

Group1

[illegible]

Group 2

TrasCS1A02G329900.1 ESNRDSARRSRSRKAA HTKELEE QVKMAFE TMKRVTCT NFPQA ISGTSRLR *IPFSGSP LDGICDN PLPTQNT SLSYLPT TTTDF_A

Group 3

Trac57D0023932800.1	MNRDGMGDKSRERKKS	YKDLST	R KSLYE	E GRRLSY	ALQCCAA	N ENMADRO	H MMLEDF	IGAHNTM	QESAVLS	ETLPLVS	LWLWLSI
Trac57A020369400.1	MNRDGMGDKSRERKKS	YKDLST	R KSLYE	E GRRLSY	ALQCCAA	N ENMADRO	H MMLEDF	IGAHNTM	QESAVLS	ETLPLVS	LWLWLSI
Trac57B002629920.1	MNRDGMGDKSRERKKS	YKDLST	R KSLYE	E GRRLSY	ALQCCAA	N ENMADRO	H MMLEDF	IGAHNTM	QESAVLS	ETLPLVS	LWLWLSI
Trac57C002151000.1	MNRDGMGDKSRERKKS	YKDLST	R KSLYE	E GRRLSY	ALQCCAA	N ENMADRO	H MMLEDF	IGAHNTM	QESAVLS	ETLPLVS	LWLWLSI
Trac57D00268500.2	LNRHESAGLSRQRKKK	YVELEEG	V KSMNS	VINDLNS	I EFFIVA	N ENMADRO	H MLSGGG	NCPPFGM	YPPGAMP	GHHFPW	PGYAMP
Trac52B0026167900.1	VNHRGASLRSRQKKK	YVELEEG	V KYAKQA	TIADLST	R ISCVTA	N ENMADRO	H QLAGAGG	ACGVPPFL	PMYPGLY	PLFPFWM	PHAYAMG
Trac52A0026142800.1	VNHRGASLRSRQKKK	YVELEEG	V KYAKQA	TIADLST	R ISCVTA	N ENMADRO	H QLAGAGG	ACGVPPFL	PMYPGLY	PLFPFWM	PHAYAMG
Trac52D0026146100.1	VNHRGASLRSRQKKK	YVELEEG	V KYAKQA	TIADLST	R ISCVTA	N ENMADRO	H QLAGAGG	ACGVPPFL	PMYPGLY	PLFPFWM	PHAYAMG
Trac56D002617800.1	LNRHVSQAQRERKKK	YVGLDVE	V KVDFLR	E KNLELE	HTSLTQN	N ENMADRO	L KNNTTT	S GGKPSGE	GK		
Trac56B002699600.1	LNRHVSQAQRERKKK	YVGLDVE	V KVDFLR	E KNLELE	HTSLTQN	N ENMADRO	L KNNTTT	S GGKPSGE	GK		
Trac56A0026175800.1	LNRHVSQAQRERKKK	YVGLDVE	V KVDFLR	E KNLELE	HTSLTQN	N ENMADRO	L KNNTTT	S GGKPSGE	GK		
Trac53D0026129800.1	LNRHVSQAQRERKKK	YVTEYLE	V KADLE	R WAELEK	V STLTQN	N ENMADRO	L KNNTTA	HAGKRRS	S GGKGDDG	GKRRHHF	GKG
Trac53A0026128900.1	LNRHVSQAQRERKKK	YVTEYLE	V KADLE	R WAELEK	V STLTQN	N ENMADRO	L KNNTTA	HAGKRRS	S GGKGDDG	GKRRHHF	GKG
Trac53C0026137800.1	LNRHVSQAQRERKKK	YVTEYLE	V KADLE	R WAELEK	V STLTQN	N ENMADRO	L KNNTTT	S GGKPGG	SGGAGG		

