

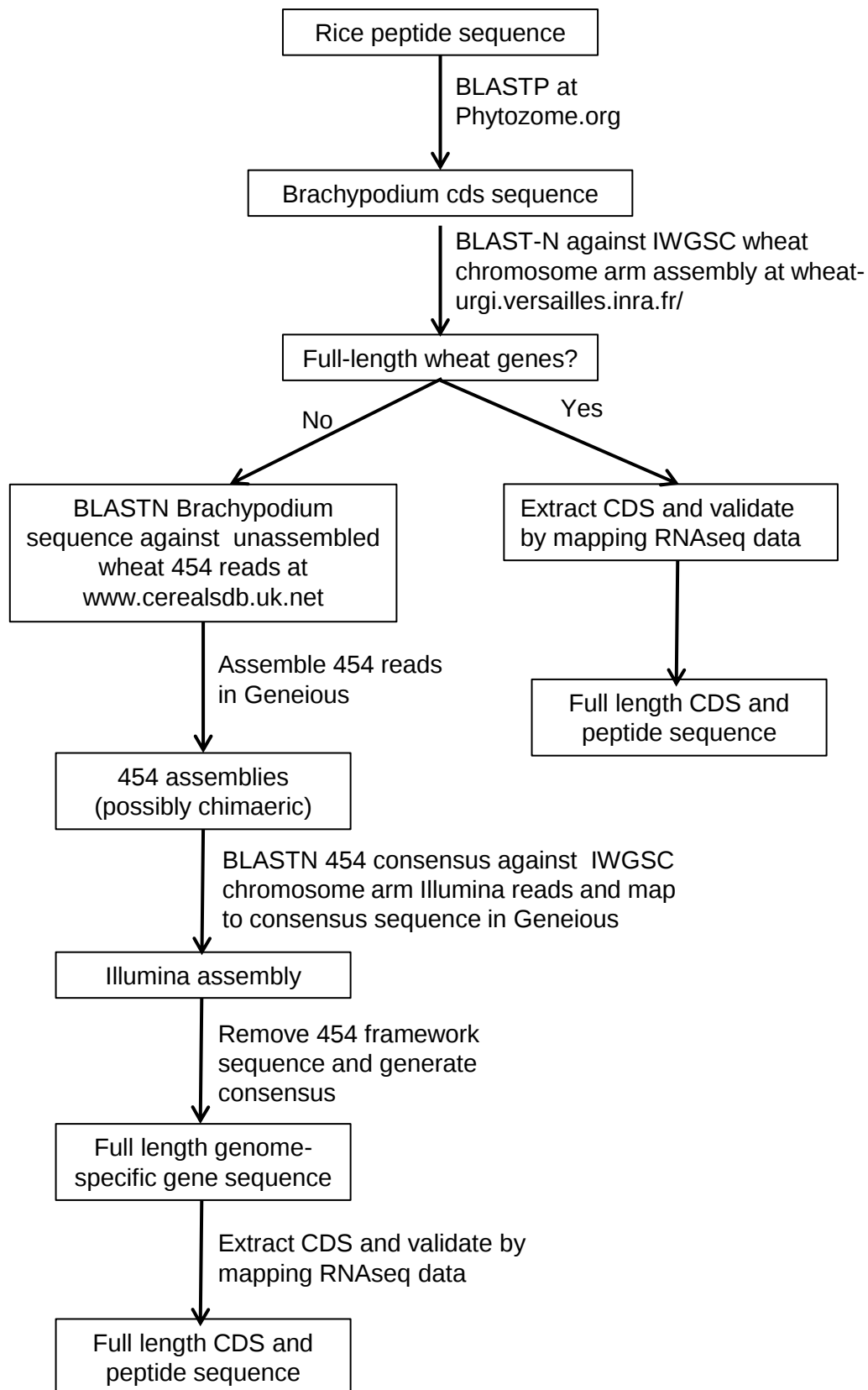


Figure S1: Workflow for identification and assembly of genes for wheat GA 2-ODDs

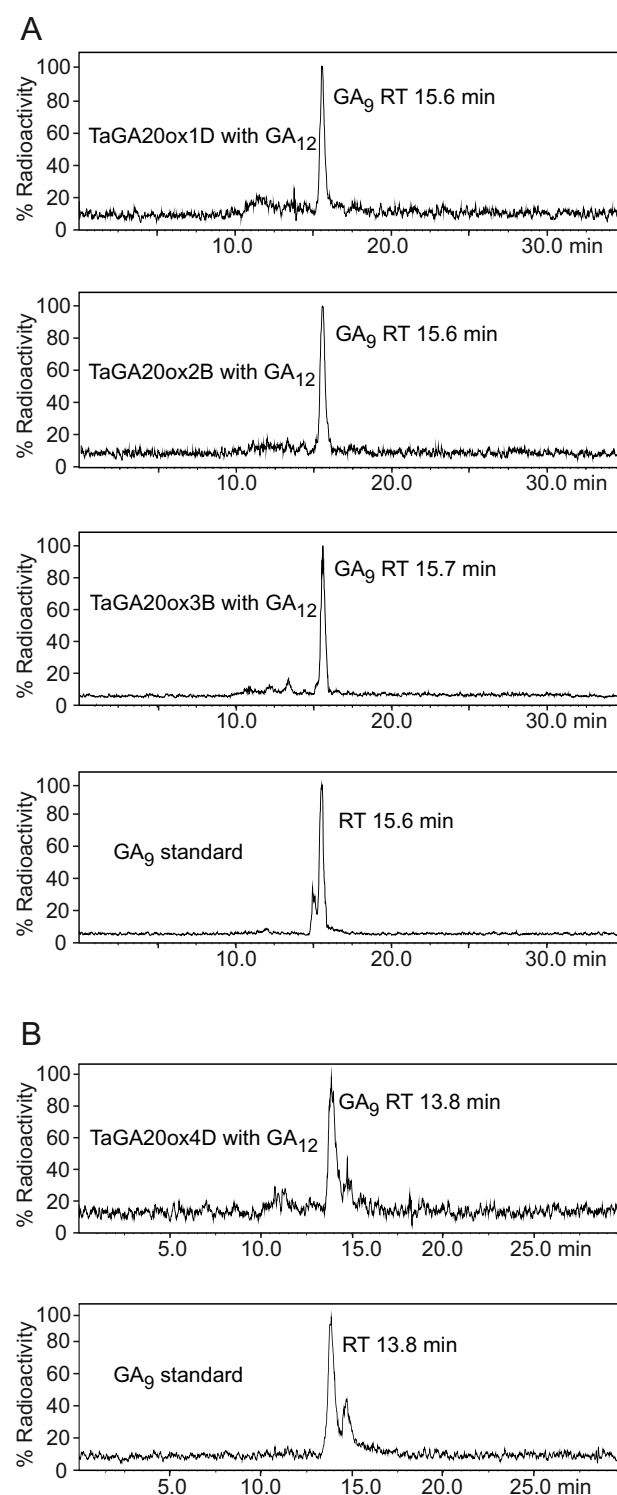


Figure S2. HPLC traces of incubations of heterologous expression products of GA20ox genes with [¹⁴C₁]GA₁₂.

A: TaGA20ox1D, TaGA20ox2B and TaGA20ox3B. B: TaGA20ox4D - note that this sample was run under different HPLC conditions and the GAs therefore have different retention times than in A. The X-axis shows HPLC retention time in minutes while the Y-axis is scaled such that the height of the largest peak of radioactivity is 100%.

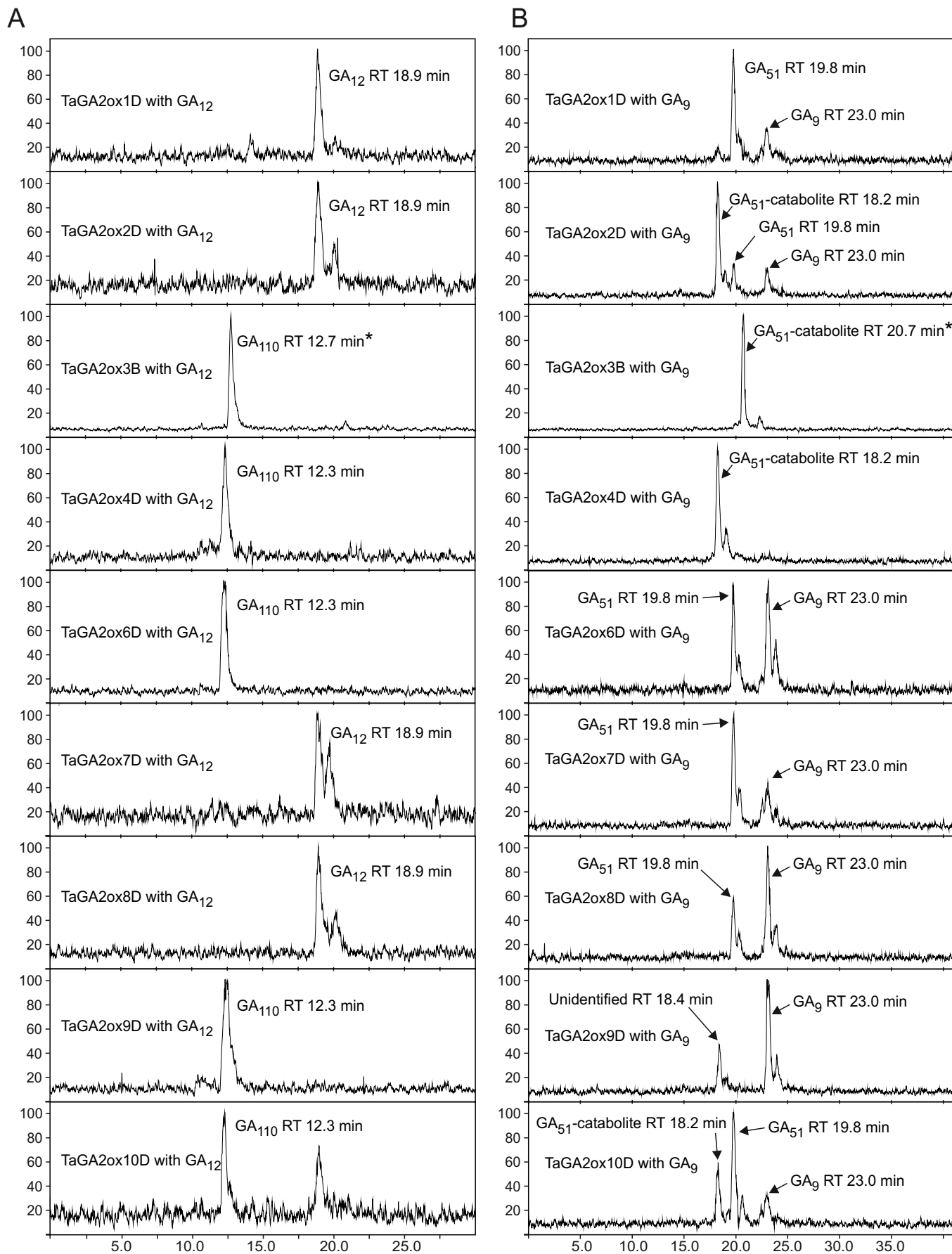


Figure S3. HPLC traces of incubations of heterologous expression products of GA2ox genes with (A) [¹⁴C₁]GA₁₂ and (B) [¹⁴C₁]GA₉. The Y-axis shows retention time in minutes. *The products from incubation of TaGA2ox3B with [¹⁴C₁]GA₉ were run under different HPLC conditions and have a longer retention time than in other panels. The X-axis shows HPLC retention time in minutes while the Y-axis is scaled such that the height of the largest peak of radioactivity is 100%.

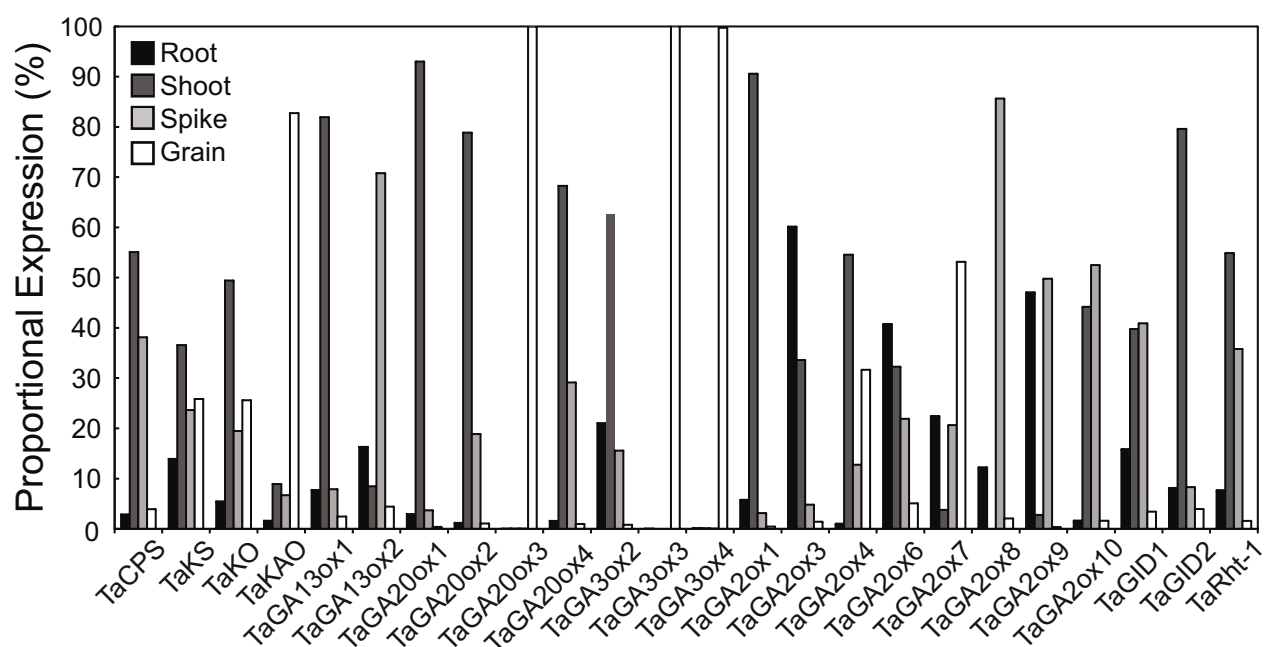


Figure S4. Relative expression of GA biosynthetic and signalling genes in durum wheat tissues determined by RT-PCR. Bars show the proportional distribution of transcripts from each gene across the four tissues.

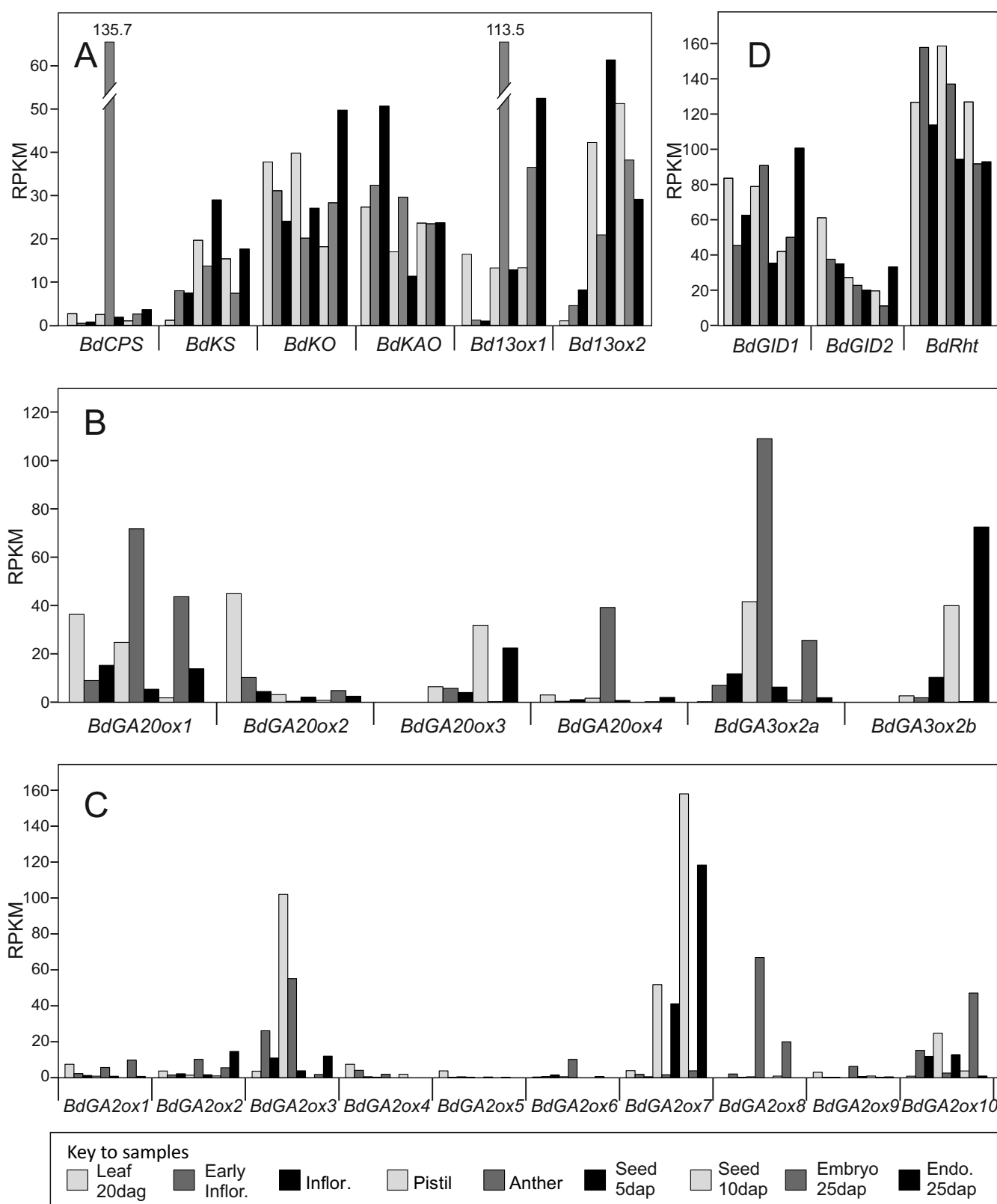


Figure S5. Transcript analysis of GA biosynthetic and signalling genes in *Brachypodium distachyon* by RNA-seq.

Unreplicated RNA-seq read samples from *Brachypodium* tissues was obtained from the Short Read Archive (<http://www.ncbi.nlm.nih.gov/sra>). Mapping to the *Brachypodium* reference transcriptome (<http://plants.ensembl.org/>) and calculation of RPKM values were carried out using BWA-mem and eXpress as described in Methods. dag: days after germination; dap: days after pollination; inflor: inflorescence; endo.: endosperm.

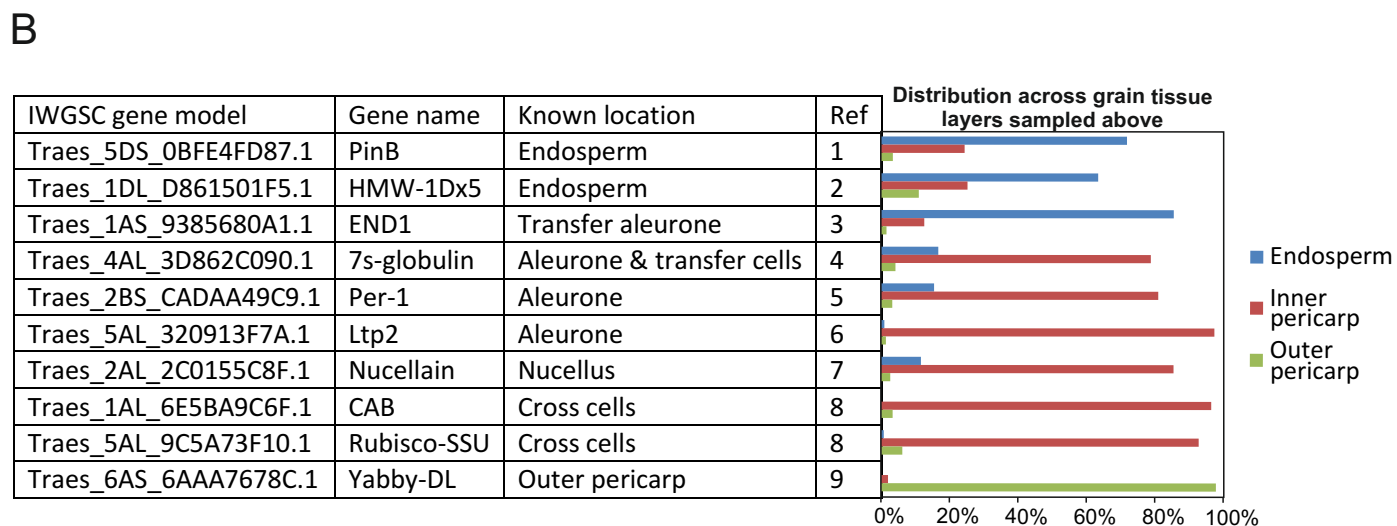
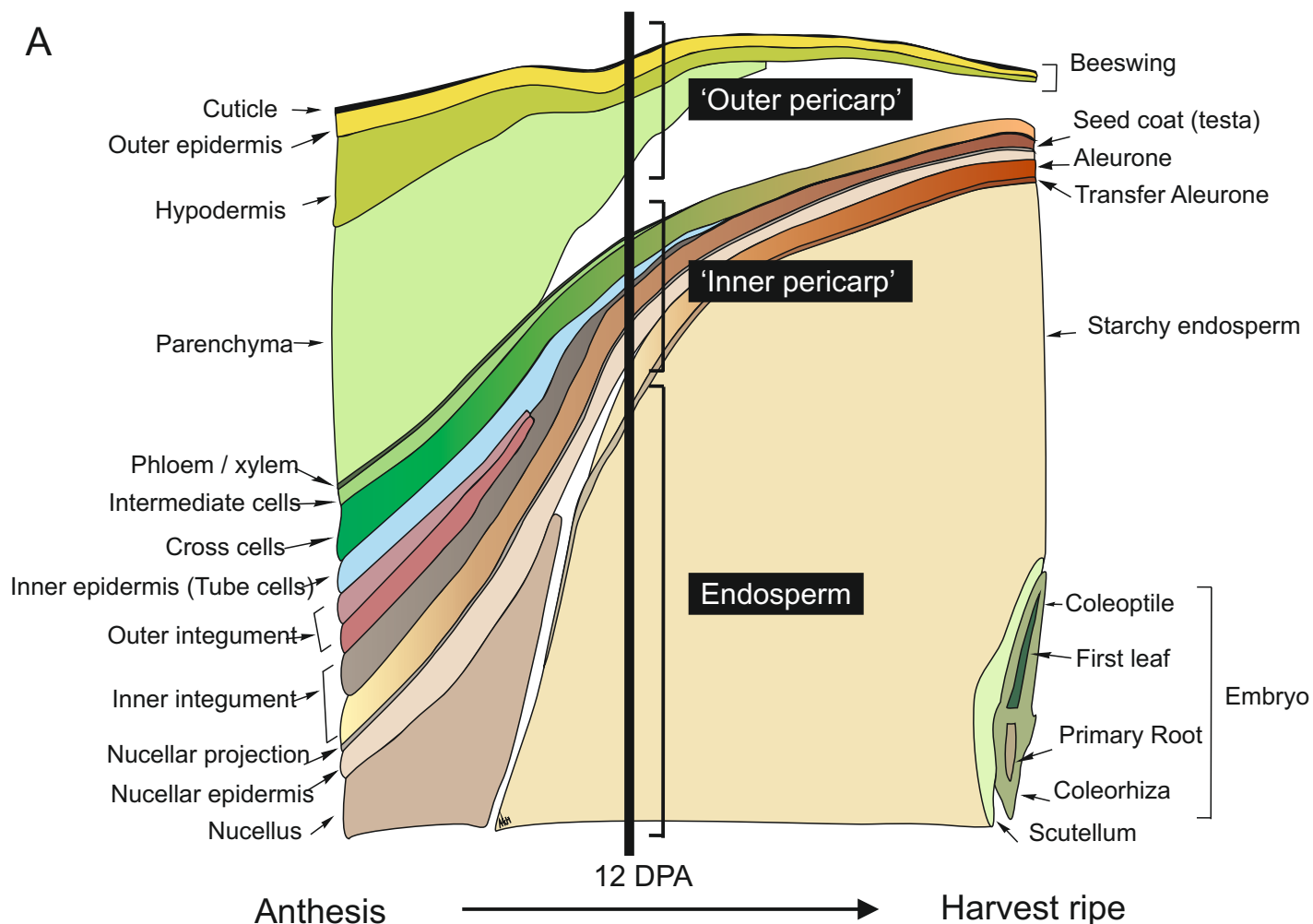


Figure S6. Dissection of tissue layers from developing grain of bread wheat.

