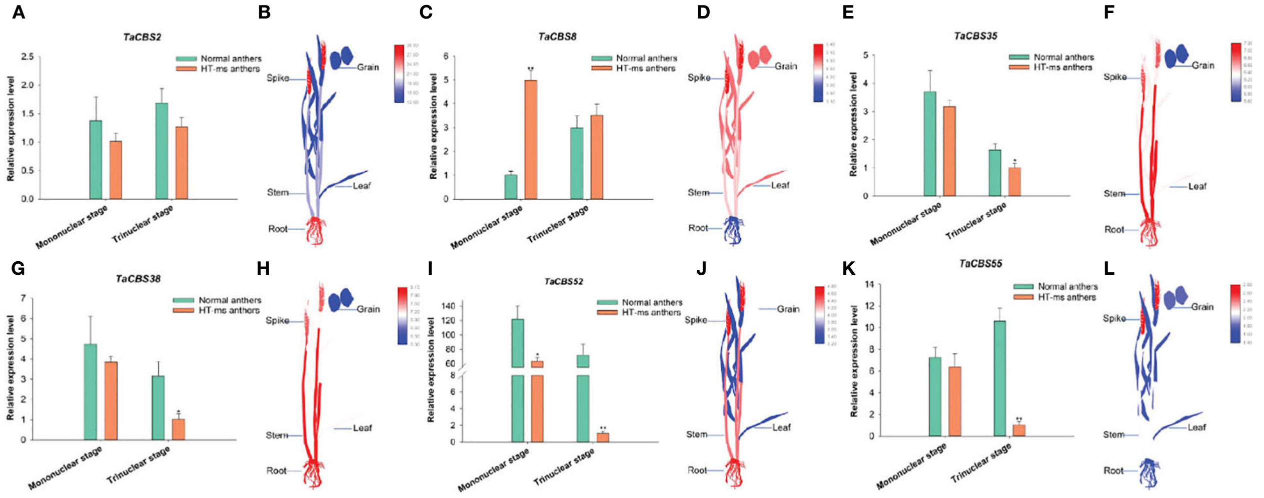

FIGURE 11
The differential expression of 6 genes encoding CDCPs in Normal and HT-ms anther tissues by qRT-PCR **(A, C, E, G, I, K)** and different tissues by RNA-seq data **(B, D, F, H, J, L)**. The x-axes and y-axes indicate the different stage in the Normal and HT-ms anthers and the relative gene expression levels, respectively. The electronic Fluorescent Pictograph (eFP) of wheat plant were visualized by Adobe Illustrator CS5 and TBtools. SPSS Statistics 23 software was used to analyze the data as means of three replicates±standard error. Tukey's method was used to test significantly different means between parameters based on analysis of variance (ANOVA) at 95% confidence levels. Capped lines indicate standard error. *P < 0.05; **P < 0.01.

conserved motif of CBS gene family heading. This heading has been corrected to **Analysis of protein domain, exon and intron structure, and conserved motif of CDCPs encoded by gene family**.

A correction has been made to the **Materials and methods**, **Cis-element prediction of CBS gene family** heading. The heading has been corrected to **Cis–element prediction of gene family encoding CDCPs**.

A correction has been made to the **Materials and methods**, **Transcriptomic data analysis of wheat CBS gene family** heading. The heading has been corrected to **Transcriptomic data analysis of wheat gene family encoding CDCPs**.

In the published article, there was in error in **Materials and methods, Transcriptomic data analysis of wheat gene family encoding CDCPs**.

The sentences previously stated:

"TBtools software was used to perform log normalization on the downloaded TPM (Transcripts Per Kilobase Million) values, and to draw the expression heatmap of wheat CBS genes."

The corrected sentence appears below:

"TBtools software was used to perform log normalization on the downloaded TPM (Transcripts Per Kilobase Million) values, and to draw the expression heatmap of wheat genes encoding CDCPs."

A correction has been made to the **Materials and methods**, **Prediction of putative miRNAs targeting TaCBS genes** heading. The heading has been corrected to **Prediction of putative miRNAs targeting genes encoding CDCPs**.

A correction has been made in **Materials and methods, Prediction of putative miRNAs targeting genes encoding CDCPs**.

This sentence previously stated:

"The miRNA target network map for *TaCBS* genes was generated by Cytoscape_v3.9.1 (Shannon et al., 2003)."

The corrected sentence appears below:

"The miRNA target network map for genes encoding CDCPs was generated by Cytoscape_v3.9.1 (Shannon et al., 2003)."

