

AmTr_v1.0_scaffold00148.15	-----	-----	MAV	AVHK	-----	-----
AmTr_v1.0_scaffold00056.60	-----	-----	MAV	TACK	-----	-----
AmTr_v1.0_scaffold00155.45	-----	-----	MAL	VLQK	-----	-----
Ara_thaPHABULOSA	-----	-----	MM	MVHS	MS	RDMMNR
Ara_thaATHB15	-----	-----	MAM	SCKD	-----	-----
Ara-thaPHAVOLUTA	-----	-----	MM	AHHS	MDD	RD
Ara_thaATHB8	-----	-----	MG	-----	-----	G
Ara_thaREVOLUTA	-----	-----	MEM	AVAN	H	RESSSD
Vit_vinHOX32-like	-----	-----	MAL	SMHK	-----	-----
The_cacXP_007022870.1	-----	-----	-----	-----	-----	-----
Ory_satHOX32	-----	-----	MAA	AMVA	AVHGVG	R QDRSSP
Pru_perppa001343mg	-----	-----	MAL	VMN	-----	RD SP
Bra_disHOX32-like	-----	-----	MAG	AMVAGL	LHG	RDRDRDRSSP
Pop_triPHABULOSA	-----	-----	MAL	SIHS	-----	-----
Pop_triPHABULOSAb	-----	-----	MAL	SMHS	-----	-----
Fra_vesHOX32-like	-----	-----	MAL	VMHK	-----	E
Gly_maxATHB-14-like	-----	-----	MAL	SMHK	-----	-----
Gly_maxREVOLUTA-like	-----	-----	MAM	VVAQ	H	RESSSS
Gly_maxREVOLUTA-likeb	-----	-----	MAM	AVAQ	H	RESSSS
Pru_perREV_IFL1	-----	-----	MAM	AVAH	H	RESSSG
Ory_satHOX33	-----	-----	MAAAAV	GGRG	ER	LSSSSP
Sol_tubATHB-14-like	-----	-----	MAL	CLQR	-----	GGGGE
The_cacXP_007022872.1	-----	-----	MAL	SMHK	-----	D
Ory_satHOX33-like	-----	-----	MAA	AA	-----	-----
Sol_lycREVOLUTA-like	-----	-----	MAM	VAQQ	H	RE SSS
Sol_lycHOX32-like	-----	-----	MAL	CLQR	-----	GEGE
Gly_maxATHB-14-likeb	-----	-----	MAL	CMQ	-----	RD SA
Pop_triXP_006378973.1	-----	-----	MAM	AVAP	QH	RESSSG
Ory_satACA64837.1	-----	-----	MAAAAV	GGRG	ER	LSSSSP
Vit_vin013992	-----	-----	MAM	AIAQ	QH	RESSSS
Ory_satOsJ_11861	-----	-----	-----	-----	-----	-----
Sol_tubREVOLUTA-like	-----	-----	MAM	VAQQ	H	RESSSG
Gly_maxATHB-14-likec	-----	-----	MAL	CMQS	QQ	RD SA
The_cacXP_007024277.1	-----	-----	MAM	SCKD	-----	-----
Vit_vinATHB-15-like	-----	-----	MAM	SCKD	-----	-----
Ric_comXP_002515977.1	-----	-----	MAM	SCKD	-----	-----
The_cacXP_007016751.1	-----	-----	MAM	AVAQ	H	RESSSG
Sol_tubHOX32-like	-----	-----	MAL	CLQR	-----	GEGE
Sol_lycATHB-14-like	-----	-----	-----	-----	-----	-----
Sol_tubATHB-14-like_X1	-----	-----	-----	-----	-----	-----
Med_truATHB-14	-----	-----	MAL	SMH	-----	-----
Zea_mayNP_001142394.1	-----	-----	MAA	VASR	-----	ERLS
Vit_vinREVOLUTA	-----	-----	MAM	AIAQ	QH	RESSSS
Ory_braHOX32-like	-----	-----	MEV	PAYQ	-----	-----
Ric_comXP_002529946.1	-----	-----	MAM	AMVQ	H	RETSSG
Tha_cacXP_007016749.1	-----	-----	MAM	AVAQ	H	RESSSG
Fra_vesREVOLUTA-like	-----	-----	MAM	AVAH	HQH	RESSSG
Zea_mayNP_001146215.1	-----	-----	MAS	SRG	-----	RLRLSP
The_cacXP_007012152.1	MLIAAEGTGK	TKAKATKNLE	WIFEVSPVIR	SCP	KVPEENE	VMMAVTSSCK
Pru_perppa001386mg	-----	-----	MMA	VTSA	-----	CKD
Pop_triAAX19057.1	-----	-----	-----	-----	-----	-----
Pop_triXP_002309538.2	-----	-----	-----	-----	-----	-----
Fra_vesATHB-8-like	-----	-----	MAV	TSSS	SC	KE LSG
Pop_triXP_002324794.1	-----	-----	-----	-----	-----	-----
Vit_vin009744	-----	-----	-----	-----	-----	-----
Gly_maxATHB-8-like	-----	-----	MMT	VSSA	C	KD
Sol_lycATHB-15-like	-----	-----	MMA	VTSS	-----	-----
Gly_maxATHB-8-likeb	-----	-----	MMA	VSSA	C	KD
Med_truXP_003603630.1	-----	-----	MAV	SSGC	-----	KD

AmTr_v1.0_scaffold00148.15	-DSSKHM-DS	SKYVRYTAEQ	VEALERVYNE	CPKPSSLRRQ	QLIRECPILC
AmTr_v1.0_scaffold00056.60	-EGKPGM-DP	GKYVRYTPEQ	VEALERLYHE	CPKPSSIIRQ	QLIRECPILS
AmTr_v1.0_scaffold00155.45	-DSNKHM-DT	SKYVRYTPEQ	VEALERVYSE	CPKPSSLRRQ	QLIRECPILS
Ara_thaPHABULOSA	ESPDKGL-DS	GKYVRYTPEQ	VEALERVYTE	CPKPSSLRRQ	QLIRECPILS
Ara_thaATHB15	-GKLGCL-DN	GKYVRYTPEQ	VEALERLYHD	CPKPSSIIRQ	QLIRECPILS
Ara-thaPHAVOLUTA	-SPDKGF-DS	GKYVRYTPEQ	VEALERVYAE	CPKPSSLRRQ	QLIRECPILC
Ara_thaATHB8	GSNNSHNMDN	GKYVRYTPEQ	VEALERLYND	CPKPSSMRRQ	QLIRECPILS
Ara_thaREVOLUTA	-SMNRHLDSS	GKYVRYTAEQ	VEALERVYAE	CPKPSSLRRQ	QLIRECSILA
Vit_vinHOX32-like	-ESKQOM-DS	SKYVRYTPEQ	VEALERVYSE	CPKPSSMRRQ	QLIRECPILS
The_cacXP_007022870.1	-----M-DS	SKYVRYTPEQ	VEALERVYSE	CPKPSSLRRQ	QLIRECPILS
Ory_sathOX32	GGGGAPQVDT	GKYVRYTPEQ	VEALERVYGE	CPKPSSLRRQ	QLIRECPILS
Pru_perppa001343mg	GSSSKQOM-DS	SKYVRYTPEQ	VEALERVYSE	CPKPSSLRRQ	QLIRECPILS
Bra_dishOX32-like	GGGGAPQVDT	GKYVRYTPEQ	VDALERVYSE	CPKPSSLRRQ	QLIRECPILS
Pop_triPHABULOSA	--KDKHM-DS	SKYVRYTPEQ	VEALERVYTE	CPKPSSLRRQ	QLIRECPILS
Pop_triPHABULOSAb	--KDKQM-DS	SKYVRYTPEQ	VEALERVYTE	CPKPSSLRRQ	QLIRECPILC
Fra_vesHOX32-like	KHNNMQM-DS	SKYVRYTPEQ	VEALERVYSE	CPKPSSLRRQ	QLIRECPILS
Gly_maxATHB-14-like	DSANNQM-DS	SKYVRYTPEQ	VEALERVYAE	CPKPSSLRRQ	QLIRECPILS
Gly_maxREVOLUTA-like	GSIDKHL-DS	GKYVRYTAEQ	VEALERVYAE	CPKPSSLRRQ	QLIRECPILS
Gly_maxREVOLUTA-likeb	GSIDKHL-DS	GKYVRYTAEQ	VEALERVYAE	CPKPSSLRRQ	QLIRECPILS
Pru_perREV_IFL1	SSINKHL-DA	GKYVRYTSEQ	VEALERVYAE	CPKPSSLRRQ	QLIRECPILS
Ory_sathOX33	TAAAPQV-DA	GKYVRYTPEQ	VEALERVYTE	CPKPSSLRRQ	QLIRECPILS
Sol_tubATHB-14-like	SGSKNDM-DN	GKYVRYTPEQ	VEALERVYAE	CPKPTSLRRQ	QLIRECPILS
The_cacXP_007022872.1	SSNNKQM-DS	SKYVRYTPEQ	VEALERVYSE	CPKPSSLRRQ	QLIRECPILS
Ory_sathOX33-like	-----	-----YTPEQ	VEALERVYTE	CPKPSSLRRQ	QLIRECPILS
Sol_lycREVOLUTA-like	GSITKHLDS	GKYVRYTAEQ	VEALERVYAE	CPKPSSLRRQ	QLIRECHILS
Sol_lycHOX32-like	SGSKNDM-DN	GKYVRYTPEQ	VEALERVYAE	CPKPTSLRRQ	QLIRESPILS
Gly_maxATHB-14-likeb	SNKQQLM-DC	GKYVRYTSEQ	VEALERVYAE	CPKPSSSRRQ	QLIRECPILS
Pop_triXP_006378973.1	GSINKHLTDN	GKYVRYTSEQ	VEALERVYAE	CPKPSSLRRQ	QLIRECPILA
Ory_satACA64837.1	TAAAPQV-DA	GKYVRYTPEQ	VEALERVYTE	CPKPSSLRRQ	QLIRECPILS
Vit_vin013992	GSINKHL-DS	GKYVRYTAEQ	VEALERVYLE	CPKPSSLRRQ	QLIRECPILS
Ory_satOsJ_11861	-----	---MPYHP--	-----IT	C-----	TLIRECPILS
Sol_tubREVOLUTA-like	-SITKHLDS	GKYVRYTAEQ	VEALERVYAE	CPKPSSLRRQ	QLIRECHILS
Gly_maxATHB-14-likec	SNK-LLM-DC	GKYVRYTPEQ	VEALERVYVE	CPKPSSSRRQ	QLIRECPILA
The_cacXP_007024277.1	-GKLGNL-DN	GKYVRYTPEQ	VEALERLYHE	CPKPSSIIRQ	QLIRECPILS
Vit_vinATHB-15-like	---GGLMDN	GKYVRYTPEQ	VEALERLYHE	CPKPSSIIRQ	QLIRECPILS
Ric_comXP_002515977.1	GKQOPANL-DN	GKYVRYTPEQ	VEALERLYHE	CPKPSSIIRQ	QLIRECPILS
The_cacXP_007016751.1	SSINKHL-DA	GKYVRYTAEQ	VEALERVYAE	CPKPSSLRRQ	QLIRECPILS
Sol_tubHOX32-like	SGSKNDM-DN	GKYVRYTPEQ	VEALERVYAE	CPKPTSLRRQ	QLIRESPILS
Sol_lycATHB-14-like	-----M-DS	SKYVRYTPEQ	VEALERVYAE	CPKPTSLKRH	QLIRECSILS
Sol_tubATHB-14-like_X1	-----M-DS	SKYVRYTPEQ	VEALERVYAE	CPKPTSLKRH	QLIRECSILS
Med_truATHB-14	----KEM-DA	GKYVRYTPEQ	VEALERVYSE	CPKPSSLRRQ	QLIRECPILS
Zea_mayNP_001142394.1	PGAAPQV-DA	GKYVRYTPEQ	VEALERVYSE	CPKPSSLRRQ	HLIRDCPILR
Vit_vinREVOLUTA	GSINKHL-DS	GKYVRYTAEQ	VEALERVYLE	CPKPSSLRRQ	QLIRECPILS
Ory_braHOX32-like	-----	-----FHAMA	M-----	-----	-----CSWDA
Ric_comXP_002529946.1	-SINKHLTDS	GKYVRYTAEQ	VEALERVYSE	CPKPSSLRRQ	QLIRECPILS
Tha_cacXP_007016749.1	SSINKHL-DA	GKYVRYTAEQ	VEALERVYAE	CPKPSSLRRQ	QLIRECPILS
Fra_vesREVOLUTA-like	SSINKHLNDA	GKYVRYTSEQ	VEALERVYAE	CPKPSSLRRQ	QLIRDCPILS
Zea_mayNP_001146215.1	RAAAPQL-DA	GKYVRYTAEQ	VDALERLAYGE	CPKPSSLRRQ	QLIRDCAVLT
The_cacXP_007012152.1	EGNKIAM-DN	GKYVRYTPEQ	VDALERLYHE	CPKPSSMRRQ	QLIRECPILA
Pru_perppa001386mg	GGMKMQM-DN	GKYVRYTPEQ	VEALERLYHE	CPKPSSMRRQ	QLIRECPILS
Pop_triAAX19057.1	-----M-DN	GKYVRYTPEQ	VEALERLYHE	CPKPSSMRRQ	QLIRECPILS
Pop_triXP_002309538.2	-----M-DN	GKYVRYTPEQ	VEALERLYHE	CPKPSSMRRQ	QLIRECPILS
Fra_vesATHB-8-like	GGMKMQM-DN	GKYVRYTPEQ	VEALERLYHE	CPKPSSMRRQ	QLIRECPILS
Pop_triXP_002324794.1	-----M-DN	GKYVRYTPEQ	VEALERLYHE	CPKPTSTRRQ	QLIRECPILS
