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**Rapid mapping of a chlorina mutant gene *cn-A1* in hexaploid wheat by bulked segregant analysis and single nucleotide polymorphism genotyping arrays**

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**Supplemental Table S1. Kompetitive Allele Specific PCR (KASP) primers used to genotype individual F2:3 for mapping *cn-A1* in B23**

Marker name (SNP ID)		Primer sequences (5'–3')	Products size(bp)
660K-7A10(AX-109851070)	Forward A_FAM	GAAGGTGACCAAGTTCATGCTaattgaagacaagcctcggT	59
	Forward B_HEX	GAAGGTTCGGAGTCAACGGATTaattgaagacaagcctcggC	
	Common reverse	gctaataactcagctGtttgcata	
660K-7A12(AX-109381813)	Forward A_FAM	GAAGGTGACCAAGTTCATGCTCgtaCagccagcTtGTttAta	93
	Forward B_HEX	GAAGGTTCGGAGTCAACGGATTcGtaCagccagcTtGTttAta	
	Common reverse	aaGaaaagacaacgggctcA	
660K-7A17(AX-94521326)	Forward A_FAM	GAAGGTGACCAAGTTCATGCTggtctgcatcaattgtggatG	75
	Forward B_HEX	GAAGGTTCGGAGTCAACGGATTggtctgcatcaattgtggatA	
	Common reverse	gtaaggattctgcacgtgTgA	
660K-7A19(AX-111685929)	Forward A_FAM	GAAGGTGACCAAGTTCATGCTgcaaGAaaCAatctccatggt	57
	Forward B_HEX	GAAGGTTCGGAGTCAACGGATTgcaaGAaaCAatctccatgg	
	Common reverse	acaagacaTcatgcTtGctacT	
660K-7A20(AX-110487260)	Forward A_FAM	GAAGGTGACCAAGTTCATGCTcGCgcacTggtgtattctacaA	60
	Forward B_HEX	GAAGGTTCGGAGTCAACGGATTcGCgcacTggtgtattctacaC	
	Common reverse	ctccaaaatgggtaagcatGG	
660K-7A21(AX-110615844)	Forward A_FAM	GAAGGTGACCAAGTTCATGCTtttaccatattttgttggttgCC	71
	Forward B_HEX	GAAGGTTCGGAGTCAACGGATTtttaccatattttgttggttgCT	
	Common reverse	gggtcaaaacacaaacaaCtaaaC	
660K-7A28(AX-111612726)	Forward A_FAM	GAAGGTGACCAAGTTCATGCTtgccaTAcacaGattgattaga	63
	Forward B_HEX	GAAGGTTCGGAGTCAACGGATTtgccaTAcacaGattgattaga	
	Common reverse	tttacagggggcaagcaA	
660K-7A30(AX-109536152)	Forward A_FAM	GAAGGTGACCAAGTTCATGCTgcccGtttgaacacagaaaaT	57
	Forward B_HEX	GAAGGTTCGGAGTCAACGGATTgcccGtttgaacacagaaaaC	
	Common reverse	gtgcttgggtTgagttttatT	

**Supplemental Table S2A. Gene models between two flanking markers 660K-7A12 and 660K-7A20 according to Chinese Spring 7AL reference sequence**