TracECS802G1422001..	LANRQAGSQRVRVKLK	YISLER	SVTGLQM	EVSALSP	WVAFIDH	QNSLTLY	GNHSHKQ	NIAALAQ	DKFPKDA	HOALQAL	EIRLRLQ	--
TracECS802G0230001..	INSHRGAQRVRVKLK	RLEDLRA	LDLAASR	GRRRLVA	WVYAAAC	NVAIVLH	ANDERHA	NIAAALS	NLEVAHA	GALALHQ	LYAAALQ	--
TracECS802G1430001..	LANRQAGSQRVRVKLK	YISLER	SVTGLQM	EVSALSP	WVAFIDH	QNSLTLY	GNHSHKQ	NIAALAQ	DKFPKDA	HOALQAL	EIRLRLQ	--
TracECS02062487001..	LANRQAGSQRVRVKLK	YISLER	SVTGLQM	EVSALSP	WVAFIDH	QNSLTLY	GNHSHKQ	NIAALAQ	DKFPKDA	HOALQAL	EIRLRLQ	--
TracECS02062497001..	LANRQAGSQRVRVKLK	YISLER	SVTGLQM	EVSALSP	WVAFIDH	QNSLTLY	GNHSHKQ	NIAALAQ	DKFPKDA	HOALQAL	EIRLRLQ	--
TracECS02062937001..	LANRQAGSQRVRVKLK	YISLER	CVTTLON	EVSLSLP	WVAFIDH	QNSLTLY	GNHSHKQ	NIAALAQ	DKFPKDA	HOALQAL	EIRLRLQ	--
TracECS02062935001..	LANRQAGSQRVRVKLK	YISLER	CVTTLON	EVSLSLP	WVAFIDH	QNSLTLY	GNHSHKQ	NIAALAQ	DKFPKDA	HOALQAL	EIRLRLQ	--
TracECS802G3824001..	LANRQAGSQRVRVKLK	YISLER	CVTTLON	EVSLSLP	WVAFIDH	QNSLTLY	GNHSHKQ	NIAALAQ	DKFPKDA	HOALQAL	EIRLRLQ	--
TracECS0206428VBRKIH	LANRQAGSQRVRVKLK	YISLER	SVTGLQM	EVSALSP	WVAFIDH	QNSLTLY	GNHSHKQ	NIAALAQ	DKFPKDA	HOALQAL	EIRLRLQ	--
TracECS0206428VBRKIH	LANRQAGSQRVRVKLK	YISLER	QVEQLSL	EVSALSP	WVAFIDH	QNSLTLY	GNHSHKQ	NIAALAQ	DKFPKDA	HOALQAL	EIRLRLQ	--
TracECS802G3918002..	VNSRGAQRSSRRRKH	QTLDEL	QVEQLSL	EVSATLF	QLTQANQ	QETTAVT	DNRIILKS	DVSTLRN	KVKMAAD	CGGLGQQ	--	
TracECS762046886002..	VNSRGAQRSSRRRKH	QTLDEL	QVEQLSL	EVSATLF	QLTQANQ	QETTAVT	DNRIILKS	DVSTLRN	KVKMAAD	CGGLGQQ	--	
TracECS02064155001..	VNSRLQAGSRRAKQK	RLEELRG	TVARFLA	EVRRLAA	HLHVAHR	HSLVAAR	QNRARLR	NIAVALR	NLEARLR	LLALQRL	QLRRS	--
TracECS02064155001..	VNSRLQAGSRRAKQK	RLEELRG	TVARFLA	EVRRLAA	HLHVAHR	HSLVAAR	QNRARLR	NIAVALR	NLEARLR	LLALQRL	QLRRS	--
TracECS02064183001..	VNSRLQAGSRRAKQK	HLDLDS	QVDQLNQ	EVSQMMN	VLGMTOT	NLVALQA	QNSVMQT	QKMELES	NLCAELG	ICCMNS	NT	--
TracECS02064052001..	VNSRLQAGSRRAKQK	RLEELRG	TVARFLA	EVRRLAA	HLHVAHR	HSLVAAR	QNRARLR	NIAVALR	NLEARLR	LLALQRL	QLRRS	--
TracECS02064179001..	VNSRGAQRSSRRRKH	HLDLDS	QVDQLNQ	EVSQMMN	VLGMTOT	NLVALQA	QNSVMQT	QKMELES	NLCAELG	ICCMNS	NT	--
TracECS02064179001..	VNSRGAQRSSRRRKH	HLDLDS	QVDQLNQ	EVSQMMN	VLGMTOT	NLVALQA	QNSVMQT	QKMELES	NLCAELG	ICCMNS	NT	--
TracECS02061657001..	LANRQAGSQRVRVKLK	YISLER	SITSLOK	EVSALSP	WVAFIDH	QNSLTLY	GNHSHKQ	NIAALAR	DKFPKDA	HOALQAL	EIRLRLQ	--
TracECS020613119002..	LANRQAGSQRVRVKLK	YISLER	SVTSLQT	EVSALSP	WVAFIDH	QNSLTLY	GNHSHKQ	NIAALAQ	DKFPKDA	HOALQAL	EIRLRLQ	--

