

		*	20	*	40	*	60	*	80	*	100								
GRF3-2A_A :	MAMPFASLSPAADHHRSSPIFFPCRSSPLYSAGEEAAQ	QQQQ	QQHAMSGARWAAARPAT	FTAAQYEELEQQALIYKYL	VAGVPVPPDLLLP	I	RRGFDSL	:	99										
GRF3-2A_B :	MAMPFASLSPAADHHRSSPIFFPCRSSPLYSAGEEAAQ	QQQQ	QQHAMSGARWAAARPAT	FTAAQYEELEQQALIYKYL	VAGVPVPPDLLLP	I	RRGFDSL	:	99										
GRF3-2A_C :	MAMPFASLSPAADHHRSSPIFFPCRSSPLYSAGEEAAQ	QQQQ	QQHAMSGARWAAARPAT	FTAAQYEELEQQALIYKYL	VAGVPVPPDLLLP	I	RRGFDSL	:	99										
GRF3-2A_D :	MAMPFASLSPAADHHRSSPIFFPCRSSPLYSAGEEAAQ	--	QQHAMSGARWAAARPAT	FTAAQYEELEQQALIYKYL	VAGVPVPPDLLLP	I	RRGFDSL	:	96										
GRF3-2B :	MAMPFASLSPAADHHRSSPIFFPCRSSPLYSVGEETA	HQQQ	QQHTMSGARWAA--RPAT	FTAAQYEELEQQALIYKYL	VAGVPVPPDLLLP	I	RRGFDSL	:	97										
GRF3-2D :	MAMPFASLSPAADHHRSSPIFFPCRSSPLYSAGEEAAQ	QQ--	QQHAMSGARWAAMRPAT	FTAAQYQEELEQQALIYKYL	VAGVPVPPDLLLP	I	RRD	FDSL	:	97									
	0	*	120	*	140	*	160	*	180	*	200								
GRF3-2A_A :	ASRFYHHHALGYGSYFGKKLD	PEPGR	CRRTDGKKWRC	SKEAAQ	DSKYCERH	MHRGRN	RSRK	PVET	QLV-----	SHSQ	LQQQ	AP---	AAAF	HGH	SPYP	:	189		
GRF3-2A_B :	ASRFYHHHALGYGSYFGKKLD	PEPGR	CRRTDGKKWRC	SKEAAQ	DSKYCERH	MHRGRN	RSRK	PVET	HLV-----	SHSQ	LQQQ	AP---	AAAF	HGH	SPYP	:	189		
GRF3-2A_C :	ASRFYHHHALGYGSYFGKKLD	PEPGR	CRRTDGKKWRC	SKEAAQ	DSKYCERH	MHRGRN	RSRK	PVET	QLV-----	SHSQ	LQQH	GP---	AAAF	HGH	SPYP	:	189		
GRF3-2A_D :	ASRFYHHHALGYGSYFGKKLD	PEPGR	CRRTDGKKWRC	SKEAAQ	DSKYCERH	MHRGRN	RSRK	PVET	QLV-----	SHSQ	LQQQ	AP---	AAAF	HGH	SPYP	:	186		
GRF3-2B :	ASRFYHHHALGYGSYFGKKLD	PEPGR	CRRTDGKKWRC	SKEAAQ	DSKYCERH	MHRGRN	RSRK	PVET	QLVATPH-H	SHSQ	LQQH	APAAS	AAAF	HSH	SPYP	:	195		
GRF3-2D :	ASRFYHHHALGYGSYFGKKLD	PEPGR	CRRTDGKKWRC	SKEAAQ	DSKYCERH	MHRGRN	RSRK	PVET	QLVATPHSH	SHSQ	LQQH	APAAT	AAAF	HSH	SPYP	:	196		
	00	*	220	*	240	*	260	*	280	*	300								
GRF3-2A_A :	AIATGAG--	APGS	FALGSTAQL	HMDNAAAP	YATAGAAGN	KDFRYSAYG	FRTSAMED	HNQFISA	AMDTAM	DNYSWRLL	PAQNSS	FSLS	SSYP	PMLSTLS	DL	:	286		