Vit_vin009744	----MAL-DN	GKYVRYTPEQ	VEALERLYHD	CPKPSSLRRQ	QLIRECPILS
Gly_maxATHB-8-like	-GSKVAL-DN	GKYVRYTPEQ	VEALERLYHE	CPKPSSLRRQ	QLIRECPILS
Sol_lycATHB-15-like	-CKDKFGMDS	GKYVRYTPEQ	VEALERLYHE	CPKPSSLRRQ	QLIRECPILS
Gly_maxATHB-8-likeb	-GSKVAL-DN	GKYVRYTPEQ	VEALERLYHE	CPKPSSLRRQ	QLIRECPILS
Med_truXP_003603630.1	-GSKIAM-DN	GKYVRYTPEQ	VEALERLYHE	CPKPTSLRRQ	QLIRECPILS

AmTr_v1.0_scaffold00148.15	NI EPKQIKVW	FQNRRCREKQ	RKEASRLQTV	NRKLTAMNKL	LMEENDRLQK
AmTr_v1.0_scaffold00056.60	NI EPKQIKVW	FQNRRCREKQ	RKEASRLQAV	NRKLTAMNKL	LMEENDRLQK
AmTr_v1.0_scaffold00155.45	NI EPKQIKVW	FQNRRCREKQ	RKEASRLQTV	NRKLTAMNKL	LMEENDRLQK
Ara_thaPHABULOSA	NI EPKQIKVW	FQNRRCREKQ	RKEAARLQTV	NRKLTAMNKL	LMEENDRLQK
Ara_thaATHB15	NI EPKQIKVW	FQNRRCREKQ	RKEASRLQAV	NRKLTAMNKL	LMEENDRLQK
Ara_thaPHAVOLUTA	NI EPKQIKVW	FQNRRCREKQ	RKEASRLQTV	NRKLTAMNKL	LMEENDRLQK
Ara_thaATHB8	NI EPKQIKVW	FQNRRCREKQ	RKEASRLQAV	NRKLTAMNKL	LMEENDRLQK
Ara_thaREVOLUTA	NI EPKQIKVW	FQNRRCREKQ	RKEASRLQSV	NRKLTAMNKL	LMEENDRLQK
Vit_vinHOX32-like	NI EPKQIKVW	FQNRRCREKQ	RKEASRLQTV	NRKLTAMNKL	LMEENDRLQK
The_cacXP_007022870.1	NI EPKQIKVW	FQNRRCREKQ	RKEASRLQTV	NRKLTAMNKL	LMEENDRLQK
Ory_satHOX32	NI EPKQIKVW	FQNRRCREKQ	RKEASRLQTV	NRKLTAMNKL	LMEENDRLQK
Pru_perppa001343mg	NI EPKQIKVW	FQNRRCREKQ	RKESSRLQTV	NRKLTAMNKL	LMEENDRLQK
Bra_disHOX32-like	NI EPKQIKVW	FQNRRCREKQ	RKEASRLQTV	NRKLTAMNKL	LMEENDRLQK
Pop_triPHABULOSA	NI EPKQIKVW	FQNRRCREKQ	RKEASRLQTV	NRKLTAMNKL	LMEENDRLQK
Pop_triPHABULOSAb	NI EPKQIKVW	FQNRRCREKQ	RKESSRLQTV	NRKLTAMNKL	LMEENDRLQK
Fra_vesHOX32-like	NI EPKQIKVW	FQNRRCREKQ	RKESSRLTTV	NRKLTAMNKL	LMEENDRLQK
Gly_maxATHB-14-like	NI EPKQIKVW	FQNRRCREKQ	RKEASRLQTV	NRKLTAMNKL	LMEENDRLQK
Gly_maxREVOLUTA-like	NI EPKQIKVW	FQNRRCREKQ	RKEASRLQTV	NRKLTAMNKL	LMEENDRLQK
Gly_maxREVOLUTA-likeb	NI EPKQIKVW	FQNRRCREKQ	RKEASRLQTV	NRKLTAMNKL	LMEENDRLQK
Pru_perREV_IFL1	NI EPKQIKVW	FQNRRCREKQ	RKESSRLQTV	NRKLTAMNKL	LMEENDRLQK
Ory_satHOX33	NI EPKQIKVW	FQNRRCREKQ	RKEASRLQTV	NRKLTAMNKL	LMEENDRLQK
Sol_tubATHB-14-like	NI EPKQIKVW	FQNRRCREKQ	RKEASRLQTV	NRKLTAMNKL	LMEENDRLQK
The_cacXP_007022872.1	NI EPKQIKVW	FQNRRCREKQ	RKEASRLQTV	NRKLTAMNKL	LMEENDRLQK
Ory_satHOX33-like	NI EPKQIKVW	FQNRRCREKQ	RKEASRLQTV	NRKLTAMNKL	LMEENDRLQK
Sol_lycREVOLUTA-like	NI EPKQIKVW	FQNRRCREKQ	RKESSRLQTV	NRKLTAMNKL	LMEENDRLQK
Sol_lycHOX32-like	NI EPKQIKVW	FQNRRCREKQ	RKEASRLQTV	NRKLTAMNKL	LMEENDRLQK
Gly_maxATHB-14-likeb	NI EPKQIKVW	FQNRRCREKQ	RKEASRLQTV	NRKLTAMNKL	LMEENDRLQK
Pop_triXP_006378973.1	NI EPKQIKVW	FQNRRCREKQ	RKESSRLQTV	NRKLTAMNKL	LMEENDRLQK
Ory_satACA64837.1	NI EPKQIKVW	FQNRRCREKQ	RKEASRLQTV	NRKLTAMNKL	LMEENDRLQK
Vit_vin013992	NI EPKQIKVW	FQNRRCREKQ	RKEASRLQTV	NRKLTAMNKL	LMEENDRLQK
Ory_satOsJ_11861	NI EPKQIKVW	FQNRRCREKQ	RKEASRLQTV	NRKLTAMNKL	LMEENDRLQK
Sol_tubREVOLUTA-like	NI EPKQIKVW	FQNRRCREKQ	RKESSRLQTV	NRKLTAMNKL	LMEENDRLQK
Gly_maxATHB-14-likec	NI EPKQIKVW	FQNRRCREKQ	RKEASRLQTV	NRKLTAMNKL	LMEENDRLQK
The_cacXP_007024277.1	NI EPKQIKVW	FQNRRCREKQ	RKEASRLQAV	NRKLTAMNKL	LMEENDRLQK
Vit_vinATHB-15-like	NI EPKQIKVW	FQNRRCREKQ	RKEASRLQAV	NRKLTAMNKL	LMEENDRLQK
Ric_comXP_002515977.1	NI EPKQIKVW	FQNRRCREKQ	RKEASRLQAV	NRKLTAMNKL	LMEENDRLQK
The_cacXP_007016751.1	NI EPKQIKVW	FQNRRCREKQ	RKEASRLQTV	NRKLTAMNKL	LMEENDRLQK
Sol_tubHOX32-like	NI EPKQIKVW	FQNRRCREKQ	RKEASRLQTV	NRKLTAMNKL	LMEENDRLQK
Sol_lycATHB-14-like	NI DPQIKVW	FQNRRCREKQ	RKEASHLQTV	NRKLTAMNKL	LMEENDRLQK
Sol_tubATHB-14-like_X1	NI DPQIKVW	FQNRRCREKQ	RKEASHLQTV	NRKLTAMNKL	LMEENDRLQK
Med_truATHB-14	NI EPKQIKVW	FQNR-----	-----	-----SFLHLL	VIV----VTK
Zea_mayNP_001142394.1	NI EPKQIKVW	FQNRRCREKQ	RKESSRLQTV	NRKLTAMNKL	LMEENDRLQK
Vit_vinREVOLUTA	NI EPKQIKVW	FQNRRCREKQ	RKEASRLQTV	NRKLTAMNKL	LMEENDRLQK
Ory_braHOX32-like	FYLTRLMLTW	DAICLCREKQ	RKEASRLQTV	NRKLTAMNKL	LMEENDRLQK
Ric_comXP_002529946.1	NI EPKQIKVW	FQNRRCREKQ	RKESSRLQTV	NRKLTAMNKL	LMEENDRLQK
Tha_cacXP_007016749.1	NI EPKQIKVW	FQNRRCREKQ	RKEASRLQTV	NRKLTAMNKL	LMEENDRLQK
Fra_vesREVOLUTA-like	NI EPKQIKVW	FQNRRCREKQ	RKESSRLQTV	NRKLTAMNKL	LMEENDRLQK
Zea_mayNP_001146215.1	NVEPRQIKVW	FQNRRCREKQ	RRESSRLQTV	NRKLTAMNKL	LMEENDRLQK
The_cacXP_007012152.1	NI EPKQIKVW	FQNRRCREKQ	RKEASRLQAV	NRKLTAMNKL	LMEENDRLQK
Pru_perppa001386mg	NI EPKQIKVW	FQNRRCREKQ	RKEASRLQTV	NRKLTAMNKL	LMEENDRLQK
Pop_triAAX19057.1	HI EPKQIKVW	FQNRRCREKQ	RKEASRLQAV	NRKLTAMNKL	LMEENDRLQK
Pop_triXP_002309538.2	HI EPKQIKVW	FQNRRCREKQ	RKEASRLQAV	NRKLTAMNKL	LMEENDRLQK
Fra_vesATHB-8-like	NI EPKQIKVW	FQNRRCREKQ	RKEASRLQTV	NRKLTAMNKL	LMEENDRLQK
Pop_triXP_002324794.1	HI EPKQIKVW	FQNRRCREKQ	RKEASRLQAV	NRKLTAMNKL	LMEENDRLQK
Vit_vin009744	NI EPKQIKVW	FQNRRCREKQ	RKEASRLQAV	NRKLTAMNKL	LMEENDRLQK
Gly_maxATHB-8-like	NI EPKQIKVW	FQNRRCREKQ	RKEASRLQAV	NRKLTAMNKL	LMEENDRLQK
Sol_lycATHB-15-like	NI EPKQIKVW	FQNRRCREKQ	RKESSRLQGV	NRKLTAMNKL	LMEENDRLQK
Gly_maxATHB-8-likeb	NI EPKQIKVW	FQNRRCREKQ	RKEASRLQAV	NRKLTAMNKL	LMEENDRLQK
Med_truXP_003603630.1	HI EPKQIKVW	FQNRRCREKQ	RKEAGRLQAV	NRKLTAMNKL	LMEENDRLQK

AmTr_v1.0_scaffold00148.15	QVAQLVYENG	YMRQOLQN	--	VSVATTD	--	TSCESVVTSG	PQQQ	--	NPTP
AmTr_v1.0_scaffold00056.60	QVSQLVYENG	YFROQTQN	--	VAITTTD	--	TSCESVVTSG	QH	---	HLTP
AmTr_v1.0_scaffold00155.45	QVSQLVYENG	YMKQQLQT	--	ASVATTD	--	TSCESVVTSG	QHQQ	--	NPTP
Ara_thaPHABULOSA	QVSNLVYENG	HMKHQIHT	--	ASGTTTD	--	NSCESVVMVSG	QHQQQN	--	PNP
Ara_thaATHB15	QVSQLVHENS	YFROHTPN	--	PSLPAKD	--	TSCESVVTSG	QH	---	QLAS
Ara-thaPHAVOLUTA	QVSNLVYENG	FMKHR IHT	--	ASGTTTD	--	NSCESVVMVSG	QQRQQN	--	PPTH
Ara_thaATHB8	QVSHLVYENS	YFROHPQN	--	QGNLATTD	--	TSCESVVTSG	QH	---	HLTP
Ara_thaREVOLUTA	QVSQLVCENG	YMKQQLTT	--	---VVND	--	PSCESVVT	---	---	TP
Vit_vinHOX32-like	QVSQLVYENG	YMRQQLQS	--	ASTATTD	--	TSCESVVMVSG	QHQQQN	--	NPTP
The_cacXP_007022870.1	QVSQLVYENG	YMRQQLQT	--	GSATTTD	N	NSCESVVMVSG	QHQQQN	--	NPTP
Ory_satHOX32	QVSRLVYENG	YMRQQLHN	--	PSVATTD	--	TSCESVVTSG	QHQQQN	--	PAA
Pru_perppa001343mg	QVSHLVYENG	FMROQLHS	--	ASGTTTD	--	NSCESVVMVSG	QHQQQN	--	NPTP
Bra_disHOX32-like	QVSRLVYENG	YMRTHLSN	--	PSVATTD	--	TSCESVVTSG	QHQQQN	--	PAV
Pop_triPHABULOSA	QVSHLVYENG	FMROQIQT	--	ASATTTD	--	NSCESVVMVSG	QHQQQN	--	NPTP
Pop_triPHABULOSAb	QVSHLVYENG	YMRQIQIT	--	ASATATD	--	NSCESVVMVSG	QHQQQN	--	NPTP
Fra_vesHOX32-like	QVSHLVYENG	FMKNKLHS	--	ASGTTTD	--	TSCESVVMNG	QHQQQN	--	NPTP
Gly_maxATHB-14-like	QVSHLVYENG	YMRQQLIHT	--	ASAGTTTD	--	NSCESVVMVSG	QNQQ	--	NPTP
Gly_maxREVOLUTA-like	QVSQLVCENG	FMROQLHT	--	PSATTTD	--	ASCDSVVT	---	---	TP
Gly_maxREVOLUTA-likeb	QVSQLVCENG	FMROQLHT	--	PSAATTD	--	ASCDSVVT	---	---	TP
Pru_perREV_IFL1	QVSQLVCENG	FMROQLHT	--	APTDD	--	ASCDSVVT	---	---	TP
Ory_satHOX33	QVSRLVYENG	YMRQQLHN	--	PSAATTD	--	TSCESVVTSG	QHQQQN	--	PAV
Sol_tubATHB-14-like	QVSQLVYENG	YMKQQLINT	--	VSSTTTD	--	TSCESVVMVSG	QQRK	--	NPTP
The_cacXP_007022872.1	QVSQLVYENG	YMRQQLQT	--	GSATTTD	N	NSCESVVMVSG	QHQQQN	--	NPTP
Ory_satHOX33-like	QVSRLVYENG	YMRQQLHN	--	PSAATTD	--	TSCESVVTSS	QHQQ	--	NPAV
Sol_lycREVOLUTA-like	QVSQLVCENG	YMRQQLQS	--	VSAATTD	--	VSCESVVT	---	---	TP
Sol_lycHOX32-like	QVSQLVYENG	YMKQQLINT	--	VSSTTTD	--	TSCESVVMVSG	QQRK	--	NPTP
Gly_maxATHB-14-likeb	QVSQLVYDNG	FMKQQLIHT	--	ASATTTTD	--	NSCESVVMVSG	QRQH	--	NPKI
Pop_triXP_006378973.1	QVSQLVCENG	FMQQLQT	--	APAAAD	--	ASCDSAVT	---	---	TP