Gene or SNP ID	Hit-start	Hit-end	Annotation
660K-7A12	670956567	670956637	
TraesCS7A02G477300	670959602	670962901	Ubiquitin conjugation factor E4, putative
TraesCS7A02G477400	671073279	671076239	WAT1-related protein
TraesCS7A02G477500	671120188	671125883	WAT1-related protein
TraesCS7A02G477700	671189814	671191125	Myb/SANT-like DNA-binding domain protein
TraesCS7A02G477800	671200949	671201263	Capsular polysaccharide phosphotransferase SacB
TraesCS7A02G477900	671218518	671219924	Glutathione S-transferase
TraesCS7A02G478000	671305678	671310622	UDP-glycosyltransferase
TraesCS7A02G478100	671412558	671417936	Glyceraldehyde-3-phosphate dehydrogenase
TraesCS7A02G478200	671419642	671420545	Ring finger protein, putative
TraesCS7A02G478300	671422517	671427535	NBS-LRR-like resistance protein
TraesCS7A02G478500	671446002	671458662	Pleiotropic drug resistance ABC transporter
TraesCS7A02G478600	671466827	671476243	DUF21 domain-containing protein
TraesCS7A02G478700	671483009	671483941	VQ motif family protein
TraesCS7A02G478800	671499443	671500877	Mediator of RNA polymerase II transcription subunit
TraesCS7A02G478900	671520794	671523243	Heptaprenylglyceryl phosphate synthase
TraesCS7A02G479000	671781074	671781526	Cyclin-D5-3
TraesCS7A02G479100	671847340	671851409	PLATZ transcription factor family protein
TraesCS7A02G479200	671925707	671928956	Thioredoxin
TraesCS7A02G479300	671937328	671938269	Ferredoxin--NADP reductase 2
TraesCS7A02G479400	672006157	672006684	NADH-ubiquinone oxidoreductase chain 4
TraesCS7A02G479500	672008531	672008839	Phosphotransferase
TraesCS7A02G479600	672013999	672016931	Ureide permease-like protein
TraesCS7A02G479700	672020422	672023238	Ureide permease-like protein
TraesCS7A02G479800	672024985	672029520	Translation initiation factor IF-2, putative
TraesCS7A02G479900	672041945	672046257	rRNA 2'-O-methyltransferase fibrillarlin 2
TraesCS7A02G480100	672069735	672075854	Copper-transporting ATPase
TraesCS7A02G480200	672148863	672149420	F-box protein
TraesCS7A02G480300	672152816	672153928	F-box protein
TraesCS7A02G480400	672316013	672317557	F-box protein
TraesCS7A02G480500	672783118	672786504	RNA polymerase-associated protein RapA
TraesCS7A02G480600	672855814	672859747	Eukaryotic aspartyl protease family protein
TraesCS7A02G480700	672872712	672874427	Mg-protoporphyrin IX chelatase

## Continued

Gene or SNP ID	Hit-start	Hit-end	Annotation
TraesCS7A02G480800	672878996	672885067	Citrate-binding protein
TraesCS7A02G480900	672950935	672951333	F-box protein
TraesCS7A02G481000	673019905	673021149	Pentatricopeptide repeat-containing protein
TraesCS7A02G481100	673126509	673127765	F-box protein
TraesCS7A02G481200	673243794	673245558	F-box protein
TraesCS7A02G481300	673401541	673403327	ATP-dependent Clp protease ATP-binding subunit C
TraesCS7A02G481400	673778418	673784059	Cytochrome c oxidase subunit 6a, mitochondrial
TraesCS7A02G481500	674015727	674020492	Allantoate amidohydrolase
TraesCS7A02G481600	674081462	674082918	Aberrant panicle organization 1 protein
TraesCS7A02G481700	674090627	674091962	Glucan endo-1,3-beta-glucosidase-like protein 3
TraesCS7A02G481800	674103803	674108136	Syntaxin
TraesCS7A02G481900	674115010	674115615	CASP-like protein
TraesCS7A02G482000	674270191	674272522	Haloacid dehalogenase-like hydrolase domain-contai
TraesCS7A02G482100	674273136	674275483	Protein DETOXIFICATION
TraesCS7A02G482200	674276643	674280959	LEM3 (Ligand-effect modulator 3)-like
660K-7A20	674279760	674279830	

**Supplemental Table S2B. Gene models between two flanking markers 660K-7A12 and 660K-7A20 according to Chinese Spring 7BL reference sequence**