A correction has been made to **Results**, **Identification characterization and phylogenetic analysis of CBS genes in wheat** heading. The heading has been corrected to **Identification, characterization and phylogenetic analysis of genes encoding CDCPs in wheat.**

A correction has been made to **Results**, **Sequence features of gene structure, motifs and conserved domains of the TaCBS gene family**, paragraph 1.

These sentences previously stated:

"The phylogenetic tree of 66 *TaCBS* gene family proteins showed that these proteins can bedivided into two major branches;"

"Intron phase 0 is present in all 66 *TaCBS* genes, with 8 being the most (such as *TaCBS11-TaCBS52* on the phylogenetic tree (Figure 2)."

"According to the classification results, 66 TaCBS proteins were classified into 6 classes, namely CBSX (25 proteins), CBSCBS (11proteins), CBSCBSCBD (6 proteins), CBSCLC (5 proteins), CBSDUF1 (1protein) and CBSCBSPB1 (18 proteins). More details are available in **Figure S1** and **Supplementary Table 3**."

The corrected sentences appear below:

"The phylogenetic tree of 66 CDCPs showed that these proteins can be divided into two major branches;"

"Intron phase 0 is present in all 66 *TaCBS* members, with 8 being the most (such as *TaCBS11-TaCBS52* on the phylogenetic tree (Figure 2)".

"According to the classification results, 66 TaCBS proteins were classified into 6 classes, namely CBSX1-25 (25 proteins), CBSCBS1-11 (11proteins), CBSCBSCBD1-6 (6 proteins), CBSCLC1-5 (5 proteins), CBSDUF1 (1protein) and CBSCBSPB1-1-18 (18 proteins). More details are available in **Figure S1** and **Supplementary Table 3**."

A correction has been made to **Results**, **Chromosome distribution and gene duplication of wheat TaCBS gene family**, paragraph 1.

These sentences previously stated:

"The distribution and density of *TaCBS* genes are uneven on 21 wheat chromosomes. Chromosomal localization of *TaCBS* genes is displayed in Figure 3, which shows that most TaCBS genes were tandemly distributed. There are 1 (in 1A, 1B, 1D, 7A, 7B, 7D), 2 (in 4D), 3 (in 4A, 4B, 5A, 6B), 4 (in 2A, 2B, 5B, 5D, 6A, 6D), 5 (in 2D, 3A) and 6 (in 3B, 3D) TaCBS genes in different chromosomes, respectively."

"These homologous genes have homologous sites on three or two partial homologous chromosomes, indicating that the wheat TaCBS gene has a large number of homologous sites, showing a high homology retention rate. The conserved positions of these fragment replication regions located on different chromosomes suggests that fragment replication events play an important role in the expansion of the number of TaCBS genes in wheat."

The corrected sentences appear below:

"The distribution and density of genes encoding CDCPs are uneven on 21 wheat chromosomes. Chromosomal localization of genes encoding CDCPs is displayed in Figure 3, which shows that most *TaCBS* members were tandemly distributed. There are 1 (in 1A, 1B, 1D, 7A, 7B, 7D), 2 (in 4D), 3 (in 4A, 4B, 5A, 6B), 4 (in 2A, 2B, 5B, 5D, 6A, 6D), 5 (in 2D, 3A) and 6 (in 3B, 3D) *TaCBS* members in different chromosomes, respectively."

"These homologous genes have homologous sites on three or two partial homologous chromosomes, indicating that the wheat genes encoding CDCPs has a large number of homologous sites, showing a high homology retention rate. The conserved positions of these fragment replication regions located on different chromosomes suggests that fragment replication events play an important role in the expansion of the number of *TaCBS* members in wheat."

A correction has been made to the **Results**, **Localization and synteny of the TaCBS genes in the wheat genome** heading. The heading has been corrected to **Localization and synteny of the genes encoding CDCPs in the wheat genome.**

A correction has been made to **Results, Localization and synteny of the genes encoding CDCPs in the wheat genome,** paragraph 1.

These sentences previously stated:

"We analyzed the collinearity of these TaCBS genes in the wheat genome by using the Bio-linux system with the two-way blast comparison analysis and the MCScanX tool, and a total of 52 pairs of collinearity genes were identified."

The corrected sentence appears below:

"We analyzed the collinearity of these genes encoding CDCPs in the wheat genome by using the Bio-linux system with the two-way blast comparison analysis and the MCScanX tool, and a total of 52 pairs of collinearity genes were identified."

A correction has been made to **Results**, **Strong purifying selection for the TaCBS gene pairs in wheat**.

This sentence previously stated:

"A further analysis of these replicated gene pairs revealed the Ka/Ks values of all wheat TaCBS genes were less than 1, with a maximum value of 0.451."