Ory_satACA64837.1	QVSRLVYENG	YMRQQLHN	--	PSAATTD	--	TSCESVVTSG	QHQQQN	--	PAV
Vit_vin013992	QVSQLVYENG	YMRQQLQT	--	ASAATTD	--	ASCESVVT	---	---	TP
Ory_satOsJ_11861	QVSRLVYENG	YMRQQLHN	--	PSVATTD	--	TSCESVVTSG	QHQQQN	--	PAA
Sol_tubREVOLUTA-like	QVSQLVCENG	YMRQQLQS	--	VSAATTD	--	VSCESVVT	---	---	TP
Gly_maxATHB-14-likec	QVSQLVYDNG	FMKQQLIHTAS	--	ATTTTTTD	--	NSCESVVMVSG	QHQP	--	NPKI
The_cacXP_007024277.1	QVSQLVYENG	YFROHTQN	--	ATLATKD	--	PSCESVVTSG	QH	---	HVTP
Vit_vinATHB-15-like	QVSQLVYENG	YFROHTQN	--	TTLATKD	--	TSCESVVTSG	QH	---	HLTP
Ric_comXP_002515977.1	QVSQLVYENG	YFROHTQN	--	TTLATKD	--	TSCDSVVTSG	QH	---	HLTP
The_cacXP_007016751.1	QVSQLVCENG	YMRQQLHT	--	VNASAATD	--	ASCDSVVT	---	---	TP
Sol_tubHOX32-like	QVSQLVYENG	YMKQQLINT	--	VSSTTTD	--	TSCESVVMVSG	QQRK	--	NPTP
Sol_lycATHB-14-like	HVSHLVYDNG	FMROQLHT	--	VNSTTTD	--	TCCESVVMVSG	QQQQ	--	NPMP
Sol_tubATHB-14-like_X1	HVSHLVYDNG	FMROQLHT	--	QVNSTTTD	--	TCCESVVMVD	QQQQ	--	NPMP
Med_truATHB-14	QVSHLVYENG	YMKQQLIHTVS	--	ASAATTTD	--	NSCDSVVMVSG	QNQQ	--	NPT
Zea_mayNP_001142394.1	QVSRLVFDNG	YMKNRLHS	--	PSVATTD	--	TSCESVVTSG	QHQQQN	--	PAV
Vit_vinREVOLUTA	QVSQLVCENG	YMRQQLQT	--	VSATTD	--	ASCESVVT	---	---	TP
Ory_braHOX32-like	QVSRLVYENG	YMRQQLHN	--	PSVATTD	--	TSCESVVTSG	QHQQQN	--	PAA
Ric_comXP_002529946.1	QVSQLVCENG	YMRQQLQT	--	ASAATD	--	ASCDSVVT	---	---	TP
Tha_cacXP_007016749.1	QVSQLVCENG	YMRQQLHT	--	VNASAATD	--	ASCDSVVT	---	---	TP
Fra_vesREVOLUTA-like	QVSQLVCENG	YMRQQLHT	--	APATD	--	ASCDSVVT	---	---	TP
Zea_mayNP_001146215.1	QVSRLVFDNG	YMKNRLHS	--	PSVATTD	--	TSCESVVTSG	QHKQQN	--	PAV
The_cacXP_007012152.1	QVSQLVYENS	YFROQTQN	--	ATLATTD	--	TSCESVVTSG	QH	---	HLTP
Pru_perppa001386mg	QVSQLVYENS	YFROQTQN	--	TNLATTD	--	TSCESVVTSG	QH	---	HLTP
Pop_triAAX19057.1	QVSQLVYENS	YFROQTQN	--	ATNLATTD	--	TSCESVVTSG	QH	---	HLTP
Pop_triXP_002309538.2	QVSQLVYENS	YFROQTQN	--	ATNLATTD	--	TSCESVVTSG	QH	---	HLTP
Fra_vesATHB-8-like	QVSHLVYENS	YFROQTQN	--	TTLATTD	--	TSCESVVTSG	QH	---	HLTP
Pop_triXP_002324794.1	QVSQLVYENS	YFROQTQN	--	ATTLATTD	--	TSCESVVTSG	QH	---	RLTP
Vit_vin009744	QVSQLVYENS	FFROQTQN	--	ATLATTD	--	TSCESVVTSG	QH	---	HLTP
Gly_maxATHB-8-like	QVSHLVYENS	FFROQTHN	--	NATLATTD	TN	TSCESVVTSG	QR	---	NLTP
Sol_lycATHB-15-like	QVSQLVYENS	FFROQTQT	--	AALATTD	N	NSCESVVTSG	QH	---	NLTP
Gly_maxATHB-8-likeb	QVSHLVYENS	FFROQTHN	N	NATLATTD	TN	TSCESVVTSG	QR	---	NLTP
Med_truXP_003603630.1	QVSHLVYENT	FFROQTQN	--	TTLATTD	--	TSCESVVTSG	QQ	---	---

AmTr_v1.0_scaffold00148.15	Q- RP -PRDAN	NPAGLLSIAE	ETLAEFLSKA	TGTAVDWVQM	PGMKPGPDSI
AmTr_v1.0_scaffold00056.60	Q-HP-PRDA-	SPAGLLSIAE	ETLAEFLSKA	TGTAVEWVQM	PGMKPGPDSI
AmTr_v1.0_scaffold00155.45	P PHP-PRDAN	NPAGLLSIAE	ETLAEFLSKA	TGTAVDWVQM	LGMKPGPDSI
Ara_thaPHABULOSA	Q-HQ-ORDAN	NPAGLLSIAE	EALAEFLSKA	TGTAVDWVQM	IGMKPGPDSI
Ara_thaATHB15	Q-NP-ORDA-	SPAGLLSIAE	ETLAEFLSKA	TGTAVEWVQM	PGMKPGPDSI
Ara-thaPHAVOLUTA	Q-HP-ORDVN	NPANLLSIAE	ETLAEFLCKA	TGTAVDWVQM	IGMKPGPDSI
Ara_thaATHB8	Q-HQ-PRDA-	SPAGLLSIAD	ETLTEFLSKA	TGTAVEWVQM	PGMKPGPDSI
Ara_thaREVOLUTA	Q- HS -LRDAN	SPAGLLSIAE	ETLAEFLSKA	TGTAVDWVQM	PGMKPGPDSV
Vit_vinHOX32-like	Q-HP-ORDAS	NPAGLLAIAE	ETLAEFLSKA	TGTAVDWVQM	IGMKPGPDSI
The_cacXP_007022870.1	Q-HP-ORDAN	SPAGLLAIAE	ETLAEFLSKA	TGTAVDWVQM	IGMKPGPDSI
Ory_satHOX32	T- RP -ORDAN	NPAGLLAIAE	ETLAEFLSKA	TGTAVDWVQM	VGMKPGPDSI
Pru_perppa001343mg	Q-HP-ORDAN	NPAGLLAIAE	ETLAEFLSKA	TGTAVDWVQM	IGMKPGPDSI
Bra_disHOX32-like	P - RP -ORDAN	NPAGLLAIAE	ETLAEFLSKA	TGTAVDWVQM	VGMKPGPDSI
Pop_triPHABULOSA	Q- QP -ORDAN	NPAGLLAIAE	ETLAEFLSKA	TGTAVDWVQM	IGMKPGPDSI
Pop_triPHABULOSAb	Q- QP -ORDAN	NPAGLLTIAE	ETLAEFLSKA	TGTAVDWVQM	IGMKPGPDSI
Fra_vesHOX32-like	Q-HP-ORDAN	NPAGLLAIAE	ETLAEFLSKA	TGTAVDWVQM	IGMKPGPDSI
Gly_maxATHB-14-like	Q-HP-NRDAN	NPAGLLAIAE	ETLAEFLSKA	TGTAVDWVQM	IGMKPGPDSI
Gly_maxREVOLUTA-like	Q-HT-LRDAS	NPAGLLSIAE	ETLTEFLSKA	TGTAVDWVQM	PGMKPGPDSV
Gly_maxREVOLUTA-likeb	Q-HT-MRDAN	NPAGLLSIAE	ETLTEFLSKA	TGTAVDWVQM	PGMKPGPDSV
Pru_perREV IFL1	Q- HS -LRDAN	NPAGLLSIAE	ETLAEFLSKA	TGTAVDWVQM	PGMKPGPDSV
Ory_satHOX33	L-HP-ORDAN	NPAGLLAIAE	ETLAEFMSKA	TGTAVEWVQM	VGMKPGPDSI
Sol_tubATHB-14-like	Q-HP-ERDAN	NPAGLLAIAE	ETLAEFLGKA	TGTAVDWVQM	IGMKPGPDSI
The_cacXP_007022872.1	Q-HP-ORDAN	SPAGLLAIAE	ETLAEFLSKA	TGTAVDWVQM	IGMKPGPDSI
Ory_satHOX33-like	L-HP-ORDAN	NPAGLLAIAE	ETLAEFMSKA	TGTAVEWVQM	VGMKPGPDSI
Sol_lycREVOLUTA-like	Q- HS -LRDAN	NPAGLLPIAE	ETLAEFLSKA	TGTAVDWVPM	PGMKPGPDSV
Sol_lycHOX32-like	Q-HP-ERDAN	NPAGLLAIAE	ETLAEFLGKA	TGTAVDWVQL	IGMKPGPDSI
Gly_maxATHB-14-likeb	Q-HP- Q WDAN	NPAGLLAIA Q	ETLAAFLSKA	TGTAVNWVQM	IGMKPGPDSI
Pop_triXP_006378973.1	Q- HS -LRDAN	NPAGLLSLAE	ETLAEFLSKA	TGTAVDWVQM	PGMKPGPDSV
Ory_satACA64837.1	L-HP-ORDAN	NPAGLLAIAE	ETLAEFMSKA	TGTAVEWVQM	VGMKPGPDSI
Vit_vin013992	Q- HS -LRDAN	NPAGLLSIAE	ETLAEFLSKA	TGTAVDWVQM	PGMKPGPDSV
Ory_satOsJ_11861	T- RP -ORDAN	NPAGLLAIAE	ETLAEFLSKA	TGTAVDWVQM	VGMKPGPDSI
Sol_tubREVOLUTA-like	Q- HS -LRDAN	NPAGLLPIAE	ETLAEFLSKA	TGTAVDWVPM	PGMKPGPDSV
Gly_maxATHB-14-likec	Q-HP- Q WDAN	NPAGLLAIA Q	ETLVEFLSKA	TGTAVNWVQM	IGMKPGPDSI
The_cacXP_007024277.1	Q-HP-PRDA-	SPAGLLSIAE	ETLAEFLSKA	TGTAVEWVQM	PGMKPGPDSI
Vit_vinATHB-15-like	Q-HP-PRDA-	SPAGLLSIAE	ETLTEFLSKA	TGTAVEWVQM	PGMKPGPDSI
Ric_comXP_002515977.1	Q-HQ-PRDA-	SPAGLLSIAE	ETLTEFLSKA	TGTAVEWVQM	PGMKPGPDSI
The_cacXP_007016751.1	Q- HS -LRDAN	NPAGLLSIAE	ETLAEFLSKA	TGTAVDWVQM	PGMKPGPDSV
Sol_tubHOX32-like	Q-HP-ERDAN	NPAGLLAIAE	ETLAEFLGKA	TGTAVDWVQL	IGMKPGPDSI
Sol_lycATHB-14-like	Q HHP-ORDAN	SPAGLLAIAE	ETLTEFLGKA	TGTAVDWVQM	IGMKPGPESI
Sol_tubATHB-14-like_X1	Q HHP-ORDAN	SPAGLLAIAE	ETLTEFLGKA	TGTAVDWVQM	IGMKPGPESI
Med_truATHB-14	Q- RP -ORDAN	NPAGLLAVAE	ETLAEFLSKA	TGTAVDWVQM	IGMKPGPESI
Zea_mayNP_001142394.1	L- HPP -ORDAN	NPAGLLAIAE	ETLAEFMSKA	TGTAVNWVQM	VGMKPGPDSV
Vit_vinREVOLUTA	Q- HS -LRDAN	NPAGLLSIAE	ETLAEFLSKA	TGTAVDWVQM	PGMKPGPDSV
Ory_braHOX32-like	A - RP -ORDAN	NPAGLLAIAE	ETLAEFLSKA	TGTAVDWVQM	VGMKPGPDSI
Ric_comXP_002529946.1	Q- HS -LRDAN	NPAGLLSIAE	ETLAEFLSKA	TGTAVDWVQM	PGMKPGPDSV
Tha_cacXP_007016749.1	Q- HS -LRDAN	NPAGLLSIAE	ETLAEFLSKA	TGTAVDWVQM	PGMKPGPDSV
Fra_vesREVOLUTA-like	Q- HS -LRDAN	NPAGLLSIAE	ETLAEFLSKA	TGTAVDWVQM	PGMKPGPDSV
Zea_mayNP_001146215.1	L- HPP -ORDAN	NPAGLLAIAE	ETLAEFMSKA	TGTAVNWVQM	VGMKPGPDSV
The_cacXP_007012152.1	Q-HP-PRDA-	SPAGLLSIAE	ETLTEFLSKA	TGTAVEWVQM	PGMKPGPDSI
Pru_perppa001386mg	Q-HP-PRDA-	SPAGLLSIAE	ETLAEFLSKA	TGTAVEWVQM	PGMKPGPDSI
Pop_triAAX19057.1	Q-HP-PRDA-	SPAGLLSIAE	ETLA Q FLSKA	TGTAVEWVQM	PGMKPGPDSI
Pop_triXP_002309538.2	Q-HP-PRDA-	SPAGLLSIAE	ETLA Q FLSKA	TGTAVEWVQM	PGMKPGPDSI
Fra_vesATHB-8-like	Q-HP-PRDA-	SPAGLLSIAE	ETLAEFLSKA	TGTAVEWVQL	PGMKPGPDSI
Pop_triXP_002324794.1	Q-HP-PRDA-	SPAGLLSIAE	ENLA Q FLSKA	TGTAVEWVQM	PGMKPGPDSI
Vit_vin009744	Q-HP-PRDA-	SPAGLLSIAE	ETLTEFLSKA	TGTAVEWVQM	PGMKPGPDSI
Gly_maxATHB-8-like	Q QHP-PRDA-	SPAGLLSIAE	ETLAEFLSKA	TGTAVEWVQM	PGMKPGPDSI
Sol_lycATHB-15-like	Q- RP -PRDA-	SPAGLLSLAE	ETLTEFLSKA	TGTAVEWVQM	PGMKPGPDSI
Gly_maxATHB-8-likeb	Q QHP-PRDA-	SPAGLLSIAE	ETLAEFLSKA	TGTAVEWVQM	PGMKPGPDSI
Med_truXP_003603630.1	-- H PPORDA-	SPAGLLSIAE	ETLAEFLSKA	TGTAVEWVQM	PGMKPGPDSI

AmTr_v1.0_scaffold00148.15	GIVAI SHS CS	GVAA---RAC	GLV SLEPT KV	VEIL KDR MSW	FRDCRN FD IL
AmTr_v1.0_scaffold00056.60	GIVAI SHG CT	GVAA---RAC	GLV GLEPT KV	SEIL KDR P TW	FRDCRS VE VL