GRF3-2A_B :	AIATGAG--	APGS	FALGSTAQL	HMDNAAAP	YATAGAAGN	KDFRYSAYG	FRTSAMED	HNQFISA	AMDTAM	DNYSWRLL	PAQNSS	FSLS	SSYP	PMLSTLS	DL	:	286		
GRF3-2A_C :	AIATGAG--	APGS	FALGSTAQL	HMDNAAAP	YATAGAAGN	KDFRYSAYG	FRTSAMED	HNQFISA	AMDTAM	DNYSWRLL	PAQNSS	FSLS	SSYP	PMLSTLS	DL	:	286		
GRF3-2A_D :	AIATGAG--	APGS	FALGSTAQL	HMDNAAAP	YATAGAAGN	KDFRYSAYG	FRTSAMED	HNQFISA	AMDTAM	DNYSWRLL	PAQNSS	FSLS	SSYP	PMLSTLS	DL	:	283		
GRF3-2B :	AIASGGG---	GSF	AVGS-AQL	HMDNAAAP	YATAGAAGN	KDFRYSAYG	FRTSAMED	HNQFISA	AMETAM	ENYSCRL	MPAQNSS	FSLS	ASYP	PMLGTL	GL	:	289		
GRF3-2D :	AIATGGGGG	AAGS	FGLGS-AQL	HMDNAAAP	YATAGAAGN	KDFRYSAYG	FRTSALE	HNQFISA	AMDTAM	DNYSWR	LMPAQNSS	AFSL	SSYP	PMLGTL	GL	:	294		
	300	*	320	*	340	*	360	*	380	*	400								
GRF3-2A_A :	QSAICSLAKTEREPLS	FFGV	GGGFDDDE	SAVKQENQ	TLRPFF	DEWPKDR	DSWP	ELQD	HDSNHN	NEAF	SATKLS	SISIP	VTSS	DFSTTAG	SRSPH	GIYSR	:	384	
GRF3-2A_B :	QSAICSLAKTEREPLS	FFGV	GGGFDDDE	SAVKQENQ	TLRPFF	DEWPKDR	DSWP	ELQD	HDSNHN	NEAF	SATKLS	SISIP	VTSS	DFSTTAG	SRSPH	GIYSR	:	384	
GRF3-2A_C :	QSAICSLAKTEREPLS	FFGV	GGGFDDDE	SAVKQENQ	TLRPFF	DEWPKDR	DSWP	ELQD	HDSNHN	NEAF	SATKLS	SISIP	VTSS	DFSTTAG	SRSPH	GIYSR	:	384	
GRF3-2A_D :	QSAICSLAKTEREPLS	FFGV	GGGFDDDE	SAVKQENQ	TLRPFF	DEWPKDR	DSWP	ELQD	HDSNHN	NEAF	SATKLS	SISIP	VTSS	DFSTTAG	SRSPH	GIYSR	:	381	
GRF3-2B :	QSAICSLAKTEREPLS	FFGG	GGGFDDDD	SAVKQENQ	TLRPFF	DEWPKDR	DSWP	ELQD	HDSN	SSNA	AF	SATKLS	SISIP	VTSS	DFSTTAG	SRSPN	GIYSR	:	387
GRF3-2D :	QSAICSLAKTEREPLS	FFGG	GGGFEDDE	SAVKQENQ	TLRPFF	DEWPKDR	DSWP	ELQD	HDSN	HSNA	AF	SATKLS	SISIP	VTSS	DFSTTAG	SRSPH	GIYSR	:	391

Figure S1. Alignment of the GRF3-2A protein isoforms with GRF3-2B and GRF3-2D proteins. The WRC domain that functions in DNA binding is highlighted in green (PEPGRCRRTDGKKWRC SKEAAQDSKYCERH MHRGRNRSRK P), while the QLQ domain involved in protein-protein interactions is highlighted in yellow (FTAAQYEELEQQAL IYKYL VAGVPVPPD LLLPI).