A: Diagrammatic representation of changes in the tissue layers of developing wheat grain with time. Samples for RNA-seq analysis were taken at 12 days post-anthesis (DPA), approximately equivalent to Zadoks stage 73. B: The tissue layers dissected from developing wheat grain were assessed by the distribution of mean FPKM values of RNA-seq reads corresponding to transcripts of known location. References: (1) Gautier et al. (1994) Plant Mol Biol 25, 43-57, (2) Lamacchia et al. (2001) J Exp Bot 52, 243-250, (3) Doan et al. (1996) Plant Mol Biol 31, 877-886, (4) Huttly et al., unpublished, (5) Stacy et al. (1996) Plant Mol Biol 31, 1205-1216, (6) Kalla et al. (1994) Plant J 6, 849-860, (7) Linnestad et al. (1998) Plant Physiol 118, 1169-1180, (8) Morrison (1976) Bot Gaz 137, 85-93, (9) Wan et al. (2008) BMC Genomics 9.

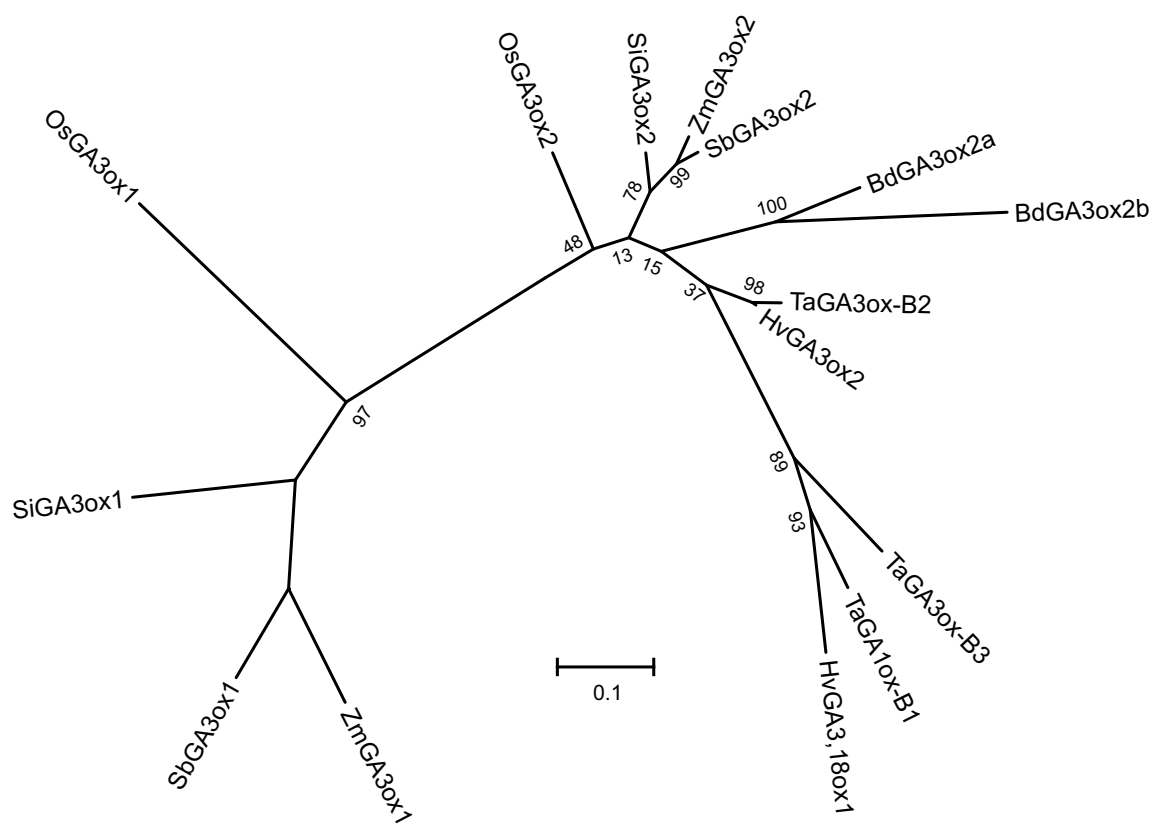


Figure S7. Phylogenetic tree of grass GA3ox-like protein sequences.

In addition to the wheat (Ta), Barley (Hv), Brachypodium (Bd) and rice (Os) sequences described in the text, the tree also contains GA3ox sequences from maize (ZmGA3ox1: GRMZM2G044358; ZmGA3ox2: GRMZM2G036340), sorghum (SbGA3ox1: Sb09g005400; SbGA3ox2: Sb03g004020) and *Setaria italica* (SiGA3ox1: Si025127m; SiGA3ox2: Si001832m); accession codes are from www.phytozome.org. Numbers show bootstrap support; the scale bar shows substitutions per site. Non-aligned residues were trimmed from the alignment prior to tree generation using PhyML within TOPALi, as reported in Materials and Methods.

Figure S8. Alignment of GA20ox protein sequences using MUSCLE with OsGA3ox2 as outgroup.

	*	20	*	40	*	60	*	80	
AtGA20ox1	:	-----MAVSFVTTSPPEEDKPKLGLGNIQTPLIFNP-----		-----SMLNLQA	:	38			
AtGA20ox2	:	-----MAILCTTTSPAEEKEHEPKQDLEKQTSPLIFNP-----		-----SLLNLQS	:	40			
AtGA20ox3	:	-----MATECIATVPQIFSE-----		-----NKTKESSIFDAKLLNQHS	:	34			
AtGA20ox4	:	-----MECIIKLPQRFNKNKSKNPLRIFDS-----		-----TVLNHQP	:	33			
AtGA20ox5	:	-----MCIYASRQTVCPYLTPFKVKRP-----		-----KSREMNSSDVNFSLLSQSQP	:	41			
BdGA20ox1	:	-----MVMQPVLFDA-----		-----AVLSGRS	:	17			
BdGA20ox2	:	-----MDTAPPLVLSP-----		-----SAPSITDTSTAKAKQSAAPVFDLRREP	:	38			
BdGA20ox3	:	-----MALEFDA-----		-----TILSRAP	:	14			
BdGA20ox4	:	-----MVDYQLSNSGEPNATTPIAAMDQVGRNPLLLFGP-----		-----ADDSKNAIIPWRQSK	:	49			
HvGA20ox1	:	-----MVQPVFDA-----		-----AVLSGRT	:	15			
HvGA20ox2	:	-----MVLQTAQQEPSLTPPPRCVASAGSPAAMDTSPATPLLLQP-----		-----PAPSIDPSAAKAAVSKGGAATAVYDLRREP	:	72			
HvGA20ox3	:	-----MASLVFDA-----		-----AVLSRKE	:	15			
HvGA20ox4	:	-----MVDVSNFVEANGNAAVSIPAMEVAGSPHVPFVP-----		-----RDANATDSKNAKDVLDLWRQKQ	:	55			
OsGA20ox1	:	-----MSMVVQQEQEVVFDA-----		-----AVLSGQT	:	22			
OsGA20ox2	:	-----MVAEHPTPPQHPQ-----		-----PPMDSTAGSGIAAPAAAACDLRMEP	:	40			
OsGA20ox3	:	-----AAVVFDA-----		-----AILSKQE	:	14			
OsGA20ox4	:	MHASPHPLQIAHDTLLLSLTHTLTCTAETGSTIRTGTAMVYISNAQDASKLIVTAKGGGGEADDAASSAAVVLDLWRQPA		:	80				
TaGA20ox-A1	:	-----MVRPVFDA-----		-----AVLSGRS	:	15			
TaGA20ox-B1	:	-----MVQPVFDA-----		-----AVLSGRA	:	15			
TaGA20ox-D1	:	-----MVQPVFDA-----		-----AVLSGRA	:	15			
TaGA20ox-A2	:	-----MDTSPATPLLLQP-----		-----PAPSIDPFAAKAAVNKNGGAATAVYDLRREP	:	44			
TaGA20ox-B2	:	-----MDTSPTTPLLLQP-----		-----PAPSIDPFAAKAAVNKNGGAATAVYDLRREP	:	44			
TaGA20ox-D2	:	-----MDTSPATPLLLQP-----		-----PAPSIDPFAAKAAVNKNGGAATAVYDLRREP	:	44			
TaGA20ox-A3	:	-----MATLVFDA-----		-----AVLSRKD	:	15			
TaGA20ox-B3	:	-----MATLVFDA-----		-----AVLSRKD	:	15			
TaGA20ox-D3	:	-----MATLVFDA-----		-----AVRSRKD	:	15			
TaGA20ox-A4	:	-----MEVARSPHLCVP-----		-----VDANATDSNSATDVLDLWRQKQ	:	35			
TaGA20ox-B4	:	-----MEVARSPHLPYVP-----		-----GDANATDSKNATDVLDLWRQKQ	:	35			
TaGA20ox-D4	:	-----MEVARSPHLCVP-----		-----VDANATDSNSATDVLDLWRQKQ	:	35			
OsGA3ox2	:	-----MPTPSHLKNP-----		-----LCFDFRAAR	:	19			

	*	100	*	120	*	140	*	160	
AtGA20ox1	:	N-IPNQFIWPD-DEKPSIN---VLE---LDVPLIDLQNLIS-----		D-PSSTLDASRLISEACKKHGFFLVVNHGISEE	:	103			
AtGA20ox2	:	Q-IPNQFIWPD-EEKPSID---IPE---LNVPFIDLSS-----		QDSTLEAPRVIAEACTKHGFFLVVNHGVSES	:	101			
AtGA20ox3	:	HHIPQFVWPD-HEKPSD---VQP---LQVPLIDLAGFLS-----		GD-SCLASEATRLVSKAATKHGFFLITNHGVDES	:	101			
AtGA20ox4	:	DHIPQEFVWPD-HEKPSKN---VPI---LQVPVIDLAGFLS-----		ND-PLLVSEAERLVSEAAKKHGFFLVVNHGVDER	:	100			
AtGA20ox5	:	N-VPAEFFWPE-KD-VAPS---EGD---LDLPIIDLSGFLN-----		GN-EAETQLAAKAVKKACMAHGFTLVVNHGFKSG	:	106			
BdGA20ox1	:	D-IPSQFIWPA-DESPTPD--AAEP---LDVPLIDIGGIVAS--		GAGDRAAAVASVARLVGDACSRHGFFQVVNHGIDAA	:	88			
BdGA20ox2	:	K-IPAPFVWPH-AE-VRPT--TAE---LGMPVVDVGLRKSRRGGD--		AAALRRVAQVAAAGATHGFFQVSGHGVDA	:	109			
BdGA20ox3	:	V-IPPQFVWPA-DE-ASPA--AVGE---IAIPVIDLAFLS-----		GSDFSGADHFAAACERHGFFQVNVHGVDP	:	78			
BdGA20ox4	:	Q-IPDSFVWPH-ADTHPPSSSTTTTTELLDVPVVDLAAALR-----		D-AAGMRDAAAQAAAACASHGFFLVTHGHGVDP	:	120			
HvGA20ox1	:	D-IPSQFIWPE-GESPTPD--ATE---MHVPLIDIGGMLS-----		GD-PRAAAEVTRLVGEACERHGFFQVVNHGIDAQ	:	82			
HvGA20ox2	:	K-IPAPFVWPH-AE-VRPT--TAQE---LAVPVVDVGLVRN--		GD-AAGIRRAVAQVAAACATHGFFQVSGHGVDNA	:	138			
HvGA20ox3	:	D-IPPQFIWPA-DEAPSVD--GVEE---IVVPVVDLAGFLA-----		GD-DAGL---NELVAACERHGFFQVVNHGVDP	:	78			
HvGA20ox4	:	Q-IPAPFIWPH-AD-ARPS--SILE---LDVPVVDIGAAALHS-----		AAGMARAAAQVAAACASHGFFQVTGHGVDP	:	120			
OsGA20ox1	:	E-IPSQFIWPA-EESPGSV--AVEE---LEVALIDVGA-----		GAERSSVVRQVGEACERHGFFLVVNHGIEAA	:	84			
OsGA20ox2	:	K-IPAPFVWPN-GD-ARPA--SAAE---LDMPVVDVGLVRD--		GD-AEGLRRAAAQVAAACATHGFFQVSEHGVDA	:	106			
OsGA20ox3	:	A-IPAQFVWPA-DEAPAADDGVVEE---IAIPVVDLAAFLA-----		SGGIG---RDVAEACERHGFFQVVNHGVDP	:	78			
OsGA20ox4	:	K-IPAPFVWPR-ADVALPP--SSPPTGELDVPVVDLAAALR-----		D-AAGMRRAVAQVAAACASHGFFQVSGHGVPPS	:	149			
TaGA20ox-A1	:	D-IPSQFIWPE-GESPTPD--AAEE---LHVPLINIGGMLS-----		GD-AAAAAEVTRLVGEACERHGFFQVVNHGIDAE	:	82			
TaGA20ox-B1	:	D-IPSQFIWPE-GESPTPD--AAEE---LHVPLIDIGGMLS-----		GD-AAAAAEVTRLVGEACERHGFFQVVNHGIDAE	:	82			
TaGA20ox-D1	:	D-IPSQFIWPE-GESPTPD--AAEE---LHVPLIDIGGMLS-----		GD-PAAAAEVTRLVGEACERHGFFQVVNHGIDAE	:	82			
TaGA20ox-A2	:	K-IPAPFVWPH-AE-VRPT--TAE---LAVPVVDVGLVRN--		GD-AAGLRRVAQVAAACATHGFFQVSGHGVDDA	:	110			
TaGA20ox-B2	:	K-IPAPFVWPH-AE-VRPT--TAE---LAMPVVDVSVLRN--		GD-AAGLRRVAQVAAACATHGFFQVSGHGVDDT	:	110			
TaGA20ox-D2	:	K-IPAPFVWPH-AE-VRPT--TAQE---LAVPVVDVGLVRN--		GD-AAGLRRVAQVAAACATHGFFQVSGHGVDEA	:	110			
TaGA20ox-A3	:	D-IPPQFVWPA-DEAPSVH--GVEE---IAPVVDIAGFLA-----		GD-GAATGGLRDAAACEKHGFFQVVNHGVDP	:	81			
TaGA20ox-B3	:	D-IPPQFVWPA-DEAPSVD--GVEE---IAPVVDIAGFLA-----		GD-GSAGAGPGLRDAAACEKHGFFQVVNHGVDP	:	82			
TaGA20ox-D3	:	D-IPPQFVWPA-DEAPSVD--GVEE---IAPVVDIAGFLA-----		GD-GSADAGGLRDAAACEKHGFFQVVNHGVDP	:	82			
TaGA20ox-A4	:	Q-IPAPFVWPH-AD-ARPS--SMLE---LDVPVVDIGAAALHS-----		AAGMGRAAAQVAAACASHGFFQVTGHGVDLA	:	100			
TaGA20ox-B4	:	Q-IPAPFVWPN-AD-ARPS--SMLE---LDVPVVDIGAAALHS-----		AAGMGRAAAQVAAACASHGFFQVTGHGVDP	:	100			
TaGA20ox-D4	:	Q-IPAPFVWPN-AD-ARPS--SMLE---LDVPVVDIGAAALHS-----		AAGMGRAAAQVAAACASHGFFQVTGHGVDP	:	100			
OsGA3ox2	:	R-VPETHAWPGLDDHPVVD--GGGGGGEDAVPVVDVGA-----		GD-----AAARVARAAEQWGAFLLVGHGVPA	:	81			

		*	180	*	200	*	220	*	240			
AtGA200x1	:	LISDAHEYTSRFFDMPLSEKQVR	LRKSGESVGYASSFTGRFSTKL	PWKETLSFRFC	----	DDMSRSKSVQDYFC	DALG	:	177			
AtGA200x2	:	LTADAHRLMESFFDMPLAGKQKA	QQRKGESCGYASSFTGRFSTKL	PWKETLSQFS	----	NDNSGSRVTQDYFSD	TLG	:	175			
AtGA200x3	:	LLSRAYLHMDSFFKAPACEKQKA	QQRKWGESSGYASSFVGRFSSKL	PWKETLSFKFS	----	PEEKIHSQTVKDFVSK	KMG	:	176			
AtGA200x4	:	LLSTAHKLMDTFFKSPNYEKLKA	QRKVGETTGYYASSFVGRFKENL	PWKETLSFSFS	----	PTEKSENYSQTVKNYISK	TMG	:	177			
AtGA200x5	:	LAEKALEISSLFFGLSKDEKLRA	YRIPGNISGYTAGHSQRFSSNL	PWNETLTLAFK	----	KGPPHVVEDFLT	SRLG	:	178			
BdGA200x1	:	LLADAHRCVDAFFKLPLAEKQRA	LRPGESEGYASSFVGRFSSKL	PWKETLSFRSS	----	PSCPDLPDLFILSNL	G	:	160			
BdGA200x2	:	LARAALDGASDFFRMLADKQARR	VQGTVSGYSAHADRFATKL	PWKETLSFGFH	----	GQDCAEAKPVVVDYFT	STLG	:	185			
BdGA200x3	:	LLAEAYRSMDAFYALPLAEKQRA	KRRRLGENHGYAGSFTGRFESRL	PWKETMSFNCS	----	DAPENASKVVVDYFVSV	LG	:	152			
BdGA200x4	:	LARAALDGAAGFFRLPLATKQRA	RRVTGSVAGYAAAHADRFAANL	PWKETLSFRHH	----	HDDDDRDVLDYFT	STLG	:	194			
HvGA200x1	:	LLADAHRCVDAFFTMPLPEKQRA	LRPGESEGYASSFTGRFASKL	PWKETLSFRSC	----	PSDPALVVDDYIVAP	LG	:	154			
HvGA200x2	:	LARAALDGASGFFRLPLAEKQRA	RRIPTVSGYSAHADRFASKL	PWKETLSFGFH	----	DRAGAAAPVVVDYFT	STLG	:	213			
HvGA200x3	:	LLAKAYRCCDAFYALPLAEKQRA	QRRRLGENHGYAGSFVGRFGSKL	PWKETMSFNCS	----	AAPESARKVVVDYFVG	VLG	:	152			
HvGA200x4	:	LAQAALDGAADFFRLPLATKQRA	RRSPGTVKGYASAHADRFAAKL	PWKETLSFIHNVHEDVGAR	SSH	-	VVDYFTSALG	:	199			
OsGA200x1	:	LEEAHRCMDAFFTLPLGEKQRA	QRRRAGSEGYASSFTGRFASKL	PWKETLSFRYS	----	SAGDEEGEEGVDEYLF	TRKL	:	160			
OsGA200x2	:	LARAALDGASDFFRLPLAEKRR	ARRVPGTVSGYSAHADRFASKL	PWKETLSFGFH	----	DRAAAPVVVDYFSST	LG	:	179			
OsGA200x3	:	LLAEAYRCCDAFYARPLAEKQRA	RRRPGENHGYASSFTGRFDCKL	PWKETMSFNCS	----	AAPGNARMVADYFVD	DALG	:	152			
OsGA200x4	:	LARAALDGAAGFFRLPPAAKQRA	RRAPGTVTGYTAHADRFVDNL	PWKETLSFGHR	----	HAN	-	AAGNNSSTVADYF	-	STLG	:	225
TaGA200x-A1	:	LLADAHRCVDAFFTMPLPEKQRA	LRPGESEGYASSFTGRFASKL	PWKETLSFRSC	----	PSDPALVVDDYIVAT	LG	:	154			
TaGA200x-B1	:	LLADAHRCVDAFFTMPLPEKQRA	LRPGESEGYASSFTGRFASKL	PWKETLSFRSC	----	PSDPALVVDDYIVAT	LG	:	154			
TaGA200x-D1	:	LLADAHRCVDAFFTMPLPEKQRA	LHPGESEGYASSFTGRFASKL	PWKETLSFRSC	----	PSDPALVVDDYIVAT	LG	:	154			
TaGA200x-A2	:	LARAALDGASGFFRLPLAEKQRA	RRVPGTVSGYSAHADRFASKL	PWKETLSFGFH	----	DRAGAAAPVVVDYFT	STLG	:	184			
TaGA200x-B2	:	LARAALDGAGGFFRLPLAEKQRA	RRIPTVSGYSAHADRFASKL	PWKETLSFGFH	----	DRAGAAAPVVVDYFT	STLG	:	184			
TaGA200x-D2	:	LARAALDGASGFFRLPLAEKQRA	RRVPGTVSGYSAHADRFASKL	PWKETLSFGFH	----	DRAGAAAPVVVDYFT	STLG	:	184			
TaGA200x-A3	:	LLAKAYRCCDAFYALPLAEKQRA	QRRRLGENHGYAGSFVGRFGSKL	PWKETVSNFCS	----	AAPEGARKVVVDYFV	AVLG	:	155			
TaGA200x-B3	:	LLAKAYRCCDAFYALPLAEKQRA	QRRRLGENHGYAGSFVGRFGSKL	PWKETMSFNCS	----	AAPEGARKVVVDYFV	GVLG	:	157			
TaGA200x-D3	:	LLAKAYRCCDAFYAMPLAEKQRA	QRRRLGENHGYAGSFVGRFGSKL	PWKETMSFNCS	----	AAPEGARKVVVDYFV	GVLG	:	156			
TaGA200x-A4	:	LARAALDGAADFFRLPLATKQRA	RRSPGTVEGYASAHADRFAAKL	PWKETLSFSHN	----	HDDVVGARGNSHVVDYFT	SALG	:	178			
TaGA200x-B4	:	LARAALDGAADFFRLPLATKQRA	RRSPGTVEGYASAHADRFAAKL	PWKETLSFSHN	----	HDDVVGARGDSHVVDYFT	SALG	:	178			
TaGA200x-D4	:	LARAALDGAADFFRLPLATKQRA	RRSPGTVEGYASAHADRFAAKL	PWKETLSFSHN	----	HDDVVGARGNSHVVDYFT	SALG	:	178			
OsGA30x2	:	LLSRVEERVAVFSLPASEKMR	AVRGPGEPCGYGSPPISSFFSKL	MWSEGYTFS	----	PSSLRSELRLRLWPK	SG	:	151			