AmTr_v1.0_scaffold00155.45	GIVAV SHN CS	GMAA---RVC	GLV SLEP AKV	AEIL KDR PSW	FRDCRS SH DVL
Ara_thaPHABULOSA	GIVAI SRN CS	GIAA---RAC	GLV SLEP MKV	AEIL KDR PSW	LRDCRS SV DTL
Ara_thaATHB15	GIIAI SHG CT	GVAA---RAC	GLV GLEPT RV	AEIV KDR PSW	FRECR A VEVM
Ara-thaPHAVOLUTA	GIVAV SRN CS	GIAA---RAC	GLV SLEP MKV	AEIL KDR PSW	FRDCR CV ETL
Ara_thaATHB8	GIVAI SHG CT	GIAA---RAC	GLV GLD PTRV	AEIL KDK PCW	LRDCR SL DIV
Ara_thaREVOLUTA	GIFAI SQR CN	GVAA---RAC	GLV SLEP MKI	AEIL KDR PSW	FRDCR S LEVF
Vit_vinHOX32-like	GIVAV SRN CS	GVAA---RAC	GLV SLEPT KV	AEIL KDR PSW	FRDCR CL DVL
The_cacXP_007022870.1	GIVAV SRN CS	GVAA---RAC	GLV SLEPT KV	AEIL KDR PSW	FRDCR CL DVL
Ory_satHOX32	GIIAV SHN CS	GVAA---RAC	GLV SLEPT KV	AEIL KDR PSW	YRDCR CV DVL
Pru_perppa001343mg	GIVAV SRN CS	GVAA---RAC	GLV SLEPT KV	AEIL KDR TSW	FRDCR CL DVL
Bra_disHOX32-like	GIIAV SHN CS	GVAA---RAC	GLV SLEPT KV	AEIL KDR PSW	YRDCR CV DVL
Pop_triPHABULOSA	GIVAV SRN CS	GVAA---RAC	GLV SLEPT KV	AEIL KDR PSW	FRDCR CL DIL
Pop_triPHABULOSAb	GIVAV SRN CS	GVAA---RAC	GLV SLEP IKV	AEIL KDR PSW	FRDCR CL DIM
Fra_vesHOX32-like	GIVAV SRN TS	GVAA---RAC	GLV SLEPT KV	AEIL KDR PSW	FRDCR CL DVL
Gly_maxATHB-14-like	GIVAV SRN CS	GVAA---RAC	GLV SLEPT KV	AEIL KDR QSW	YRDCR CV DVL
Gly_maxREVOLUTA-like	GIFAI SQS CS	GVAA---RAC	GLV SLEPT KI	AEIL KDR PSW	FRDCR S LEVF
Gly_maxREVOLUTA-likeb	GIFAI SQS CS	GVAA---RAC	GLV SLEPT KI	AEIL KDR PSW	FRDCR S LEVF
Pru_perREV_IFL1	GIFAI SQS CS	GVAA---RAC	GLV SLEPT KI	AEIL KDR PSW	FRDCR S LEVF
Ory_satHOX33	GIIAV SHN CS	GVAA---RAC	GLV SLEPT KV	AEIL KDR PSW	YRDCR CV DI I
Sol_tubATHB-14-like	GIVAV SRN CS	GVAA---RAC	GLV SLEPT KV	AEIL KDR PSW	YRDCR CL NVL
The_cacXP_007022872.1	GIVAV SRN CS	GVAA---RAC	GLV SLEPT KV	AEIL KDR PSW	FRDCR CL DVL
Ory_satHOX33-like	GIIAV SHN CS	GVAA---RAC	GLV SLEPT KV	AEIL KDR PSW	YRDCR CV DI I
Sol_lycREVOLUTA-like	GIFAI SHS CS	GVAA---RAC	GLV SLEPT KI	ADIL KDR PSW	FRDCR N VEVI
Sol_lycHOX32-like	GIVAV SRN CS	GVAA---RAC	GLV SLEPT KV	AEIL KDC PSW	YRDCR CL NVL
Gly_maxATHB-14-likeb	GIVAV SRN CS	GVAA---RAC	GLV SLEPT KV	AEIL KDR PSW	YRDCR CL NVL
Pop_triXP_006378973.1	GIFAI SQR CS	GVAA---RAC	GLV SLEPT KL	AEIL KDR QSW	FRDCR N LEVF
Ory_satACA64837.1	GII TV SHNCS	GVAA---RAC	GLV SLEPT KV	AEIL KDR PSW	YRDCR CV DI I
Vit_vin013992	GIFAI SHS CS	GGSS SM RSC	K FRT LK---	-EIL KDR PSW	FRDCR S LEVF
Ory_satOsJ_11861	GIIAV SHN CS	GVAA---RAC	GLV SLEPT KV	AEIL KDR PSW	YRDCR CV DVL
Sol_tubREVOLUTA-like	GIFAI SHS CS	GVAA---RAC	GLV SLEPT KI	AEIL KDR PSW	FRDCR N VEVI
Gly_maxATHB-14-likec	GIVAV SRN CS	GVAA---RAC	GLV SLEPT KV	AEIL KDR PSW	YRDCR CL NVL
The_cacXP_007024277.1	GIVAI SHG CT	GVAA---RAC	GLV GLEPT RV	AEIL KDR PSW	FRDCR AV DVL
Vit_vinATHB-15-like	GIVAI SHG CT	GVAA---RAC	GLV GLEPT RV	AEIL KDR PSW	FRDCR AV DVL
Ric_comXP_002515977.1	GIIAI SHG CT	GVAA---RAC	GLV GLEPT RV	AEIL KDR PSW	FRDCR AV DVL
The_cacXP_007016751.1	GIFAI SQS CS	GVAA---RAC	GLV SLEPT KI	AEIL KDR PSW	FRDCR N LEVF
Sol_tubHOX32-like	GIVAV SRN CS	GVAA---RAC	GLV SLEPT KV	AEIL KDC PSW	YRDCR CL NVL
Sol_lycATHB-14-like	GIVAV SRN CN	GVAA---RAC	GLV SLEP MKV	AEIL KDR PSW	YRDCR CL DIL
Sol_tubATHB-14-like_X1	GIVAV SRN CN	GVAA---RAC	GLV SLEP MKV	AEIL KDR PSW	YRDCR CL DIL
Med_truATHB-14	GIVAV SRN SS	GIAA---RAC	GLV SLEPT KV	AEIL KDR LSW	YRDCR CV DVL
Zea_mayNP_001142394.1	GIIAV SHN CS	GVAA---RAC	GLV SLEPT KV	AEIL KDR ASW	YRDCR HV DVL
Vit_vinREVOLUTA	GIFAI SHS CS	GVAA---RAC	GLV SLEP SKI	AEIL KDR PSW	FRDCR S LEVF
Ory_braHOX32-like	GIIAV SHN CS	GVAA---RAC	GLV SLEPT KV	AEIL KDR PSW	YRDCR CV DVL
Ric_comXP_002529946.1	GIFAI SQS CS	GVAA---RAC	GLV SLEPT KI	AEIL KDR PSW	FRDCR S LEVF
Tha_cacXP_007016749.1	GIFAI SQS CS	GVAA---RAC	GLV SLEPT KI	AEIL KDR PSW	FRDCR N LEVF
Fra_vesREVOLUTA-like	GIFAI SQS CS	GVAA---RAC	GLV SLEPT KI	AEIL KDR PSW	FRDCR S LEVF
Zea_mayNP_001146215.1	GIIAV SHN CS	GVAA---RAC	GLV SLEPT KV	AEIL KDR ASW	YRDCR RV DIL
The_cacXP_007012152.1	GIVAI SHG CT	GVAA---RAC	GLV GLD PTRV	AEIL KDR PSW	FRDCR AV DVM
Pru_perppa001386mg	GIVAI SHG CT	GVAA---RAC	GLV GLEPT RV	AEIL KDR PSW	FR N CR S VDVL
Pop_triAAX19057.1	GIVAI SHG CT	GVAA---RAC	GLV GLEPT RV	AEIL KDR PSW	FRDCR AV DVV
Pop_triXP_002309538.2	GIVAI SHG CT	GVAA---RAC	GLV GLEPT RV	AEIL KDR PSW	FRDCR AV DVV
Fra_vesATHB-8-like	GIVAI SHG CT	GVAA---RAC	GLV GLEPT RV	SEIL KDR PSW	FR N CR S VDVL
Pop_triXP_002324794.1	GIVAI SHG CT	GVAA---RAC	GLV GLEPT RV	AEIL KDR PSW	FRDCR AV DVI
Vit_vin009744	GIVAI SHG CT	GVAA---RAC	GLV SLEPT RV	AEIL KDR PSW	YRDCR N VDVL
Gly_maxATHB-8-like	GIVAI SHG CP	GVAA---RAC	GLV GLEP ARV	AEIL KDR LSW	FRDCR T VDVL
Sol_lycATHB-15-like	GIIAI SHG CS	GVAS---RAC	GLV GLEPT RV	AEIL KDR PSW	FRDCR AV DVL
Gly_maxATHB-8-likeb	GIVAI SHG CP	GVAA---RAC	GLV GLEPT RV	AEIL KDR LSW	FRDCR T VDVL
Med_truXP_003603630.1	GIVAI SHG SP	GVAA---RAC	GLV GLEP ARV	AEIL KDR LSW	YRDCR T VDVL

AmTr_v1.0_scaffold00148.15	TVLP	IGSGGT	IELIYMQT	--	YAPTTLA	---	----	PARDFW	TLRYTCGLED
AmTr_v1.0_scaffold00056.60	TALST	GNGGT	IELLYMQM	--	YAPTTLA	---	----	SARDFW	LLRYTSVLED
AmTr_v1.0_scaffold00155.45	TVFP	PAGNGGT	IELIYMQT	--	YAPTTLA	---	----	AARDFW	TLRYTTGLDD
Ara_thaPHABULOSA	SVI	PAGNGGT	IELIYTQM	--	YAPTTLA	---	----	AARDFW	TLRYSTCLED
Ara_thaATHB15	NVLPT	TANGGT	VELLYMQL	--	YAPTTLA	---	----	PPRDFW	LLRYTSVLED
Ara-thaPHAVOLUTA	NVI	PTGNGGT	IELVNTQI	--	YAPTTLA	---	----	AARDFW	TLRYSTSLED
Ara_thaATHB8	NVLST	ANGGT	LELIYMQL	--	YAPTTLA	---	----	PARDFW	MLRYTSVMED
Ara_thaREVOLUTA	TMFP	PAGNGGT	IELVYMQT	--	YAPTTLA	---	----	PARDFW	TLRYTTSLDN
Vit_vinHOX32-like	SVI	PTGNGGT	IELIYMQT	--	YAPTTLA	---	----	SARDFW	TLRYTTSLED
The_cacXP_007022870.1	SVI	PTGNGGT	IELIYMQT	--	YAPTTLA	---	----	AARDFW	TLRYTTSLED
Ory_sathOX32	HVI	PTGNGGT	IELIYMQT	--	YAPTTLA	---	----	APRDFW	TLRYTSGLED
Pru_perppa001343mg	SLI	PAGNGGT	IELIYMQT	--	YAPTTLA	---	----	AARDFW	TLRYTTSLED
Bra_disHOX32-like	QII	PTGNGGT	IELIYMQT	--	YAPTTLA	---	----	APRDFW	ILRYTSGLED
Pop_tripHABULOSA	SVI	PTGSGGT	IELIYMQT	--	YAPTTLA	---	----	AARDFW	TLRYTTTLED
Pop_tripHABULOSAb	SVI	PTGSGGT	IELIYMQT	--	YAPTTLA	---	----	AARDFW	TLRYTTTLED
Fra_vesHOX32-like	SI	PAGNGGT	IELLYMQI	--	YAPTTLA	---	----	AARDFW	TLRYTTTLED
Gly_maxATHB-14-like	SIV	PTGNGGT	IELMYMQT	--	YAPTTLA	---	----	AARDFW	TLRYTTSLED
Gly_maxREVOLUTA-like	TMFP	PAGNGGT	IELVYTQT	--	YAPTTLA	---	----	PARDFW	TLRYTTSLEN
Gly_maxREVOLUTA-likeb	TMFP	PAGNGGT	IELVYTQT	--	YAPTTLA	---	----	PARDFW	TLRYTTSLEN
Pru_perREV_IFL1	TMFP	PAGNGGT	IELIYTQT	--	YAPSTLA	---	----	PARDFW	TLRYTTSLDN
Ory_sathOX33	HVI	PTGNGGT	IELIYMQT	--	YAPTTLA	---	----	APRDFW	TLRYTSGLED
Sol_tubATHB-14-like	SVI	PTGNGGT	IELIYLQT	--	YAPTTLA	---	----	TARDFW	TLRYTTSLED
The_cacXP_007022872.1	SVI	PTGNGGT	IELIYMQT	--	YAPTTLA	---	----	AARDFW	TLRYTTSLED
Ory_sathOX33-like	HVI	PTGNGGT	IELIYMQT	--	YAPTTLA	---	----	APRDFW	TLRYTSGLED
Sol_lycREVOLUTA-like	TMFP	PAGNGGT	VELLYTQI	--	YAPTTLA	---	----	PARDFW	TLRYTTTLDN
Sol_lycHOX32-like	SVI	PTGNGGT	IELIYLQT	--	YAPTTLA	---	----	TARDFW	TLRYTTSLED
Gly_maxATHB-14-likeb	SVI	PTGNGGT	IELMYMQT	--	YAPTTLA	---	----	AARDFW	TLRYTTSLED
Pop_triXP_006378973.1	TVFP	PAGNGGT	IELLYSQI	--	YAPTTLA	---	----	PARDFW	TLRYTINLEN
Ory_satACĀ64837.1	HVI	PTGNGGT	IELIYMQT	--	HAPTTLA	---	----	APRDFW	TLRYTSGLED
Vit_vin013992	TMFP	PAGNGGT	VELLYTQI	--	YAPTTLA	---	----	PARDFW	TLRYTTSLDN