Trac5C5802612120002	QSNRSGARSRSRRLKQA	RMEELAQ	ASRLVLA	ENKALVE	RLKVLK	RYDELVS	ENAVLRD	NVDGDKH	TEADG	DNKHLKS	GDDSG	---
Trac5C5140027626001	LNHRGARSRSRRAKQ	RMEELIA	ASRLVLA	ENKALVE	QLCAVTT	RLTKVDV	ENAVLRD	HESELAG	RLQALG	VLIEFVQ	AGAPVDI	---
Trac5C54002611526001	LNHRGARSQRTLLRQA	IRDELAR	VADILAS	ENRMKQ	QDMYLE	QYTLTLE	TNQLQK	QAHHLSL	SFLA			---
Trac5C54002612666001	LNHRGARSQRTLLRQA	IRDELAR	VADILAS	ENRMKQ	QDMTAMQ	QYTLTQE	TNQLQK	QVIAKTA	QAPPV	VTSMDDT	PPAEQRA	---
Trac5C5400261740002	LNHRGARSQRTLLRQA	IRDELAR	VADILAS	ENRMKQ	QDMVYLE	QYTLTLE	TNQLQK	QVAKTTK	QSSPT	EATQATQ	APFAAQA	---
Trac5C5002613410001	LNHRGARSQRTLLRQA	VRDELAR	VADILAS	ENRMKQ	QDMTVMQ	QYTLTQE	TNQLQK	QARHRLP	LPFL	ATMDI	APFAARA	---
Trac5C5802611258001	LNHRGARSQRTLLRQA	IRDELAR	VADILAS	ENRMKQ	QDMTVMQ	QYTLTQE	TNQLQK	QVIAKTA	QAPPV	VTSMDDT	PPAEQRA	---
Trac5C500261350001	VSNRGARSRSRRAKQ	QLESLWA	QVHLDA	ENKALVE	QLCAVTT	RYDELVS	ENAVLRD	QKALCE	QLESLFA	VPAAVAV	AVEGEAG	---
Trac5C5002610130001	VSNRGARSRSRRAKQ	HLREQRA	AAATLRA	ENRHLAE	RLRVARA	RAGLTIL	ANARLRA	QGQALG	RLAAARQ	ALALRLQ	YAAASAS	---
Trac5C5002610612001	VSNRGARSRSRRAKQ	HLREQRA	AAATLRA	ENRHLAE	RLRVARA	RAGLTIL	ANARLRA	QGQALR	RLDAARQ	ALALRLQ	YAAASAS	---
Trac5C5002612626001	ENRSLAGRSRRAKLL	QVDELEA	CAAVAA	AQAQAAR	RCVAVQA	ENRHLRA	RLDELQA	RESEDA		LQITDA	YAAAGAS	---
Trac5C580261350001	VSNRGARSRSRRAKQ	RMEELIA	ASRLVLA	ENKALVE	QLCAVTT	RLKVLK	ENAVLRD	HESELAG	HQALGQ	VLIEFHV	AGAPVDI	---
Trac5C5002610500001	VSNRGARSRSRRAKQ	QLESLWA	QVHLDA	ENKALVE	QLCAVTT	RYDELVS	ENAVLRD	QKALCE	QLESLFA	QAOQSNN	ASSEPE	---
Trac5C7402639180001	ASHRGARSRSRMRRR	QDELLEA	ASRLVLA	ENKALVE	QLCAVTT	RYDELVS	ENAVLRD	QKALCE	QLESLFA	AARDGAD	QAAAAAR	---
Trac5C500261350001	VSNRGARSRSRRAKQ	QDELLEA	ASRLVLA	ENKALVE	QLCAVTT	RYDELVS	ENAVLRD	QKALCE	QLESLFA	ADRDGAD	QAAAAAR	---
Trac5C5002613930001	LNHRGARSRSRMRRR	QDELLEA	ASRLVLA	ENKALVE	QLCAVTT	RYDELVS	ENAVLRD	QKALCE	QLESLFA	VLIEFVQ	AGAPVDI	---
Trac5C5100260750001	LNHRGARSRSRRAKQ	RMEELIA	ASRLVLA	ENKALVE	QLCAVTT	RLTKVDV	ENAVLRD	HESELAG	RLQALG			---
Trac5C5300262030001	ENRSLAGRSRRAKLL	QVDELEA	CAAVAA	AQAQAAR	RCVAVQA	ENRHLRA	RLDELQA	RESEDA		LQIYMDA	RAAHGAS	---
Trac5C580261350001	QSNRSGARSRSRRLKQA	QLESLWA	QVHLDA	ENKALVE	QLCAVTT	RYDELVS	ENAVLRD	QKALCE	QLESLFA	QVTVTLT	QVLEAP	---
Trac5C580261740001	QSNRSGARSRSRRAKQ	HLNELEA	QVQVLQ	ENSLIRL	QLDANQV	RYNGGAAV	DNKRVLR	QVETLRA	KVKMAAD	SVKRVTG	*GLFLFA	---
Trac5C5802614440002	QSNRSGARSRSRRLKQA	HLVELET	QVQVLQ	ENSLIRL	QLDANQV	RYNGGAAV	DNKRVLR	QVETLRA	KVKMAAD	NKARGAM	QGLHGL	---
Trac5C5802614440002	QSNRSGARSRSRRLKQA	HLNELEA	QVQVLQ	ENSLIRL	QLDANQV	RYNGGAAV	DNKRVLR	QVETLRA	KVKMAAD	SVKRVTG	*GLFLFA	---
Trac5C7402612115001	QSNRSGARSRSRRLKQA	QQLQGLWA	QVHLDA	ENKALVE	QLCAVTT	RYDELVS	ENAVLRD	QKALCE	QLESLFA	VDGADGE	GVAVGQ	---
Trac5C5802612105001	QSNRSGARSRSRRLKQA	QQLQGLWA	QVHLDA	ENKALVE	QLCAVTT	RYDELVS	ENAVLRD	QKALCE	QLESLFA	QAOQSTK	*SEPE	---
Trac5C5802612050001	QSNRSGARSRSRRLKQA	QQLQGLWA	QVHLDA	ENKALVE	QLCAVTT	RYDELVS	ENAVLRD	QKALCE	QLESLFA	QVTVTLT	*GVPMQ	---
Trac5C5802614040001	QSNRSGARSRSRRLKQA	QQLQGLWA	QVHLDA	ENKALVE	QLCAVTT	RYDELVS	ENAVLRD	QKALCE	QLESLFA	QVTVTLT	*GVPMQ	---
Trac5C5802611855001	QSNRSGARSRSRRLKQA	QQLQGLWA	QVHLDA	ENKALVE	QLCAVTT	RYDELVS	ENAVLRD	QKALCE	QLESLFA	QVTVTLT	*GVPMQ	---
Trac5C5802611825001												