		*	260	*	280	*	300	*	320		
AtGA200x1	:	HGF-QPFGKVYQEYCEAMSSLSL	KIMELLGSLGV	---	K-RD	--	YFREFFEENDSIMRLN	YPPCKIPDLTLGTGPHCDP	:	250	
AtGA200x2	:	QEF-EQFGKVYQDYCEAMSSLSL	KIMELLGSLGV	---	N-RD	--	YFRGFFEENDSIMRLN	YPPCQTPDLTLGTGPHCDP	:	248	
AtGA200x3	:	DGY-EDFGKVYQEYAEAMNTSL	KIMELLGMSLGV	---	E-RR	--	YFKEFFEDSDSIFRLN	YPPCKQPELALGTGPHCDP	:	249	
AtGA200x4	:	DGY-KDFGSVYQEYAEAMNTSL	KIMELLGMSLGI	---	K-RE	--	HFREFFEDNESIFRLN	YPPCKQPDVLGTGPHCDP	:	250	
AtGA200x5	:	NHR-QEIGQVQEFCDAMNGLVMD	LMELLGISLGL	---	KDRT	--	HYRRFFEDGSGIFRCN	YPPCKQPEKALGVGPHNDP	:	252	
BdGA200x1	:	EEH-RRLGEVYARYCEMSRVSLE	IMEVLGESLGV	---	G-RS	--	HYRSFFEGNDSIMRLN	YPPCQRPYETLGTGPHCDP	:	233	
BdGA200x2	:	QDF-EPMGRVYQEYCEKMKELSL	TIMELLESLGV	---	E-RG	--	YYREFFADSSSIMRCN	YPPCPEPERTLGTGPHCDP	:	258	
BdGA200x3	:	EEY-RQMGVWQEYCDVMTRLALD	VTDLAVLGL	---	G-RG	--	ALRGFFAGGDSVMRLN	YPPCQRPHTLGTGPHRDP	:	225	
BdGA200x4	:	DDF-KPLGEVYQEYCGAMEAASL	AIMEVLGSLGV	---	G-RG	--	HYRDFADGSSVMRCN	YPPCPEPDRTLGTGPHCDP	:	267	
HvGA200x1	:	EDH-RRLGEVYARYCEMSRVSLE	IMEVLGESLGV	---	G-RA	--	HYRRFFEGNDSIMRLN	YPPCQRPLETLGTGPHCDP	:	227	
HvGA200x2	:	PDY-EPMGRVYQEYCGKMKELSL	RIMELLESLGV	---	E-KRG	--	YYRDFADSSSIMRCN	YPPCPEPERTLGTGPHCDP	:	287	
HvGA200x3	:	EEY-RHMGDVWQEYCNEMTRLALD	VTDLVLAACLGL	---	D-RG	--	ALRGFFAGDDSLMRLN	YPPCCKPHLTLGTGPHHDP	:	225	
HvGA200x4	:	DDF-MHLGEVYQEYCEAMEDASL	AIMEVLGSLGL	---	G-RG	--	YYRDFADGSSIMRCN	YPPRCPEPDRTLGTGPHCDP	:	272	
OsGA200x1	:	AEHGRRLGEVYSRYCHEMSRSL	SLEIMEVLGESLGI	VDGR	-	RH	-	YFRFFQNRNDSIMRLN	YPPACQRPDLTLGTGPHCDP	:	237
OsGA200x2	:	PDF-APMGRVYQKYCEEMKELSL	TIMELLESLGV	---	E-RG	--	YYREFFADSSSIMRCN	YPPCPEPERTLGTGPHCDP	:	252	
OsGA200x3	:	EEY-RHMGVWQEYCDVMTRLALD	VTDLVLAACLGL	---	G-RG	--	ELRGFFADGDPVMRLN	YPPCQRPHTLGTGPHRDP	:	225	
OsGA200x4	:	DDF-KHLGEVYQEYCEAMEEVT	KAIMAVLGESLGV	---	G-GG	--	YYREFFEDSSSIMRCN	YPPCPEPERTLGTGPHCDP	:	298	
TaGA200x-A1	:	EDH-RRLGEVYARYCEMSRVSLE	IMEVLGESLGV	---	G-RA	--	HYRRFFEGNDSIMRLN	YPPCQRPLETLGTGPHCDP	:	227	
TaGA200x-B1	:	EDH-RRLGEVYARYCEMSRVSLE	IMEVLGESLGV	---	G-RA	--	HYRRFFEGNDSIMRLN	YPPCQRPLETLGTGPHCDP	:	227	
TaGA200x-D1	:	EDH-RRLGEVYARYCEMSRVSLE	IMEVLGESLGV	---	G-RA	--	HYRRFFEGNDSIMRLN	YPPCQRPLETLGTGPHCDP	:	227	
TaGA200x-A2	:	PDY-EPMGRVYQEYCEKMKELSL	RIMELLESLGV	---	E-KRG	--	YYRDFADSSSIMRCN	YPPCPEPERTLGTGPHCDP	:	258	
TaGA200x-B2	:	PDY-EPMGRVYQEYCGKMKELSL	TIMELLESLGV	---	E-KRG	--	YYREFFADSSSIMRCN	YPPCPEPERTLGTGPHCDP	:	258	
TaGA200x-D2	:	PDY-EPMGRVYQEYCGKMKELSL	RIMELLESLGV	---	E-KRG	--	YYREFFADSSSIMRCN	YPPCPEPERTLGTGPHCDP	:	258	
TaGA200x-A3	:	EEY-RDMGEVWQEYCDMTRLALD	VDVLAACLGL	---	G-RG	--	ALRGFFAGDASLMRLN	YPPCQPHLTLGTGPHHDP	:	227	
TaGA200x-B3	:	EEY-RDMGEVWQEYCDMTRLALD	VDVLAACLGL	---	R-HG	--	ALRGFFAGDDSLMRLN	YPPCQPHLTLGTGPHHDP	:	230	
TaGA200x-D3	:	EEF-RYMGEVWQEYCDMTRLALD	VDVLAACLGL	---	G-RG	--	SLRGFFAGDDSLMRLN	YPPCQPHLTLGTGPHHDP	:	229	
TaGA200x-A4	:	DDF-KHLGEVYQEYCEAMEEASL	AIMEVLGSLGL	---	G-RG	--	YYRDFADGSSIMRCN	YPPRCPEPDRTLGTGPHCDP	:	251	
TaGA200x-B4	:	GDF-KHLGEVYQEYCEAMEDASL	AIMEVLGSLGL	---	G-RG	--	YYRDFADGSSIMRCN	YPPRCPEPDRTLGTGPHCDP	:	251	
TaGA200x-D4	:	DDF-KHLGEVYQEYCEAMEEASL	AIMEVLGSLGL	---	G-RG	--	YYRDFADGSSIMRCN	YPPRCPEPDRTLGTGPHCDP	:	251	
OsGA30x2	:	DDY-LLFCDVMEEFHKEMRRLA	DELLRLFLRALGLTGEEVAG	VEAERRIGERMTATVHLN	WYPRCPEPRRALGLIAHTDS	:	230				

	*	340	*	360	*	380	*	400	
AtGA200x1	:	TSLTILHQD-HVNGLQVFVE-----N--QWRSIRPNPKAFVFNIGDTFMALSNDRYKSCSLHRAVVNSESEKSLAFFLC	:	321					
AtGA200x2	:	SSLTILHQD-HVNGLQVFVD-----N--QWQSIRPNPKAFVFNIGDTFMALSNIGFKSCLHRAVVNRESARKSMAFFLC	:	319					
AtGA200x3	:	TSLTILHQD-QVGGLQVFVD-----N--KWQSIPPNPHAFVFNIGDTFMALTNGRYKSCSLHRAVVNSERERKTFAFFLC	:	320					
AtGA200x4	:	TSLTILQD-QVSGLQVFVD-----N--QWQSIPPIQALVFNIGDTLMALTNIGYKSCSLHRAVVNGETTRKTLAFFLC	:	321					
AtGA200x5	:	TAITVLLQD-DVVGLEVFVA-----G--SWQTVRPRPGALVFNIGDTFMALSNNGYRSCYHRAVVNKEKVRRLVFFSC	:	323					
BdGA200x1	:	TSLTILHQD-AVGGLQVHVD-----G--RWRRAIPRQDAFVFNIGDTFMALSNNGRYKSCSLHRAVVNSKVPKSLAFFLC	:	304					
BdGA200x2	:	TALTILLQD-DVGGLQVLVD-----G--DWRPVRPVP GAMVINIGDTFMALSNNGRYKSCSLHRAVVNRQERRSLAFFLC	:	329					
BdGA200x3	:	TSLTLLHQD-LVGGLQVFG-----G--EWRVVRPRDAFVFNIGDTFAALVDGRHASCLHRAVVNGAAARRSLTFFLN	:	296					
BdGA200x4	:	SALTLLMQDGGVDGLQVLVD-----G--GWRPVRPKPDELVFNIGDTFMALSNNGRYKSCSLHRAVVHREKERRSLAYFLC	:	339					
HvGA200x1	:	TSLTILHQD-DVGGLQVHTD-----G--RWRIRPRADAFVFNIGDTFMALSNNGRYKSCSLHRAVVNSRVPRKSLAFFLC	:	298					
HvGA200x2	:	TALTILLQD-DVGGLQVLVD-----G--DWRPVRPVP GAMVINIGDTFMALSNNGRYKSCSLHRAVVNRQERRSLAFFLC	:	358					
HvGA200x3	:	TALTLLHQD-DVGGLQVFTG-----G--AWRAVRPRSDAFVFNIGDTFSALTNGRHVSCLHRAVVNGSLARRALTFFLN	:	296					
HvGA200x4	:	SALTILLQDGEVDGLQVLVD-----G--AWRSVRPKPGELVFNIGDTFMALSNNGRYKSCSLHRAVVHREKERRSLAYFLA	:	344					
OsGA200x1	:	TSLTILHQD-HVGGLQVWAE-----G--RWRRAIPRPGALVFNIGDTFMALSNARYRSCSLHRAVVNSKVPKSLAFFLC	:	308					
OsGA200x2	:	TALTILLQD-DVGGLQVLVD-----G--EWRPVSPPVPGAMVINIGDTFMALSNNGRYKSCSLHRAVVNRQERRSLAFFLC	:	323					
OsGA200x3	:	TSLTLLHQD-DVGGLQVLPDDAAAAAG--GWRVVRPRADAFVFNIGDTFAALTNGRHASCLHRAVVNGVARRSLTFFLN	:	302					
OsGA200x4	:	SALTILLQDGGVDGLQVLVA-----G--AWRPVRPLPGAFVFNIGDTFMALTNNGRYKSCSLHRAVVHREKERRSLAFFLC	:	370					
TaGA200x-A1	:	TSLTILHQD-DVGGLQVHTE-----G--RWRIRPRADAFVFNIGDTFMALSNNGRYKSCSLHRAVVNSRVPRKSLAFFLC	:	298					
TaGA200x-B1	:	TSLTILHQD-NVGGLQVHTE-----G--RWRIRPRADAFVFNIGDTFMALSNNGRYKSCSLHRAVVNSKVPKSLAFFLC	:	298					
TaGA200x-D1	:	TSLTILHQD-NVGGLQVHTE-----G--RWRIRPRADAFVFNIGDTFMALSNNGRYKSCSLHRAVVNSRVPRKSLAFFLC	:	298					
TaGA200x-A2	:	TALTILLQD-DVGGLQVLVD-----G--DWRPVRPVP GAMVINIGDTFMALSNNGRYKSCSLHRAVVNRQERRSLAFFLC	:	329					
TaGA200x-B2	:	TALTILLQD-DVGGLQVLVD-----G--DWRPVRPVP GAMVINIGDTFMALSNNGRYKSCSLHRAVVNRQERRSLAFFLC	:	329					
TaGA200x-D2	:	TALTILLQD-DVGGLQVLVD-----G--DWRPVRPVP GAMVINIGDTFMALSNNGRYKSCSLHRAVVNRQERRSLAFFLC	:	329					
TaGA200x-A3	:	TSLTLLHQD-DVGGLQVFTG-----G--AWRAVRPRGDAFVFNIGDTFSALTNGRHISCLHRAVVNSLARRSLTFFLN	:	298					
TaGA200x-B3	:	TSLTLLHQD-DVGGLQVFTG-----G--AWRAVRPRSDAFVFNIGDTFSALTNGRHISCLHRAVVNSLARRSLTFFLN	:	301					
TaGA200x-D3	:	ASLTLLHQD-DVGGLQVFTG-----G--AWRAVRPRSDAFVFNIGDTFSALTNGRHISCLHRAVVNSLARRSLTFFLN	:	300					
TaGA200x-A4	:	SALTILLQDGGVDGLQVLVD-----G--AWRFVRPKTGELVFNIGDTFMALSNNGRYKSCSLHRAVVHREKERRSLAYFLS	:	323					
TaGA200x-B4	:	SALTILLQDGEVDGLQVLVD-----G--AWRFVRPKTGELVFNIGDTFMALSNNGRYKSCSLHRAVVHREKERRSLAYFLS	:	323					
TaGA200x-D4	:	SALTILLQDGGVDGLQVLVD-----G--AWRFVRPKTGELVFNIGDTFMALSNNGRYKSCSLHRAVVHREKERRSLAYFLA	:	323					
OsGA30x2	:	GFFTFLVQS-LVPLQLFRR-----GPDRAWVAVAGAFVFNIGDLFHILNNGRFHSVYHRAVVNRDRDVSLSGYFLG	:	303					

	*	420	*	440	*	460	*	480	
AtGA200x1	:	PKKDRVVTTPRELL---DSITSRRYPDFTWSMFLEFTQKHYRADMNTLQAFSDWLT KPI-----	:	377					
AtGA200x2	:	PKKDKVVKPPSDIL---EKMKTRKYPDFTWSMFLEFTQKHYRADVNTLDSFSNWNITNNNPI-----	:	378					
AtGA200x3	:	PKGEKVVKPPPEELVNG--VKSGERKYPDFTWSMFLEFTQKHYRADMNTLDEFSIWLKNRRSF-----	:	380					
AtGA200x4	:	PKVDKVVKPPSELE-----GERAYPDFTWSMFLEFTMKHYRADMNTLEEFTNWLKNKGSF-----	:	376					
AtGA200x5	:	PREDKIIVPPPELVE---GEEASRKYPDFTWAQLQKFTQSGYRVDNNTLHNFSWLVNS------	:	380					
BdGA200x1	:	PEMDKTIVAPPGLV---DEENPRVYPDFTWRALLDFTQKHYRADMKTLEVFSGWVLQQQ-----K	:	361					
BdGA200x2	:	PRQDRVVRPPLAVV---SSSAPRQYPDFTWADLMRFTQRHYRADTRTLDAFTQWLAPSSSSSSSSPAPSAAPPPVAS	:	405					
BdGA200x3	:	PPLDRVVSPPQGLLVAKDGGAINRKYPGFTWREFLEFTQKHYRSDTNTMEAFVDWIKQGRRGAFQHG-----A	:	365					
BdGA200x4	:	PRKDRVVRPPPT---TAPAPRLYPDFTWADLSRFTQKHYRADARTLDAFARWLGPAK-----	:	394					
HvGA200x1	:	PEMDKVVAPPGLTV---DAANPRAYPDFTWRSLLDFTQKHYRADMKTLEVFSSWVVQQQ-----	:	354					
HvGA200x2	:	PREDRVVRPPPSLR-----SPRQYPDFTWADLMRFTQRHYRADTRTLDAFTQWF-----S	:	408					
HvGA200x3	:	PQLDRPVTPPAELLA---IDGRPRVYPDFTWREFLEFTQKHYRSDSRTLDFAVAVINQGHG-----	:	355					
HvGA200x4	:	PREDRVVRPPPS-----PAPAPRLYPDFTWAEMLRFTQRHYRADARTLDAFACWLDLPSCPTTP-----	:	403					
OsGA200x1	:	PEMDTVVRPPEELV---DDHPRVYPDFTWRALLDFTQRHYRADMRTLQAFSDWLNHHRH-----L	:	366					
OsGA200x2	:	PREDRVVRPPP-----SAATPQHYPDFTWADLMRFTQRHYRADTRTLDAFTRWLAPPAADAAAT-----A	:	383					
OsGA200x3	:	PRLDRVVSPPPALV---DAAHPRAFDPDFTWREFLEFTQRHYRSDTNTMDAFVAVIKQRNG-----Y	:	360					
OsGA200x4	:	PREDRVVRPPAGA-----GAGERRLYPDFTWADFMRFTQRHYRADTRTLDAFARWLPPAC---SGAAPVVG--PPTTA	:	439					
TaGA200x-A1	:	PEMDKVVAPPGLTV---DASNPRAYPDFTWRSLLDFTQKHYRADMKTLEVFSSWIVQQQGLL-----A	:	359					
TaGA200x-B1	:	PEMDKVVAPPGLTV---DAANPRAYPDFTWRSLLDFTQKHYRADMKTLEVFSSWIVQQQGLLAL-----Q	:	361					
TaGA200x-D1	:	PEMDKVVAPPGLTV---DAANPRAYPDFTWRSLLDFTQKHYRADMKTLEVFSSWIVQQQ-----Q	:	355					
TaGA200x-A2	:	PREDRVVRPPGLR-----SPRRYPDFTWADLMRFTQRHYRADTRTLDAFTQWFSSSTSPPPPA-----P	:	389					
TaGA200x-B2	:	PREARVVRPPGLR-----SPRQYPDFTWADLMRFTQRHYRADTRTLDAFTQWFSSSS-----S	:	384					
TaGA200x-D2	:	PREDRVVRPPGLR-----SPRRYPDFTWADLMRFTQRHYRADTRTLDAFTQWFSSSS-----S	:	383					
TaGA200x-A3	:	PQLDCPVAPPAELLA---IDGRPRVYPDFTWREFLEFTQKHYRSDWRTLDAFAAWINQGRKG-----	:	356					
TaGA200x-B3	:	PQLDRLVAPPAELLA---VDGRPRVYPDFTWREFLEFTQKHYRSDWRTLDAFASWINQGRKG-----	:	360					
TaGA200x-D3	:	PQLDRPVAPTELLA---IDGRPRAYPDFTWREFLEFTQKHYRSDWRTLDAFAAWINQGRKG-----	:	359					
TaGA200x-A4	:	PREDRVVRPPPS-----PAPAPRLYPDFTWAEMLRFTQRHYRADSRTRLDAFARWLDPPSFSAAPLPHGP-----A	:	388					
TaGA200x-B4	:	PREDRVVRPPPS-----PAPAPRLYPDFTWAEMLRFTQRHYRADSRTRLDAFARWLDPPSFSAAPLPHGP-----A	:	388					
TaGA200x-D4	:	PREDRVVRPPPS-----PAPAPRLYPDFTWAEMLRFTQRHYRADARTLDAFARWLDPPSTCSATPLSHGP-----A	:	388					
OsGA30x2	:	PPDAEVAPLPEAV---PAGRSPAYRAVTWPEYMAVRKKAFAATGGSALKMVSTDAADAAEHDDVAA-----A	:	368					

AtGA200x1	:	-----	:	-
AtGA200x2	:	-----	:	-
AtGA200x3	:	-----	:	-
AtGA200x4	:	-----	:	-
AtGA200x5	:	DKKST-	:	385
BdGA200x1	:	QKQLGS	:	367
BdGA200x2	:	TAQEAA	:	411
BdGA200x3	:	GQAEKN	:	371
BdGA200x4	:	-AQEIV	:	399
HvGA200x1	:	PASART	:	360
HvGA200x2	:	SAQEAA	:	414
HvGA200x3	:	-----	:	-
HvGA200x4	:	QAQGTV	:	409
OsgA200x1	:	QPTIYS	:	372
OsgA200x2	:	QVEAAS	:	389
OsgA200x3	:	ESLDKY	:	366
OsgA200x4	:	TQAATV	:	445
TaGA200x-A1	:	LQPAMT	:	365
TaGA200x-B1	:	PQPART	:	367
TaGA200x-D1	:	PQPART	:	361
TaGA200x-A2	:	AAQQAA	:	395
TaGA200x-B2	:	SAQEAA	:	390
TaGA200x-D2	:	SAQEAA	:	389
TaGA200x-A3	:	-----	:	-
TaGA200x-B3	:	-----	:	-
TaGA200x-D3	:	-----	:	-
TaGA200x-A4	:	QAQGTV	:	394
TaGA200x-B4	:	QAQGTV	:	394
TaGA200x-D4	:	QAQGTV	:	394
OsgA30x2	:	ADVHA-	:	373

Figure S9. Alignment of GA3ox-related protein sequences using MUSCLE with OsGA2ox1 as outgroup.

		*	20	*	40	*	60	*	80																																																							
AtGA3ox1	:	-----	MPAMLT	DFVRGHP	IIHLPHSHIP	DFTS	LR	ELPDSYK	--	TPKDDL	LF	SAAPS	P	PATGEN	----	IPLIDL	DH	:	64																																													
AtGA3ox2	:	-----	MSSTL	SDVFRSH	PIHIPL	SNPPDF	---	KSLPDSY	TW	--	TPKDDL	LF	----	SASAS	DET	----	LPLIDL	SD	:	57																																												
AtGA3ox3	:	-----	MSSVT	QLFKNN	PVNRDRI	IP	LDFT	NTKTLP	DSHW	----	SKPEP	ET	TSGP	-----	IPVIS	LSN	:	54																																														
AtGA3ox4	:	-----	MPSLA	EEICIG	-----	NLGSL	QTL	PESFTW	KLTA	ADSL	LR	PSSAV	S	FD	AVEES	----	IPVID	LSN	:	56																																												
BdGA3ox2a	:	-----	MPTASH	L	-TS	----	PR	--	YDFRA	ARGV	P	ESHAW	--	PGLHD	HPV	V	DGGAG	AG	EDD	AD	DRV	P	V	D	M	R	A	D	:	60																																		
BdGA3ox2b	:	-----	MPTATH	L	-----	DFQA	A	RGV	P	ETHEW	--	PVLHD	HPV	V	DG	--	GAGAG	E	D	----	VPV	D	L	R	D	A	:	49																																				
HvGA3, 18ox1	:	-----	MPSQL	NKD	----	PHNRY	F	D	LGA	A	R	E	V	P	D	T	HAW	--	DGQ	H	E	L	P	V	D	G	--	G	V	G	A	G	E	D	A	:	55																											
AtGA3ox2	:	-----	MPTPS	HL	SKD	----	PH	--	YDFRA	A	R	R	V	P	E	T	HAW	--	PGLHD	HPV	V	D	G	--	GAGG	P	D	A	----	VPV	D	M	R	D	:	56																												
OsGA3ox1	:	MQIMT	SS	TS	S	P	T	S	P	L	A	A	A	D	N	G	V	A	A	Y	F	N	R	G	A	E	R	V	P	E	S	H	W	--	K	G	M	H	E	K	D	T	A	P	V	A	A	A	D	A	D	G	G	D	A	----	VPV	D	M	S	G	G	:	75
OsGA3ox2	:	-----	MPTPS	HL	-KN	----	PL	--	CFD	FRA	A	R	R	V	P	E	T	HAW	--	PGLD	D	H	P	V	D	G	--	G	-	G	G	G	E	D	A	----	VPV	D	V	G	A	----	VPV	D	V	G	A	----	VPV	D	M	R	D	:	54									
TaGA1ox-B1	:	-----	MPTPS	K	L	NKD	----	PHNHY	F	D	LGA	A	R	Q	V	P	E	T	HAW	--	EGLH	E	H	P	V	D	G	--	G	V	G	A	G	E	D	A	----	VPV	D	M	Q	D	----	VPV	D	M	R	D	:	57														
TaGA3ox-A2	:	-----	MPTPS	HL	SKD	----	PR	--	YDFRA	A	R	R	V	P	E	T	HAW	--	PGLHD	HPV	V	D	G	--	GAGG	P	D	A	----	VPV	D	M	R	D	----	VPV	D	M	R	D	----	VPV	D	M	R	D	----	VPV	D	M	R	D	:	56										
TaGA3ox-A3	:	-----	MSAPS	Q	L	SKD	----	PHNDY	F	D	FGA	A	R	Q	V	P	E	T	HAW	--	EGLY	E	H	P	L	V	D	G	--	G	V	G	A	A	E	D	A	----	VPV	D	L	R	D	----	VPV	D	M	R	D	:	57													
TaGA3ox-B2	:	-----	MPTPA	H	L	SKD	----	PH	--	YDFRA	A	R	R	V	P	E	T	HAW	--	PGLHD	HPV	V	D	G	--	GAGG	P	D	A	----	VPV	D	M	R	D	----	VPV	D	M	R	D	----	VPV	D	M	R	D	:	56															
TaGA3ox-B3	:	-----	MSAPS	Q	L	SKD	----	PRNNY	F	D	FGA	A	R	Q	V	P	E	T	HAW	--	EGLY	E	H	P	V	D	G	--	G	V	R	A	G	E	D	A	----	VPV	D	M	Q	D	----	VPV	D	M	R	D	:	57														
TaGA3ox-D2	:	-----	MPTPA	H	L	SKD	----	PR	--	YDFRA	A	R	R	V	P	E	T	HAW	--	PGLHD	HPV	V	D	G	--	GAGG	P	D	A	----	VPV	D	M	R	D	----	VPV	D	M	R	D	----	VPV	D	M	R	D	:	56															
TaGA3ox-D3	:	-----	MSAPS	Q	L	SKH	----	PHNNY	F	D	FGA	A	R	Q	V	P	E	T	HAW	--	EGLY	E	H	P	L	V	D	G	--	G	V	G	A	A	E	D	A	----	VPV	D	L	R	D	----	VPV	D	M	R	D	:	57													
OsGA2ox1	:	-----	MVVP	S	A	T	T	P	A	R	Q	-----	ETVVA	A	A	P	A	A	A	A	S	-----	G	V	V	G	G	G	G	V	T	----	I	A	T	V	D	M	S	A	E	:	45																					