Ory_satOsJ_11861	HVI	PTGNGGT	IELIYMQT	--	YAPTTLA	---	----	APRDFW	ILRYTSGLED
Sol_tubREVOLUTA-like	TIF	PAGNGGT	VELLYTQI	--	YAPTTLA	---	----	PARDLW	TLRYTTTLDN
Gly_maxATHB-14-likec	SVV	SAGNGGT	IELMYMQT	--	YAPTTLA	---	----	AARDFW	TLRYSTSLED
The_cacXP_007024277.1	NVLPT	TANGGT	IELLYMQL	--	YAPTTLA	---	----	PARDFW	LLRYTSVLED
Vit_vinATHB-15-like	NVLPT	TANGGT	IELLYMQL	--	YAPTTLA	---	----	PARDFW	LLRYTSVMED
Ric_comXP_002515977.1	NVLPT	TANGGT	IELLYMQL	--	YAPTTLA	---	----	PARDFW	LLRYTSVLED
The_cacXP_007016751.1	TMFP	PAGNGGT	IELVYTQT	--	YAPTTLA	---	----	PARDFW	TLRYTTTLEN
Sol_tubHOX32-like	SVI	PTGNGGT	IELIYLQT	--	YAPTTLA	---	----	TARDFW	TLRYTTSLED
Sol_lycATHB-14-like	NVI	PTGNGGT	IELIYLQT	--	YAPTTLA	---	----	PARDFW	TLRYTTSLED
Sol_tubATHB-14-like_X1	NVI	PTGNGGT	IELIYLQT	--	YAPTTLA	---	----	PARDFW	TLRYTTSLED
Med_truATHB-14	SIV	PTGGG	IELMYMQVLF	--	YSTKELTMPF	---	----	LFLLSRDFW	TLRYTTSLED
Zea_mayNP_001142394.1	HVI	PTGNGGT	IELIYMQT	--	YALTTLA	---	----	EPRDFW	TLRYTSGLDD
Vit_vinREVOLUTA	TMFP	PAGNGGT	VELLYTQI	--	YAPTTLA	---	----	PARDFW	TLRYTTSLDN
Ory_braHOX32-like	HVI	PTGNGGT	IELIYMQT	--	YAPTTLA	---	----	APRDFW	TLRYTSGLED
Ric_comXP_002529946.1	TMFP	PAGNGGT	IELVYSQV	--	YAPTTLA	---	----	PARDFW	TLRYTSSLDN
Tha_cacXP_007016749.1	TMFP	PAGNGGT	IELVYTQT	--	YAPTTLA	---	----	PARDFW	TLRYTTTLEN
Fra_vesREVOLUTA-like	TMFP	PAGNGGT	IELIYTQT	--	YAPTTLA	---	----	PARDFW	TLRYTTSLDN
Zea_mayNP_001146215.1	HVI	PTGNGGT	IELIYMQT	--	YALTTLA	---	----	EPRDFW	TLRYTSGLDD
The_cacXP_007012152.1	NVLST	GNGGT	IELLYMQL	--	YAPTTLA	---	----	PARDFW	LLRYTSVLED
Pru_perppa001386mg	NVLST	GNGGT	IELLYMQL	--	YAPTTLA	---	----	PARDFW	LLRYTSVLED
Pop_triAAX19057.1	NALST	GSGGT	IELLYMQL	--	YAPTTLA	---	----	PARDFW	LLRYTSVLED
Pop_triXP_002309538.2	NALST	GSGGT	IELLYMQL	--	YAPTTLA	---	----	PARDFW	LLRYTSVLED
Fra_vesATHB-8-like	NVLST	GNGGT	IELLYMQL	--	YAPTTLA	---	----	PARDFW	LLRYTSVLED
Pop_triXP_002324794.1	NAMST	TANGGT	IELLYMQL	--	YAPTTLA	---	----	PARDFL	LLRYTSVLED
Vit_vin009744	NVLST	GNGGT	IELLYMQL	--	YAPTTLA	---	----	PARDFW	LLRYTSVLED
Gly_maxATHB-8-like	NVMST	GNGGT	IELLYMQL	--	YAPTTLA	---	----	PGRDFW	LLRYTSLLED
Sol_lycATHB-15-like	NVMST	GNGGT	IELLYMQL	--	YAPTTLA	---	----	PARDFW	LMRYTSVMED
Gly_maxATHB-8-likeb	NVMST	GNGGT	IELLYMQL	--	YAPTTLA	---	----	PGRDFW	LLRYTSLLED
Med_truXP_003603630.1	NVMST	GNGGT	IELLYMQL	--	YAPTTLA	---	----	PGRDFW	LLRYTSLLED

AmTr_v1.0_scaffold00148.15	GSLVVCERSL	TSSNGSPHGQ	PVPNFVRAEM	LPSGYLIRPC	EGGGSIIHIV
AmTr_v1.0_scaffold00056.60	GSLVVCERSL	SNTQGGPSMP	PVQFVRAEM	HPSGYLIRPC	EGGGSIIHLV
AmTr_v1.0_scaffold00155.45	GSLVVCERSL	TSSTGGPSGP	TSLSFVRAEM	MPSGYLIRPC	EGGGSIIHIV
Ara_thaPHABULOSA	GSYVVCERSL	TSATGGPTGP	PSSNFVRAEM	KPSGFLIRPC	DGGGSILHIV
Ara_thaATHB15	GSLVVCERSL	KSTQNGPSMP	LVQNFVRAEM	LSSGYLIRPC	DGGGSIIHIV
Ara-thaPHAVOLUTA	GSYVVCERSL	TSATGGPNGP	LSSSFVRAKM	LSSGFLIRPC	DGGGSIIHIV
Ara_thaATHB8	GSLVICERSL	NNTQNGPSMP	PSPHFVRAEI	LPSGYLIRPC	EGGGSILHIV
Ara_thaREVOLUTA	GSFVVCERSL	SGSGAGPNA	SASQFVRAEM	LSSGYLIRPC	DGGGSIIHIV
Vit_vinHOX32-like	GSLVICERSL	TSSTGGPTGP	PASSYIRAEM	LPSGYLIRPC	EGGGSIIHIV
The_cacXP_007022870.1	GSLVICERSL	TSSTGGPTGP	PTSSFVRAEM	LPSGFLIRPC	EGGGSIIHIV
Ory_satHOX32	GSLVICERSL	TQSTGGPSGP	NTPNFVRAEV	LPSGYLIRPC	EGGGSMIHIV
Pru_perppa001343mg	GSLVVCERSL	TSSTGGPTGP	PSASFVRAEM	LPSGYLIRPC	EGGGSIIHIV
Bra_disHOX32-like	GSLVICERSL	TQATGGPSGP	NTPNFVRAEV	LPSGYLIRPC	EGGGSMIHIV
Pop_triPHABULOSA	GSLVICERSL	TSSTGGPTGP	PPSSFIRAEM	LPSGYLIRPC	EGGGSIIHIV
Pop_triPHABULOSAb	GSLVICERSL	TSSTGGPTGP	PSSSFVRADM	LPSGYLIRPC	EGGGSIIHIV
Fra_vesHOX32-like	GSLVICERSL	TSSTGGPTGT	PSPSFVRAEM	LPSGYLIRPC	EGGGSIIHIV
Gly_maxATHB-14-like	GSLVICERSL	TSSTGGPAGP	PSTTFVRAEM	LPSGFLIRPC	EGGGSIIHIV
Gly_maxREVOLUTA-like	GSLVVCERSL	SGSGTGPNPA	AAAQFVRAET	LPSGYLIRPC	EGGGSIIHIV
Gly_maxREVOLUTA-likeb	GSLVVCERSL	SGSGTGPNPA	AAAQFVRAET	LPSGYLIRPC	EGGGSIIHIV
Pru_perREV_IFL1	GSFVVCERSL	SGSGAGPNA	SAAQFVRAEM	LPSGYLIRPC	EGGGSIIHIV
Ory_satHOX33	GSLVICERSL	TQSTGGPSGP	NTPNFIRAEM	LPSGYLIRPC	EGGGSMIYIV
Sol_tubATHB-14-like	GSLVICERSL	TTATGGPTGP	PATSFVRAEM	LPSGYLIRPC	EGGGSMIHIV
The_cacXP_007022872.1	GSLVICERSL	TSSTGGPTGP	PTSSFVRAEM	LPSGFLIRPC	EGGGSIIHIV
Ory_satHOX33-like	GSLVICERSL	TQSTGGPSGP	NTPNFIRAEM	LPSGYLIRPC	EGGGSMIYIV
Sol_lycREVOLUTA-like	GSLVVCERSL	SGNGGPNPT	AASQFVRAQM	LPSGYLIRPC	DGGGSIIHIV
Sol_lycHOX32-like	GSLVICERSL	TTATGGPTGP	PATSFVRAEM	LPSGYLIRPC	EGGGSMIHIV
Gly_maxATHB-14-likeb	GSLVICERSL	TSSTGGPTGP	AASNFVRAEM	LPSGYLIRSC	EGGGSIVHIV
Pop_triXP_006378973.1	GSLVVCERSL	SGSGAGPNA	AAAQFVRAEM	LPSGYLIRPC	EGGGSIIHIV
Ory_satACA64837.1	GSLVICERSL	TQSTGGPSGP	NLNFIRAEM	LPSGYLIRPC	EGGGSMIYIV
Vit_vin013992	GSLVVCERSL	SGSGAGPNTA	AAAQFVRAEM	LPSGYLIRPC	EGGGSIIHIV
Ory_satOsJ_11861	GSLVICERSL	TQSTGGPSGP	NTPNFVRAEV	LPSGYLIRPC	EGGGSMIHIV
Sol_tubREVOLUTA-like	GSLVVCERSL	SGNGGPNPA	AASQFVRAQM	LPSGYLIRPC	DGGGSIIHIV
Gly_maxATHB-14-likec	GSLVICERSL	TSSTGGPTGP	AASNFIRAEM	LPSGYLIRSC	EGGGSIIHIV
The_cacXP_007024277.1	GSLVVCERSL	KNTQNGPSMP	AVQHFVRAEM	LPSGYLIRPC	EGGGSIIHIV
Vit_vinATHB-15-like	GSLVVCERSL	KNTQNGPSMP	PVQHFVRAEM	LPSGYLIRPC	EGGGSIIHIV
Ric_comXP_002515977.1	GSLVICERSL	KNTQNGPSMP	PVQHFVRAEM	LPSGYLIRPC	EGGGSIIHIV
The_cacXP_007016751.1	GSLVVCERSL	SGSGAGPSAA	AAAQFVRAEM	LPSGYLIRPC	EGGGSIIHIV
Sol_tubHOX32-like	GSLVICERSL	TTATGGPTGP	PATSFVRAEM	LPSGYLIRPC	EGGGSMIHIV
Sol_lycATHB-14-like	GSLVICERSL	TSNTGGPVGP	PATSSVRAKM	LPSGFLIRPC	EGGGSIIHIV
Sol_tubATHB-14-like_X1	GSLVICERSL	TSNTGGPVGP	PATSSVRAKM	LPSGFLIRPC	EGGGSIIHIV
Med_truATHB-14	GSLVICERSL	NASTGGPTGP	SPSNFVRAEM	LPSGFLIRPC	EGGGSIIHIV
Zea_mayNP_001142394.1	GSLVICERSL	TQSTGGPSGP	NTPNFIRAEM	LPSGYLIRPC	DGGGSMIYIV
Vit_vinREVOLUTA	GSLVVCERSL	SGSGAGPNTA	AAAQFVRAEM	LPSGYLIRPC	EGGGSIIHIV
Ory_braHOX32-like	GSLVICERSL	TQSTGGPSGP	NTPNFVRADV	LPSGYLIRPC	EGGGSMIHIV
Ric_comXP_002529946.1	GSLVVCERSL	SGSGAGPNA	AAAQFVRAEM	LPSGYLIRPC	DGGGSIIHIV
Tha_cacXP_007016749.1	GSLVVCERSL	SGSGAGPSAA	AAAQFVRAEM	LPSGYLIRPC	EGGGSIIHIV
Fra_vesREVOLUTA-like	GSFVVCERSL	SGSGAGPSGA	SAAQFVRAEM	LPSGYLIRPC	EGGGSIIHIV
Zea_mayNP_001146215.1	GSLVICERSL	THSTGGPSGP	KTPDFIRAEM	LPSGYLIRPC	DGGGSMIYIV
The_cacXP_007012152.1	GSLVVCERSL	NNTQNGPSIP	PAANFVRAEM	LPSGYLIRPC	EGGGSIIHIV
Pru_perppa001386mg	GSLVVCERSL	NNTQNGPSMP	PVQNFVRAEM	LPSGYLIRPC	EGGGSIIHIV
Pop_triAAX19057.1	GSLVVCERSL	NNTQNGPSMP	PTQHFVRAEM	LPSGYLIRPC	EGGGSIIHVV
Pop_triXP_002309538.2	GSLVVCERSL	NNTQNGPSMP	PTQHFVRAEM	LPSGYLIRPC	EGGGSIIHVV
Fra_vesATHB-8-like	GSLVVCERSL	NNTQNGPSMP	PVQNFVRAEM	LPSGYLIRPC	EGGGSIIHIV
Pop_triXP_002324794.1	GSLVVCERSL	NNTQNGPSMP	PTQHFVRAEM	LPSGYLIRPC	EGGGSIIHIV
Vit_vin009744	GSLVVCERSL	NNTQNGPSMP	PVQYFVRAEK	LPSGYLIRPC	EGGGSIIHIV
Gly_maxATHB-8-like	GSLVVCERSL	NNTQNGPAMP	PVQHFVRADM	LASGYLIRPC	EGGGSIIHIV
Sol_lycATHB-15-like	GSLVICERSL	NNTQNGPSMP	PVQSFVRADI	LPSGYLIRPC	EGGGSIIHIV
Gly_maxATHB-8-likeb	GSFVVCERSL	NNTQNGPAMP	PVQHFVRADM	LPSGYLIRPC	EGGGSIIHIV
Med_truXP_003603630.1	GSLVVCERSL	NNTQNGPSMP	PVPHFVRAEV	LPSGYLIRPC	EGGGSIIHIV

AmTr_v1.0_scaffold00148.15	DHLNLEAWSV	PEVLRPLYES	SKVLAQKMTI	AALRHIRQIA	QEMSGEV--V
AmTr_v1.0_scaffold00056.60	DHMDLEPWSV	PEVLRPLYES	STVLAQKMTM	AALRHRLRQIA	QEVSQNT--V
AmTr_v1.0_scaffold00155.45	DHVDLEAWN	PEVLRPLYES	SKILAQKMTL	AALRHIRQIA	HEASGEV--N
Ara_thaPHABULOSA	DHVDLDAWSV	PEVLRPLYES	SKILAQKMTV	AALRHVRQIA	QETSQGEV--Q
Ara_thaATHB15	DHMDLEACSV	PEVLRPLYES	PKVLAQKTTM	AALRQLKQIA	QEVTQTNSSV