Trac558026142200.1	LANRQSGAQRVRVRLK	SVTGLGM	VYSLSP	VYAFIDH	QRLTLY	GNHHKQ	RIAAALQ	DKPFKD	HQALRK	IERLQ	--
Trac5580263000.1	INRSGARSRRAHRLK	RKLDLRA	LAATLGR	GRRLVLA	QVAIVLH	GNHHKQ	RIAAALR	DKPFKD	GAIALAQ	LYAAALQ	--
Trac55A026143300.1	LANRQSGAQRVRVRLK	YISELER	SVTGLGM	VYSLSP	VYAFIDH	QRLTLY	GNHHKQ	RIAAALQ	DKPFKD	HQALRK	IERLQ
Trac558026148700.1	LANRQSGAQRVRVRLK	YISELER	SVTGLGM	VYSLSP	VYAFIDH	QRLTLY	GNHHKQ	RIAAALQ	DKPFKD	HQALRK	IERLQ
Trac558026167500.1	LANRQSGAQRVRVRLK	YISELER	SVTSLQT	VYSLSP	VYAFIDH	QRLTLY	GNHHKQ	RIAAALQ	DKPFKD	HQALRK	IERLQ
Trac558026293500.1	LANRQSGAQRVRVRLK	YISELER	SVTGLGM	VYSLSP	VYAFIDH	QRLTLY	GNHHKQ	RIAAALQ	DKPFKD	HQALRK	IERLQ
Trac558026328400.1	LANRQSGAQRVRVRLK	YISELER	SVTTLGN	VYSLSP	VYAFIDH	QRLTLY	GNHHKQ	RIAAALQ	DKPFKD	HQALRK	IERLQ
Trac558026348200.1	LANRQSGAQRVRVRLK	YISELER	SVTSLQT	VYSLSP	VYAFIDH	QRLTLY	GNHHKQ	RIAAALQ	DKPFKD	HQALRK	IERLQ
Trac55802635000.1	LANRQSGAQRVRVRLK	YISELER	SVTGLGM	VYSLSP	VYAFIDH	QRLTLY	GNHHKQ	RIAAALQ	DKPFKD	HQALRK	IERLQ
Trac558026391800.2	VSNRSGARSRRRHRLK	QTLTDEL	QVEQLRS	QATLTK	QLTANQ	QPTTAVT	DNRIKLS	DVETLRI	VYKMAED	MVARGAV	CGLGQ
Trac55C7024638600.2	VSNRSGARSRRRHRLK	QTLTDEL	QVEQLRS	QATLTK	QLTANQ	QPTTAVT	DNRIKLS	DVETLRI	VYKMAED	MVARGAV	CGLGQ
Trac55C0026415300.1	VSNRSGARSRRAHQK	RLEELRG	TVARFLE	QREELA	HLAVAR	HLAVAR	QNARLR	RAVLR	LRERLR	LLALQRL	QILRS
Trac55C0026415300.1	VSNRSGARSRRAHQK	RLEELRG	TVARFLE	QREELA	HLAVAR	HLAVAR	QNARLR	RAVLR	LRERLR	LLALQRL	QILRS
Trac55C00264183500.1	VSNRSGARSRVRKQK	HLDDLSL	QVQLDNL	QGMNMN	VGLMGTQ	NIALQQA	QNVVMT	QKMELES	LCALGE	ICCMMS	STANP*
Trac55C5A026405200.1	VSNRSLGAQRRAHQK	RLEELRG	TVARLRA	QREELA	HLAVAR	HLAVAR	QNARLR	RAVLR	LRERLR	LRLTQQL	ARRP*
Trac55C5A026479000.1	ESNRSGARSRVRKQK	HLDDLSL	QVQLDNL	QGMNMN	VGLMGTQ	NIALQQA	QNVVMT	QKMELES	LCALGE	ICCMMS	STANP*
Trac55C5A02649090.1	LANRQSGAQRVRVRLK	YISELER	SVTGLGM	VYSLSP	VYAFIDH	QRLTLY	GNHHKQ	RIAAALR	DKPFKD	HQALRK	IERLQ
Trac55C5A02649090.1	LANRQSGAQRVRVRLK	YISELER	SVTGLGM	VYSLSP	VYAFIDH	QRLTLY	GNHHKQ	RIAAALQ	DKPFKD	HQALRK	IERLQ
Trac55C5A026491900.2	LANRQSGAQRVRVRLK	YISELER	SVTSLQT	VYSLSP	VYAFIDH	QRLTLY	GNHHKQ	RIAAALQ	DKPFKD	HQALRK	IERLQ

Trac5C80262120002.1	QSNRDRGARRRLRQKA	ECEELAQ	ASLVYDQ	ENSMKKD	QVSRNRK	RYDYLTK	KNSELRK	NYVDGRKH	KTDEAGL	DNRKLQHS	GDSBQ	---
Trac5C54026072600.1	LSNRGARSRRRAHQK	RHEMLTA	ASRLDA	ENSMKKK	QVGRATF	ENYDNRK	KNSELRK	NYVDGELAG	KLQALQG	VLRFIVQ	AGAPVDI	---
Trac5C5402616600.1	LSNRGARSQTLRLRQK	REDELAR	AVADLDS	ENSMKKK	QVETAMQ	QVYLTLQ	KNSELRK	QVIATKAT	KAPPVP	VTSMDTT	PFAEQRA	---
Trac5C54026198100.2	LSNRGARSQTLRLRQK	REDELAR	AVADLDS	ENSMKKK	QKDKVLE	QVYLTLQ	KNSELRK	QKPSSTP	AITPMDI	APPAQSA	EATFPQT	---
Trac5C480260117400.2	LSNRGARSQTLRLRQK	REDELAR	AVADLDS	ENSMKKK	QNVHMLE	QVYLTLQ	KNSELRK	QVAKTTTK	KFSSTP	AITPMDI	APPAQSA	---
Trac5C54026198100.1	LSNRGARSQTLRLRQK	REDELAR	AVADLDS	ENSMKKK	QKVTVMQ	QVYLTLQ	KNSELRK	QVIATKAT	KAPPVP	VTSMDTT	PFAEQRA	---
Trac5C6A026289800.1	LSNRGARSRRMRQK	QISELVA	QVHVLHG	ENSRQLD	QINRVIR	DGCRVLR	DNSELGR	KAKLQEV	LEELFA	VPAAVAV	AVEGEA	---
Trac5C540260215200.1	LSNRGARSQTLRLRQK	REDELAR	AVADLDS	ENSMKKK	QNVHMLE	QVYLTLQ	KNSELRK	QAHHLSL	SFLIA	---	---	---
Trac5C540260215200.2	LSNRGARSRRRAHQK	REDELAR	AVADLDS	ENSMKKK	QNVHMLE	QVYLTLQ	KNSELRK	QAHHLSL	SFLIA	---	---	---
Trac5C54026016200.1	LSNRGARSRRRAHQK	HLEEQRA	AAATLTA	ENSRHLA	KSRVRAA	RAGLVAL	ANARRAA	QGQALSR	LDPAARQ	ALALRLQ	YAAASAS	---
Trac5C5402622600.1	ESNRLSGAQSRPAKLL	QVDELEA	AAALALA	RCAVAAA	AQGEAAR	RCAVQVA	RNLEHAA	RALELGA	LESLEAE	LQIYDIA	AAMGAS	---
Trac5C78026293700.1	LSNRGARSRRMRMR	QVDELEA	AAELAA	RCARLVV	ENENRAE	RAQVQAR	RNRARRR	VRERDGR	RLAAEE	TRDRDAG	DEAAAAA	---
Trac5C18026091500.1	LSNRGARSRRRAHQK	RHEMLTA	ASRLDA	ENSMKKK	QVGRATF	ENYDNRK	KNSELRK	NYVDGELAG	KLQALQG	VLRFIVQ	AGAPVDI	---
Trac5C54026198100.1	LSNRGARSQTLRLRQK	REDELAR	AVADLDS	ENSMKKK	QVETAMQ	QVYLTLQ	KNSELRK	QVIATKAT	KAPPVP	VTSMDTT	PFAEQRA	---
Trac5C74026391800.1	ESNRGARSRRMRMR	QVDELEA	AAELAA	RCARLVV	ENENRAE	RAQVQAR	RNRARRR	VRERDGR	RLAAEE	AADRAG	DEAAAAA	---
Trac5C3402602000.1	ESNRLSGAQSRPAKLL	QVDELEA	AAALALA	RCAVAAA	AQGEAAR	RCAVQVA	RNLEHAA	RALELGA	LESLEAE	LQIYDIA	AAMGAS	---
Trac5C78026293900.1	LSNRGARSRRMRMR	QVDELEA	AAELAA	RCARLVV	ENENRAE	RAQVQAR	RNRARRR	VRERDGR	RLAAEE	AADRAG	DEAAAAA	---

