

1 **Supplementary table 4. Putative candidate genes and molecular functions in the 100 kb Region of linked SNPs**

Trait	SNP	Chromosome	Position	Transcript ID	Protein	Function
ALL_CL	AX-94583923	2D	476696204	<i>TraesCS2D02G372500</i>	Peptidase S10, serine carboxypeptidase	Serine carboxypeptidase plays an important role in the drought tolerance of coleoptiles and the roots of spring wheat [1]
				<i>TraesCS2D02G372700</i>	DNA-binding pseudobarrel domain superfamily	The B3 DNA-binding superfamily plays a significant role in the response to stresses in plants, as well as in the development of different parts of the plant [2]
ALL_CL	AX-95017965	2B	19070631	<i>TraesCS2B02G042000</i>	UDP-glucuronosyl/UDP-glucosyltransferase	UDP-glucuronosyl/UDP-glucosyltransferase confer drought tolerance in spring wheat [3]
ALL_CL	AX-94773224	6B	650596466	<i>TraesCS6B02G375700</i>	Zinc finger, SIAH-type	Up-regulated gene induced by drought stress in Tibetan hulless barley [4]
ALL_SDW	AX-94699286	4A	660988520	<i>TraesCS4A02G383100</i>	O-methyltransferase domain	Overexpression of the wheat <i>TaCOMT</i> gene enhances drought tolerance and increases the content of melatonin in transgenic <i>Arabidopsis</i> [5]
ALL_SDW	AX-95103885	6D	13975625	<i>TraesCS6D02G032900</i>	Alpha/Beta hydrolase fold	Plays a critical role in mediating lipid mobilization during seed germination and growth [6]
				<i>TraesCS6D02G033100</i>	RmlC-like cupin domain superfamily	The <i>Arabidopsis</i> cupin domain protein AtPirin1 interacts with the G protein alpha-subunit GPA1 and regulates seed germination and early seedling development [7]
ALL_RD	AX-94446435	3D	43020473	<i>TraesCS3D02G085400</i>	Pyridoxal phosphate-dependent transferase	Up-regulated by drought stress in maize [8]
ALL_RD	AX-94470331	4D	5694858	<i>TraesCS4D02G012200</i>	26S proteasome non-ATPase regulatory subunit Rpn12	RPN12a is part of the <i>Arabidopsis</i> 26S proteasome that controls the stability of one or more of the factors involved in cytokinin regulation [9]

ALL_RD	AX-95234949	3A	56390763	<i>TraesCS3A02G087200</i>	AP2/ERF domain	Dehydration responsive element-binding factors (DBFs) belong to the AP2/ERF superfamily and play vital regulatory roles in abiotic stress responses in plants [10]
ALL_RD	AX-94811606	4D	53243459	<i>TraesCS4D02G079200</i>	P-type ATPase, subfamily IIB	Role during root epidermis development and early seedling development via sucrose signalling [11]
C_MGT	AX-94471577	4A	1890138	<i>TraesCS4A02G002000</i>	WD40-repeat-containing domain superfamily	-
				<i>TraesCS4A02G002200</i>	Protein DCL-like	-
D_SDW	AX-94742835	2D	90243264	<i>TraesCS2D02G148700</i>	Transcription elongation factor, TFIIS/CRSP70, N-terminal, sub-type	Transcription factors (TFs) are involved in drought stress tolerance and response via an ABA signalling pathway [12]
D_SDW	AX-94394580	5A	700443596	<i>TraesCS5A02G545500</i>	EF-hand domain	Plays a principal role in calcium signalling events in plants which is an essential nutrient for the normal development of the plant root and shoot tips and more specifically in cell division [13]
				<i>TraesCS5A02G545800</i>	Invertase/pectin methylesterase inhibitor domain superfamily	Early development of wheat grain endosperm and outer Layers [14]
				<i>TraesCS5A02G546200</i>	MFS transporter superfamily	Role in nitrate signalling and seedling vigour [15]
D_SVI-II	AX-94926133	5A	584713681	<i>TraesCS5A02G387800</i>	RNA-binding domain superfamily	Function in the regulation of shoot stem cell fates, root growth, gravitropic responses and embryo development [16]
				<i>TraesCS5A02G387700</i>	Helicase superfamily 1/2, ATP-binding domain	play crucial roles in plant growth, development, and abiotic stress responses by regulating the degree of membrane lipid peroxidation [17]
S1C_AUC	AX-95194336	2B	9620943	<i>TraesCS2B02G020200</i>	P-loop containing nucleoside triphosphate hydrolase	-