Ara-thaPHAVOLUTA	DHVDLDVSSV	PEVLRPLYES	SKILAQKMTV	AALRHVRQIA	QETSQGEV--Q
Ara_thaATHB8	DHFDLEPWSV	PEVLRSLYES	STLLAQRTTM	AALRYLRQIS	QEISQPN--V
Ara_thaREVOLUTA	DHLNLEAWSV	PDVLRPLYES	SKVVAQKMTI	AALRYIRQLA	QESNGEV--V
Vit_vinHOX32-like	DHVDLDAWSV	PEVLRPLYES	SKILAQKTTV	AALRHIRQIA	QETSQGEI--Q
The_cacXP_007022870.1	DHVDLDVWSV	PEVLRPLYES	SKILAQKMTI	AALRHIRQIA	QETSQGEI--Q
Ory_satHOX32	DHVDLDAWSV	PEVLRPLYES	PKILAQKMTI	AALRHIRQIA	HESSGEM--P
Pru_perppa001343mg	DHVDLDAWSV	PEVLRSLYES	SKILAQKMTI	SALRHIRQIA	QETSQGEI--Q
Bra_disHOX32-like	DHVDLDAWSV	PEVLRPLYES	PKILAQKMTI	AALRHIRQIA	HESSGEM--P
Pop_tripHABULOSA	DHVDLDVWSV	PEVLRPLYES	SKILAQKMTM	AALRHIRQIA	QETSQGEI--Q
Pop_tripHABULOSAb	DHVDLDVWSV	PEVLRPLYES	SKILAQKMTM	AALRYIRQIA	QETSQGEI--Q
Fra_vesHOX32-like	DHVDLDAWSV	PEVLRSLYES	SKIIAQKMTV	AALRHIRQIA	QEATQGEI--Q
Gly_maxATHB-14-like	DHIDLDVWSV	PEVLRPLYES	SKILAQKLT	AALOHIRQIA	LESSQGEI--Q
Gly_maxREVOLUTA-like	DHLNLEAWSV	PEVLRPLYES	SKVVAQKMTI	AALRYIRQIA	QETSQGEV--V
Gly_maxREVOLUTA-likeb	DHLNLEAWSV	PEVLRPLYES	SKVVAQKMTI	AALRYIRQIA	QETSQGEV--V
Pru_perREV IFL1	DHLNLEAWSV	PEVLRPLYES	SKVVAQKMTI	AALRYIRQIA	QETSQGEV--V
Ory_satHOX33	DHVDLDAWSV	PEVLRPLYES	PKILAQKMTI	AALRHIRQIA	HESSQGEI--P
Sol_tubATHB-14-like	DHIDLDAWSV	PEVLRPLYES	SKILAQKMTM	AALRHIRQIA	QETSQGEI--Q
The_cacXP_007022872.1	DHVDLDVWSV	PEVLRPLYES	SKILAQKMTI	AALRHIRQIA	QETSQGEI--Q
Ory_satHOX33-like	DHVDLDAWSV	PEVLRPLYES	PKILAQKMTI	AALRHIRQIA	HESSQGEI--P
Sol_lycREVOLUTA-like	DHLNLEAWSA	PEILRPLYES	SKVVAQKMTI	AALRYARQLA	QETSQGEV--V
Sol_lycHOX32-like	DHIDLDAWSV	PEVLRPLYES	SKILAQKTTM	AALRHIRQIA	QETSQGEI--Q
Gly_maxATHB-14-likeb	DHVDLDVWSV	PEVLRPLYES	PKFLAQKLT	AALRNVRQIA	QESSQGEV--Q
Pop_tripX_006378973.1	DHLNLAQWSV	PEVLRPLYES	SKAVAQKVTI	TALRHVRQIA	HETSQGEV--V
Ory_satACA64837.1	DHVDLDAWSV	PEVLRPLYES	PKILAQKMTI	AALRHIRQIA	HESSQGEI--P
Vit_vin013992	DHLNLEAWSV	PEVLRPLYES	SRVVAQKMTI	AALRYIRQIA	QETSQGEV--V
Ory_satOsJ_11861	DHVDLDAWSV	PEVLRPLYES	PKILAQKMTI	AALRHIRQIA	HESSGEM--P
Sol_tubREVOLUTA-like	DHLNLEAWSA	PEILRPLYES	SKVVAQKMTI	AALRYARQLA	QETSQGEV--V
Gly_maxATHB-14-likec	DHVDLDVWSV	PEVLRPLYES	PKFLAQKLT	AALRHARQIA	QESSQGDV--H
The_cacXP_007024277.1	DHMDLEPWRV	PEVLRPLYES	STVLAQKTTM	AALRQLRQIA	QEVSQSN--V
Vit_vinATHB-15-like	DHMDLEPWSV	PEVLRPLYES	STVLAQKTTM	AALRQLRQIA	QEVSQSN--V
Ric_comXP_002515977.1	DHMDLEPWSV	PEVLRPLYES	STVLAQKTTM	AALRHRLRQIA	QEASQSN--V
The_cacXP_007016751.1	DHMNLEAWSV	PEVLRPLYES	SKVIAQKMTI	AALRYIRQIA	QETSQGEV--V
Sol_tubHOX32-like	DHIDLDAWSV	PEVLRPLYES	SKILAQKTTM	AALRHIRQIA	QETSQGEI--Q
Sol_lycATHB-14-like	DHIDLDACSV	PEVLRPLYES	SKILAQKLT	AAFRYIRQIA	QETSQGEI--Q
Sol_tubATHB-14-like_X1	DHIDLDACSV	PEVLRPLYES	SKILAQKMTM	AAFRYIRQIA	QETSQGEI--Q
Med_truATHB-14	DHVDLDVWSV	PEVLRPLYES	SKILAQKLT	AALOHIKQIA	QESSQGEI--Q
Zea_mayNP_001142394.1	DHVNLAQWSV	PEVLRPLYES	PKILAQKMTA	AALRHIRQIA	HESSQGEI--P
Vit_vinREVOLUTA	DHLNLEAWSV	PEVLRPLYES	SRVVAQKMTI	AALRYIRQIA	QETSQGEV--V
Ory_braHOX32-like	DHVDLDAWSV	PEVLRPLYES	PKILAQKMTI	AALRHIRQIA	HESSGEM--P
Ric_comXP_002529946.1	DHLNLEAWSV	PEVLRPLYES	SKVVAQKMTI	AALRFIRQIA	QETSQGEV--V
Tha_cacXP_007016749.1	DHMNLEAWSV	PEVLRPLYES	SKVIAQKMTI	AALRYIRQIA	QETSQGEV--V
Fra_vesREVOLUTA-like	DHLNLEAWSV	PEVLRPLYES	SKVVAQKRTI	AALRYIRQIA	QETSQGEV--V
Zea_mayNP_001146215.1	DHVDLNACSV	PEVLRPLYES	PKILAQKMTA	AALRHIRQIA	HESSQGEI--P
The_cacXP_007012152.1	DHMDLEPWSV	PEVLRPLYES	STLLAQKTTM	AALRHRLRQIS	QEISQPN--V
Pru_perppa001386mg	DHMDLEPWSV	PEVLRPLYES	STLLAQKTTM	AALRNLRQIS	QEVSQPN--A
Pop_triAAX19057.1	DHMDLEPWSV	PEVLRPLYES	STLLAQKTTM	AALRHRLRQIS	QEVSQPN--V
Pop_triXP_002309538.2	DHMDLEPWSV	PEVLRPLYES	STLLAQKTTM	AALRHRLRQIS	QEVSQPN--V
Fra_vesATHB-8-like	DHMDLEPWNV	PEVLRPLYES	STLLAQKTTM	AALRNLRQIS	QEVSQPN--T
Pop_triXP_002324794.1	DHMDLEPWSV	PEVLRPLYES	STLLAQKTTM	AALRHRLRQIS	QEISQPN--V
Vit_vin009744	DHMDLEPWSV	PEVLRPLYES	STLLAQKTTM	AALRHRLRQIS	QEVSQPN--N
Gly_maxATHB-8-like	DHMDLEPWSV	PEVLRPLYES	SMLLAQRTTM	AALRHRLRQIS	QEVSQPT--V
Sol_lycATHB-15-like	DHMDLEPWSV	PEVLRPLYES	STLLSQRTTM	AALRHRLRQIS	QEISHPT--V
Gly_maxATHB-8-likeb	DHMDLEPWSV	PEVLRPLYES	SMLLAQRTTM	AALRHRLRQIS	QEVSQPS--V
Med_truXP_003603630.1	DHMDLEPWSV	PEVLRPLYES	SMLLAQRTTM	AALRHRLRQIS	QEVSQPS--V

AmTr_v1.0_scaffold00148.15	FGWGRQPAVL	RTFSQRLSRG	FNDVAVNGFAD	DGWS-LMSSD	GVEDVSVVIN
AmTr_v1.0_scaffold00056.60	VGWGRQPAAL	RALSQRLSKG	FNEALNGFTD	DGWS-LLGND	GMDDVTILVN
AmTr_v1.0_scaffold00155.45	YGGGRQPAVL	RTFSQRLSRG	FNDVAVNGFAD	DGWS-LMSSD	GVEDVTIVLN
Ara_thaPHABULOSA	YGGGRQPAVL	RTFSQRLCRG	FNDVAVNGFVD	DGWS-PMGSD	GAEDVTVMIN
Ara_thaATHB15	NGWGRRPAAL	RALSQRLSRG	FNEAVNGFTD	EGWS-VIG-D	SMDDVTITVN
Ara-thaPHAVOLUTA	YSGGRQPAVL	RTFSQRLCRG	FNDVAVNGFVD	DGWS-PMSSD	GGEDITIMIN
Ara_thaATHB8	TGWGRRPAAL	RALSQRLSKG	FNEAVNGFSD	EGWS-ILLES	GIDDVTLVLN
Ara_thaREVOLUTA	YGLGRQPAVL	RTFSQRLSRG	FNDVAVNGFGD	DGWS-TMHCD	GAEDIIVAIN
Vit_vinHOX32-like	YGGGRQPAVL	RTFSQRLCRG	FNDVAVNGFAD	DGWS-LMGSD	GVEDVTIVIN
The_cacXP_007022870.1	YGGGRQPAVL	RTFSQRLCRG	FNDVAVNGFAD	DGWS-LMGSD	GVEDVTIMIN
Ory_sathOX32	YGGGRQPAVL	RTFSQRLSRG	FNDVAVNGFPD	DGWS-LMSSD	GAEDVTIAFN
Pru_perppa001343mg	YGGGRQPAVL	RTFCQRLCRG	FNDVAVNGFAD	DGWS-LMGSD	GVEDVTITIN
Bra_dishOX32-like	YGGGRQPAVL	RTFSQRLSRG	FNDVAVNGFLD	DGWS-LMSSD	GAEDVTIAIN
Pop_tripHABULOSA	YGGGRQPAVL	RTFSQRLCRG	FNDVAVNGFTD	DGWS-LLGSD	GGDDVTIVIN
Pop_tripHABULOSAb	YGGGRQPAVL	RTFSQRLCRG	FNDVAVNGFTD	SGWS-LLDGD	GGDDVTIVIN
Fra_vesHOX32-like	YAGGRQPAVL	RTFSQRLCRG	FNDVAVNGFAD	DGWS-LLGSD	GAEDVTIAIN
Gly_maxATHB-14-like	YGGGRQPAVL	RTFSQRLCRG	FNDVAVNGFVD	DGWS-LMGTD	GVEDVTIAIN
Gly_maxREVOLUTA-like	YGLGRQPAVL	RTFSQRLSRG	FNDVAVNGFND	DGWT-VLNCD	GAEDVIAVN
Gly_maxREVOLUTA-likeb	YGLGRQPAVL	RTFSQRLSRG	FNDVAVNGFND	DGWT-VLNCD	GAEDVFIIVN
Pru_perREV_IFL1	YSLGRQPAVL	RTFSQRLIRG	FNDVAVNGFND	DGWS-LINCD	GAEDVIAVN
Ory_sathOX33	YGAGROPVAVF	RTFSQRLSRG	FNDVAVSGFPD	DGWS-LLSSD	GSEDITISVN
Sol_tubATHB-14-like	YTGGROPVAVL	RALSQRLCRG	FNDVAVSGFVD	DGWT-IMDSD	GVEDVTIAIN
The_cacXP_007022872.1	YGGGRQPAVL	RTFSQRLCRG	FNDVAVNGFAD	DGWS-LMGSD	GVEDVTIMIN
Ory_sathOX33-like	YGAGROPVAVF	RTFSQRLSRG	FNDVAVSGFPD	DGWS-LLSSD	GSEDITISVN
Sol_lycREVOLUTA-like	YGLGRQPAVL	RTFSQRLCRG	FNDVAVNGFGD	DGWS-MLSSD	GAEDVIVAVN
Sol_lycHOX32-like	YSGGRQPAVL	RALSQRLCRG	FNDVAVNGFVD	DGWT-ITDSD	GVEDVTIAIN
Gly_maxATHB-14-likeb	YGGGRQPAVL	RTFSQRLCKG	FNDVAVNGFVD	DGWS-LMGN	GVEDVTIGIN
Pop_triXP_006378973.1	YGLGRQPAVL	RTFSQRLSRG	FNDVAVNGFND	DGWS-LMNSD	GAEDVIAVN
Ory_satACA64837.1	YGAGROPVAVF	RTFSQRLSRG	FNDVAVSGFPD	DGWS-LLSSD	GSEDITISVN
Vit_vin013992	YGLGRQPAVL	RTFSQRLSRG	FNDVAVNGFND	DGWS-LMSCD	GAEDVIAVN
Ory_satOsJ_11861	YGGGRQPAVL	RTFSQRLSRG	FNDVAVNGFPD	DGWS-LMSSD	GAEDVTIAFN
Sol_tubREVOLUTA-like	YGLGRQPAVL	RTFSQRLCRG	FNDVAVNGFGD	DGWS-MLSSD	GAEDVIVAVN
Gly_maxATHB-14-likec	YGGGRQPAVL	RTFSQRLCKG	FNDVAVNGFVD	DGWS-LMGN	GVEDVTIAIN
The_cacXP_007024277.1	TGWGRRPAAL	RALSQRLSRG	FNEALNGFTD	EGWS-MMGND	GMDDVTILVN
Vit_vinATHB-15-like	TGWGRRPAAL	RALSQRLSRG	FNEALNGFTD	EGWS-MMGND	GIDDVTLVLN
Ric_comXP_002515977.1	TNWGRRPAAL	RALSQRLSRG	FNEALNGFTD	EGWS-MMGND	GMDDVTILVN
The_cacXP_007016751.1	YGLGRQPAVL	RTFSQRLSRG	FNDVAVNGFND	DGWS-IMNCD	GAEDVIAIN
Sol_tubHOX32-like	YSGGRQPAVL	RALSQRLCRG	FNDVAVNGFVD	DGWT-ITDSD	GVEDVTIAIN
Sol_lycATHB-14-like	YAGGRQPAVL	RAFSQRLCRG	FNNVAVSGFID	DGWT-IMGSD	GVEDVTIIVN