Group 8

Traes-ids	DNA binding region	L0 gabdef	L1 gabdef	L2 gabdef	h2IP region	L3 gabdef	L4 gabdef	L5 gabdef	L6 gabdef	L7 gabdef	L8 gabdef	L9 gabdef
TraesC53D02G203300.1	ESNRLSAQSPARKLL	QVDELEA	GAAALRA	LNCAVAA	AAQAAAR	AAQAAAR	BCAVVQA	ENLILHA	RALELGA	LESLEAE	LIQYMDA	AAAMGAS--
TraesC56B02G318700.1	VSNRSAARRSRMRKQ	QLSELWA	QVVHLRG	ANRQLLD	QLNRRIR	DCDRVLR	DNSSLRA	QOABLRE	RIEFLPA	VPVAVAV	BAAGQVE	
TraesC55D02G473000.1	QSNRSGARRSRRLKQ	ECEELAQ	QVSELTG	ANTGLDS	EDDQMLG	DCCKTCT	ENRQLMG	RIEFLPA	KMQQSEB	*LQVVTTL	STQVEAP	
TraesC55B02G444100.2	QSNRSGARRSRRLKQ	HUNELEA	QVSQILRV	DNSSLIR	EDDQMLG	DCCKTCT	ENRQLMG	RIEFLPA	KMQQSEB	*LQVVTTL	STQVEAP	
TraesC56D02G144400.2	VSNRSAARRSRRLKQ	HUNELEA	QVSQILRV	DNSSLIR	QLTDANQ	QFTTAVT	DNRLILS	DVEALRV	KVKLARD	MVARGAM	*GGLGHL	
TraesC55D02G447500.1	QSNRSGARRSRRLKQ	HUNELEA	QVSQILRV	DNSSLIR	QLTDANQ	QFTTAVT	DNRLILS	DVEALRV	KVKLARD	MVARGAM	*GGLGHL	
TraesC55A02G440400.1	QSNRSGARRSRRLKQ	HUNELEA	QVSQILRV	DNSSLIR	QLTDANQ	QFTTAVT	DNRLILS	DVEALRV	KVKLARD	MVARGAM	*GGLGHL	
TraesC57A02G211500.1	VSNRSAARRSRRLKQ	QLGQLWA	QVVHLRD	ANRDLLD	LNRAVIT	YDGRVVR	DNRRMRD	ERAELOA	RIEFLPV	VDAGDAE	GVAVGSD	
TraesC55D02G258000.1	VSNRSAARRSRMRKQ	QISELWA	RVAHLRG	ANRRLLD	LNRRMR	SCQDVVR	DNDRLGA	ERAELOA	RIEFLPV	QAQOSTK	*SEEP	
TraesC34A02G120500.1	TSNRLSAQSRITKQ	REDNLVV	RAAQLEI	DNRRMR	QLTFLVQ	QSLVRQ	DNRRVLA	DARCLYS	LLQQQNS	QLRMLGQ	*ITGVFMD	
TraesC53B02G404200.1	TSNRSAARRSPARKQ	YVELEA	QVHLRE	KNARAA	ERTITLL	TSQMLV	QNVIEQS	KNVNAK	EGCTLSR	EGGCTWA		
TraesC54D02G185500.1	TSNRLSAQSRVRKQ	REDNLAA	RVAQLSI	DNRRMR	TSGLVQV	QSLVRQ	DNRRVLA	DARCLYS	LLQQQNS	QLRMLGQ	*ITGVFMD	
TraesC55B02G470600.1	QSNRSGARRSRRLKQ	ECEELAQ	QVSELTG	ANTGLDS	EDDQMLG	DCCKTCT	ENRQLMG	RIEFLPA	KMQQSEB	*LQVVTTL	STQVEAP	
TraesC56B02G182500.1	VSNRSAARRSRRLKQ	HUNELEA	QVSQILRV	DNSSLIR	QLTDANQ	QFTTAVT	DNRLILS	DVEALRV	KVKLARD	MVARGAM	*GGLGHL	
TraesC57B02G118500.1	VSNRSAARRSRRLKQ	QLGQLWA	QVVHLRD	ANRDLLD	LNRAVIT	YDGRVVR	DNRRMRD	ERAELOA	RIEFLPV	VDAGDAE	GVAVGSD	
TraesC57D02G213200.1	VSNRSAARRSRRLKQ	QLGQLWA	QVVHLRD	ANRDLLD	LNRAVIT	YDGRVVR	DNRRMRD	ERAELOA	RIEFLPV	VDAGDAE	GVAVGSD	
TraesC55D02G100700.1	LSNRSAARRSRRLKQ	HUNELEA	QVSQILRV	DNSSLIR	QLTDANQ	QFTTAVT	DNRLILS	DVEALRV	KVKLARD	MVARGAM	*GGLGHL	