The corrected sentence appears below:

"A further analysis of these replicated gene pairs revealed the Ka/Ks values of all wheat *TaCBS* members were less than 1, with a maximum value of 0.451."

A correction has been made to **Results, Synteny analysis of TaCBS genes between wheat and four representative pplant species** heading. The heading has been corrected to **Synteny analysis of genes encoding CDCPs between wheat and four representative plant species.**

A correction has been made to the **Results**, **Expression pattern analysis of wheat CBS gene in different tissues** heading. The heading has been corrected to **Expression pattern analysis of wheat genes encoding CDCPs in different tissues**.

A correction has been made to **Results, Expression pattern analysis of wheat genes encoding CDCPs in different tissues**, paragraph 1.

This sentence previously stated:

"According to the expression data of the heatmap, we found *TaCBS* genes showed different expression patterns in roots, stems, leaves, spikelets, and grains."

The corrected sentence appears below:

"According to the expression data of the heatmap, we found genes encoding CDCPs showed different expression patterns in roots, stems, leaves, spikelets, and grains."

A correction has been made to **Results, Expression pattern analysis of wheat genes encoding CDCPs in different tissues**, paragraph 2.

These sentences previously stated:

"The *TaCBS* genes of group 1 showed high expression in all tissues, especially in roots, stems, spikelets and grains."

"This suggests that *TaCBS* genes play an important role in wheat growth and development, which also implies that there may be a certain degree of biofunctional differentiation among different TaCBS members."

The corrected sentences appear below:

"The genes encoding CDCPs of group 1 showed high expression in all tissues, especially in roots, stems, spikelets and grains."

"This suggests that genes encoding CDCPs play an important role in wheat growth and development, which also implies that there may be a certain degree of biofunctional differentiation among different TaCBS members."

A correction has been made to **Results**, **Identifying miRNA targets for TaCBS genes throughout the genome,** paragraph 1, These sentences previously stated:

"In order to better understand the posttranscriptional alteration of TaCBS genes by miRNAs, we identified 29 miRNAs that target 41 genes (Figure 9A; **Supplementary Table 10**)."

The corrected sentence appears below:

"In order to better understand the posttranscriptional alteration of *TaCBS* members by miRNAs, we identified 29 miRNAs that target 41 genes (Figure 9A, **Supplementary Table 10**)."

A correction has been made to **Results**, **The connection between wheat CBS family and another sterility initiated by high temperature and qRT-PCR investigation**, paragraph 2.

These sentences previously stated:

"To further explore the function of *TaCBS* gene in wheat, we investigated the expression levels of *TaCBS* gene in Normal and HT-ms anthers at the mononuclear and trinuclear stages."

"In contrast, the *TaCBS8* gene showed elevated expression at both the mononuclear and trinuclear stages of HT-ms anthers compared with Normal anthers (Figure 11)."

The corrected sentence appears below:

"To further explore the function of genes encoding CDCPs in wheat, we investigated the expression levels of these genes in Normal and HT-ms anthers at the mononuclear and trinuclear stages."

"In contrast, the *TaCBS8* member showed elevated expression at both the mononuclear and trinuclear stages of HT-ms anthers compared with Normal anthers (Figure 11)."

A correction has been made to **Discussion**, paragraph 4.

These sentences previously stated:

"The 66 CBS genes in this study were unequally distributed on 21 chromosomes, with chromosomes 3A, 3B, and 3D being the most abundant (Figure 3)."

"These results suggest that the TaCBS genes shared by these several species may have been highly conserved during evolution."

"In addition, the genes of *TaCBS38* and *TaCBS35*, which are homologous pairs in all three species except barley, showed a highly expressed state in roots, stems, leaves, spikelets, and grains (Figure 7)."

The corrected sentences appear below:

"The 66 *TaCBS* members in this study were unequally distributed on 21 chromosomes, with chromosomes 3A, 3B, and 3D being the most abundant (Figure 3)."

"These results suggest that the *TaCBS* members shared by these several species may have been highly conserved during evolution."

"In addition, the members of *TaCBS38* and *TaCBS35*, which are homologous pairs in all three species except barley, showed a highly expressed state in roots, stems, leaves, spikelets, and grains (Figure 7)."

A correction has been made to **Discussion**, paragraph 5.

This sentence previously stated:

"In the present study, most of the CBS genes identified had these JA and IAA-related cis-acting elements in the upstream region (Figure 6), suggesting that the expression of CBS genes is closely related to these cis-acting elements, which may have a relationship with high temperature induced male sterility."