Sol_tubATHB-14-like_X1	YAGGRQPAVL	RAFSQRLCRG	FNNVAVSGFID	DGWT-IMGSD	GVEDVTIIVN
Med_truATHB-14	YGGGRQPAVL	RTFSQRLCRG	FNDVAVNGFVD	DGWS-LLGND	GVEDVTIIVN
Zea_mayNP_001142394.1	YGAGROPVAVL	RTFSQRLSRG	FNDVAVSGFPD	DGWS-CLLNTD	GAEDITVTIN
Vit_vinREVOLUTA	YGLGRQPAVL	RTFSQRLSRG	FNDVAVNGFND	DGWS-LMSCD	GAEDVIAVN
Ory_braHOX32-like	YGGGRQPAVL	RTFSQRLSRG	FNDVAVNGFPD	DGWS-PMSSD	GAEDVTIAFN
Ric_comXP_002529946.1	YGLGRQPAVL	RTFSQRLSRG	FNDVAVNGFND	DGWS-LMSCD	GAEDVIVTIN
Tha_cacXP_007016749.1	YGLGRQPAVL	RTFSQRLSRG	FNDVAVNGFND	DGWS-IMNCD	GAEDVIAIN
Fra_vesREVOLUTA-like	YSLGRQPAVL	RTFSQRLIRG	FNDVAVNGFND	DGWS-LINCD	GAEDIMAVN
Zea_mayNP_001146215.1	YGAGROPVAVL	RTFSQRLSRG	FNDVAVSGFPD	DGWS-LLSSD	GAEDISITIN
The_cacXP_007012152.1	TGWGRRPAAL	RALSQRLSKG	FNEAVNGFTD	EGWS-MLES	GVEDVTLLVN
Pru_perppa001386mg	AGWGRRPAAL	RALSQRLSKG	FNEAVNGFTD	EGWS-ILES	GVEDVTLLVN
Pop_triAAX19057.1	TGWGRRPAAL	RALSQRLSKG	FNEAVNGFAD	EGWS-MLES	GIDDVTVLVN
Pop_triXP_002309538.2	TGWGRRPAAL	RALSQRLSKG	FNEAVNGFAD	EGWS-MLES	GIDDVTVLVN
Fra_vesATHB-8-like	NGWGRRPAAL	RALSQRLSKG	FNEAVNGFTD	EGWS-ILES	GVEDVTLLVN
Pop_triXP_002324794.1	TGWGRRPAAL	RALSQRLSKG	FNEAVNGFAD	EGWS-LLES	GIDDVTVLVN
Vit_vin009744	TGWGRRPAAL	RALGQRLTKG	FNEAVNGFTD	EGWS-MMES	GIDDVTVLVN
Gly_maxATHB-8-like	TGWGRRPAAL	RALSQRLSKG	FNEAVNGFAD	DGWS-MLES	GIDDVTVLVN
Sol_lycATHB-15-like	SGWGRRPAAL	RALGQRLSKG	FNEAVNGFTD	EGWS-MLES	GVEDVTLLVN
Gly_maxATHB-8-likeb	TGWGRRPAAL	RALSQRLSKG	FNEAVNGFAD	DGWS-MLES	GIDDVTVLVN
Med_truXP_003603630.1	TGWGRRPAAL	RALSQRLSKG	FNEAVNGFTD	DGWS-MLDSD	GIDDVTVLVN

AmTr_v1.0_scaffold00148.15	TSPNKHVG--	-----	MSGGILCAKS	SMLL	-----
AmTr_v1.0_scaffold00056.60	SSPAKIMAAN	LTS-TNGFPT	VCGAVLCAKA	SMLL	-----
AmTr_v1.0_scaffold00155.45	TNPSKLFAN	VNS-AAAIST	FGGGILCAKA	SMLL	-----
Ara_thaPHABULOSA	LSPGKFGGSQ	YGN--SFLPS	FGSGVLCACA	SMLL	-----
Ara_thaATHB15	SSPDKLMGLN	LTF-ANGFAP	VSNVVLCAKA	SMLL	-----
Ara-thaPHAVOLUTA	SSSAKFAGSQ	YGS--SFLPS	FGSGVLCACA	SMLL	-----
Ara_thaATHB8	SSPTKMMMTS	SLPFANGYTS	MPSAVLCAKA	SMLL	-----
Ara_thaREVOLUTA	STK-----H	LNNISNSLSF	L-GGVLCAKA	SMLL	-----
Vit_vinHOX32-like	SSPSKFLGPQ	YNS--TMFPT	FGGGVLCACA	SMLL	-----
The_cacXP_007022870.1	SSPGKFLGSQ	YNT--SMFPS	FGGGVLCACA	SMLL	-----
Ory_satHOX32	SSPNKLVGSH	VNS-SQLFSA	IGGGILCAKA	SMLL	-----
Pru_perppa001343mg	SSPNKFLGSQ	YNA--SIFPT	FGGGVLCACA	SMLL	-----
Bra_disHOX32-like	SSPNKLVGSH	VNS-SQLFSA	IGGGILCAKA	SMLL	-----
Pop_triPHABULOSA	SSPNKFLGSQ	YNA--SMFPT	FGGGVLCACA	SMLL	-----
Pop_triPHABULOSAb	SSPTKFLGSQ	YNA--SISPT	F-GGVLCAKA	SMLL	-----
Fra_vesHOX32-like	SSPNKFLGSQ	YNT--SIFPS	FGGGVLCACA	SMLL	-----
Gly_maxATHB-14-like	SSPNKFLGSN	YNA--SMFPA	FGGGVLCACA	SMLL	-----
Gly_maxREVOLUTA-like	STKN--LSGT	SNP-ASSLTF	L-GGILCAKA	SMLL	-----
Gly_maxREVOLUTA-likeb	STKN--LSGT	SNP-ASSLTF	L-GGILCAKA	SMLL	-----
Pru_perREV IFL1	STKN--L-TT	SNP-ANSLAL	IGGGVLCACA	SMLL	-----
Ory_satHOX33	SSPNKLVGSH	VSP-NPLFST	VGGGILCAKA	SMLL	-----
Sol_tubATHB-14-like	SSSSKFLGSQ	YNT-LSILPT	F-GGVLCAKA	SMLL	-----
The_cacXP_007022872.1	SSPGKFLGSQ	YNT--SMFPS	FGGGVLCACA	SMLL	-----
Ory_satHOX33-like	SSPNKLVGSH	VSP-NPLFST	VGGGILCAKA	SMLL	-----
Sol_lycREVOLUTA-like	SRKN--LATT	SIP---LSP	L-GGVLCAKA	SMLL	-----
Sol_lycHOX32-like	SSSSKFLGSQ	YNT-LSILPT	F-GGVLCAKA	SMLL	-----
Gly_maxATHB-14-likeb	SSPNKFFSSH	YNT--SMLPA	FGGGVLCACA	SMLL	-----
Pop_triXP_006378973.1	TTKN--LISA	NNP-AHLSLF	L-GGILCAKA	SMLL	-----
Ory_satACA64837.1	SSPNKLVGSH	VSP-NPLFST	VGGGILCAKA	SMLL	-----
Vit_vin013992	STKN--LNTT	SNP-ANSL-S	LPGGVLCACA	SMLL	-----
Ory_satOsJ_11861	SSPNKLVGSH	VNS-SQLFSA	IGGGILCAKA	SMLL	-----
Sol_tubREVOLUTA-like	SRKN--LATT	SVP---LSS	L-GGILCAKA	SMLL	-----
Gly_maxATHB-14-likec	SSPNKFFGSH	YNT--SMLPA	FGGGVLCACA	SMLL	-----
The_cacXP_007024277.1	SSPDKLMGLN	LSF-ANGFPA	VSNVVLCAKA	SMLL	-----
Vit_vinATHB-15-like	SSPEKLTGLN	LSF-ANGFPA	VSNVVLCAKA	SMLL	QVSFIS CSDVLFTH
Ric_comXP_002515977.1	SSPEKLMGLN	LSF-SNGFPA	VSNVVLCAKA	SMLL	-----
The_cacXP_007016751.1	SSKN--LSSS	SNP-ANALSF	L-GGVLCAKA	SMLL	-----
Sol_tubHOX32-like	SSSSKFLGSQ	YNT-LSILPT	F-GGVLCAKA	SMLL	-----
Sol_lycATHB-14-like	SSPSKFLDAQ	YNT-LSILPT	F-GGVLCAKA	SMLL	-----
Sol_tubATHB-14-like_X1	SSPSKFLDAQ	YNT-LSILPT	F-GGVLCAKA	SMLL	-----
Med_truATHB-14	SSPNKFLGSN	YSS--MFPT	FGGGVLCACA	SMLL	-----
Zea_mayNP_001142394.1	SSPNKLVGSH	VSA-SPLFSA	MGGGIMCAKA	SMLL	-----
Vit_vinREVOLUTA	STKN--LNTT	SNP-ANSL-S	LPGGVLCACA	SMLL	-----
Ory_braHOX32-like	SSPNKLVGSH	VNS-SQLFSA	IGGGILCAKA	SMLL	-----
Ric_comXP_002529946.1	STKN--LSST	SNA-ANSFAF	L-GGILCAKA	SMLL	-----
Tha_cacXP_007016749.1	SSKN--LSSS	SNP-ANALSF	L-GGVLCAKA	SMLL	-----
Fra_vesREVOLUTA-like	STKN--L-TT	TNP-ANSFAF	L-GGILCAKA	SMLL	-----
Zea_mayNP_001146215.1	SSPNKLIGSD	VSP-SPFFSA	MGGGIMCAKA	SMLL	-----
The_cacXP_007012152.1	SSPGKMMGAN	LSY-SNGFPS	MSNAVLCAKA	SMLL	-----
Pru_perppa001386mg	SSPGKMMGAN	LYA--NGVPS	MSNAVLCAKA	SMLL	-----
Pop_triAAX19057.1	SSPAKMMGVN	FSY-ANGFPS	MSNAVLCAKA	SMLL	-----
Pop_triXP_002309538.2	SSPAKMMGVN	FSY-ANGFPS	MSNAVLCAKA	SMLL	-----
Fra_vesATHB-8-like	SSPGKMMGAN	LYA--NGVPS	MSNAVLCAKA	SMLL	-----
Pop_triXP_002324794.1	SSPTKTMGVN	FSY-DNGFPS	MNAVLCAKA	SMLL	-----
Vit_vin009744	SSPAKMMGVN	LSY-ASGFPS	MSNAVLCAKA	SMLL	-----
Gly_maxATHB-8-like	SSPSKMMGVN	LGYNNGFPS	VSSLLCAKA	SMLL	-----
Sol_lycATHB-15-like	SSPSKLMGAN	ISY-ANGFPS	MSSAVLCAKA	SMLL	-----
Gly_maxATHB-8-likeb	SSPSKMMGVS	LVYNNMGFPS	VSSSVLCAKA	SMLL	-----
Med_truXP_003603630.1	SSPSKMMGLN	LGY--NNGFPS	VTSSVLCACA	SMLL	-----

AmTr_v1.0_scaffold00148.15	-QNVPPALLI	RFLREHRSEW	ADSNIDAYCA	ASLKANPFAI	PGSGPSRFTG
AmTr_v1.0_scaffold00056.60	-QNVPPALLI	RFLREHRSEW	ADSNIDAYS	AALKSNPGTL	PTSRMGGF-G
AmTr_v1.0_scaffold00155.45	-QNVPPALLV	RFLREHRSEW	ADSGVDAYAA	SSMRTGQFVV	PGSRTGSFPG
Ara_thaPHABULOSA	-QNVPPAVLV	RFLREHRSEW	ADYGVDAYAA	ASLRASPFVAV	PCARAGGFPS
Ara_thaATHB15	-QNVPPAILL	RFLREHRSEW	ADNNIDAYLA	AAVKVGPCS-	--ARVGGF-G
Ara-thaPHAVOLUTA	-QNVPPPLVI	RFLREHRAEW	ADYGVDAYS	ASLRATPYAV	PCVRTGGFPS
Ara_thaATHB8	-QNVPPSILL	RFLREHRQEW	ADNSIDAYS	AAIKAGPCSL	PIPRPGSF-G
Ara_thaREVOLUTA	-QNVPPAVLI	RFLREHRSEW	ADFNVDAYS	ATLKAGSFAY	PGMRPTRFTG
Vit_vinHOX32-like	-QNVPPALLV	RFLREHRSEW	ADYGVDAYS	ACLKASPYEV	PCARPGGFPS
The_cacXP_007022870.1	-QNVPPALLV	RFLREHRSEW	ADYGVDITYSA	ACLKASPYAV	PCARPGGFPS
Ory_satHOX32	-QNVPPALLV	RFLREHRSEW	ADPGVDAYS	AALRASPYAV	PGLRAGGFMG
Pru_perppa001343mg	-QSVPPALLV	RFLREHRSEW	ADYGVDAYS	ACLKASPYAV	PCARPGGFPS
Bra_disHOX32-like	-QNVPPALLV	RFLREHRSEW	ADPGVDAYS	AALRASPYAV	PGLRASGFMG
Pop_triPHABULOSA	-QNVPPALLV	RFLREHRSEW	ADYGVDAYS	ACLKASPYAV	PCARPGGFPS
Pop_triPHABULOSAb	-QNVPPALLV	RFLREHRSEW	ADYGVDVYS	ACLKASPYAV	PCARPGGFPS
Fra_vesHOX32-like	-QSVPPALLV	RFLREHRSEW	ADYGVDAYS	ACLKASPYAV	PCARPGGFPS
Gly_maxATHB-14-like	-QNVPPALLV	RFLREHRSEW	ADYGVDAYS	ACLKASPYAV	PCARPGGFPS
Gly_maxREVOLUTA-like	-QNVPPAVLV	RFLREHRSEW	ADFNVDAYS	ASLKAGTYAY	PGMRPTRFTG
Gly_maxREVOLUTA-likeb	-QNVPPAVLV	RFLREHRSEW	ADFSVDAYS	ASLKAGTYAY	PGMRPTRFTG
Pru_perREV_IFL1	-QNVPPAVLV	RFLREHRSEW	ADFNVDAYS	ASLKAGSYAY	PGMRPTRFTG
Ory_satHOX33	-QNVPPALLV	RFLREHRSEW	ADPGVDAYS	ASLRASPYAV	PGLRTSGFMG
Sol_tubATHB-14-like	-QNVPPALLV	RFLREHRSEW	ADYGVDAYSS	ASLKASPYAV	PCARPGGFPS
The_cacXP_007022872.1	-QNVPPALLV	RFLREHRSEW	ADYGVDITYSA	ACLKASPYAV	PCARPGGFPS
Ory_satHOX33-like	-QNVPPALLV	RFLREHRSEW	ADPGVDAYS	ASLRASPYTV	PGLRTSGFMG
Sol_lycREVOLUTA-like	-QNVPPAVLV	RFLREHRSEW	ADFNVDVFA	SALKSCPITY	PGMRPTRFTG