Gene or SNP ID	Hit-start	Hit-end	Annotation
660K-7A12	643349145	643349213	
TraesCS7B02G378900	643350213	643356059	Ubiquitin conjugation factor E4, putative
TraesCS7B02G379000	643375236	643382071	WAT1-related protein
TraesCS7B02G379100	643462228	643463424	Peroxidase
TraesCS7B02G379200	643500478	643503335	F-box/RNI-like/FBD-like domains-containing protein
TraesCS7B02G379300	643566510	643569705	WAT1-related protein
TraesCS7B02G379400	643624344	643627584	WAT1-related protein
TraesCS7B02G379500	644183619	644195648	Vacuolar protein sorting-associated protein 8-like protein
TraesCS7B02G379600	644298678	644300586	BTB/POZ domain containing protein, expressed
TraesCS7B02G379700	644447666	644447920	NADH-ubiquinone oxidoreductase chain 5
TraesCS7B02G379800	644463935	644464577	Ribosomal protein S1
TraesCS7B02G379900	644466628	644466882	BnaCnng55980D protein
TraesCS7B02G380000	644529738	644530989	B3 domain protein (DUF313)
TraesCS7B02G380100	644545334	644555458	O-fucosyltransferase family protein
TraesCS7B02G380200	645105512	645106162	F-box domain containing protein
TraesCS7B02G380300	645256055	645260821	Glutathione S-transferase
TraesCS7B02G380400	645257327	645257659	PKS-NRPS hybrid synthetase CHGG_01239
TraesCS7B02G380500	645384979	645390477	Glyceraldehyde-3-phosphate dehydrogenase
TraesCS7B02G380600	645391794	645392851	Ring finger protein, putative
TraesCS7B02G380700	645394973	645396033	Disease resistance protein (NBS-LRR class) family
TraesCS7B02G380800	645397875	645399572	Polypyrimidine tract-binding protein
TraesCS7B02G380900	645400592	645403325	Disease resistance protein (NBS-LRR class) family
TraesCS7B02G381000	645500837	645520989	Drug resistance transporter-like ABC domain protein
TraesCS7B02G381100	645514427	645515837	Tetratricopeptide repeat (TPR)-like superfamily protein
TraesCS7B02G381200	645588688	645605482	Pleiotropic drug resistance ABC transporter
TraesCS7B02G381300	646063708	646074390	DUF21 domain-containing protein
TraesCS7B02G381400	646209569	646210468	VQ motif family protein
TraesCS7B02G381500	646680061	646684266	PLATZ transcription factor family protein
TraesCS7B02G381600	646999012	647002412	Thioredoxin
TraesCS7B02G381700	647009804	647011918	Phosphoglycerate kinase
TraesCS7B02G381800	647069750	647071486	Polyubiquitin
TraesCS7B02G381900	647132483	647134229	transmembrane protein
TraesCS7B02G382000	647751459	647754258	Ureide permease-like protein

Continued

Gene or SNP ID	Hit-start	Hit-end	Annotation
TraesCS7B02G382100	647758196	647762061	Translation initiation factor IF-2, putative
TraesCS7B02G382200	648042287	648045080	rRNA 2'-O-methyltransferase fibrillarlin 2
TraesCS7B02G382300	648103932	648109965	Copper-transporting ATPase
TraesCS7B02G382400	648139017	648139633	F-box protein
TraesCS7B02G382500	648378414	648380051	F-box protein
TraesCS7B02G382600	648428874	648429586	DNA topoisomerase
TraesCS7B02G382700	648656041	648661260	Eukaryotic aspartyl protease family protein
TraesCS7B02G382800	648668890	648670928	Mg-protoporphyrin IX chelatase
TraesCS7B02G382900	648704534	648710175	Citrate-binding protein
TraesCS7B02G383000	648719578	648720863	gamma-irradiation and mitomycin c induced 1
TraesCS7B02G383100	648909136	648911013	F-box protein
TraesCS7B02G383200	648916626	648917868	F-box protein
TraesCS7B02G383300	649013409	649015142	F-box protein
TraesCS7B02G383400	649153880	649154329	myosin 2
TraesCS7B02G383500	649211354	649212593	F-box protein
TraesCS7B02G383600	649247335	649248923	F-box protein
TraesCS7B02G383700	649403927	649407953	F-box protein
TraesCS7B02G383800	649458044	649465824	F-box protein
TraesCS7B02G383900	649844927	649849556	Allantoate amidohydrolase
TraesCS7B02G384000	649950255	649951851	Aberrant panicle organization 1 protein
TraesCS7B02G384100	649991532	649992802	Glucan endo-1,3-beta-glucosidase-like protein 3
TraesCS7B02G384200	650124948	650127266	Haloacid dehalogenase-like hydrolase domain-containing protein 3
TraesCS7B02G384300	650128138	650130058	Protein DETOXIFICATION
660K-7A20	650135774	650135844	

**Supplemental Table 2C. Gene models between two flanking markers 660K-7A12 and 660K-7A20 according to Chinese Spring 7DL reference sequence**