TraesC55A02G088300.1	LSNRSAARRSRRLKQ	HUNELEA	QVSQILRV	DNSSLIR	QLTDANQ	QFTTAVT	DNRLILS	DVEALRV	KVKLARD	MVARGAM	*GGLGHL	
TraesC54B02G184500.1	TSNRLSAQSRMRKQ	REDNLAA	RAAQLEI	DNRRMR	QLTFLVQ	QSLVRQ	DNRRVLA	DARCLYS	LLQQQNS	QLRMLGQ	*ITGVFMD	
TraesC31A02G409800.2	QSNRSGARRSRRLKQ	ECEELAT	QVSELTG	ANTGLDS	EDDQMLG	DCCKTCT	ENRQLMG	RIEFLPA	KMQQSEB	*LQVVTTL	STQVEAP	
TraesC55A02G460800.2	QSNRSGARRSRRLKQ	ECEELAT	QVSELTG	ANTGLDS	EDDQMLG	DCCKTCT	ENRQLMG	RIEFLPA	KMQQSEB	*LQVVTTL	STQVEAP	
TraesC52A02G245700.2	QSNRSGARRSRRLKQ	ECEELSR	QVSELTG	ANTGLDS	EDDQMLG	DCCKTCT	ENRQLMG	RIEFLPA	KMQQSEB	*LQVVTTL	STQVEAP	
TraesC55D02G068800.1	LSNRSAARRSRRLKQ	HONDIES	QVQELTA	DNRRMR	QLTFLVQ	QSLVRQ	DNRRVLA	DARCLYS	LLQQQNS	QLRMLGQ	*ITGVFMD	
TraesC55A02G057500.2	LSNRSAARRSRRLKQ	HONDIES	QVQELTA	DNRRMR	QLTFLVQ	QSLVRQ	DNRRVLA	DARCLYS	LLQQQNS	QLRMLGQ	*ITGVFMD	
TraesC55B02G059200.1	QSNRSGARRSRRLKQ	ECEELAT	QVSELTG	ANTGLDS	EDDQMLG	DCCKTCT	ENRQLMG	RIEFLPA	KMQQSEB	*LQVVTTL	STQVEAP	
TraesC31B02G439800.1	QSNRSGARRSRRLKQ	ECEELAT	QVSELTG	ANTGLDS	EDDQMLG	DCCKTCT	ENRQLMG	RIEFLPA	KMQQSEB	*LQVVTTL	STQVEAP	
TraesC52B02G269600.2	QSNRSGARRSRRLKQ	ECEELSR	QVQELTA	DNRRMR	QLTFLVQ	QSLVRQ	DNRRVLA	DARCLYS	LLQQQNS	QLRMLGQ	*ITGVFMD	
TraesC31D02G17100.1	QSNRSGARRSRRLKQ	ECEELAT	QVSELTG	ANTGLDS	EDDQMLG	DCCKTCT	ENRQLMG	RIEFLPA	KMQQSEB	*LQVVTTL	STQVEAP	
TraesC52D02G136200.3	QSNRSGARRSRRLKQ	ECEELSR	QVQELTA	DNRRMR	QLTFLVQ	QSLVRQ	DNRRVLA	DARCLYS	LLQQQNS	QLRMLGQ	*ITGVFMD	
TraesC56A02G087400.2	LSNRSAARRSRRLKQ	ECEELGQ	QVSELTG	ANTGLDS	EDDQMLG	DCCKTCT	ENRQLMG	RIEFLPA	KMQQSEB	*LQVVTTL	STQVEAP	
TraesC54A02G073000.2	QSNRSGARRSRRLKQ	ECEELGQ	QVSELTG	ANTGLDS	EDDQMLG	DCCKTCT	ENRQLMG	RIEFLPA	KMQQSEB	*LQVVTTL	STQVEAP	
TraesC54D02G230200.2	QSNRSGARRSRRLKQ	ECEELGQ	QVSELTG	ANTGLDS	EDDQMLG	DCCKTCT	ENRQLMG	RIEFLPA	KMQQSEB	*LQVVTTL	STQVEAP	
TraesC54B02G29100.1	QSNRSGARRSRRLKQ	ECEELGQ	QVSELTG	ANTGLDS	EDDQMLG	DCCKTCT	ENRQLMG	RIEFLPA	KMQQSEB	*LQVVTTL	STQVEAP	
TraesC56B02G110100.1	QSNRSGARRSRRLKQ	ECEELGQ	QVSELTG	ANTGLDS	EDDQMLG	DCCKTCT	ENRQLMG	RIEFLPA	KMQQSEB	*LQVVTTL	STQVEAP	
TraesCU02G019200.1	LSNRSAARRSRRLKQ	ECEELGQ	QVSELTG	ANTGLDS	EDDQMLG	DCCKTCT	ENRQLMG	RIEFLPA	KMQQSEB	*LQVVTTL	STQVEAP	
TraesC55B02G094300.1	LSNRSAARRSRRLKQ	ECEELGQ	QVSELTG	ANTGLDS	EDDQMLG	DCCKTCT	ENRQLMG	RIEFLPA	KMQQSEB	*LQVVTTL	STQVEAP	