		*	100	*	120	*	140	*	160																																																																					
AtGA3ox1	:	-P-DAT	NQIGH	ACRTW	GA	FQIS	NH	GV	PLG	--	LLQD	I	E	F	L	T	G	S	L	F	G	L	P	V	Q	R	K	L	K	S	A	R	S	E	--	T	G	V	S	G	Y	G	V	A	R	I	A	S	F	F	N	K	Q	M	W	S	:	139																				
AtGA3ox2	:	-I-HV	ATLV	G	H	A	C	T	T	W	G	A	F	I	T	N	H	G	V	P	S	R	--	LLDD	I	E	F	L	T	G	S	L	F	R	L	P	V	Q	R	K	L	K	A	R	S	E	--	N	G	V	S	G	Y	G	V	A	R	I	A	S	F	F	N	K	K	M	W	S	:	132								
AtGA3ox3	:	-P-EE	H	L	L	R	Q	A	C	E	E	W	G	V	F	H	I	D	H	G	V	S	H	--	LLHN	V	D	C	Q	M	K	R	L	F	S	L	P	M	H	R	K	I	L	A	V	R	S	P	--	D	E	S	T	G	Y	G	V	V	R	I	S	M	F	Y	D	K	L	M	W	S	:	129						
AtGA3ox4	:	-P-DV	T	T	L	I	G	D	A	S	K	T	W	G	A	F	L	I	A	N	H	G	I	S	Q	--	LLDD	I	E	S	L	S	K	T	L	F	D	M	P	S	E	R	K	L	E	A	S	S	D	--	K	G	V	S	G	Y	G	E	P	R	I	S	P	F	F	E	K	K	M	W	S	:	131					
BdGA3ox2a	:	PS-AAAA	A	V	A	R	A	A	E	T	W	G	A	F	L	L	E	G	H	G	V	P	E	S	--	LLAR	V	E	E	R	V	A	G	M	F	A	L	P	A	P	E	K	M	R	A	V	R	G	R	--	G	E	S	C	G	Y	G	S	P	P	I	S	S	F	F	A	K	S	M	W	S	:	136					
BdGA3ox2b	:	DPAK	V	A	A	A	M	A	R	A	E	Q	W	G	A	F	L	L	L	G	H	G	V	P	A	D	--	LVAR	V	E	E	R	I	E	A	M	F	A	L	P	A	S	E	K	T	R	A	V	R	G	R	--	G	E	S	C	G	Y	G	S	P	P	I	S	S	G	F	F	D	K	S	M	W	S	:	126		
HvGA3, 18ox1	:	-P-RA	AE	A	V	A	R	A	S	E	Q	W	G	A	F	L	L	E	G	H	G	V	P	T	E	--	LLAR	V	E	A	G	I	A	G	M	F	A	L	P	T	P	E	K	M	R	A	A	R	H	D	--	G	D	L	Y	G	Y	G	P	L	I	A	S	Y	S	K	N	M	W	S	:	130						
AtGA3ox2	:	-P-CA	AE	A	V	A	L	A	A	Q	D	W	G	A	F	L	L	Q	H	G	V	P	L	E	--	LLAR	V	E	A	A	I	A	G	M	F	A	L	P	A	S	E	K	M	R	A	V	R	R	P	--	G	D	S	C	G	Y	G	S	P	P	I	S	S	F	F	S	K	M	W	S	:	131						
OsGA3ox1	:	DD-AA	V	A	V	A	R	A	A	E	E	W	G	G	F	L	L	V	G	H	G	V	T	A	E	--	ALAR	V	E	A	Q	A	A	R	L	F	A	L	P	A	D	D	K	A	R	G	A	R	R	P	G	G	G	N	T	G	Y	G	V	P	P	Y	L	L	R	Y	P	K	Q	M	W	A	:	152				
OsGA3ox2	:	-G-DAA	A	R	V	A	R	A	E	Q	W	G	A	F	L	L	V	G	H	G	V	P	A	A	--	LLSR	V	E	E	R	V	A	R	V	F	S	L	P	A	S	E	K	M	R	A	V	R	G	P	--	G	E	P	C	G	Y	G	S	P	P	I	S	S	F	F	S	K	L	M	W	S	:	129					
TaGA1ox-B1	:	-P-HA	AE	A	V	A	R	A	S	E	Q	W	G	A	F	L	L	Q	H	G	V	P	R	E	--	LLAR	V	E	A	G	I	A	G	M	F	A	L	P	K	T	D	K	M	R	A	A	R	Q	G	--	G	D	P	Y	G	Y	G	L	P	H	I	A	L	Y	F	S	K	T	M	W	S	:	132					
TaGA3ox-A2	:	-P-CA	AE	A	V	A	L	A	A	Q	D	W	G	A	F	L	L	Q	H	G	V	P	L	E	--	LLAR	V	E	A	A	I	A	G	M	F	A	L	P	A	S	E	K	M	R	A	V	R	R	P	--	G	D	S	C	G	Y	G	S	P	P	I	S	S	F	F	S	K	M	W	S	:	131						
TaGA3ox-A3	:	-P-HA	AE	A	V	A	R	A	S	E	Q	W	G	T	F	L	L	E	G	H	G	I	P	S	E	--	LLAR	V	E	A	R	I	A	S	V	F	A	L	P	A	S	E	K	M	R	A	A	R	Q	D	--	G	Q	S	H	G	Y	G	L	P	P	I	A	S	Y	F	P	K	T	T	W	S	:	132				
TaGA3ox-B2	:	-P-FA	AE	A	V	G	L	A	A	Q	D	W	G	A	F	L	L	V	G	H	G	V	P	L	D	--	LLVR	V	E	A	A	I	A	G	M	F	A	L	P	A	S	E	K	M	R	A	V	R	R	P	--	G	D	S	C	G	Y	G	S	P	P	I	S	S	F	F	S	K	M	W	S	:	131					
TaGA3ox-B3	:	-P-RA	AE	A	V	A	R	A	S	E	Q	W	G	V	F	L	L	E	G	H	G	I	P	S	E	--	LLAR	V	E	A	G	I	A	G	M	F	A	L	P	T	P	E	K	M	R	A	E	R	Q	D	--	G	E	P	Y	G	Y	G	L	P	H	I	A	S	Y	S	S	K	A	T	W	S	:	132				
TaGA3ox-D2	:	-P-CA	AE	A	V	A	L	A	A	Q	D	W	G	A	F	L	L	E	G	H	G	V	P	L	E	--	LLAR	V	E	A	A	I	A	G	M	F	A	L	P	A	S	E	K	M	R	A	V	R	R	P	--	G	D	S	C	G	Y	G	S	P	P	I	S	S	F	F	S	K	M	W	S	:	131					
TaGA3ox-D3	:	-P-HA	AE	A	V	A	R	A	S	E	Q	W	G	T	F	L	L	E	G	H	G	I	P	S	E	--	LLAR	V	E	A	G	I	A	S	M	F	A	L	P	A	S	E	K	M	R	A	A	R	Q	D	--	G	Q	S	H	G	Y	G	L	P	P	I	A	S	Y	F	P	K	T	T	R	S	:	132				
OsGA2ox1	:	RG-A	V	A	R	Q	V	A	T	A	C	A	A	H	G	F	F	R	C	V	G	H	G	V	P	A	A	A	P	V	A	A	R	L	D	A	A	T	A	A	F	F	A	M	A	P	A	E	K	Q	R	A	--	G	P	-	A	S	P	L	G	Y	G	C	R	S	I	G	--	F	N	G	D	V	G	E	:	119

		*	180	*	200	*	220	*	240																																																																
AtGA3ox1	:	EGFT	I	T	G	S	P	L	N	-D	F	R	K	L	W	P	Q	----	H	H	L	N	Y	C	D	I	V	E	E	E	E	H	M	K	K	L	A	S	K	L	M	W	L	A	L	N	S	L	G	V	S	E	E	D	I	E	W	A	S	L	S	S	D	L	N	W	A	Q	A	----	AL	:	212
AtGA3ox2	:	EGFT	V	I	G	S	P	L	H	-D	F	R	K	L	W	P	S	--	H	H	L	K	Y	C	E	I	I	E	E	E	E	H	M	Q	K	L	A	A	K	L	M	W	F	A	L	G	S	L	G	V	E	E	K	D	I	Q	W	A	G	P	N	S	D	F	Q	G	T						

	*	260	*	280	*	300	*	320	
AtGA3ox1	:	QLNHYPVCPEPDR-----		-----AMGLAAHTDSTLLTILYQNNTAGLQV---		FRDDL---		GWV	: 259
AtGA3ox2	:	QLNHYPKCPEPDR-----		-----AMGLAAHTDSTLMTILYQNNTAGLQV---		FRDDV---		GWV	: 252
AtGA3ox3	:	QLNSYPVCPDPHL-----		-----AMGLAPHTDSSLTILYQGNIPGLEIESPQEEGS---		RWI			: 256
AtGA3ox4	:	RLNHYPVCPEPER-----		-----AMGLAAHTDSTILILHQSNTGGLQV---		FREES---		GWV	: 254
BdGA3ox2a	:	HLNWYPRCPDPKR-----		-----ALGLIPHTDSGYFTFVLQSQVPGQL---		FRRGP---		DRWV	: 262
BdGA3ox2b	:	HLNWYPKCPDPKR-----		-----AVGLIAHTDSGYFTFVLQSMVPGQL---		FRREP---		DRWV	: 249
HvGA3, 18ox1	:	HLNWYPKCPDPTR-----		-----ALGLKGHTDSGFFTFVMQSQVPGHL---		FRHGPPADRWV			: 258
HvGA3ox2	:	HLNWYPKCPDPKR-----		-----ALGLIAHTDSGFFTFVLQSLVPGQL---		FRHGP---		DRWV	: 257
OsGA3ox1	:	HLNMFPKCPDPDR-----		-----VVGLAAHTDSGFFTFILQSPVPGQL---		LRHRP---		DRWV	: 278
OsGA3ox2	:	HLNWYPRCPEPRR-----		-----ALGLIAHTDSGFFTFVLQSLVPGQL---		FRRGP---		DRWV	: 255
TaGA1ox-B1	:	HLNWYPKCPDPKR-----		-----ALGMAHTDSGFFALLMQSQVPGHL---		FRHGPPADRWV			: 260
TaGA3ox-A2	:	HLNWYPKCPDPKR-----		-----ALGLIAHTDSGFFTFVLQSLVPGQL---		FRHGP---		DRWV	: 257
TaGA3ox-A3	:	HLNWYPKCPDPKR-----		-----TLGLAIHTDSGFFTFMLQSHVSGQL---		FRHGP---		DRWV	: 255
TaGA3ox-B2	:	HLNWYPKCPDPKR-----		-----ALGLIAHTDSGFFTFVLQSLVPGQL---		FRHGP---		DRWV	: 257
TaGA3ox-B3	:	HLNWYPKCPDPKR-----		-----ALGMTHTDSGFFTFVMQSHVPGMQL---		FRRGP---		DRWV	: 260
TaGA3ox-D2	:	HLNWYPKCPDPKR-----		-----ALGLIAHTDSGFFTFVLQSLVPGQL---		FRHGP---		DRWV	: 257
TaGA3ox-D3	:	HLNWYPKCPDPKR-----		-----TLGLATHTDSGFFTFVMQSHVSGQL---		FRRGP---		DRWV	: 255
OsGA2ox1	:	RINHYPSCNIHKLHDDQCNIKSLVSTKASNGGNLMAGGRIGFGEHSDPQILSLLRANDVEGLQVFPDHEGK--				EMWV			: 272

	*	340	*	360	*	380	*	400	
AtGA3ox1	:	TVPFPFGLVNVNVDLFIHLSNGLFKSVLHRAVNQTRARLSVAFLW-GPQSDIKISPVKLVSPVES-PLYQSVTWKEY							: 337
AtGA3ox2	:	TAPPVPGSLVNVNVDLLHILTNGIFPSVLHRAVNVHRSRFSMAYLW-GPPSDIMISPLPKLVDPQLS-PLYPSLTWKQY							: 330
AtGA3ox3	:	GVEPIEGLVVMGDLSHIISNGQFRSTMHRAVNVKTHHRVSAAYFA-GPPKNLQIGPLTS--DKNHP-PIYRRLIWEED							: 332
AtGA3ox4	:	TVEPAPGLVNVNIGDLFIHLSNGKIPSVVHRAKVNHTSRISIAYLWGGPAGDVQIAPISKLTGPAEP-SLYRSITWKEY							: 333
BdGA3ox2a	:	AVPAVPGAFVNVNVDLFIHLSNGLFKSVLHRAVNVKESHRSVSLGYFL-GPPAQTRVGPLEEALTPARPKPMYRPVTWPEY							: 341
BdGA3ox2b	:	AVPAMPGAFVINVDLFIHLSNGLFKSVLHRAVNVSRSHRSVSLGYFL-GPPAQAVVAPLDEALTDRPRPAYRPPVWREY							: 328
HvGA3, 18ox1	:	EVPAPVPGALIVNIGDLFIHLSNGLFKSVLHRAVNVNRERERISVAYFL-IPPAVVKVAPLKEVVGSGK--PVYRALTWSES							: 335
HvGA3ox2	:	TVPAPVPGAMVNVNVDLFIHLSNGLFKSVLHRAVNVNRSDRISLGYFL-GPPAHVKVAPLREAL-AGTP-AAYRAVTWPEY							: 334
OsGA3ox1	:	TVPGTGALIVNVNVDLFIHLSNGLFKSVLHRAVNVNRDRISMPYFL-GPPADMKVTPLVAAAGSPESK-AVYQAVTWPEY							: 356
OsGA3ox2	:	AVPAVAGAFVNVNVDLFIHLSNGLFKSVLHRAVNVNRDRVSLGYFL-GPPPDAAEVAPLPEAVPAGRS-PAYRAVTWPEY							: 333
TaGA1ox-B1	:	EVPAPVPGALVNVNIGDLFIHLSNGLFKSVLHRAVNVNRDRERISLAYFL-GPAANAKVGPLKEVVGSGK--PAYRALTWPEY							: 337
TaGA3ox-A2	:	TVPAPVPGAMVNVNVDLFIHLSNGLFKSVLHRAVNVNRSDRISLGYFL-GPPAHVKVAPLREAL-AGTP-AAYRAVTWPEY							: 334
TaGA3ox-A3	:	GVP--PGALIVNIGDLFIHLSNGLFKSVLHRAVNVNRDRISVAYHL-GPPADAKVAPLREAVGSGK--PAYRTVTWREY							: 330
TaGA3ox-B2	:	TVPAPVPGAMVNVNVDLFIHLSNGLFKSVLHRAVNVNRSDRISLGYFL-GPPAHVKVAPLREAL-AGTP-AAYRAVTWPEY							: 334
TaGA3ox-B3	:	GVP--PGALIVNIGDLFIHLSNGLFKSVLHRAVNVNRDNARVSVAYHL-GPPADVKVAPLREAVGAGK--PAYRTVTWREY							: 335
TaGA3ox-D2	:	TVPAPVPGAMVNVNVDLFIHLSNGLFKSVLHRAVNVNRSDRISLGYFL-GPPAHVKVAPLREAL-AGTP-AAYRAVTWPEY							: 334
TaGA3ox-D3	:	--PGH??ALIVNISDLFIHLSNGLFKSVLHRAVNVNRDSTRVSVAYHL-GPPAGVKVAPLREAVGCGK--PAYRTVTWREY							: 328
OsGA2ox1	:	QVPSPSAIFVNVNVDLQALTNGLRLISIRHVIATACRPLSTIYFA-SPPLHARISALPETITASSP-RRYRSFTWAEY							: 350

	*	420	*	440	*	
AtGA3ox1	:	LRTKATHFNK-----		ALSMIR-----		NHREE----- : 358
AtGA3ox2	:	LATKATHFNQ-----		SLSIIR-----		: 346
AtGA3ox3	:	LAAKATHFNK-----		ALTLCRC-----		: 349
AtGA3ox4	:	LQIKYEVFDK-----		AMDAIRVVNPTN-----		: 355
BdGA3ox2a	:	MTVRKKAFAT-----		GDSALQMVAVDQD-DDDDAQTKLANRKIKVSGEAY		: 385
BdGA3ox2b	:	MGLREKALFV-----		GESALKMIAVAKD-DAPQTPKLHETS-----		: 363
HvGA3, 18ox1	:	IVVRKEAFANHGADLEFGKGRALTDMLSISSDEDDGAEHHRD-----				: 377
HvGA3ox2	:	MGVRKKAFAT-----		GASALKMVAISTD-DAADVLPDVLSS-----		: 369
OsGA3ox1	:	MAVRDKLFGT-----		NISALSMIRVAKEEDKES-----		: 384
OsGA3ox2	:	MAVRKKAFAT-----		GGSALEKVMVSTDA-AAAEDHDDVAAAADVHA----		: 373
TaGA1ox-B1	:	IIVRKEAFANGGADLEFTKGGTALEMVSNPDDDDGMDQGDISS-----				: 382
TaGA3ox-A2	:	MGVRKKAFAT-----		GASALKMVAISTDNDAAANDTDDLIS-----		: 370
TaGA3ox-A3	:	FLVRKEAFTT-----		GGSALEKVMVSLSPG-DHDDDGADQISEISS----		: 370
TaGA3ox-B2	:	MGVRKKAFAT-----		GASALKMVAISTD-DAANDTDDLILS-----		: 369
TaGA3ox-B3	:	IVVRKEAFAT-----		GGSALEKVMVSLSPD-DHDDEGDGADHISEIPS----		: 375
TaGA3ox-D2	:	MGVRKKAFAT-----		GASALKMVAISTDNDAAANDTDDLIS-----		: 370
TaGA3ox-D3	:	FLVRKEAFAT-----		GGSALEKVMVSLSPG-DHKNHGDGADQISEISS----		: 368
OsGA2ox1	:	---KTTMYSLR-----		LSHSRLELFKIDDD-DSDNASEGKA-----		: 382

Figure S10. Alignment of GA2ox protein sequences using MUSCLE with OsGA3ox2 as outgroup.