Gene or SNP ID	Hit-start	Hit-end	Annotation
660K-7A12	579146821	579146887	
TraesCS7D02G464800	579148968	579152855	Ubiquitin conjugation factor E4, putative
TraesCS7D02G464900	579196300	579199193	WAT1-related protein
TraesCS7D02G465000	579247587	579253624	WAT1-related protein
TraesCS7D02G465100	579324498	579327188	FBD-associated F-box protein
TraesCS7D02G465200	579342572	579343390	E3 ubiquitin-protein ligase SINA-like 10
TraesCS7D02G465300	579362406	579362717	1-hydroxy-2-methyl-2-E-butenyl 4-diphosphate reductase
TraesCS7D02G465400	579535302	579536399	Glutathione S-transferase
TraesCS7D02G465500	579749059	579754613	Glyceraldehyde-3-phosphate dehydrogenase
TraesCS7D02G465600	579756244	579757036	Ring finger protein, putative
TraesCS7D02G465700	579759216	579760925	NBS-LRR-like resistance protein
TraesCS7D02G465800	579761084	579764000	Disease resistance protein (NBS-LRR class) family
TraesCS7D02G465900	579789649	579799088	Pleiotropic drug resistance ABC transporter
TraesCS7D02G466000	579823603	579831619	DUF21 domain-containing protein
TraesCS7D02G466100	579961074	579961946	VQ motif family protein
TraesCS7D02G466200	580002545	580005934	Mediator of RNA polymerase II transcription subunit 1
TraesCS7D02G466300	580111172	580111441	Tyrosine--tRNA ligase
TraesCS7D02G466400	580263133	580267375	PLATZ transcription factor family protein
TraesCS7D02G466500	580316370	580320107	Thioredoxin
TraesCS7D02G466600	580380727	580382342	Polyubiquitin
TraesCS7D02G466700	580478154	580479470	Pleiotropic drug resistance protein 1
TraesCS7D02G466800	580481451	580484320	Ureide permease-like protein
TraesCS7D02G466900	580490978	580493503	Ureide permease-like protein
TraesCS7D02G467000	580552330	580555764	rRNA 2'-O-methyltransferase fibrillarlin 2
TraesCS7D02G467100	580570228	580576400	Copper-transporting ATPase
TraesCS7D02G467200	580576572	580577111	F-box protein
TraesCS7D02G467300	580741687	580743262	F-box protein
TraesCS7D02G467400	580763412	580765072	F-box protein
TraesCS7D02G467500	580852973	580854606	Mg-protoporphyrin IX chelatase
TraesCS7D02G467600	581021880	581022606	Citrate-binding protein
TraesCS7D02G467700	581039584	581041323	F-box protein
TraesCS7D02G467800	581271392	581273186	F-box protein
TraesCS7D02G467900	581284101	581285330	F-box protein

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Gene or SNP ID	Hit-start	Hit-end	Annotation
TraesCS7D02G468000	581289578	581290876	F-box protein
TraesCS7D02G468100	581384524	581386094	F-box protein
TraesCS7D02G468200	581452646	581453521	F-box protein
TraesCS7D02G468300	581637866	581638585	F-box protein
TraesCS7D02G468400	582043026	582055154	F-box protein
TraesCS7D02G468500	582089065	582089646	Ethylene-responsive transcription factor
TraesCS7D02G468600	582115629	582120318	Allantoate amidohydrolase
TraesCS7D02G468700	582136884	582138473	Aberrant panicle organization 1 protein
TraesCS7D02G468800	582162964	582164339	Glucan endo-1,3-beta-glucosidase-like protein 3
TraesCS7D02G468900	582298930	582301236	Haloacid dehalogenase-like hydrolase domain-containing protein 3
TraesCS7D02G469000	582301738	582304043	Protein DETOXIFICATION
660K-7A20	582307811	582307881	

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**Supplemental Table S3. The physical genomic region in Chinese Spring delimited by flanking markers of chlorina mutant genes and identification of candidate genes.**

Species	Ploidy	Chlorina mutant <sup>a</sup>	Chromosome	Flanking SSR markers or candidate genes	Physical position of makers or genes	Annatation
<i>Triticum aestivum</i>	hexaploid	<i>cn-A1</i>	7AL	Xbarc292	648.68Mb	
				TraesCS7A01G480700.1	672.87Mb	Magnesium chelatase, subunit ChII
				Xgwm282	681.39Mb	
<i>Triticum durum</i>	tetraploid	<i>cn-A1</i>	7AL	Xbarc192	667.98Mb	
				TraesCS7A01G480700.1	672.87MB	Magnesium chelatase, subunit ChII
				Xgwm282	681.39Mb	
<i>Triticum monococcum</i>	diploid	<i>cn-A1</i>	7AL	Xgwm748 <sup>b</sup>		
				TraesCS7A01G480700.1	672.87Mb	Magnesium chelatase, subunit ChII
				Xwmc116	694.92Mb	

<sup>a</sup> Kosuge, K., N. Watanabe and T. Kuboyama (2011) Comparative genetic mapping of homoeologous genes for the chlorina phenotype in the genus *Triticum*. *Euphytica* 179: 257-263.

<sup>b</sup> The marker sequence is not available in the database