S1C_AUC	AX-95194973	7B	105011342	<i>TraesCS7B02G090900</i>	Aspartic peptidase domain superfamily	Role in gluten breakdown [18]
S1D_AUC	AX-94953183	6D	16295427	<i>TraesCS6D02G039600</i>	Papain-like cysteine peptidase superfamily	Play a role in seed germination, plant growth and development, organ senescence, immunity, and stress response [19]
				<i>TraesCS6D02G039700</i>	Leucine-rich repeat domain superfamily	The leucine-rich repeat receptor like kinases (LRRK) constitute the largest subfamily of receptor-like kinases (RLK), which play critical roles in plant development and stress responses [20]
S1D_SDW	AX-94620141	2D	14772793	<i>TraesCS2D02G040700</i>	Protein kinase-like domain superfamily	Role in various plant processes, including growth, development, and stress response [21]
S1D_SDW	AX-95094238	5A	510891163	<i>TraesCS5A02G302000</i>	AAA+ ATPase domain	Abiotic stress tolerance [22]
S1D_SDW	AX-94574509	1A	9580120	<i>TraesCS1A02G018800</i>	The domain of unknown function DUF4220	DUF genes are associated with seedling development, root development, plant cell growth, and chloroplast movement [23]
				<i>TraesCS1A02G018900</i>	Zinc finger C2H2 superfamily	Key regulator of drought tolerance [24]
				<i>TraesCS1A02G019000</i>	V-ATPase proteolipid subunit C, eukaryotic	Role in root growth [25]
S1D_SDW	AX-95232641	5B	449131902	<i>TraesCS5B02G265100</i>	C2 domain superfamily	Upregulated during drought and osmotic stress [26]
S1D_SDW	AX-94873710	3A	20004183	<i>TraesCS3A02G036400</i>	ABC transporter-like, ATP-binding domain	It is essential for both root growth and shoot growth in plants [27]
S1D_SVI-II	AX-94485323	2D	577599376	<i>TraesCS2D02G474800</i>	F-box-like domain superfamily	The F-box-like domain superfamily plays specific roles in protein degradation by post-translational modification in several biological processes including seed germination and seedling development [28]

				<i>TraesCS2D02G474900</i>	APO domain	APO expressed greater in early vigorous wheat cultivars [29]
S2C_AUC	AX-94491917	3D	429632555	<i>TraesCS3D02G316300</i>	LysM domain superfamily	LysM domain-containing proteins modulate stress response and signalling in wheat [30]
S2C_SL	AX-94515822	1B	638930477	<i>TraesCS1B02G413800</i>	Bile acid: sodium symporter/arsenical resistance protein Acr3	BILE ACID: SODIUM SYMPORTER FAMILY PROTEIN 2 (BASS2) repress ABI4 expression during seedling development by binding to its promoter [31]

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4 **Note;** ALL- control and Moisture deficit stress condition across the season, Combined, C: Control, D: Moisture deficit stress condition (PEG-6000 treatment), S1-Season 1,  
5 S2- Season 2; AUC: area under the curve; CL: coleoptile length (cm); SL: seedling length (cm); SDW: seedling dry weight (mg); SVI.I: seedling vigour index-I; SVI.II:  
6 seedling vigour index-II, RD: average root diameter (mm)

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