		*	20	*	40	*	60	*	80		
AtGA2ox1	:	MAV-LSK	-----PVAIPK	-----	-----SGF	-----	SLIPVIDMSDP	----	:	26	
AtGA2ox2	:	MVV-LPQ	-----PVTLDN	-HISLIP	-----	TYKPPVPL	-----	TSHSIPVVNLADP	----	39	
AtGA2ox3	:	MVI-VLQ	-----PASFDS	-----NLYV	-----	NPKCKPRP	-----	VLIPVIDLTDS	----	35	
AtGA2ox4	:	MVKGSQK	-----IVAVDQ	-----	-----	-----	-----	DIPIDMSQE	----	23	
AtGA2ox6	:	MVL-PSS	-----TPLQTT	-----	-----	GKKTISSP	-----	EYNFPVIDFSLN	----	32	
AtGA2ox7	:	MAS	-----QPPFKTN	-FCSIFG	-----	SSFPNSTSESNTNTSTIQTSGIKLPVIDLSHL	----	:	48		
AtGA2ox8	:	MDPPFNE	-----IYNNLLYNQITK	-----	-----	KNDVSEIPFSFSVTAVVEEVELPVIDVSRL	----	:	50		
BdGA2ox1	:	MVVPSTT	-----TPARQE	-----	-----	IATAAAL	-----	QLPAIPTVDMSAP	----	34	
BdGA2ox10	:	MVV-LAQ	-----GELEQ	-----IALPA	-----	VQKAAPPL	-----	ADVPEIDLAAA	----	35	
BdGA2ox2	:	MVM	-----PASTAS	-----	-----	SAACRDTA	-----	SGAGIPTVDMSAP	----	30	
BdGA2ox3	:	MVV-LAS	-----PPAADH	-IPLLR	-----	SPDPGDYF	-----	SGMPVIDLCSP	----	36	
BdGA2ox4	:	MVV-LAK	-----PAALEQ	-----ISLLR	-----	TPEPWESF	-----	AGVPAVDLSAP	----	36	
BdGA2ox5	:	MEDHEYEQ	-----DESNPPLLAT	-YKHLLD	-----	GEHRRRLPLGVVAGDEEDDQCDLPVIDLAPL	----	:	54		
BdGA2ox6	:	MPALFAD	-----GATSDPPLADS	-YRALLR	-----	SGGIAHPPEESL	-----	SPVLERDLPMDIECL	----	52	
BdGA2ox7	:	MVV-LAK	-----GELEQ	-----IALPA	-----	AQSP	-----	ANVQAVDLSSA	----	32	
BdGA2ox8a	:	MAAITMTA	-----LPSSVDHQVVIPLLK	-----	-----	CPIAAAAA	-----	AAMIPTVDLSSP	----	43	
BdGA2ox8b	:	MVA-IKA	-----PSSIDH	-ANPLTK	-----	SPKAAAAA	-----	AAAIPTVDLSSP	----	38	
BdGA2ox9	:	MPA-FAE	-----SAAEPPLADS	-YHALLR	-----	RAGADGRNKDAHCTPTVHADHVLPA	-----	PDMAVSECELPMDIVGCL	----	65	
HvGA2ox1	:	MVV-PS	-----TTPARQE	-TATLLP	-----	QAQPSGG	-----	GAIPTVDMSAP	----	38	
HvGA2ox10	:	MVV-LAK	-----GELEQ	-----IALPA	-----	VHKTAPPL	-----	ADLPEVDLSVA	----	35	
HvGA2ox2	:	MVASTAA	-----PASSSA	-AAV	-----	APACRGMA	-----	PAGIPTIDMSAP	----	36	
HvGA2ox3	:	MVV-LAG	-----TPAVDH	-IPLLR	-----	SPDPGDNF	-----	SGMPVVDLSRP	----	36	
HvGA2ox4	:	MVV-LAK	-----PAALEQ	-----IALMR	-----	TPEPWESF	-----	SGVPAVDLSSP	----	36	
HvGA2ox6	:	MPA-FAE	-----PAIDPPLADS	-YRALLR	-----	SDERAGIAAAPATGSVAVLERDLPMDLRL	----	:	53		
HvGA2ox7	:	MVV-LAK	-----GELEQ	-----IALPA	-----	AQP	-----	PLAHVRAIDL SAA	----	32	
HvGA2ox8	:	TVA-ITV	-----PISVDT	-IPLLK	-----	CVNAATAA	-----	VPSVDLSAP	----	34	
HvGA2ox9	:	MPA-FAE	-----STAEPLSDS	-YYALLR	-----	RGNKVDECASVPPPGCQVLPVAECELPMIDVGL	----	:	56		
OsGA2ox1	:	MVVPSTT	-----TPARQE	-TVVAA	-----	APPAAAAA	-----	GVVGGGGVVTIATVDMSAE	----	45	
OsGA2ox10	:	MVV-LAK	-----GELEQ	-----IALPA	-----	AVQKAAPP	-----	LADVPEVDLGGG	----	36	
OsGA2ox2	:	MVVPAAA	-----APECGR	-----	-----	REAAAAAAAVFCRRGRGVVPTVDMASAP	----	:	42		
OsGA2ox3	:	MVV-LAG	-----PPAVDH	-IPLLR	-----	SPDPGDVF	-----	SGVPVVDLGGP	----	36	
OsGA2ox4	:	MVV-LAK	-----PAALEQ	-----ISLVR	-----	SPSVEDNF	-----	GAGLPVVDLAAD	----	37	
OsGA2ox5	:	MEEHDYD	-----SNS	-NPPLMST	-YKHLFV	-----	EQHRLDMD	-----	MGADVDCECLPVIDLAGL	----	50
OsGA2ox6	:	MPA-FAD	-----IAIDPPLADSYRALALLR	-----	-----	RDRDGGIAPPAVQMV	-----	GSAGVAVLERDLPMDLRL	----	58	
OsGA2ox7	:	MVV-LAK	-----GELEQ	-----IALPA	-----	AHPPP	-----	ADVRAIDL SAT	----	32	
OsGA2ox8	:	MVA-ITA	-----PSSIEH	-IPLVR	-----	CPKGANAG	-----	PQAVIPCIDL SAP	----	38	
OsGA2ox9	:	MPA-IAD	-----CAADPPLADS	-YYTLLR	-----	LGGDDDDACTKVTTTPQPVSECELPMDIVGLTAP	----	:	58		
TaGA2ox-A1	:	MVVPSTT	-----SARQET	-ATMLLP	-----	PPCPGGGA	-----	IPTVDMASAP	----	36	
TaGA2ox-A10	:	MVV-LAK	-----GELEQ	-----IALPA	-----	VHKTAPPL	-----	ADVPEVDLSVA	----	35	
TaGA2ox-A11	:	MLA-FAE	-----GTSCCTTDPPLADS	-YRALLC	-----	RGELEGVGAASAHAVESLAMLERDLPIDLERL	----	:	59		
TaGA2ox-A3	:	MVV-LAG	-----SPAVDH	-IPLLR	-----	SPDPGDNF	-----	SGMPVVDLSSP	----	36	
TaGA2ox-A4	:	MVV-LAK	-----PAALEQ	-----IALLR	-----	TPEAWESF	-----	SGVPAVDLSGP	----	36	
TaGA2ox-A6	:	MPA-FAE	-----PAI	-DPPLADS	-YRALLRTDQLRRGGIAPALSPAVPESVAVL	-----	ERDLPMDLKLRL	----	58		
TaGA2ox-A7	:	MVV-LAK	-----GELEQ	-----IALPA	-----	AQP	-----	PLAHVRAVDLSAA	----	32	
TaGA2ox-A8	:	MVA-ITV	-----PISVEA	-IPLVK	-----	CAHAAAAA	-----	VPSVDLSAP	----	34	
TaGA2ox-A9	:	MPA-FAE	-----STAEPLADS	-YYALLR	-----	GGNKADECASAPPPGCQAPPVSECELPMDIVGCL	----	:	56		
TaGA2ox-B1	:	MVVPSTT	-----PARQET	-VTLLP	-----	PPCPGGGA	-----	IPTVDMASAP	----	36	
TaGA2ox-B10	:	MVV-LAK	-----GELEQ	-----IALPA	-----	VHKTAPPL	-----	ANMPEVDLAVA	----	35	
TaGA2ox-B11	:	MLA-FAK	-----RTSCCTTDPPLADS	-YRALLC	-----	RGKLEGGGAASAHAVESLAMLERDLPIDLKLRL	----	:	59		
TaGA2ox-B12	:	MPA-SGE	-----GGTSDPPLVDS	-YRTLLR	-----	KGGGDGFVPALAAESLAVLECDLPMDLRL	----	:	55		
TaGA2ox-B13	:	MAA-FDE	-----NGTT	-DPPLADS	-YRKLLR	-----	RDELGGAL	-----	ARES LAVLERDLPMDLKLRL	----	51
TaGA2ox-B2	:	MVASSAA	-----PASSSA	-----	-----	APACRGMA	-----	PAGIPTIDMSAP	----	33	
TaGA2ox-B3	:	MVV-LAS	-----TPAVDH	-IPLLR	-----	SPDPGDYF	-----	SGMPVVDLSSP	----	36	
TaGA2ox-B4	:	MVV-LAK	-----PAALEQ	-----ITLLR	-----	TPEPWESF	-----	SGIPAVDLSGP	----	36	
TaGA2ox-B6	:	MPA-FAE	-----PAIDPPLADS	-YRALLR	-----	SDQLHRGGIAPALSPAV	-----	LESVAVLERDLPMDLKLRL	----	58	
TaGA2ox-B7	:	MVV-LAK	-----GELEQ	-----IALPA	-----	AQPP	-----	LAHVRAIDL SAA	----	32	
TaGA2ox-D1	:	MVVPSTT	-----PARQET	-ATMLLP	-----	PPSAGGGA	-----	IPTVDMASAP	----	36	
TaGA2ox-D10	:	MVV-LAK	-----GELEQ	-----IALPA	-----	VHKTAPPL	-----	ADVPEVDLAVA	----	35	
TaGA2ox-D11	:	MLA-FAE	-----GTSCCTTDPPLADS	-YRALLC	-----	RGELEGGAAPAHAVESLAMLERDLPIDLKLHL	----	:	59		
TaGA2ox-D2	:	MVASSAA	-----PASSSA	-----	-----	AAPACRMA	-----	PAGIPTIDMSAP	----	34	
TaGA2ox-D3	:	MVV-LAS	-----TPAVDH	-IPLLR	-----	SPDPGDYF	-----	SGMPVVDLSSP	----	36	
TaGA2ox-D4	:	MVV-LAK	-----PAALEQ	-----ITLLR	-----	PPEPWESF	-----	SGVPAVDLSGP	----	36	
TaGA2ox-D6	:	MPA-FAE	-----PAIDPPLADS	-YRALLR	-----	SDQLRRGGIAPAPASESVAVLERALPMDLKLRL	----	:	55		
TaGA2ox-D7	:	MELTCKQYWRKAFD	-----CQKMTVEVNDLLA	-----	-----	IVLKALTELSFLEVCTA	----	:	46		
TaGA2ox-D8	:	MVG-ITV	-----PMSMDK	-IPLVK	-----	CANAAAAA	-----	AVPTVDLSAG	----	35	
TaGA2ox-D9	:	MPA-FAE	-----STAEPLADS	-YYALLR	-----	GGNKADECASAPPPGCQAPPVSECELPMDIVGCL	----	:	56		
OsGA3ox2	:	MPT-PSHL	-----K	-----NPLCFDF	-----RAARR	-----	VPETHAWP	-----	GLDDHPVVDGGGG	----	41

		*	100	*	120	*	140	*	160	
AtGA20x1	:	-----	ESKHALVKACEDFGFFKVINHG	--V--	SAELVSVLEHETVDFFSLPKSEK	---	TQV	----	:	75
AtGA20x2	:	-----	EAKTRIVKACEEFGFFKVVNHG	--V--	RPELMTRLEQEAIQGFGLPQSLK	---	NR	----	:	87
AtGA20x3	:	-----	DAKTQIVKACEEFGFFKVINHG	--V--	RPDLLTQLEQEAINFFALHHSK	---	DK	----	:	83
AtGA20x4	:	-----	RSQVSMQIVKACESLGFFKVINHG	--V--	DQTTISRMEQESINFFAKPAHEK	---	KS	----	:	73
AtGA20x6	:	-----	DRSKLSEKIVKACEVNGFFKVINHG	--V--	KPEIIKRFEHEGEEFFNKPESDK	---	LR	----	:	83
AtGA20x7	:	-----	TSGEEVKRKRCVKQMVAACEWGFQVINHG	--I--	PKDVFEMMLLEKKLFDQPFVSK	---	VRERF	----	:	108
AtGA20x8	:	-----	IDGAEEREKCKEAIARASREWGFFQVINHG	--I--	SMDVLEKMRQEQRVRFREPFDDK	---	SK	----	:	107
BdGA20x1	:	-----	RGLLSRQVARACAEQGFRAVNHGVLVPGPAPAARQLDAATAAFFALPAHEK	---	QR	----	:	:	:	88
BdGA20x10	:	-----	GAGGSAAGRAAAAKAVAAACEEHGFFKVTGHG	--V--	ASGLLARVEAAAAFFALPQREK	---	EAAMAMAM	----	:	99
BdGA20x2	:	-----	WGRAELSRQMVEAFAERGFVKVNHG	--V--	PPRAPATLDAATAAFFERPAPKEK	---	QA	----	:	82
BdGA20x3	:	-----	GAPRAIADACERFGFFKLVNHG	--V--	ATDAMDRLESEAVTFFSQPADK	---	DR	----	:	84
BdGA20x4	:	-----	GAADDVVRACERFGFFSVVNHG	--V--	ARGVVERLEHEAALFFSWPQADK	---	DA-SA	----	:	86
BdGA20x5	:	LLDLES	DQTRNNGSSSAACRAAMVRAASEWGFFQVTNHG	--V--	PQPLLDELHGQQLRAFRFPFHRK	---	LAP	----	:	122
BdGA20x6	:	---	ITTGEGGASMRKKKACADAMARAASEWGFFQVTNHG	--V--	GKELLEMRKEQARLRLPFETK	---	RK	----	:	116
BdGA20x7	:	-----	RRSGPGRAAAARALVAACEEQGFFKVTGHG	--V--	APALVRALDAAAAFFALPQAEK	---	EA-A	----	:	89
BdGA20x8a	:	-----	GAARAVAEACRGVGFRRATNHG	--V--	PSSLAATLEADAMAFFALPDKDK	---	QSTT	----	:	93
BdGA20x8b	:	-----	GAARAVADACRGVGFRRATNHG	--I--	PSSLAAALEARAMAFFALPHEDK	---	VDA	----	:	87
BdGA20x9	:	-----	TTGGGSAEERAACAAIAGAEAGFFQVNVNHG	--V--	KQELLEAMRREQTRLRLPFPEAK	---	AT	----	:	124
HvGA20x1	:	-----	RGRGALSQVARACAEQGFRAVNHG	--V--	PPAGPPARLDAATSAFFALAAHDK	---	QR	----	:	91
HvGA20x10	:	-----	RSGSEGRAAAARAVAAACEEHGFFKVTGHG	--V--	PAELLARVENAAAAFFALSQRDK	---	EAAMSA	----	:	95
HvGA20x2	:	-----	AGRAEMSRQMVEAFAERGFVKVNHG	--V--	PPRASARLDAASAFFARPAAEK	---	QE	----	:	88
HvGA20x3	:	-----	GAPRAIADACERFGFFKLVNHG	--V--	ALDAMDRLESEAVRFFSLPQADK	---	DR	----	:	84
HvGA20x4	:	-----	GAADDVVRACERFGFFSVVNHG	--V--	PAGVVDRLAEAEVRFFASTQAEK	---	DA	----	:	84
HvGA20x6	:	-----	RSGDARERKACADAMAAAASEWGFFQVTNHG	--V--	GRQLLEEMRREQARLRLPFDTK	---	EK	----	:	110
HvGA20x7	:	-----	PGPGRDAAARALVSACEEQGFFKVTGHG	--V--	PLELVRAVEAAAAEFFALPQAEK	---	EA-A	----	:	87
HvGA20x8	:	-----	GAAAADACRAVGFRRATNHG	--V--	PAALTDALAEERAAFFALPHKDKMDASA	---	:	----	:	85
HvGA20x9	:	-----	TTGGGGEEERAACAAIASAAAEWGFFQVNVNHG	--V--	KQELLEAMRREQVRLRLPFPEAK	---	AT	----	:	115
OsGA20x1	:	-----	RGAVARQVATACAAGHGFRCVGHG	--V--	VPAAAPVAARLDAATAAFFAMAPAEK	---	QR	----	:	97
OsGA20x10	:	-----	ACRADAARAVVAAACEGHGFFKVTGHG	--V--	PAGLLARVEAAAAFFAMAPQPEK	---	EA-AAAA	----	:	92
OsGA20x2	:	-----	AGRGELSRQVARACAGSGFFRAVNHG	--V--	PPRVSAMDAGAAFFARAGAEK	---	QL	----	:	94
OsGA20x3	:	-----	GAARAVVDACERYGFFKVVNHG	--V--	ATDTMDKAESEAVRFFSQTPDK	---	DR	----	:	84
OsGA20x4	:	-----	GAAGEVVRACERFGFFKVVSHG	--V--	GEGVVGRLEAEVRFFASQPAK	---	DA	----	:	85
OsGA20x5	:	-----	MEAEQVCRADMVRAASEWGFFQVTNHG	--V--	PQALLRELHDAQVAVFRFPFQEK	---	VTERRLLG	----	:	108
OsGA20x6	:	-----	TRGGAGERKACAGAMARAASEWGFFQLTNHG	--V--	GRELMEEMRREQARLRLPFETK	---	EK	----	:	115
OsGA20x7	:	-----	GPARAAEARALVAACEEQGFFRVTVNHG	--V--	PGLVRAAEAAAAFFALSQRDK	---	EA-A	----	:	86
OsGA20x8	:	-----	GAAAADACRTLGFFKATNHG	--V--	PAGLADALESSAMAFFALPHQEK	---	LDM	----	:	87
OsGA20x9	:	TGAAAA	AAVGGQHQAEERAACAAIAAAAEWGFFQVNVNHG	--V--	AQELLEAMRREQARLRLPFPEAK	---	SS	----	:	125
TaGA20x-A1	:	-----	RGRGALSQVARACTEQGFFRAVNHG	--V--	PPAGPAARLDAATSAFFALAAHDK	---	QR	----	:	89
TaGA20x-A10	:	-----	GSGSDGRAAAARALVACEEHGFFKVTGHG	--V--	PAELLTRVENAAAAFFALSQRDK	---	EA	----	:	91
TaGA20x-A11	:	-----	ASRDSRESKACADAMARAASEWGFFQVNVNHG	--V--	GRDLLLEEMRREQAKLRLPFRTK	---	DK	----	:	116
TaGA20x-A3	:	-----	GAPRAIADACERFGFFKLVNHG	--V--	PADTMDRLESEAVRFFSLPQADK	---	DR	----	:	84
TaGA20x-A4	:	-----	GAAADVVRACERYGFFSVVNHG	--V--	PAGMVDRLAEAEVRFFASSQADK	---	DA	----	:	84
TaGA20x-A6	:	-----	TSGDAGERKACADAMARAASEWGFFQVNVNHG	--V--	GRELLEEMRREQARLRLPFDTK	---	EK	----	:	115
TaGA20x-A7	:	-----	PGPGRAAAARALVTACEEQGFCVTVGHG	--V--	PPELVRAVEAAAAEFFALPQADK	---	EA-A	----	:	87
TaGA20x-A8	:	-----	GAAAADACRAVGFRRVTVNHG	--V--	PAALADALEERAAFFALPHKDKLEASA	---	:	----	:	85
TaGA20x-A9	:	-----	TACGGGTEERAACAAIASAAAEWGFFQVNVNHG	--V--	KQELLEAMRREQVRLRLPFPEAK	---	AT	----	:	115
TaGA20x-B1	:	-----	HGRGALSQVARACAEQGFRAVNHG	--V--	PPAGPAARLDAATSAFFALAAHDK	---	QR	----	:	89
TaGA20x-B10	:	-----	GSGSDGRAAAAGRAVAAACEEHGFFKVTGHR	--V--	PAELLARVENAAAAFFALSQRDK	---	EA	----	:	91
TaGA20x-B11	:	-----	ASRDARESKACAEAMARAASEWGFFQVNVNHG	--V--	GRELLEEMRREQARLRLPFGTK	---	DK	----	:	116
TaGA20x-B12	:	-----	MMGDARERGVCMDAMASAASEWGFFQVINHG	--V--	GQELLEEMRREQARLHQPFNIK	---	EK	----	:	112
TaGA20x-B13	:	-----	TSGDARERDVCADAMASAASEWGFFQVINHG	--V--	GRELLEEMRREQARLHQPFDTK	---	EK	----	:	108
TaGA20x-B2	:	-----	AGRAELSGQMVEAFAERGFVKVNHG	--V--	PPRVSARLDAASAFFARPAPAEK	---	QE	----	:	85
TaGA20x-B3	:	-----	GAPRAIADACERFGFFKLVNHG	--V--	PADTMDRLESEAVRFFSLPQADK	---	DR	----	:	84
TaGA20x-B4	:	-----	DAAADVVRACERFGFFSVVNHG	--V--	PAGVVDRLAEAEVRFFASSQAEK	---	DA	----	:	84
TaGA20x-B6	:	-----	TSGDAWERKACADAMACAASEWGFFQVINHG	--V--	GRELLEEMRREQARLRLPFDTK	---	EK	----	:	115
TaGA20x-B7	:	-----	PGPGRAAAARALVSACEEQGFFKVTGHG	--V--	PPELVRAAEAAAAEFFALPQAEK	---	EA	----	:	86
TaGA20x-D1	:	-----	RGRGALSQVARACAEQGFRAVNHG	--V--	PPAGPPARLDAATSAFFALAAHDK	---	QR	----	:	89
TaGA20x-D10	:	-----	GRGSEGRAAAARAVAAACEEHGFFKVTGHG	--V--	PAELLARVENAAAAFFALSQRDK	---	EA	----	:	91
TaGA20x-D11	:	-----	TSRDARESKACADAMARAASEWGFFQVNVNHG	--V--	GRELLEEMRREQARLRLPFGTK	---	DK	----	:	116
TaGA20x-D2	:	-----	AGRAELSRQMVEAFAERGFVKVNHG	--V--	PPRVSARLDAASAFFARPAPAEK	---	QQ	----	:	86
TaGA20x-D3	:	-----	GAPRAIADACERFGFFKLVNHG	--V--	PADTMDRLESEAVRFFSLPQADK	---	DR	----	:	84
TaGA20x-D4	:	-----	DAAADVVRACERFGFFSVVNHG	--V--	PAGVVDRLAEAEVRFFASSQAEK	---	DA	----	:	84
TaGA20x-D6	:	-----	TSGDAGERKACADAMATAASEWGFFQVINHD	--V--	GRELLEEMRREQARLRLPFDTK	---	EK	----	:	112
TaGA20x-D7	:	-----	RQSARNIQRLLYQPSGGPGFFKVTGHG	--V--	PPELVRAAEAAAAEFFALPQAEK	---	EA-A	----	:	101
TaGA20x-D8	:	-----	AAAAVEQACRSVGFIRATNHG	--V--	PTALTDALEAGAAFFALPHKKK	---	LEASA	----	:	85
TaGA20x-D9	:	-----	TACGGGTEERAACAAIASAAAEWGFFQVNVNHG	--V--	KQELLEAMRREQVRLRLPFPEAK	---	AT	----	:	115
OsGA30x2	:	-GGED-	-AVPVVDVGAGDAAARVARAAEQWGAFLLVGHG	--V--	PAALLSRVEERVARVFSLPASEK	---	MRAVR	----	:	106