Group 9

TraesC57A02G268700.1	LANRQSAARRSRMRK	YIQELEH	QVQVLOT	EAATLSA	QLTMMQR	DSGLLAT	QNHLELI	RLQAMEQ	QAQLRDA	INEALTG	EVORLEI	
TraesC57D02G269300.1	LANRQSAARRSRMRK	YIQELEH	QVQVLOT	EAATLSA	QLTMMQR	DSGLLAT	QNHLELI	RLQAMEQ	QAQLRDA	INEALTG	EVORLEI	
TraesC55A02G308400.1	LNRLSAARRSRMRK	YIYELEG	QVQVLOG	EAATLSA	QLTMMQR	DSGLLAT	QNHLELI	RLQAMEQ	QAQLRDA	INEALTG	EVORLEI	
TraesC55B02G308800.1	LNRLSAARRSRMRK	YIYELEG	QVQVLOG	EAATLSA	QLTMMQR	DSGLLAT	QNHLELI	RLQAMEQ	QAQLRDA	INEALTG	EVORLEI	
TraesC55D02G315400.1	LNRLSAARRSRMRK	YIYELEG	QVQVLOG	EAATLSA	QLTMMQR	DSGLLAT	QNHLELI	RLQAMEQ	QAQLRDA	INEALTG	EVORLEI	
TraesC52D02G105400.1	LANRQSAARRSRMRK	YIYELEG	QVQVLOG	EAATLSA	QLTMMQR	DSGLLAT	QNHLELI	RLQAMEQ	QAQLRDA	INEALTG	EVORLEI	
TraesC54D02G105700.1	LANRQSAARRSRMRK	YIYELEG	QVQVLOG	EAATLSA	QLTMMQR	DSGLLAT	QNHLELI	RLQAMEQ	QAQLRDA	INEALTG	EVORLEI	
TraesC54B02G113400.1	LANRQSAARRSRMRK	YIYELEG	QVQVLOG	EAATLSA	QLTMMQR	DSGLLAT	QNHLELI	RLQAMEQ	QAQLRDA	INEALTG	EVORLEI	
TraesC54D02G116900.1	LANRQSAARRSRMRK	YIYELEG	QVQVLOG	EAATLSA	QLTMMQR	DSGLLAT	QNHLELI	RLQAMEQ	QAQLRDA	INEALTG	EVORLEI	
TraesC54D02G116900.1	LANRQSAARRSRMRK	YIYELEG	QVQVLOG	EAATLSA	QLTMMQR	DSGLLAT	QNHLELI	RLQAMEQ	QAQLRDA	INEALTG	EVORLEI	
TraesC55A02G491600.1	LANRQSAARRSRMRK	YIYELEG	QVQVLOG	EAATLSA	QLTMMQR	DSGLLAT	QNHLELI	RLQAMEQ	QAQLRDA	INEALTG	EVORLEI	
TraesC31A02G186000.1	LANRQSAARRSRMRK	YIYELEG	QVQVLOG	EAATLSA	QLTMMQR	DSGLLAT	QNHLELI	RLQAMEQ	QAQLRDA	INEALTG	EVORLEI	
TraesC52A02G352100.1	MANRQSAARRSRMRK	YIYELEG	QVQVLOG	EAATLSA	QLTMMQR	DSGLLAT	QNHLELI	RLQAMEQ	QAQLRDA	INEALTG	EVORLEI	
TraesC31D02G19100.1	LANRQSAARRSRMRK	YIYELEG	QVQVLOG	EAATLSA	QLTMMQR	DSGLLAT	QNHLELI	RLQAMEQ	QAQLRDA	INEALTG	EVORLEI	
TraesC54B02G20400.1	LANRQSAARRSRMRK	YIYELEG	QVQVLOG	EAATLSA	QLTMMQR	DSGLLAT	QNHLELI	RLQAMEQ	QAQLRDA	INEALTG	EVORLEI	
TraesC54D02G110900.1	LANRQSAARRSRMRK	YIYELEG	QVQVLOG	EAATLSA	QLTMMQR	DSGLLAT	QNHLELI	RLQAMEQ	QAQLRDA	INEALTG	EVORLEI	
TraesC54D02G171700.2	LANRQSAARRSRMRK	YIYELEG	QVQVLOG	EAATLSA	QLTMMQR	DSGLLAT	QNHLELI	RLQAMEQ	QAQLRDA	INEALTG	EVORLEI	
TraesC55D02G132300.1	LANRQSAARRSRMRK	YIYELEG	QVQVLOG	EAATLSA	QLTMMQR	DSGLLAT	QNHLELI	RLQAMEQ	QAQLRDA	INEALTG	EVORLEI	
TraesC55A02G124600.1	LANRQSAARRSRMRK	YIYELEG	QVQVLOG	EAATLSA	QLTMMQR	DSGLLAT	QNHLELI	RLQAMEQ	QAQLRDA	INEALTG	EVORLEI	
TraesC54A02G135600.2	LANRQSAARRSRMRK	YIYELEG	QVQVLOG	EAATLSA	QLTMMQR	DSGLLAT	QNHLELI	RLQAMEQ	QAQLRDA	INEALTG	EVORLEI	
TraesC54D02G352100.1	MANRQSAARRSRMRK	YIYELEG	QVQVLOG	EAATLSA	QLTMMQR	DSGLLAT	QNHLELI	RLQAMEQ	QAQLRDA	INEALTG	EVORLEI	
TraesC55B02G124200.1	LANRQSAARRSRMRK	YIYELEG	QVQVLOG	EAATLSA	QLTMMQR	DSGLLAT	QNHLELI	RLQAMEQ	QAQLRDA	INEALTG	EVORLEI	
TraesC52B02G122700.1	LANRQSAARRSRMRK	YIYELEG	QVQVLOG	EAATLSA	QLTMMQR	DSGLLAT	QNHLELI	RLQAMEQ	QAQLRDA	INEALTG	EVORLEI	
TraesC31B02G193800.1	LANRQSAARRSRMRK	YIYELEG	QVQVLOG	EAATLSA	QLTMMQR	DSGLLAT	QNHLELI	RLQAMEQ	QAQLRDA	INEALTG	EVORLEI	
TraesC54B02G113400.1	LANRQSAARRSRMRK	YIYELEG	QVQVLOG	EAATLSA	QLTMMQR	DSGLLAT	QNHLELI	RLQAMEQ	QAQLRDA	INEALTG	EVORLEI	
TraesC54A02G209900.1	LANRQSAARRSRMRK	YIYELEG	QVQVLOG	EAATLSA	QLTMMQR	DSGLLAT	QNHLELI	RLQAMEQ	QAQLRDA	INEALTG	EVORLEI	
TraesC55A02G299400.1	WANRQSAARRSRMRK	YIYELEG	QVQVLOG	EAATLSA	QLTMMQR	DSGLLAT	QNHLELI	RLQAMEQ	QAQLRDA	INEALTG	EVORLEI	
TraesC55B02G301900.1	WANRQSAARRSRMRK	YIYELEG	QVQVLOG	EAATLSA	QLTMMQR	DSGLLAT	QNHLELI	RLQAMEQ	QAQLRDA	INEALTG	EVORLEI	
TraesC55D02G308600.1	WANRQSAARRSRMRK	YIYELEG	QVQVLOG	EAATLSA	QLTMMQR	DSGLLAT	QNHLELI	RLQAMEQ	QAQLRDA	INEALTG	EVORLEI	
TraesC57A02G266400.1	WANRQSAARRSRMRK	YIYELEG	QVQVLOG	EAATLSA	QLTMMQR	DSGLLAT	QNHLELI	RLQAMEQ	QAQLRDA	INEALTG	EVORLEI	
TraesC57B02G166100.1	WANRQSAARRSRMRK	YIYELEG	QVQVLOG	EAATLSA	QLTMMQR	DSGLLAT	QNHLELI	RLQAMEQ	QAQLRDA	INEALTG	EVORLEI	