The corrected sentence appears below:

"In the present study, most of the *TaCBS* members identified had these JA and IAA-related cis-acting elements in the upstream region (Figure 6), suggesting that the expression of genes encoding CDCPs is closely related to these cis-acting elements, which may have a relationship with high temperature induced male sterility."

A correction has been made to **Discussion**, paragraph 6.

This sentence previously stated:

"In the present study, a total of 29 putative tae-miRNAs have been identified, with 41 *TaCBS* genes being targeted by these miRNAs."

The corrected sentence appears below:

"In the present study, a total of 29 putative tae-miRNAs have been identified, with 41 *TaCBS* members being targeted by these miRNAs."

A correction has been made to **Discussion**, paragraph 7.

These sentences previously stated:

"According to qRT-PCR results, five CBS genes were underexpressed in the mononuclear and trinuclear anthers of HT-ms compared with Normal anthers. The TaCBS8 gene showed an elevated expression trend in both the mononuclear and trinuclear stages of sterile anthers compared with the same period in Normal anthers, especially showing a highly significant difference in the mononuclear stage (Figure 11)."

"Another example is that the genes *TaCBS35* and *TaCBS38* had almost identical expression trends (Figure 11), and their motifs and gene structures were found to be extremely similar by analysis, and the evolutionary trees were clustered to the same branch (Figure 2). And to go further, the TaCBS8 gene is not involved in synteny, whereas the TaCBS35 and TaCBS38 genes are a pair of paralogous homologs and are orthologous homologous to other species (Figure 4), which indirectly suggests that the functions of these genes may have diverged somewhat."

"Similarly, the down-regulation of the majority of *TaCBS* genes in the expression of HT-ms anthers in the present study suggests an association of CBS genes with sterility caused by high-temperature induction in wheat."

The corrected sentences appear below:

"According to qRT-PCR results, five *TaCBS* members were under-expressed in the mononuclear and trinuclear anthers of HT-ms compared with Normal anthers. The *TaCBS8* member showed an elevated expression trend in both the mononuclear and trinuclear stages of sterile anthers compared with the same period in Normal anthers, especially showing a highly significant difference in the mononuclear stage (Figure 11)."

"Another example is that the members *TaCBS35* and *TaCBS38* had almost identical expression trends (Figure 11), and their motifs and gene structures were found to be extremely similar by analysis, and the evolutionary trees were clustered to the same branch (Figure 2). And to go further, the *TaCBS8* member is not involved in synteny, whereas the *TaCBS35* and *TaCBS38* members are a pair of paralogous homologs and are orthologous homologous to other species (Figure 4), which indirectly suggests that the functions of these genes may have diverged somewhat."

"Similarly, the down-regulation of the majority of genes encoding CDCPs in the expression of HT-ms anthers in the present study suggests an association of genes encoding CDCPs with sterility caused by high-temperature induction in wheat."

A correction has been made to **Conclusions**.

These sentences previously stated:

"In this study, we identified 66 CBS genes in wheat."

"Based on protein motifs, gene structure, chromosomal location, Ka/Ks analysis, cis-acting elements, putative miRNAs analysis, synteny analysis and expression pattern analysis, *TaCBS* genes are conservative and diversified."

"Twenty-nine miRNAs targeting 41 *TaCBS* genes were identified, and the analysis of the regulatory relationships between these miRNAs and *TaCBS* gene interactions further increased our understanding of *TaCBS* genes."

"These outcomes indicate that the wheat CBS gene family may have some relationship with high temperature-induced male sterility."

"In addition, the abnormal expression of these CBS genes may be one of the reasons why HT-ms anthers develop small and with no dehiscence, which may be one of the factors that eventually lead to anther abortion."

The corrected sentences appear below:

"In this study, we identified 66 genes encoding CDCPs in wheat."

"Based on protein motifs, gene structure, chromosomal location, Ka/Ks analysis, cis-acting elements, putative miRNAs analysis, synteny analysis and expression pattern analysis, *TaCBS* members are conservative and diversified."

"Twenty-nine miRNAs targeting 41 *TaCBS* members were identified, and the analysis of the regulatory relationships between these miRNAs and *TaCBS* gene interactions further increased our understanding of *TaCBS* genes."

"These outcomes indicate that the wheat gene family encoding CDCPs may have some relationship with high temperature-induced male sterility."

"In addition, the abnormal expression of these *TaCBS* members may be one of the reasons why HT-ms anthers develop small and with no dehiscence, which may be one of the factors that eventually lead to another abortion."

The authors apologize for these errors and state that these do not change the scientific conclusions of the article in any way. The original article has been updated.

Publisher's note