	*	180	*	200	*	220	*	240	
AtGA2ox1	:	---A-----G----	YPFGYGNISKI	-GRNGDVGWVEYLLMNA	NHDS---	GSGLFPSPLLK-----			: 118
AtGA2ox2	:	---A-----GPP---	EPYGYGNKRI	-GPNGDVGWIEYLL	LLNA-NPQ---	LSSPKTSAVFR-----		Q---	: 132
AtGA2ox3	:	---A-----GPP---	DPFGYGTKRI	-GPNGDLGWLEYILL	NA-NLC---	LESHKTTAIFR-----		H---	: 128
AtGA2ox4	:	---V-----RPVN---	QPFYGFRTI	-GLNGDSGEVEYLL	FHTNDPA---	FRSQLSF-----			: 115
AtGA2ox6	:	---A-----GPA---	SPFGYGCKNI	-GFNGDLGELEYLL	LLHA-NPT---	AVADKSETISH-----		D---	: 128
AtGA2ox7	:	---S-----DLSK---	NSYRWGNPSA	-TSPAQYSVSEAFH	IILSEVS---	RISD-----			: 147
AtGA2ox8	:	-----SEKFSAGSYRWG	TPSA-TSIRQLSWSEAFH	VPMPTDIS---	DNK-----				: 146
BdGA2ox1	:	---ARGVQGGPPS---	SPLGYGCRTI	-GFGSDVGELEYLL	LHNDPA---	YKAASIHAH-----			: 138
BdGA2ox10	:	APAA-----AAAGS-	SPFGYASKRI	-GSNGDLGWVEYLL	LGVTAA	GPLVPSS-----		A---	: 147
BdGA2ox2	:	---A-----GPP---	DPLGYGSRSI	-GSHGDVGELEYLL	THA-DPA---	AVARRAVADR-----		E---	: 127
BdGA2ox3	:	---S-----GPA---	YPFGYGSKRI	-GLNGDMGWLEYLL	LAVDDSA---	SLSGA-----		V---	: 124
BdGA2ox4	:	---S-----GPA---	DPFGYGSKRI	-GRNGDMGWLEYLL	LLAI-DRE---	SLSKASP-----		A---	: 127
BdGA2ox5	:	---GDGDEDEDQLLL	SPEAYRWGNPTA	-TCLHQLSWSEAYH	VPITTPS---	PETK-----			: 169
BdGA2ox6	:	---A-----GLLN---	GSYRWGNPTA	-TSLRQLSWSEAFH	VPL-ASI---	SGRDCDY-----		G---	: 158
BdGA2ox7	:	---A-----G----	RPVGYASKRI	-GTAGDLGWIEYLL	LCVAPGAGQAL	PVPASAFSTLPCAAAA		ASLSGSEP	: 154
BdGA2ox8a	:	-----TTTTAPGPGSAR	PLSGYSRRI	-GSNGDVGWIEYLL	LSGNS---	V-----			: 137
BdGA2ox8b	:	---T-----IAAAARR	PFYGSRSI	-GSNGDVGWIEYLL	LSGNSNS	SSSIPGASS-----			: 134
BdGA2ox9	:	---A-----GLLN---	HSYRWGTPTA	-TSPAQLSWSEAFH	VPLAAVS---	GDPPCNY-----		G---	: 167
HvGA2ox1	:	---A-----GPP---	SPLGYGCRSI	-GFNGDVGELEYLL	LLHA-NPA---	AVAHRASSIDT-----		N---	: 136
HvGA2ox10	:	---A-----TPG---	SPFGYASKRI	-GNGDGLWVEYLL	LLGV-TAAGA	EAGAPLSVPEEVPS		A---	: 146
HvGA2ox2	:	---A-----GPP---	DPLGYGSRSI	-GSHGDVGELEYLL	THT-DPE---	VVARKARAYDR-----		D---	: 133
HvGA2ox3	:	---S-----GPA---	YPFGYGSKRI	-GLNGDMGWLEYLL	LAV-DSA---	SLPAASA-----		V---	: 125
HvGA2ox4	:	---S-----GPA---	DPFGYGSKRI	-GRNGDMGWVEYLL	LLAI-DRD---	TLKASP-----		A---	: 125
HvGA2ox6	:	---A-----GLLN---	GSYRWGNPTA	-TSLRHLSWSEAFH	VPL-ATI---	SREDCDY-----		G---	: 152
HvGA2ox7	:	---A-----G----	RPLGYGSKRI	-GVSGDLGWIEYLL	LGVTAG---	ALPAASFASWTLPCAGA		AVASSS	: 143
HvGA2ox8	:	-----RPFYGSKNI	-GCNGDVGWIEYILL	SVRSGS---	VAAAS-----				: 120
HvGA2ox9	:	---A-----GLLN---	DSYRWGSPTA	-TSPRQLSWSEAFH	VPL-AGI---	SGSPCSY-----		G---	: 157
OsGA2ox1	:	---A-----GPA---	SPLGYGCRSI	-GFNGDVGELEYLL	LLHA-NPA---	AVAHARTIDA-----		M---	: 142
OsGA2ox10	:	AAAA-----VPG---	SPFGYGSKRI	-GCNGDLGWVEYLL	LGVA	AAA-----		AAPLPAHGE	: 142
OsGA2ox2	:	---A-----GRP---	TPLGYGSRSI	-GANGDVGELEYLL	THA-SPD---	AVARKASADR-----		E---	: 139
OsGA2ox3	:	---S-----GPA---	YPFGYGSKRI	-GFNGDMGWIEYLL	LALDDAS---	LADACTV-----			: 125
OsGA2ox4	:	---H-----GPA---	SPFGYGSKRI	-GRNGDMGWIEYLL	LLAI-DGA---	SLSRSS-----		A---	: 126
OsGA2ox5	:	---F-----SP----	ESYRWGTPTA	-KCLEQLSWSEAYH	IPMTTPR---	PSTSIRA-----			: 148
OsGA2ox6	:	---A-----GLLN---	GSYRWGNPTA	-TSLRHLSWSEAFH	VPL-ASI---	SGADCDF-----		G---	: 157
OsGA2ox7	:	---A-----G----	APLGYASKRI	-GSAGDLGWIEYLL	LCL-APAAAA	AALPCAATSPT-----			: 131
OsGA2ox8	:	---S-----GPA---	RPLGYGSKSI	-GSNGDVGWIEYLL	LSAGAAS---	SGGAA-----			: 126
OsGA2ox9	:	---A-----GLLN---	DSYRWGTPTA	-TSLRQLSWSEAFH	LPL-AGI---	SGKSCNY-----		G---	: 167
TaGA2ox-A1	:	---A-----GPP---	SPLGYGCRSI	-GFNGDVGELEYLL	LLHA-NPA---	AVAHRASSIDTN-----			: 134
TaGA2ox-A10	:	---AMSAATPG-----	SPFGYASKRI	-GNGDGLWVEYLL	LLGV-SAA---	TSGPLSVPEGVVPSA			: 143
TaGA2ox-A11	:	---A-----GLLN---	GSYRWGNPTA	-TSLGQLSWSESFH	VPL-PSI---	SREDCDY-----		G---	: 158
TaGA2ox-A3	:	---S-----GPA---	YPFGYGSKRI	-GLNGDMGWIEYLL	LAVD	AAAS-----		V---	: 125
TaGA2ox-A4	:	---S-----GPA---	DPFGYGSKRI	-GRNGDMGWIEYLL	LLAI-ERD---	ALSKASP-----		A---	: 125
TaGA2ox-A6	:	---A-----GLLN---	GSYRWGNPTA	-TSLRHLSWSEAFH	VPL-ASI---	SREDCDY-----		G---	: 157
TaGA2ox-A7	:	---A-----G----	RPLGYGSKRI	-GVSGDLGWIEYLL	MLGV-TPG---	ALPASFASWTLPCAAD		AVAASLS	: 142
TaGA2ox-A8	:	-----RPLGYGSKSI	-GCNGDVGWIEYILL	SVGSGS---	VAAAS-----				: 120
TaGA2ox-A9	:	---A-----GLLN---	DSYRWGSPTA	-TSPRQLSWSEAFH	VPL-AGI---	SGSPCSY-----		G---	: 157
TaGA2ox-B1	:	---A-----GPP---	SPLGYGCRSI	-GFNGDGELEYLL	LLHA-NPA---	AVAHRASSIDTN-----			: 134
TaGA2ox-B10	:	---AMSAATPG-----	SPFGYASKRI	-GNGDGLWVEYLL	LLGV-TAS---	TGGPLSVPEGVVPSA			: 143
TaGA2ox-B11	:	---A-----GLLN---	GSYRWGNPTA	-TSLGQLSWSFESFH	VPL-PSI---	SREDCDR-----		G---	: 158
TaGA2ox-B12	:	---A-----GLLN---	GSYRWGTPTA	-TSLRQLSWSEAFH	VPLASIS---	GEDDCG-----		A---	: 155
TaGA2ox-B13	:	---A-----GLLN---	GSYRWGNATA	-TSLRQLSWSEAFH	VPLASIS---	EEDA-----			: 147
TaGA2ox-B2	:	---A-----GPP---	DPLGYGSRSI	-GSHGDVGELEYLL	THT-DPE---	VVARKARADR-----		D---	: 130
TaGA2ox-B3	:	---S-----GPA---	YPFGYGSKRI	-GLNGDMGWIEYLL	LAVESAS---	LSGACTV-----			: 125
TaGA2ox-B4	:	---S-----GPA---	DPFGYGSKRI	-GRNGDMGWIEYLL	LLAI-ERD---	ALSKASP-----		A---	: 125
TaGA2ox-B6	:	---A-----GLLN---	GSYRWGNPTA	-TSLRHLSWSEAFH	VPL-ASI---	SREDCDY-----		G---	: 157
TaGA2ox-B7	:	-----AAG---	RPLGYGSKRI	-GVSGDLGWIEYV	MLGVTPAG---	ALPAASFTSWTLPCAGA		AV	: 142
TaGA2ox-D1	:	---A-----GPP---	NPLGYGCRSI	-GFNGDVGELEYLL	LLHA-NPA---	AVAHRASSIDTN-----			: 134
TaGA2ox-D10	:	---AMSAATPG-----	SPFGYGSKRI	-GNGDGLWVEYLL	LLGV-TAA---	TGGPLSVPEGVVPSA			: 143
TaGA2ox-D11	:	---A-----GLLN---	GSYRWGNPTA	-TSLGQLSWSESFH	VPL-PSI---	SREDCDY-----		G---	: 158
TaGA2ox-D2	:	---A-----GPP---	DPLGYGSRSI	-GSHGDVGELEYLL	THT-DPD---	VVARKARADR-----		D---	: 131
TaGA2ox-D3	:	---S-----GPA---	YPFGYGSKRI	-GLNGDMGWIEYLL	LAVDSAS---	LSGACAV-----			: 125
TaGA2ox-D4	:	---S-----GPA---	DPFGYGSKRI	-GRNGDMGWIEYLL	LLAI-ERD---	TLKASP-----		A---	: 125
TaGA2ox-D6	:	---A-----GLLN---	GSYRWGNPTA	-TSLRHLSWSEAFH	VPL-ASI---	SREDCDY-----		G---	: 154
TaGA2ox-D7	:	---A-----G----	RPLGYDSKRI	-GVSGDLGWIEYLL	MLGVTPAG---	ALPAASFASWTLPCAGA		AVASLS	: 157
TaGA2ox-D8	:	-----NPLGYGSKSI	-GRNGDVGWIEYILL	SVS-GSG---	PVAAA-----			S---	: 120
TaGA2ox-D9	:	---A-----GLLN---	DSYRWGSPTA	-TSPRQLSWSEAFH	VPL-AGI---	SGTPCSY-----		G---	: 157
OsGA2ox-D10	:	---G-----PG----	EPCGYGSPPTSS	FFSKLMWSEGYTF---	SPS-----	SLRSELRLRLWPKSG		D---	: 152

		*	260	*	280	*	300	*	320				
AtGA20x1	:	-SPGTF	-RNALEEYTTSVRKMTFDVLEKITDG	-LGI	---	KPRNT	-LSKLVSDQN	---	TDSILRLNHYP	--PCPLSN	---	: 182	
AtGA20x2	:	-TPQIF	-RESLEEYMKIEKVSXKVLMEVAAEE	-LGI	---	EPRDT	-LSKM-LRDE	---	K-SDSCLRLNHYP	--AAEEEA	---	: 196	
AtGA20x3	:	-TPAIF	-REAVEEYIKEMKRMSSKFLEMVEEE	-LKI	---	EPKEK	-LSRL-VKVK	---	E-SDSCLRMNHYP	--EKEETP	---	: 192	
AtGA20x4	:	-----	-SSAVNCYIEAVKQLAREILDLTAEGLHV	---	PPHS	-FSRLISSVD	---	SDSVLRVNHYP	--PSDQFF	---	: 173		
AtGA20x6	:	-DPFKF	-SSATNDYIRTVRDLACEIIDLTIENTLWGQ	---	KSSE	-VSEL-IRDV	-R-SDSILRLNHYP	---	PAPYAL	---	: 192		
AtGA20x7	:	-DRNNL	-RTIVETYVQEIARVAQMICEILGKQ	-VNV	---	SSEY-FEN	---	IFEL	---	ENSFLRLNKYH	--PSVFGS	---	: 208
AtGA20x8	:	-DFTTL	-SSTMEKFASESEALAYMLAEVLAEK	---	SGQNSSFFK	-ENCV	-R-NTCYLRMNRYP	---	PCPKPS	---	: 207		
BdGA20x1	:	-DPKHF	-SCVVNEYVEAVKQLACDILDLLGEG	-LGL	---	EDPRS	-FSKLITEPD	---	SDSLLRINHYP	--PSCTVHKLD	: 205		
BdGA20x10	:	-SLCAF	-RELLDEYTVAVRRMTCVLELMAEA	-LGM	---	EKDE	-FTRL-VLEE	-D-SDSMLRVNHYP	PAPPELK	---	: 212		
BdGA20x2	:	-DPSRF	-SEAVNEYVGAVRRACQILDLLGEG	-LGL	---	EDPTA	-LSKIITVSD	---	SDSIIRINHYP	--PSSAAA	---	: 191	
BdGA20x3	:	-PSGSAFRRALNEYIGAVRKVAVRVMEAMAEG	-LGI	---	APLDA	-LSKM-VTAA	-G-SDQVFRVNHYP	---	PCAALQ	---	: 189		
BdGA20x4	:	-PSSSL	-RDAINEYVGAMRGLARTVLEMAVEG	-LGV	---	SPRGA	-LADM-VTGE	-A-SDQVFRVNHYP	---	PCPLLQ	---	: 191	
BdGA20x5	:	-TTTAT	-RRVIHEVSAAMSKLARRILSVLAAE	-HG	---	PPPET	-----	ETTTCFRLRNRY	--QAPGSG	---	: 225		
BdGA20x6	:	-KLSSL	-RGVMQEVADAMSRVADAVAGALAEK	-LGQ	---	EAGSA	---	LFPAGCD	-G-TTCFRLRNRY	--ACPFAP	---	: 221	
BdGA20x7	:	ESSCPL	-RGLLEEYAAALRRMACEVLELMAEG	-LGL	---	APSDA	-ISRL-VSDG	-G-SDNMLRVNHYP	---	PRPELQ	---	: 219	
BdGA20x8a	:	-LPASL	-RLALHEYTRAVRELSGRVLELMAEG	-LGIVGETERG	-LRRMVAGSE	---	EELVRVNHYP	---	PPPTTER	---	: 203		
BdGA20x8b	:	-LPPSL	-RAALEEYTGAVRNASGKVLLELMAEG	-LGM	---	QERCA	-LRRM-VDGS	---	EEELVRVNHYP	--PTKEED	---	: 197	
BdGA20x9	:	-QLTTL	-RDVTQEVATAMSKLANTLARVLAES	-LGH	---	AGE	---	RFPEGCD	-E-RTCFRLRNRY	--PCPLSP	---	: 228	
HvGA20x1	:	-DPSRF	-SSVVNEYVEAVKQLACDILDLLGEG	-LGL	---	EDPRL	-FSKL-VTEA	-D-SDSLLRINHYP	---	PSCTVHKLD	: 203		
HvGA20x10	:	-SLCSF	-RDLLNEYTVAVRRMTCQVLELMAEG	-LGM	---	EDRDA	-FTRL-VLHK	-E-SDSMLRVNHYP	---	PRPELK	---	: 210	
HvGA20x2	:	-DPSRF	-SEAVNEYVQAVRHLACRILDMLELMAEG	-LGL	---	RDPAS	-LSRLITTTD	---	GDSLVRINHYP	--ASAAGD	---	: 197	
HvGA20x3	:	-PSCALFRAALNEYIAAVRKVAVRVMEAMAEG	-LGI	---	APADA	-LSAM-VAAE	-G-SDQVFRVNHYP	---	PCHALQ	---	: 190		
HvGA20x4	:	-PSSAL	-RAAINAYVSAMRGLARTVLEMAVEG	-LGV	---	SPRGA	-LADM-VTGE	-A-SDQVFRVNHYP	---	PCPLLQ	---	: 189	
HvGA20x6	:	-KLSSL	-REVMQEVADAMSCVADTVAGALAE	-LGH	---	AAGGG	-ESTFPAGCD	-G-TTCFRLRNRY	--ACPFAP	---	: 217		
HvGA20x7	:	-HPCPL	-RDLLEEYAAAVRRMACGVLELMAEG	-LGI	---	GPADA	-LSRL-VSDG	-E-SDNMLRVNHYP	---	PRPEMQ	---	: 207	
HvGA20x8	:	-LPPSL	-RAALEEYTDVAREVGARVLELMADG	-LGV	---	AEHHRGV	-LRRMVAPDDAGG	-ADEMVRVNHYP	---	PCPSSL	---	: 189	
HvGA20x9	:	-ELTSI	-RDVTQEVAKAMSKLANTLARVLAES	-LGH	---	TAGQG	---	FPEGCD	-E-STCFRLRNRY	--PCPFSP	---	: 219	
OsGA20x1	:	-DPSRF	-SAIVNEYIEAMKKLACEILDLLGEG	-LGL	---	KDPRY	-FSKL-TTNA	-D-SDCLLRINHYP	---	PSCNIHKLD	: 209		
OsGA20x10	:	PSYGSF	-RDILNEYVVAVRAMMEVLKLELMAEG	-LGL	---	KEKDA	-LVRL-VSHE	-E-SDSVLRVNHYP	---	PHPELK	---	: 207	
OsGA20x2	:	-DPRRF	-SQVVNDYVEAVRQLACHVLDLLGEG	-LGL	---	RDPTS	-LTRITATD	---	NDSLIRINHYP	--PSCAAA	---	: 203	
OsGA20x3	:	-PSCAVFRAALNEYISGVRKVAVRVMEAMSEG	-LGI	---	ADQDA	-LSAL-VTAE	-G-SDQVFRVNHYP	---	PCRALQ	---	: 190		
OsGA20x4	:	-PSSSL	-RDAANKYVGAMRGMAVLEMAVEG	-LGV	---	APRGA	-LADM-VVGDGAA	-SDQILRLNHYP	---	PCPPLL	---	: 192	
OsGA20x5	:	-----	-RAVIEEVSRAAMYELAQKLAELLMRGLPGA	---	GEGET	-M	---	VTTR	-E-ETCFRLRNRY	--PCAMAM	---	: 205	
OsGA20x6	:	-DLTSL	-RGVMQEVAEAMSRVANTVAAALAEELTGR	---	GGGGASAAPWF	-FAGCD	---	E-TTCFRLRNRY	--ACPFAP	---	: 225		
OsGA20x7	:	-PPCPL	-RAVMEQEVADAMSRVADTVAAALAE	-LGH	---	DAGGG	-EPAFPAGCD	-G-TTCFRLRNRY	--ACPFAP	---	: 222		
OsGA20x8	:	-LPAAL	-RAAVEAYTGAVRGVGRVMELMAEG	-LGL	---	GASEEGRCVLR	-LRRMVVGC	-E-SDMLRVNHYP	---	PCLLPP	---	: 195	
OsGA20x9	:	-DLTSL	-RDVTREVADAMSRALARALAESELLGH	---	AAGER	---	FPEGCD	-D-ATCFRLRNRY	--PCPFPP	---	: 230		
TaGA20x-A1	:	-DPSRF	-SSVVNEYVEAVKQLACDILDLLGEG	-LGL	---	EDPRL	-FSKLITETD	---	SDSLLRINHYP	--PSCTVH-KL	: 200		
TaGA20x-A10	:	-SLCSF	-RDLLNEYTVAVRRMTCQALELMAEG	-LGM	---	DDRDA	-FTRLVLHKE	---	SDSMLRVNHYP	--PRPELK	---	: 207	
TaGA20x-A11	:	-KLNSL	-RGVMQVADAMSRVAYTVAGTLAEN	-LGH	---	EAGGG	-EPVFPAGCD	-G-TTCFRLRNRY	--ACPFAP	---	: 223		
TaGA20x-A3	:	-PSCALFRAALNEYIAAVRKVAVRVMEAMAEG	-LGI	---	APVDA	-LSAM-VTAE	-G-SDQVFRVNHYP	---	PCHALQ	---	: 190		
TaGA20x-A4	:	-PTSAL	-RDAINDYVGAMRGLARTVLEMAVEG	-LGV	---	SPRGA	-LADM-VTGD-AA	-SDQVFRVNHYP	---	PCPLLQ	---	: 190	
TaGA20x-A6	:	-KLSSL	-RAVMQEVADAMSRVADTVAAALAE	-LGH	---	DAGGG	-EPAFPAGCD	-G-TTCFRLRNRY	--ACPFAP	---	: 222		
TaGA20x-A7	:	-PPCPL	-RDLLEEYAAAVRRMACGVLELMAEG	-LGV	---	APADA	-LSRL-VSDA	-E-SDSMLRVNHYP	---	PRPELQ	---	: 206	
TaGA20x-A8	:	-LPASL	-RAALEEYTDVAREVGARVLELMADG	-LGV	---	AEHHRGV	-LRRM-VAPD	-E-ADEMVRVNHYP	PPCPCLAA	---	: 188		
TaGA20x-A9	:	-ELTSI	-RDVTQEVANAMSKLANTLARVLASS	-LGH	---	TAGQR	---	FPEGCD	-E-RTCFRLRNRY	--PCPFSP	---	: 219	
TaGA20x-B1	:	-DPSRF	-SSVVNEYVEAVKQLACDILDLLGEG	-LGL	---	EDPRL	-FSKLITETD	---	SDSLLRINHYP	--PSCTVH-KL	: 200		
TaGA20x-B10	:	-SLCSF	-RDLLNEYTVAVRRMTCQVLELMAEG	-LRM	---	EDRDA	-FTRLVLHKE	---	SDSMLRVNHYP	--PRPELK	---	: 207	
TaGA20x-B11	:	-KLSTL	-RGVMQEVADAMSRVAGTVAGTLAEN	-LGH	---	EAGGE	-SAFPAGCD	-G-TTCFRLRNRY	--ACPFAP	---	: 222		
TaGA20x-B12	:	-ELSSL	-RGVMQEVAAAMSRVADTVAGTLAKN	-LGH	---	ESTFP	---	AAAGCD	-G-TTCFRLRNRY	--ACPFAP	---	: 217	
TaGA20x-B13	:	-KLSSL	-RGMMQEVADAMSRVAETVAGTLAKN	-LG	---	QAGST	-FPAA-AGCD	-G-TTCFRLRNRY	--ACPFAP	---	: 210		
TaGA20x-B2	:	-DPSRF	-SEAVNVVQAVRHLACQILDLLGEG	-LGL	---	RDPAS	-LSRLVTTTD	---	SDSLVRINNY	--PSAASD	---	: 194	
TaGA20x-B3	:	-PSCALFRAALNEYIAAVRKVAVRVMEAMAEG	-LGI	---	APVDA	-LSAMVTAGG	---	SDQVFRVNHYP	---	PCHALQ	---	: 190	
TaGA20x-B4	:	-PTSAL	-RDAINAYVGAMRGLARTVLEMAVEG	-LGV	---	SPRGA	-LADM-VTGD-VA	-SDQVFRVNHYP	---	PCPLLQ	---	: 190	
TaGA20x-B6	:	-KLSSL	-RGVMQEVADAMSHVADTVAAALAE	-LGH	---	DAGGG	-EPAFPAGCD	-G-TTCFRLRNRY	--ACPFAP	---	: 222		
TaGA20x-B7	:	EPPCPL	-RDLLEEYAAAVRRMACGVLELMAEG	-LGV	---	APADA	-LSRL-VSDA	-E-SDSMVRVNHYP	---	PRPELQ	---	: 207	
TaGA20x-D1	:	-DPSRF	-SSVVNEYVEAVKQLACDILDLLGEG	-LGL	---	EDPRL	-FSKLITETD	---	SDSLLRINHYP	--PSCTVH-KL	: 200		
TaGA20x-D10	:	-SLCSF	-RDLLNEYTEVVRMTCQVLELMAEG	-LGM	---	DDRDA	-FTRLVLHKE	---	SDSMLRVNHYP	--PRPELK	---	: 207	
TaGA20x-D11	:	-KLSTL	-RGVMQEVADAMLRVADTVAGTLAEN	-LGH	---	EAGGS	-ESAFPAGCD	-G-TTCFRLRNRY	--ACPFAP	---	: 223		
TaGA20x-D2	:	-DPSRF	-SEAVNEYVQAVRHLACQILDLLGEG	-LGL	---	RDPAS	-ISRLVTTTD	---	SDSLVRINNY	--PSATGD	---	: 195	
TaGA20x-D3	:	-PSCALFRAALNEYIAAVRKVAVRVMEAMAEG	-LGI	---	AAVDA	-LSGM-VTAE	-G-SDQVFRVNHYP	---	PCHALQ	---	: 190		
TaGA20x-D4	:	-PSTAL	-RDAINAYVGAMRGLARTVLEMAVEG	-LGV	---	SPRGA	-LADM-VTGD	-VASDQVFRVNHYP	---	PCPLLQ	---	: 190	
TaGA20x-D6	:	-KLSSL	-RGVMQEVADAMSRVADTVAAALAE	-LGH	---	DAGGG	-EPAFPAGCD	-G-TTCFRLRNRY	--ACPFAP	---	: 219		
TaGA20x-D7	:	-PPCPL	-RDLLEEYAAAVRRMACGVLELMAEG	-LGI	---	APADA	-LSRL-VADA	-E-SDSMLRVNHYP	---	PRPELQ	---	: 221	
TaGA20x-D8	:	-LPPSL	-RAALEEYTDVAREVGARVLELMADG	-LGL	---	AEENRGV	-LRRV-VASD	-E-ADKMVRVNHYP	PPWPCLAA	---	: 188		
TaGA20x-D9	:	-ELASI	-RDVTQEVANAMSKLANTLARVLAES	-LGH	---	TAGQR	---	FPKGCD	-E-RTCFRLRNRY	--PCPFSP	---	: 219	
OsGA30x2	:	-DYLLF	-CDVMEEFHKEMRRLADELLRLFLRA	-LGLTGEEVAGV	-EAER-RIGE	-R-MTATVHLNWYP	---	RCPEPR	---	: 219			