Group 10

TraesC55B02G176700.1	ESNRSAARRSRKQ	LDLSSQ	VDQLKNQ	SQQLSMV	LGMTTQN	LVALQAQ	NSVMQTO	MELESR	LICALG	ICMNSI	*TNAANPA
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Group 11

TraesC55A02G115300.1	QSNRDSARRSRRLKQA	ECEELAQ	QVSELTG	EAATLSA	QLTMMQR	DSGLLAT	QNHLELI	RLQAMEQ	QAQLRDA	INEALTG	EVORLEI	
TraesC31B02G43500.1	ESNRDSARRSRRLKQA	HANELEA	QVSELTG	EAATLSA	QLTMMQR	DSGLLAT	QNHLELI	RLQAMEQ	QAQLRDA	INEALTG	EVORLEI	
TraesC31D02G332200.1	ESNRDSARRSRRLKQA	HANELEA	QVSELTG	EAATLSA	QLTMMQR	DSGLLAT	QNHLELI	RLQAMEQ	QAQLRDA	INEALTG	EVORLEI	
TraesC56D02G087400.1	LSNRDSARRSRRLKQA	HANELEA	QVSELTG	EAATLSA	QLTMMQR	DSGLLAT	QNHLELI	RLQAMEQ	QAQLRDA	INEALTG	EVORLEI	
TraesC54D02G096300.1	LSNRDSARRSRRLKQA	HANELEA	QVSELTG	EAATLSA	QLTMMQR	DSGLLAT	QNHLELI	RLQAMEQ	QAQLRDA	INEALTG	EVORLEI	
TraesC56B02G124700.1	LSNRDSARRSRRLKQA	HANELEA	QVSELTG	EAATLSA	QLTMMQR	DSGLLAT	QNHLELI	RLQAMEQ	QAQLRDA	INEALTG	EVORLEI	

Supplementary figure 1: Amino acid sequence of all identified TabZIPs

in bread wheat. Protein sequences are aligned into sub-families demarcated with groups in first column clustered based on the similarity in sequence. Second column contains Traes ids. Third column has n-terminal region of bZIP domain and c-terminal leucine zipper region is divided into heptads (a,b,c,d,e,f and g). Primarily, the placement of N at 'a' position was considered for classification and it was coloured black at the respective 'a' position. Secondly, for the g-e' interactions, we used four colours (provided on the below right side). The attractive acidic-basic pairs (E↔R', E↔K', D↔R', D↔K') were coloured orange, and the attractive basic-acidic pairs (R↔E, K↔E') were coloured green. We coloured the repulsive basic pairs (K↔K', R↔K') with blue and repulsive acidic pairs (E↔E', D↔D', E↔D') with red. We have coloured the polar residues black at 'a' and 'd' position and charged residues at 'a' and 'd' positions were coloured purple. The candidate genes have been divided into five groups. We have used (*) symbol for potential helix break, due to the presence of proline or glycine. Symbol (^) denotes the natural end of a bZIP protein, and (--) shows that it is a longer protein and we have only shown the 9 heptads in the coloured