		*	340	*	360	*	380	*	400					
AtGA2ox1	:	-----	KKTNGGKNVIGFGEHTDPQIISVLR	----	SNNTSGLQINL	----	ND	----	G	-----	SWISVPP	:	228	
AtGA2ox2	:	-----	EKMVKVGFGEHTDPQIISVLR	----	SNNTAGLQICV	----	KD	----	G	-----	SWAVVPP	:	238	
AtGA2ox3	:	-----	VKEEIGFGEHTDPQLISLLR	----	SNDTEGLQICV	----	KD	----	G	-----	TWVDVTP	:	233	
AtGA2ox4	:	-----	GEANLSDQSVSLTRVGFGEHTDPQLITVLR	----	SNGVGGGLQVSN	----	SD	----	G	-----	MWVSVSP	:	224	
AtGA2ox6	:	-----	SGVGQIGFGEHSDPQLITVLR	----	SNDVDGLEICS	----	RD	----	G	-----	LWIPIPS	:	234	
AtGA2ox7	:	-----	EVFGLVPHTDTSFLTILS	----	QDQIGGLELE	----	NN	----	G	-----	QWISVKP	:	246	
AtGA2ox8	:	-----	EVYGLMPHTDSDFLTILY	----	QDQVGGGLQLIK	----	DN	----	G	-----	RWIAVKP	:	245	
BdGA2ox1	:	HDGQCKLKGTACRAKAGNGGNPTGGGRIGFGEHSDPQLISLLR	----	ANDVDGLQVLL	----	PD	----	----	VNGKEVWIQVPA	----	:	273		
BdGA2ox10	:	-----	QQLQHGGNGRVTGFGHEHTDPQIISVLR	----	SNATSGLEIAL	----	RD	----	G	-----	TWVSVPP	:	260	
BdGA2ox2	:	-----	SSVGFGEHSDPQLISVLR	----	ANDVDGLQVLL	----	PD	----	GRGQD	----	TWVQVPA	:	234	
BdGA2ox3	:	-----	GLGCSATGFGEHTDPQLVSVLR	----	SNGTSGLQIAL	----	QDG	----	G	-----	QWVSVPS	:	233	
BdGA2ox4	:	-----	GLPPNCSTVGFEHTDPQLVSVLR	----	SNATAGLQIAL	----	HGD	----	GDAQ	----	KWVSVPP	:	240	
BdGA2ox5	:	-----	GGHGHGVLGCGHTDSDFLTILR	----	QDDHVGGGLQLL	----	DDKDGG	----	----	----	RWRTVRP	:	274	
BdGA2ox6	:	-----	DTFGLVPHTDSDFLTILC	----	QDQVGGGLQLMK	----	DS	----	----	----	RWLAVKP	:	259	
BdGA2ox7	:	-----	AGKNQLLTGFGEHTDPQIISVLR	----	SNGTSGLEIAS	----	PRD	----	G	-----	AWASVPP	:	264	
BdGA2ox8a	:	-----	DEDDGCVGITGFGEHTDPQLISLLR	----	SNRTAGYQILL	----	QEADEA	----	----	----	RWVNVAP	:	253	
BdGA2ox8b	:	-----	CVAGMTGFGEHTDPQIISLLR	----	SNRTAGLQIKLQGP	----	PD	----	A	-----	PWVNVAP	:	241	
BdGA2ox9	:	-----	DAFGLVPHTDSDFLTIVLC	----	QDQVGGGLQLMK	----	GS	----	----	----	RWLAVKP	:	266	
HvGA2ox1	:	HDDQCKLKGLIA	----	RTKAGNGANPGAGGRIGFGEHSDPQLISLLR	----	ANDVDGLQVLL	----	PD	----	----	VNGKDAWIQVPA	:	270	
HvGA2ox10	:	-----	QHHGGRVTGFGHEHTDPQIISVLR	----	SNATSGLEIAL	----	RD	----	G	-----	DWVSVPP	:	254	
HvGA2ox2	:	-----	GGVKAASSVGFEHTDPQLISVLR	----	ANDVDGLQVLL	----	PD	----	GRGED	----	AWVQVPA	:	246	
HvGA2ox3	:	-----	GLGCSATGFGEHTDPQLISVLR	----	SNGTSGLQIAL	----	QS	----	G	-----	HWVSVPS	:	233	
HvGA2ox4	:	-----	GLPPNCSTVGFEHTDPQLVSVLR	----	SNGTAGLQVAL	----	HD	----	G	-----	RWVSVPP	:	234	
HvGA2ox6	:	-----	DTFGLVPHTDSDFLTILC	----	QDQVGGGLQLM	----	KD	----	A	-----	RWVAVKP	:	255	
HvGA2ox7	:	-----	GRLLMGFGEHTDPQIISVLR	----	SNGTSGLEICA	----	RD	----	G	-----	EWTSVPP	:	248	
HvGA2ox8	:	-----	AAGQRGVTGFEHTDPQIISVLR	----	SNRTAGFQIML	----	PD	----	G	-----	RWVPVAP	:	233	
HvGA2ox9	:	-----	DAFGLVPHTDSDFLTIVLC	----	QDQVGGGLQLMK	----	GS	----	----	----	RWLAVKP	:	257	
OsGA2ox1	:	HDDQCNIKSLV	----	STKASNGGNLMAGGRIGFGEHSDPQLISLLR	----	ANDVEGLQVVF	----	PDHEGK	----	E	-----	MWVQVPS	:	276
OsGA2ox10	:	-----	QGHGRLTGFEHTDPQIISVLR	----	SNDTSGLEISL	----	RD	----	G	-----	SWASVPP	:	251	
OsGA2ox2	:	-----	AGDHKSGGGPAPTAAIGFGEHTDPQLISVLR	----	ANDADGLQLLPDA	----	----	----	AAAGDSVWVPVPP	----	:	261		
OsGA2ox3	:	-----	GLGCSVTGFGEHTDPQLVSVLR	----	SNGTSGLQIAL	----	RD	----	G	-----	QWVSVPS	:	233	
OsGA2ox4	:	-----	QNLMPNCSTPGFEHTDPQLISILH	----	SNSTSGLQVAL	----	HHH	----	ADAGDHQWVTVP	----	:	244		
OsGA2ox5	:	-----	GGFGLCPHTDSDLLTIVHQQDQTVGGGLQLK	----	G	----	----	----	G	-----	RWVAVKP	:	245	
OsGA2ox6	:	-----	DTFGLVPHTDSDFLTIVLC	----	QDQVGGGLHLMK	----	DS	----	----	----	RWVAVRP	:	263	
OsGA2ox7	:	-----	GGGGPNLTGFGEHTDPQIISVLR	----	SNGAPGLEISL	----	RD	----	G	-----	AWVSVPHD	:	241	
OsGA2ox8	:	-----	GRDRDECGVTGFGEHTDPQIISVLR	----	SNCTAGLQILL	----	RGDYSSP	----	A	-----	RWVPVPP	:	246	
OsGA2ox9	:	-----	DDAFGLVPHTDSDFLTIVLC	----	QDHVGGGLQLMK	----	GS	----	----	----	RWVAVKP	:	269	
TaGA2ox-A1	:	DHDDQCKLKGVARTKAGSGGNPAAGGRIGFGEHSDPQLISLLR	----	ANDVDGLQVLL	----	PD	----	----	INGKDTWIQVPA	----	:	268		
TaGA2ox-A10	:	-----	LLQQQHHGGGGRVTGFGHEHTDPQIISVLR	----	SNATSGLEIAL	----	RD	----	G	-----	AWVSVPP	:	258	
TaGA2ox-A11	:	-----	DDFGMPHTDSDFLTILC	----	QDQVGGGLQIL	----	KD	----	S	-----	HWVAVKP	:	261	
TaGA2ox-A3	:	-----	GLGCSATGFGEHTDPQLISVLR	----	SNGTSGLQIAL	----	QN	----	G	-----	QWVSVPS	:	233	
TaGA2ox-A4	:	-----	GLPPNCSTVGFEHTDPQLVSVLR	----	SNGTPGLQVAL	----	HD	----	G	-----	RWVSVPP	:	235	
TaGA2ox-A6	:	-----	DTFGLVPHTDSDFLTILC	----	QDQVGGGLQLMK	----	DS	----	----	----	RWVAVKP	:	260	
TaGA2ox-A7	:	-----	GRLLTGFEHTDPQIISLLR	----	SNGTSGLEICA	----	RD	----	G	-----	SWAAVPP	:	247	
TaGA2ox-A8	:	-----	GQRGVTGFGEHTDPQIISVLR	----	SNRIGGLQIML	----	PD	----	G	-----	RWVPVAP	:	230	
TaGA2ox-A9	:	-----	DAFGLVPHTDSDFLTIVLC	----	QDQVGGGLQLMK	----	GS	----	----	----	QWVAVKP	:	257	
TaGA2ox-B1	:	DHDDQCKLKGVARTKAGNGGNPAAGGRIGFGEHSDPQLISLLR	----	ANDVDGLQVLL	----	PD	----	----	INGKDTWIQVPA	----	:	268		
TaGA2ox-B10	:	-----	LLQQQHHGGGGRVTGFGHEHTDPQIISVLR	----	SNATSGLEIAL	----	RD	----	G	-----	AWVSVPP	:	256	
TaGA2ox-B11	:	-----	DSFGMPHTDSDFLTILC	----	QDQVGGGLQIL	----	KD	----	S	-----	RWVAVKP	:	260	
TaGA2ox-B12	:	-----	DTLGMVPHTDSDFLTIVLC	----	QDQVGGGLEIMK	----	DS	----	----	----	HWVAVKP	:	255	
TaGA2ox-B13	:	-----	DTFGMPHTDSDFLTIVLC	----	QDQVGGGLEIMK	----	DS	----	----	----	HWVAVKP	:	248	
TaGA2ox-B2	:	-----	GGVKAASSVGFEHSDPQLISVLR	----	ANDVDGLQVLL	----	PD	----	GRGED	----	AWVQVPA	:	243	
TaGA2ox-B3	:	-----	GLGCSATGFGEHTDPQLISVLR	----	SNGTSGLQIAL	----	QN	----	G	-----	QWVSVPS	:	233	
TaGA2ox-B4	:	-----	GLPPNCSTVGFEHTDPQLVSVLR	----	SNGTPGLQVAL	----	HD	----	G	-----	RWVSVPP	:	235	
TaGA2ox-B6	:	-----	DTFGLVPHTDSDFLTILC	----	QDQVGGGLQLM	----	KD	----	S	-----	RWVAVKP	:	260	
TaGA2ox-B7	:	-----	GRLLTGFEHTDPQIVSVLR	----	SNGTSGLEICA	----	RD	----	G	-----	SWTAVPP	:	248	
TaGA2ox-D1	:	DHDDQCKLKGVARTKAGSGGNPAAGGRIGFGEHSDPQLISLLR	----	ANDVDGLQVLL	----	PD	----	----	INGKDTWIQVPA	----	:	268		
TaGA2ox-D10	:	-----	LLQQQHHGGGGRVTGFGHEHTDPQIISVLR	----	SNATSGLEIAL	----	RD	----	G	-----	AWVSVPP	:	255	
TaGA2ox-D11	:	-----	DSLGMVPHTDSDFLTILC	----	QDQVGGGLQLIK	----	DS	----	----	----	RWVAVKP	:	261	
TaGA2ox-D2	:	-----	GGVKAASAVGFGEHSDPQLISVLR	----	ANDVDGLQVLL	----	PD	----	GRGED	----	AWVQVPA	:	244	
TaGA2ox-D3	:	-----	GLGCSATGFGEHTDPQLISVLR	----	SNGTSGLQIAL	----	QN	----	G	-----	QWVSVPS	:	233	
TaGA2ox-D4	:	-----	GLPPNCSTVGFEHTDPQLVSVLR	----	SNGTPGLQVAL	----	HD	----	G	-----	RWVSVPP	:	235	
TaGA2ox-D6	:	-----	DTFGLVPHTDSDFLTILC	----	QDQVGGGLQLM	----	KD	----	S	-----	RWVAVKP	:	257	
TaGA2ox-D7	:	-----	GRLLTGFEHTDPQIVSVLR	----	SNGTSGLEICA	----	RD	----	G	-----	SWAAVPP	:	262	
TaGA2ox-D8	:	-----	GQRGVTGFGEHTDPQIVSVLR	----	SNRT	----	GLQIML	----	PD	----	RWVPVAP	:	231	
TaGA2ox-D9	:	-----	DAFGLVPHTDSDFLTIVLC	----	QDQVGGGLQLMK	----	GS	----	----	----	RWVAVKP	:	257	
OsGA3ox2	:	-----	RALGLIAHTDSGFFTFVL	----	QSLVPGLQLFR	----	----	----	RGPD	----	RWVAVPA	:	259	

		*	420	*	440	*	460	*	480				
AtGA20x1	:	-DHTSFFNVGDSLQVMTNGRFSKSVHRV	-LA	-N-CKKSRVSMIYFAGPSLTQRI	-APLTCLI	-----	DNEDERLYE	:	295				
AtGA20x2	:	-DHSSFFINVGDALQVMTNGRFSKSVKHRV	-LA	-D-TRRSRSMIYFGGPHLSQKI	-APLPCLV	-----	PEQDDWLYK	:	305				
AtGA20x3	:	-DHSSFFVLVGDTLQVMTNGRFSKSVKHRV	-VT	-N-TKRSRSMIYFAGPPLSEKI	-APLSCLV	-----	PKQDDCLYN	:	300				
AtGA20x4	:	-DPSAFCVNVGDLQVMTNGRFSVRHRA	-LT	-Y-GEESRLSTAYFAGPPLQAKI	-GPLSAMV	-----	MTMNQPRLYQ	:	292				
AtGA20x6	:	-DPTCCFVLVGDCQLALTNGRFTSVRHRV	-LA	-NTAKKPRMSAMYFAAPPLEAKI	-SPLPKMV	-----	SPENPRRYN	:	302				
AtGA20x7	:	-CLEALTVNIGDMFQALSNGVYQSVRHRV	-IS	-P-ANIERMSIAFFVCPYLETEI	-DCF	-----	GYPKKYR	:	307				
AtGA20x8	:	-NPKALIINIGDLFQAWSNGMYKSVEHRV	-MT	-N-PKVERFSTAYFMCPSYDAVIECS		-----	SDRPAYR	:	306				
BdGA20x1	:	-DSSAFFNVGDLQALTNGKLLSVRHRV	-IA	-S-ACRPRLSTIYFAAPPLHARI	-SALPETV	-----	TAGSPRRYR	:	340				
BdGA20x10	:	-DHTSFFNVV	-----	LTNGRFRSVRHRV	-MV	-N-SVRSRVSVIFFGGPAPGKTL	-APLPRMV	----	GE	----	GGSSRYR	:	321
BdGA20x2	:	-DPAAFFINVGDLLQALTNGRLVSVIRHRV	-MA	-S-TSKPRLSTIYFAAPALHALI	-SALPETV	-----	TSAPRRYR	:	301				
BdGA20x3	:	-DRDALFVNVDGDLQVLTNGRFSKSVKHRV	-VA	-N-SLKSRSVSLIYFGGPPLTQRI	-APLPQLL	----	GE	----	GEQSLYT	:	300		
BdGA20x4	:	-NRDAFFNVVDGDLQVLTNGRLKSVRHRV	-VA	-GSGRKSRSVMIYFGGPPVAQRI	-APLPQLL	----	QAE	----	QQLPIYR	:	309		
BdGA20x5	:	-NPGALTVNVGDLQAWTNDVYASVEHRV	-VA	-R-PDRERFSVAFFLCPSYDTLIRPPLPGKT		-----	TTSQVYR	:	340				
BdGA20x6	:	-HPDALIVNIGDLFQAWSNNRYKSVEHKV	-VA	-N-AKAERFSVAYFLCPSYDAPV	-GTC	-----	GEPSPYR	:	320				
BdGA20x7	:	-DADSSFFINVGDVQLVLTNGRFRSVKHRV	-VV	-N-SERPRSMIIFGGPPGERL	-APLRELL	----	GDD	----	GGRSRYR	:	332		
BdGA20x8a	:	-DPDSFFNVVDGDLQVLTNGRFRSVKHRVLVAPERGGKASRLSVIYFGGPAPAQRI	-APLPELM	-----	REGERSLYR	:	324						
BdGA20x8b	:	-DPDSLFFNVVDGDLQVLTNGRFRSVKHRV	-VAPEG	-AQASRLSVIYFGGPAPAQRI	-APLPELM	-----	REGEQSLYR	:	310				
BdGA20x9	:	-IPNALIVNIGDLFQAWSNNRYKSVEHKV	-VT	-N-ATTERYSVAYFLCPSYDSPI	-GAC	-----	GEPSPYR	:	327				
HvGA20x1	:	-DSSAYFNVVDGDLQALTNGRLVSVIRHRV	-IA	-S-ACRPRLSTIYFAAPPLHARI	-SALPEMV	-----	TASSPRRYR	:	337				
HvGA20x10	:	-DQTSFFNVVDGDLQVLTNGRFRSVRHRV	-MV	-N-NIQPRVSVIFFGGPPPRETL	-APLPQLV	----	GE	----	GGRSRYK	:	321		
HvGA20x2	:	-DPAAFFINVGDLLQALTNGKLVSVIRHRV	-MA	-S-SSKPRLSAIYFAAPALHERI	-SAFPETV	-----	TAAAPRRYR	:	313				
HvGA20x3	:	-DRDALFVNVDGDLQVLTNGRFRSVKHRV	-VA	-N-SLKSRSVMIYFGGPALTQRI	-APLPQLL	----	RE	----	GEQSLYK	:	300		
HvGA20x4	:	-NRDAFFNVVDGDLQVLTNGRLRSVRHRV	-VA	-GNGLKSRSVMIYFAGPPLAQRI	-APLQQLL	----	AGT	----	QSLPLYR	:	303		
HvGA20x6	:	-HPDALIVNVGDLFQAWSNNRYKSVEHKV	-VA	-N-YKAERFSVAYFLCPSYDSPV	-GTC	-----	SESPYR	:	316				
HvGA20x7	:	-DPDAFFNVVDALQVLTNGRFSVSVKHRV	-VV	-S-SERPRVSMIIFGGPPMGERL	-APLRQLL	----	GD	----	GGRSKYR	:	315		
HvGA20x8	:	-DTSDFVNVDGDLQVLTNGRFRSVKHRV	-VAPE	-GQPRLSVIYFGGPAPTQRI	-APLPELM	-----	REGEQSLYR	:	302				
HvGA20x9	:	-IPNALIVNIGDLFQAWSNNRYKSVEHKV	-IT	-N-ATTERYSVAYFLCPSYDSPI	-GAC	-----	GEPSPYR	:	318				
OsGA20x1	:	-DPSAIFNVVDGDLQALTNGRLSVIRHRV	-IA	-T-ACRPRLSTIYFASPPLHARI	-SALPETI	----	TA	----	SSPRRYR	:	343		
OsGA20x10	:	-DRKSFFNVVDGDLQVLTNGRFRSVRHRV	-MV	-S-SPRPRVSVIFFAGPPPRERL	-APLPWL	----	AED	----	GGRRRYR	:	319		
OsGA20x2	:	-DPSAFFNVVDGDLQALTNGRLVSVIRHRV	-VV	-G-TGKPRLSIYFAAPPLHARI	-SALPETV	-----	AAGAPRRYR	:	328				
OsGA20x3	:	-DRDSFFNVVDGDLQVLTNGRFSKSVKHRV	-VA	-N-SLKSRSVSIYFGGPPLAQRI	-APLPQLL	-----	GEGEQSLYK	:	300				
OsGA20x4	:	-DPASFLVIVGDSLQVMTNGRMRSVRHRV	-VA	-N-KLKSRSVMIYFGGPPLEQRI	-APLRQLLVAGVGNGEEEEQSRYE	:	318						
OsGA20x5	:	-SPSTLIVNVGDLQAWSNDVYKSVEHRV	-MA	-N-ATLERFSMAFFLCPSYHTLI	-IPSSSHVH	-----	DDDAHRY	:	311				
OsGA20x6	:	-RPDALVNVIGDLFQAWSNNRYKSVEHKV	-VA	-N-AKTDRLSVAYFLCPSYDSL	-GTC	-----	GEPSPYR	:	324				
OsGA20x7	:	GDGDSFFNVVDGDLQVLTNGRFRSVKHRV	-VV	-N-SEKSRVSMVYFGGPPGERL	-APLPALL	----	GD	----	GGRSRYR	:	309		
OsGA20x8	:	-DPDSFFNVVDGDLQVLTNGRFRSVKHRV	-LA	-PEGEESRLSVIYFGGPAASQRI	-APLEQVM	----	RE	----	GEQSLYR	:	314		
OsGA20x9	:	-IPGALIVNIGDLFQAWSNNRYKSVEHRV	-MT	-N-ATTERYSVAYFLCPSYDSPI	-GTC	-----	REPSYK	:	330				
TaGA20x-A1	:	-DSSAYFNVVDGDLQALTNGRLVSVRHRV	-IA	-S-ACRPRLSTIYFAAPPLHARI	-SALPEMV	-----	TADSPRRYR	:	335				
TaGA20x-A10	:	-DQTSFFNVVDGDLQVLTNGRFRSVRHRV	-MV	-N-SVRPRVSVIFFGGPPPRETL	-APLPQLV	-----	GEGGRSRYR	:	325				
TaGA20x-A11	:	-RADALIVNVGDLFQAWSNNRYKSVEHKV	-VA	-N-SKAERFSIAYFMCPLSDSPV	-GT	-----	GEPSYK	:	322				
TaGA20x-A3	:	-DRDAFFNVVDGDLQVLTNGRFSKSVKHRV	-VA	-N-SLKSRSVMIYFGGPAMTQRI	-APLPQLL	----	GA	----	GEQSLYK	:	300		
TaGA20x-A4	:	-NRDAFFNVVDGDLQVLTNGRLRSVRHRV	-VA	-GNGLKSRSVMIYFGGPPLAQRI	-APLPQLL	----	AGTQSLPLYR	:	304				
TaGA20x-A6	:	-RPDALIVNIGDLFQAWSNNRYKSVEHKV	-VA	-N-AKAERLSVAYFLCPSYDSL	-GTC	-----	GEPSPYR	:	321				
TaGA20x-A7	:	-DPDAFFNVVDALQVLTNGRFRSVRHRV	-VV	-S-SERPRVSMIIFGGPPMGERL	-APLRQLL	----	GD	----	GGRSRYR	:	314		
TaGA20x-A8	:	-DPDSLFFNVVDGDLQVLTNGRFSVSVKHRV	-VAPAE	-GQQSRLSVIYFGGPAPAQRI	-APLPELM	-----	REGERSLYR	:	299				
TaGA20x-A9	:	-IPGALIVNIGDLFQAWSNNRYKSVEHKV	-VT	-N-ATTERYSVAYFLCPSYDSPI	-GAC	-----	EESPYR	:	318				
TaGA20x-B1	:	-DSSAYFNVVDGDLQALTNGRLVSVIRHRV	-IT	-S-ACRPRLSTIYFAAPPLHARI	-SALPEMV	-----	TAGSPRRYR	:	335				
TaGA20x-B10	:	-DQTSFFNVVDGDLQVLTNGRFRSVRHRV	-MV	-N-SVRPRVSVIFFGGPAPRETL	-APLRQLV	-----	GEGGRSRYR	:	323				
TaGA20x-B11	:	-HADALIVNVGDLFQAWSNNRYKSVEHKV	-VA	-N-SKAERFSVAYFLCPSDSSV	-GTC	-----	GEPSYK	:	321				
TaGA20x-B12	:	-HAHALMVNVGDLFQAWSNNRYKSVEHRV	-VA	-N-SKAERFSVAYFMCPPCDSPV	-GTC	-----	AEPSYK	:	316				
TaGA20x-B13	:	-HADALIVNVGDLFQAWSNNRYKSVEHKV	-LA	-N-SKAERFSIAYFMCPSHDSLI	-GTC	-----	GGPSPYR	:	309				
TaGA20x-B2	:	-DPAAFFINVGDLLQALTNGKLVSVIRHRV	-MA	-S-TSKPRLSAIYFAAPALHECI	-SALPETV	-----	TAAAPRRYR	:	310				
TaGA20x-B3	:	-DRDAFFNVVDGDLQVLTNGRFSKSVKHRV	-VA	-N-SLKSRSVMIYFGGPAMTQRI	-APLPQLL	-----	GAGEQSLYK	:	300				
TaGA20x-B4	:	-NRDAFFNVVDGDLQVLTNGRLRSVRHRV	-VA	-GNGLKSRSVMIYFGGPPLAQRI	-APLPQLL	-----	AGTPLYR	:	301				
TaGA20x-B6	:	-RPDALIVNIGDLFQAWSNNRYKSVEHKV	-VA	-N-PKAERLSVAYFLCPSYDSPV	-STC	-----	GEPSAYR	:	321				
TaGA20x-B7	:	-DADSSFFNVVDGDLQVLTNGRFRSVRHRV	-VV	-S-SERPRVSTIFFGGPPFGERL	-GPRRQL	----	GDGGRSRYR	:	315				
TaGA20x-D1	:	-DSSAYFINVGDLLQALTNGRLVSVRHRV	-IA	-S-ACRPRLSTIYFAAPPLHARI	-SALPEMV	-----	TAGSPRRYR	:	335				
TaGA20x-D10	:	-DHTSFFNVVDGDLQVLTNGRFRSVRHRV	-MV	-N-SARPRVSVIFFGGPPPRETL	-APLPQLV	-----	GEGGRSRYR	:	322				
TaGA20x-D11	:	-HADALIVNVGDLFQAWSNNRYKSVEHKV	-VA	-N-SKAERFSVAYFLCPSDSSV	-GTC	-----	GEPSYK	:	322				
TaGA20x-D2	:	-DPAAFFINVGDLLQALTNGKLVSVIRHRV	-MA	-S-TSKPRLSAIYFAAPALHESI	-SALPETV	-----	TADAPRRYR	:	311				
TaGA20x-D3	:	-DRDAFFNVVDGDLQVLTNGRFSKSVKHRV	-VA	-N-SLKSRSVMIYFGGPAMTQRI	-APLPQLL	-----	GAGEQSLYK	:	300				
TaGA20x-D4	:	-NRDAFFNVVDGDLQVLTNGRLRSVRHRV	-VA	-GNGLKSRSVMIYFGGPPLAQRI	-APLPQLL	----	AGTQSLPLYR	:	304				
TaGA20x-D6	:	-RSDALIVNIGDLFQAWSNNRYKSVEHKV	-VA	-N-AKAERLSVAYFLCPSYDSPV	-GTC	-----	GEPSPYR	:	318				
TaGA20x-D7	:	-DPDSFFNVVDALQVLTNGRFRSVRHRV	-VV	-S-SERPRVSMIIFGGPPFGQL	-APLRQLL	----	GD	----	GGRSRYR	:	329		
TaGA20x-D8	:	-DPDSLFFNVVDGDLRLVLTNGRFSVSVKHRV	-VAP	-AEGQQSRLSVIYFGGPAPTQRI	-APLPELM	----	RE	----	GEQSLYR	:	300		
TaGA20x-D9	:	-IPGALIVNIGDLFQAWSNNRYKSVEHKV	-VT	-N-ATTERYSVAYFLCPSYDSPI	-GAC	-----	EESPYR	:	318				
OsGA30x2	:	-VAGAFVNVVDLFIHILTNGRFSVYHRA	-VV	-N-RDRDRVSLGYFLGPPDAEV	-APLPEAV	----	P-A	----	GRSPAYR	:	326		

		*	500	*	520	*	540	*		
AtGA20x1	:	EFTWSEY	--KNSTYNSRLSDNRLQQFERK	----	----	----	----	TIKNLLN	----	: 329
AtGA20x2	:	EFTWSQY	--KSSAYKSKLGDYRLGLFEKQ	----	----	----	----	PLLNHHKTLV	----	: 341
AtGA20x3	:	EFTWSQY	--KLSAYKTKLGDYRLGLFEKR	----	----	----	----	PPFSLSNV	----	: 335
AtGA20x4	:	TFTWGEY	--KKRAYSLRLSDNRLDMFRTCKD	----	----	----	----	----	----	: 321
AtGA20x6	:	SFTWGDY	--KKATYSLRLDVPRLFEFFKTL	----	----	----	----	----	----	: 329
AtGA20x7	:	RFSFREYK	--EQSEHDVKETGDKVGLSRFLI	----	----	----	----	----	----	: 336
AtGA20x8	:	NFSFREFR	--QQVQEDVKKFGFKVGLPRFL	----	----	----	----	NHVV	----	: 338
BdGA20x1	:	SFTWAEY	--KTTMYSRLSLSHSRLDLFCVH	----	----	----	----	DDDDNSSDVSKEK	----	: 380
BdGA20x10	:	EFTWREY	--KASAYRTKLAENRLCHFETTS	----	----	----	----	----	----	: 349
BdGA20x2	:	PFTWAEY	--KKNMYTLLSLSHNRLLEYNAV	----	----	----	----	NADAGEARPRSGIAS	----	: 343
BdGA20x3	:	EFTWSEY	--KKAAYKSRLGDNRLAQFQK	----	----	----	----	----	----	: 326
BdGA20x4	:	EFTWGEY	--KKAAYRSRLGDNRLAPFQMT	----	----	----	----	LVELQAHADAAGLHRS	----	: 354
BdGA20x5	:	NFTFGEYR	--SQVREDVRLTGRKVGLPRFR	----	----	----	----	RHVSPSPASLTHQLS	----	: 383
BdGA20x6	:	SFTFGEYR	--RKVQDDVKRTGKKIGLPNFL	----	----	----	----	KHPPIVDGLK	----	: 358
BdGA20x7	:	EFTWKEY	--KSTGCRGRLAEDRLCLFEN	----	----	----	----	----	----	: 358
BdGA20x8a	:	DFTWGEY	--KAAAYKTRLGDHRLGPFVQV	----	----	----	----	LLPPAAAKA	----	: 360
BdGA20x8b	:	DFTWGEY	--KAAAYKTRLGDNRLGPYELRNVDNPTALITASKEPTAADHCCSNSSSSSAACVVVQPPHVAQVH	----	----	----	----	----	----	: 383
BdGA20x9	:	TFTFGEYR	--RRVQEDVKKTGKKVGLPGFLL	----	----	----	----	----	----	: 356
HvGA20x1	:	SFTWAEY	--KTAMYSRLSLSHSRLDLF--H	----	----	----	----	VDDDESGNGSKGK	----	: 375
HvGA20x10	:	EFTWCEY	--KASAYGKLAANRLCHFETTN	----	----	----	----	----	----	: 349
HvGA20x2	:	PFTWAEY	--KKTMYTLRLSHNRLDLFAVV	----	----	----	----	GDSGEDKPRI	----	: 350
HvGA20x3	:	DFTWGEY	--KKAAYNSRLGDNRLAHFHR	----	----	----	----	----	----	: 326
HvGA20x4	:	DFTWGEY	--KKAAYRSRLGDNRLAPFETP	----	----	----	----	LVAMPHAAHRS	----	: 342
HvGA20x6	:	PFTFGEYR	--RKVQDDVKRTGKKIGLPNFL	----	----	----	----	KHSPVHGLSS	----	: 354
HvGA20x7	:	EFTWKEY	--KSSTHKGRLATDRCLSFEN	----	----	----	----	----	----	: 341
HvGA20x8	:	DFTWAEY	--KKAAYKSRLGDHRLGPFELP	----	----	----	----	AAATAQESTTKADHYCCSNAAVQAPAAAPHVARVH	----	: 364
HvGA20x9	:	TFTFGEYR	--RRVQEDVKKTGKKIGLPNFLL	----	----	----	----	----	----	: 347
OSGA20x1	:	SFTWAEY	--KTTMYSRLSLSHSRLDLFKID	----	----	----	----	DDSDNASEGKA	----	: 382
OSGA20x10	:	EFTWREY	--KASAYRTKLAENRLCHFETEAD	----	----	----	----	----	----	: 348
OSGA20x2	:	AFTWAEY	--KRTMYTLRLSHNRLDLFHAG	----	----	----	----	DGDGDAGVGDDDDHE	----	: 370
OSGA20x3	:	EFTWDEY	--KKAAYKSRLGDNRLAQFEKK	----	----	----	----	----	----	: 327
OSGA20x4	:	EFTWGEY	--KKAAYLSRLSDNRLAPFHRQ	----	----	----	----	PPPVANPLA	----	: 354
OSGA20x5	:	SFTFGEYR	--KQIMEDVRSTGRKIGLHFRFTR	----	----	----	----	----	----	: 341
OSGA20x6	:	AFTFGEYR	--KKVQEDVRTTGKKIGLPNFF	----	----	----	----	KHSSVQ	----	: 358
OSGA20x7	:	EFTWKEY	--KGSQCKGRLADDRLCRFEN	----	----	----	----	----	----	: 335
OSGA20x8	:	EFTWGEY	--KKAAYKTRLGDNRLGPYELQ	----	----	----	----	HAAANDEAATKK	----	: 353
OSGA20x9	:	AFTFGEYR	--RRVQEDVKKTGKKIGTGLSNFLV	----	----	----	----	----	----	: 359
TaGA20x-A1	:	SFTWAEY	--KTAMYSRLSLSHSRLDLFHVD	----	----	----	----	DDESGNGSKGK	----	: 373
TaGA20x-A10	:	EFTWREY	--KASAYRTKLAANRLCHFETTS	----	----	----	----	----	----	: 353
TaGA20x-A11	:	PFTFEEYR	--RSVRDDVERTGKKIGLPNFL	----	----	----	----	KRSTVHGLDDDDIMDLSS	----	: 367
TaGA20x-A3	:	DFTWGEY	--KKAAYNSRLGDNRLAHFHR	----	----	----	----	----	----	: 326
TaGA20x-A4	:	DFTWGEY	--KKAAYRSRLGDNRLAPFEAP	----	----	----	----	PVATPHADRHRS	----	: 343
TaGA20x-A6	:	PFTFGEYR	--RKVQDDVKRTGKKIGLPNFL	----	----	----	----	KQSPVDAMNHSCT	----	: 363
TaGA20x-A7	:	DFTWKEY	--KSSTHKGRLAADRLCSFEN	----	----	----	----	----	----	: 340
TaGA20x-A8	:	DFTWAEY	--KKAAYKSRLGDHRLGPFELP	----	----	----	----	AAKETNSSDHHCCSNAVQPPARAPPHVATVY	----	: 357
TaGA20x-A9	:	TFTFGEYR	--RRVQEDVKMGKKIGLPNFLL	----	----	----	----	----	----	: 347
TaGA20x-B1	:	SFTWAEY	--KTAMYSRLSLSHSRLDLFHVD	----	----	----	----	DDESGNGSKGK	----	: 373
TaGA20x-B10	:	EFTWREY	--KASAYRTKLAANRLGHFETTS	----	----	----	----	----	----	: 351
TaGA20x-B11	:	PFTFGEYR	--RSVQDDVKRTGKKIGLPNFL	----	----	----	----	KRSTVHGLDDDDTMDLSS	----	: 366
TaGA20x-B12	:	PFTFGEYR	--RKVQEDVRTTGKKIGLNSNFL	----	----	----	----	KGSTFDGLAE	----	: 354
TaGA20x-B13	:	PFTFEEYR	--RKVQDDVRTTGKKIGLPNFL	----	----	----	----	KRSTIS	----	: 343
TaGA20x-B2	:	PFTWAEY	--KKTMYTLRLSHNRLDLFKVI	----	----	----	----	LVGDVGEAGAGEDRSRI	----	: 353
TaGA20x-B3	:	DFTWGEY	--KKAAYNSRLGDNRLAQFHR	----	----	----	----	----	----	: 326
TaGA20x-B4	:	EFTWGEY	--KKAAYRSRLGDNRLAPFETP	----	----	----	----	LVAMAHADHRS	----	: 340
TaGA20x-B6	:	PFTFGEYR	--RKVQDDVKRTGKKIGLPNFL	----	----	----	----	KQSPVDGMNHTLCS	----	: 363
TaGA20x-B7	:	EFTWKEY	--KSSTHKGRLATDRCLSFEN	----	----	----	----	----	----	: 341
TaGA20x-D1	:	SFTWAEY	--KTAMYSRLSLSHSRLDLFHVD	----	----	----	----	DDESGNGSKGK	----	: 373
TaGA20x-D10	:	EFTWREY	--KASAYRTKLAANRLCHFETTS	----	----	----	----	----	----	: 350
TaGA20x-D11	:	PFTFGEYR	--RSVHDDVERTGKKIGLPNFL	----	----	----	----	KRSTVHGLDDDDTMDLSS	----	: 367
TaGA20x-D2	:	PFTWAEY	--KKTMYTLRLSHNRLDLFKVV	----	----	----	----	GEGGGDSGEDKSRI	----	: 352
TaGA20x-D3	:	DFTWGEY	--KKAAYNSRLGDNRLAQFHR	----	----	----	----	----	----	: 326
TaGA20x-D4	:	DFTWGEY	--KKAAYRSRLGDNRLAPFEAP	----	----	----	----	PVATPDADRHRS	----	: 343
TaGA20x-D6	:	PFTFGEYR	--RKVQDDVKRTGKKIGLPNFL	----	----	----	----	KQSPVDAMNHGLCF	----	: 360
TaGA20x-D7	:	EFTWKEY	--KSSTHKGRLATDRCLSFEN	----	----	----	----	----	----	: 355
TaGA20x-D8	:	DFTWAEY	--KKAAYKSRLGDNRLGPFELF	----	----	----	----	PSAAQDCSNAVQPPAPAPPHVAPVH	----	: 353
TaGA20x-D9	:	TFTFGEYR	--RRVQEDVKKTGKKIGLPNFLL	----	----	----	----	----	----	: 347
OSGA30x2	:	AVTWPEYMAVRKKAFAATGGSALKMVSTDA	----	----	----	----	----	AAAEHDDVAAAADVHA	----	: 373

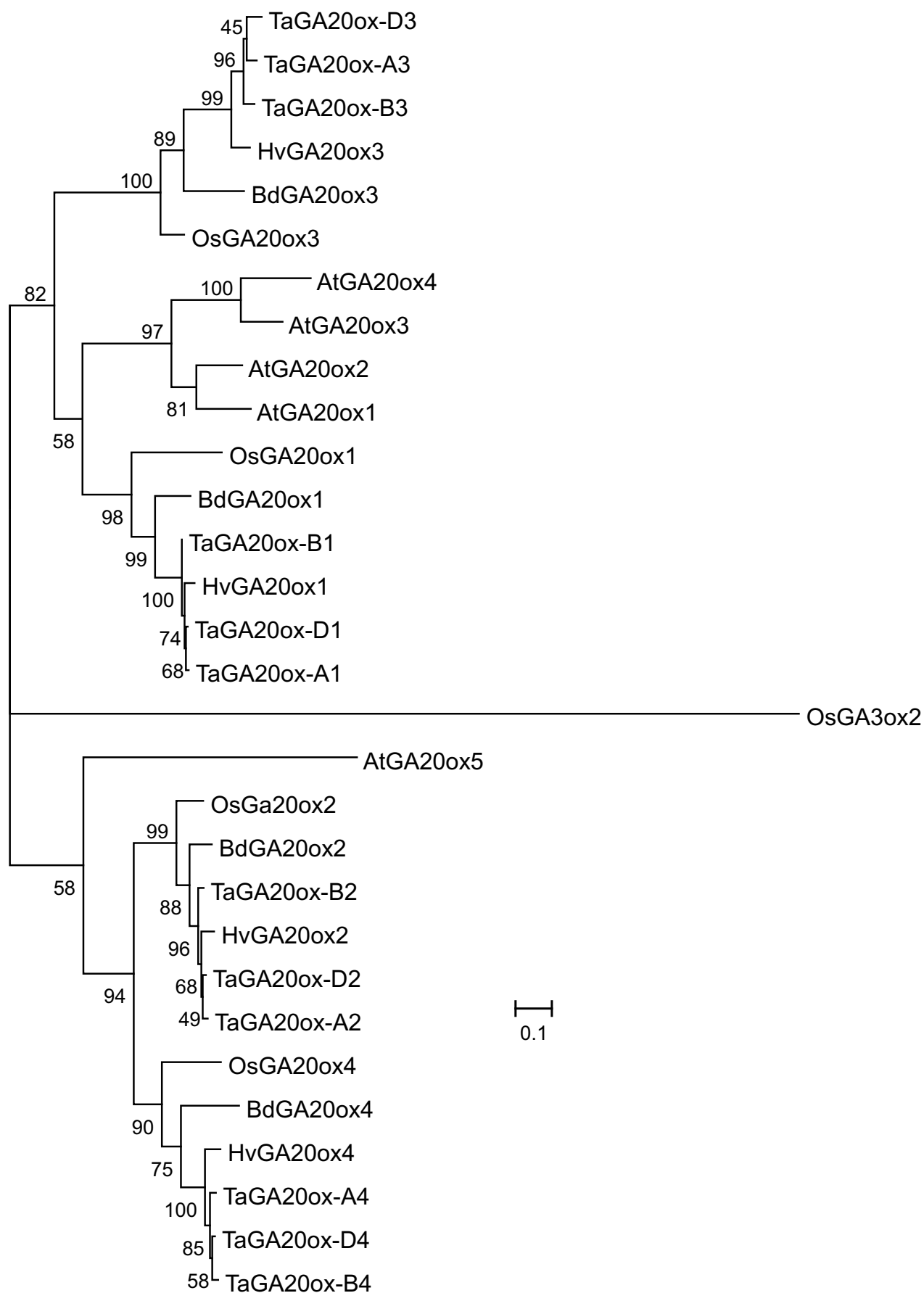


Figure S11. PHYML tree of GA20ox proteins sequences from Arabidopsis, rice, Brachypodium, wheat and barley using OsGA3ox2 as outgroup. Numbers show bootstrap support; the scale bar shows substitutions per site. Non-aligned residues were trimmed from the alignment prior to tree generation using PhyML within TOPALi as reported in Materials and Methods.

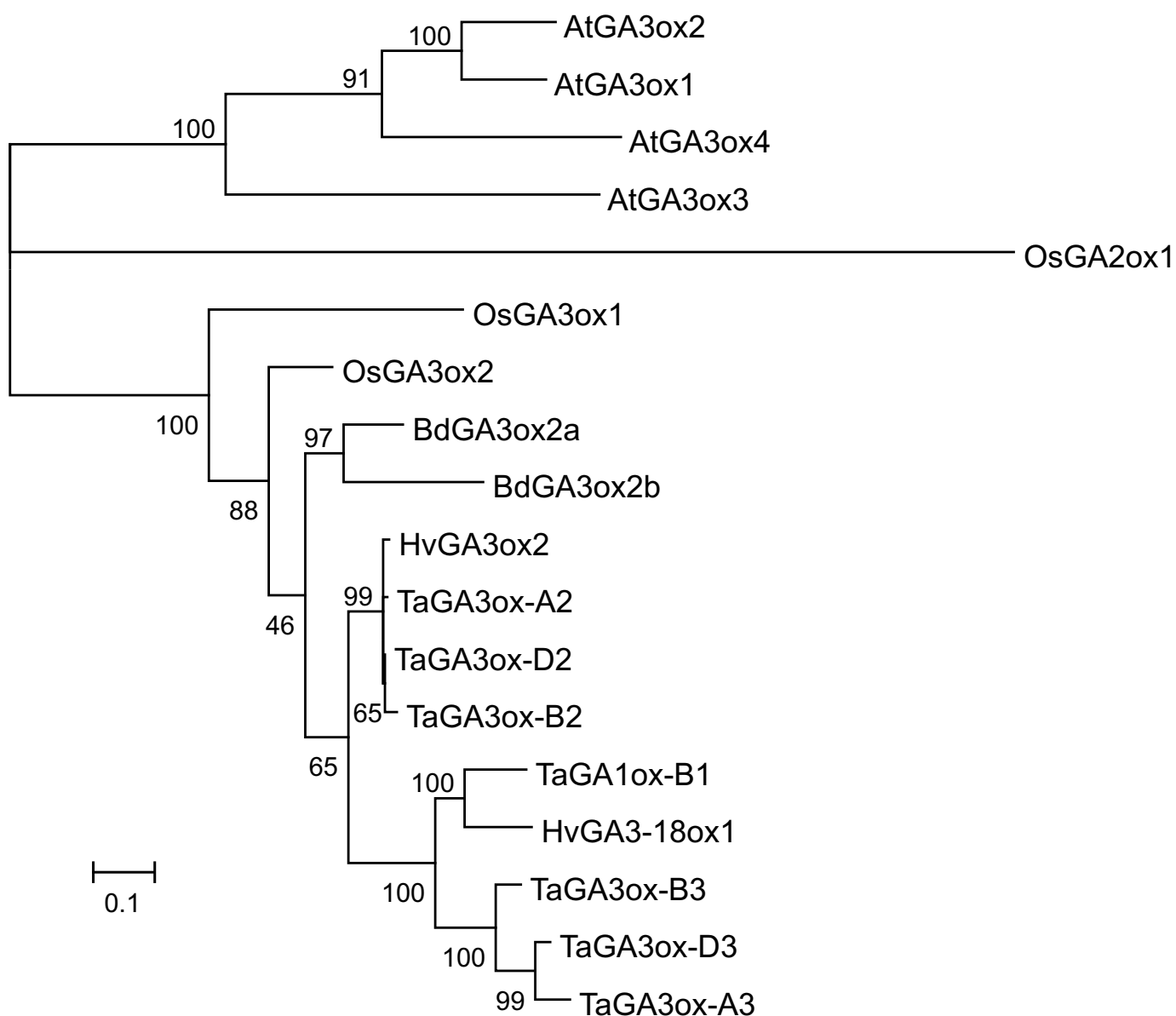


Figure S12. PHYML tree of GA3ox proteins sequences from Arabidopsis, rice, Brachypodium, wheat and barley using OsGA2ox1 as outgroup. Numbers show bootstrap support; the scale bar shows substitutions per site. Non-aligned residues were trimmed from the alignment prior to tree generation using PhyML within TOPALi as reported in Materials and Methods.

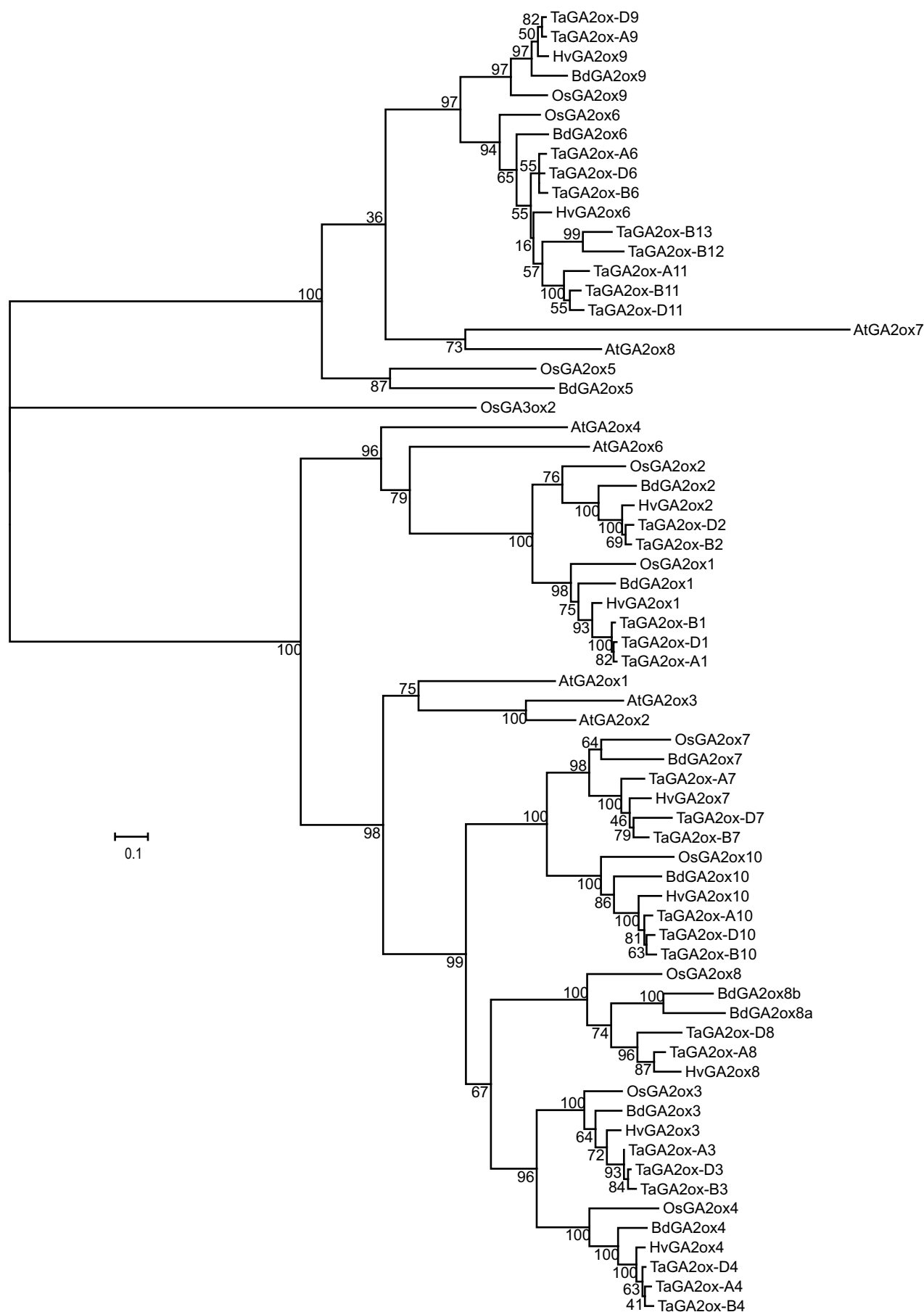


Figure S13. PHYML tree of GA2ox proteins sequences from Arabidopsis, rice, *Brachypodium*, wheat and barley using OsGA3ox2 as outgroup. Numbers show bootstrap support; the scale bar shows substitutions per site. Non-aligned residues were trimmed from the alignment prior to tree generation using PhyML within TOPALi as reported in Materials and Methods.