Sol_lycHOX32-like	-QNVPPALLV	RFLREHRSEW	ADYGVDAYSS	ASLKASPYAV	PCARPGGFPS
Gly_maxATHB-14-likeb	-QNVPPALLV	RFLREHRSEW	ADYGVDAYSS	ACLKASPYAV	PCARPSGFPS
Pop_triXP_006378973.1	-QNVPPAVLV	RFLREHRSEW	ADFSVDAYS	ASLKAGSYAY	PGMRSMRFTG
Ory_satACA64837.1	-QNVPPALLV	RFLREHRSEW	ADPGVDAYS	ASLRASPYAV	PGLRTSGFMG
Vit_vin013992	-QNVPPAVLV	RFLREHRSEW	ADFSVDAYS	ASLKASPYSY	PGMRPTRFTG
Ory_satOsJ_11861	-QNVPPALLV	RFLREHRSEW	ADPGVDAYS	AALRASPYAV	PGLRAGGFMG
Sol_tubREVOLUTA-like	-QNVPPAVLV	RFLREHRSEW	ADFNVDVFA	SALKSCPITY	PGMRPTRFTG
Gly_maxATHB-14-likec	-QNVPPALLV	RFLREHRSEW	ADYEVDAYSS	ACLKASPYAV	PCARPSGFPS
The_cacXP_007024277.1	RFLREHRSEW	ADSSIDAYS	AAVKVGPCSL	PGSRVGGF-G	
Vit_vinATHB-15-like	FQNVPPAILL	RFLREHRSEW	ADNNIDAYS	AAVKVGPCSL	PGSRVGGF-G
Ric_comXP_002515977.1	-QNVPPAILL	RFLREHRSEW	ADNNIDAYS	AAIKVGPCTL	PGTRIGSF-G
The_cacXP_007016751.1	-QNVPPAVLV	RFLREHRSEW	ADFNVDAYS	ASLKAGTYSY	PGMRPTRFTG
Sol_tubHOX32-like	-QNVPPALLV	RFLREHRSEW	ADYGVDAYSS	ASLKASPYAV	PCARPGGFPS
Sol_lycATHB-14-like	-QDVCPALLV	RFLREHRSEW	ADYGVDAYSS	ASLKASPYAV	PCARPGVFP
Sol_tubATHB-14-like_X1	-QDVCPALLV	RFLREHRSEW	ADYGVDAYSS	ASLKASPYAV	PCARPGVFP
Med_truATHB-14	-QNVPPALLV	RFLREHRSEW	ADYGVDAYS	TCLKSSPYAV	PCPRPGGFPS
Zea_mayNP_001142394.1	-QNVPPALLV	RFLREHRSEW	ADPGIDAYSV	ASLRANPYTV	PGLRAGGFMG
Vit_vinREVOLUTA	-QNVPPAVLV	RFLREHRSEW	ADFSVDAYS	ASLKASPYSY	PGMRPTRFTG
Ory_braHOX32-like	-QNVPPALLV	RFLREHRSEW	ADPGVDAYS	AALRASPYAV	PGLRAGGFMG
Ric_comXP_002529946.1	-QNVPPAVLV	RFLREHRSEW	ADFNVDAYS	ASLKAGSYAF	PGMRPTRFTG
Tha_cacXP_007016749.1	-QNVPPAVLV	RFLREHRSEW	ADFNVDAYS	ASLKAGTYSY	PGMRPTRFTG
Fra_vesREVOLUTA-like	-QNVPPAVLV	RFLREHRSEW	ADFNVDAYS	ASLKSGSYAY	PGMRPTRFTG
Zea_mayNP_001146215.1	-QNVPPALLV	RFLREHRSEW	ADPGVDAYS	ASLRANPYAV	PGLRAGGFMG
The_cacXP_007012152.1	-QNVPPAILL	RFLREHRSEW	ADSGIDAYS	AAVKAGPCSL	PVSRGGSF-G
Pru_perppa001386mg	-QNVPPAILL	RFLREHRSEW	ADRSIDAYS	AAIKPGPCGL	LGSRAGGF-G
Pop_triAAX19057.1	-QNVPPAILL	RFLREHRSEW	ADSGIDAYAA	AAVKAGPCSL	PMSRAGNF-G
Pop_triXP_002309538.2	-QNVPPAILL	RFLREHRSEW	ADSGIDAYAA	AAVKAGPCSL	PMSRAGNF-G
Fra_vesATHB-8-like	-QNVPPAILL	RFLREHRSEW	ADRSIDAYS	AAIKAGPCGM	IGSRAGSF-G
Pop_triXP_002324794.1	-QNVPPAILL	RFLREHRSEW	ADNGIDAYAA	SAIKAGPCSL	PVSRAGNF-G
Vit_vin009744	-QNVPPAILL	RFLREHRSEW	ADSSIDAYS	AAVKAGCTL	PVSRAGGY-G
Gly_maxATHB-8-like	-QNVPPAILL	RFLREHRSEW	ADSSIDAYS	AAIKAGPCSL	PGARPGGF-G
Sol_lycATHB-15-like	-QNVPPPILL	RFLREHRSEW	ADSGIDAYS	AAVKAGPCSI	PVTRTGSF-G
Gly_maxATHB-8-likeb	-QNVPPAILL	RFLREHRSEW	ADSSIDAYS	AAIKAGPCSL	PGARSGGF-G
Med_truXP_003603630.1	-QNVPPAILL	RFLREHRSEW	ADTSIDAYS	AAIKAGPCSL	PGARTGAF-G

AmTr_v1.0_scaffold00148.15	SQIILPLAHT	VENEE	-----	FVEV	IRLEGHGFPO	EEAVVC	RDL
AmTr_v1.0_scaffold00056.60	GQVILPLAHT	VEHEE	-----	FLEV	IKLENHGLVQ	DDSIIP	RDM
AmTr_v1.0_scaffold00155.45	SQVILPLAQT	VEHEE	-----	FLEV	IRLEGHGFSQ	DDAVLP	RDM
Ara_thaPHABULOSA	NQVILPLAQT	VEHEE	-----	SLEV	VRLEGHAYSP	EDMGLA	RDM
Ara_thaATHB15	GQVILPLAHT	IEHEE	-----	FMEV	IKLEGLGHSP	EDAIVP	RDI
Ara-thaPHAVOLUTA	NQVILPLAQT	LEHEE	-----	FLEV	VRLEGGHAYSP	EDMGLS	RDM
Ara_thaATHB8	GQVILPLAHT	IENEE	-----	FMEV	IKLESGLGHYQ	EDMMMP	ADI
Ara_thaREVOLUTA	SQIIMPLGHT	IEHEE	-----	MLEV	VRLEGHSLAQ	EDAFMS	RDV
Vit_vinHOX32-like	SQVILPLAHT	VEHEE	-----	FLEV	VRLEGHAFSP	EDVALT	RDM
The_cacXP_007022870.1	SQVILPLAHT	VEHEE	-----	FLEV	VRLEGHAFTP	EDVALA	RDM
Ory_satHOX32	SQVILPLAHT	LEHEE	-----	FLEV	IRLEGHSLCH	DEVVLS	RDM
Pru_perppa001343mg	SQVILPLAQT	VENEE	-----	FLEV	VRLEGHAFSP	EDVALA	RDM
Bra_disHOX32-like	SQVILPLAHT	LEHEE	-----	FLEV	IRLEGHSLCH	DEVVLS	RDM
Pop_triPHABULOSA	SQVILPLAHT	MEHEE	-----	FLEV	VRLEGHAFSP	EDVALA	RDM
Pop_triPHABULOSAb	SQVILPLAHT	VEHEE	-----	FLEV	VRLEGHAFSP	EDVALA	QDM
Fra_vesHOX32-like	SQVILPLAHT	VENEE	-----	FLEV	VRLEGHAFSP	EDVALA	RDM
Gly_maxATHB-14-like	TQVILPLAHT	IEHEE	-----	FLEV	VRIEGHAFSP	EDVAMA	RDM
Gly_maxREVOLUTA-like	SQIIMPLGHT	IEHEE	-----	MLEV	IRLEGHSLAQ	EDAFVS	RDI
Gly_maxREVOLUTA-likeb	SQIIMPLGHT	IEHEE	-----	MLEV	IRLEGHSLAQ	EDAFVS	RDI
Pru_perREV_IFL1	GQIIMPLGHT	IEHEE	-----	LLEV	VRLEGHSLTQ	EDAFAS	RDI
Ory_satHOX33	SQVILPLAHT	LEHEE	-----	FLEV	IRLEGHGFSH	DEVLLS	RDM
Sol_tubATHB-14-like	SQVILPLAQT	VEHEE	-----	FLEV	VRLEGPAPSP	EDIALS	RDM
The_cacXP_007022872.1	SQVILPLAHT	VEHEE	-----	FLEV	VRLEGHAFTP	EDVALA	RDM
Ory_satHOX33-like	SQVILPLAHT	LEHEE	-----	FLEV	IRLEGHGFSH	DEVLLS	RDM
Sol_lycREVOLUTA-like	SQIIMPLGHT	IEHEE	-----	MLEV	IRLEGHSIGQ	EDAFMP	RDI
Sol_lycHOX32-like	SQVILPLAQT	VEHEE	-----	FLEV	VRLEGPAPSP	EDIALS	RDM
Gly_maxATHB-14-likeb	SHVIIPLAHT	IEHEE	-----	FLEV	VRIEGNAFPP	DDVALA	CDM
Pop_triXP_006378973.1	SQIIMPLGHT	IEQEE	-----	LLEV	IRLEGHSAFQ	EDAFVS	RDI
Ory_satACA64837.1	SQVILPLAHT	LEHEE	-----	FLEV	IRLEGHGFSH	DEVLLS	RDM
Vit_vin013992	SQIIMPLGHT	IEHEE	-----	LLEV	IRLEGHSLAH	EDAFMS	RDI
Ory_satOsJ_11861	SQVILPLAHT	LEHEE	-----	FLEV	IRLEGHSLCH	DEVVLS	RDM
Sol_tubREVOLUTA-like	SQIIMPLGHT	IEHEE	-----	MLEV	IRLEGHSIGQ	EDAFMP	RDI
Gly_maxATHB-14-likec	SHVIIPLAHT	IEHEE	-----	FLEV	VRIEGNAFPP	DDVAWA	CDM
The_cacXP_007024277.1	GQVILPLAHT	IEHEE	-----	FLEV	IKLEGVHSP	EDAIMP	RDV
Vit_vinATHB-15-like	SQVILPLAHT	IEHEE	-----	FLEV	IKLEGVGHCP	EDAMMP	RDM
Ric_comXP_002515977.1	GQVILPLAHT	IEHEE	-----	FLEV	IKLEGGHSP	EDPIMP	RDM
The_cacXP_007016751.1	SQIIMPLGHT	IEHEE	-----	LLEV	IRLEGHSLAQ	EDAFLS	RDI
Sol_tubHOX32-like	SQVILPLAQT	VEHEE	-----	FLEV	VRLEGPAPSP	EDIALS	RDM
Sol_lycATHB-14-like	SQVILPLAQT	VEHEE	-----	FLEV	VRLEGHAFSP	EDIALS	RDM
Sol_tubATHB-14-like_X1	SQVILPLAQT	VEHEE	-----	FLEV	VRLEGHAFSP	EDIALS	RDM
Med_truATHB-14	SQVILPLAHT	IEHEE	-----	FLEV	VRIEGHAFSP	EDVALA	RDM
Zea_mayNP_001142394.1	NQVILPLART	LEHEE	-----	SLEV	IRLEGHGFSH	EEVLMS	RDM
Vit_vinREVOLUTA	SQIIMPLGHT	IEHEE	-----	LLEV	IRLEGHSLAH	EDAFMS	RDI
Ory_braHOX32-like	SQVILPLAHT	LEHEE	-----	FLEV	IRLEGHSLCH	DEVVLS	RDM
Ric_comXP_002529946.1	SQIIMPLGHT	IEHEE	-----	LLEV	IRLEGHSLVQ	EDAFVS	RDI
Tha_cacXP_007016749.1	SQIIMPLGHT	IEHEE	-----	LLEV	IRLEGHSLAQ	EDAFLS	RDI
Fra_vesREVOLUTA-like	GQIIMPLGHT	IEQEE	-----	LLEV	VRLEGHSAFQ	EEAFAS	RDI
Zea_mayNP_001146215.1	NQVILPLART	VEHEE	-----	CLEV	IRLQGHGFSH	DEVLLS	PDM
The_cacXP_007012152.1	GQVILPLAHT	IEHEE	-----	FMEV	IKLENMGHYR	DDMIMP	GDI
Pru_perppa001386mg	DQVIHPLAHT	IEHEE	-----	FMEV	IKIENMGHYR	EDMIMPAADI	
Pop_triAAX19057.1	GQVILPLAHT	IEHEEAS	-----	TSMFMEV	IKLENMGY-R	EDMLMP	GDV
Pop_triXP_002309538.2	GQVILPLAHT	IEHEEAS	-----	TSMFMEV	IKLENMGY-R	EDMLMP	GDV
Fra_vesATHB-8-like	DQVILPLAHT	IEHEE	-----	FMEV	IKIENMGHYR	DDMMMPAADI	
Pop_triXP_002324794.1	GQVILPLAHT	IENEE	-----	AKV	IKLENMGY-R	EDMLMP	GDV
Vit_vin009744	GQVILPLAHT	IEHEEANLIR	FNCLQQ	FMEV	IKLENVDHYR	EDLMMS	GDV
Gly_maxATHB-8-like	GQVILPLAHT	IEHEE	-----	FMEV	IKLENMGYYR	DDMIMP	GDV
Sol_lycATHB-15-like	GQIILPLAHT	IEHEE	-----	FMEV	IRLESIGHYQ	DDMIMP	SDI
Gly_maxATHB-8-likeb	GQVILPLAHT	IEHEE	-----	FMEV	IKLENMGYYR	DDMSIP	GDV
Med_truXP_003603630.1	GQVILPLAHT	IEHEE	-----	FMEV	IKLENMGYYR	DDMTMP	GDI

AmTr_v1.0_scaffold00148.15	YLLQLCSGVD	ENAVGAI SQL	VFAPIDDSFA	DDAPLLPSGF	RVIPLDSKT
AmTr_v1.0_scaffold00056.60	FLLQLCSGVD	ENAVGACAEL	VFAPIDPSFA	DDAPLLPSGF	RIIPLDNGV
AmTr_v1.0_scaffold00155.45	FLLQLCSGVD	ENAVGACAQL	VFAPIDESFA	DDAPLLPSGF	RVIPLDSKS
Ara_thaPHABULOSA	FLLQLCSGVD	ENVVGGCAQL	VFAPIDESFA	DDAPLLPSGF	RIIPLDOKS
Ara_thaATHB15	FLLQLCSGMD	ENAVGTCAEL	IFAPIDASFA	DDAPLLPSGF	RIIPLDSAK
Ara_thaPHAVOLUTA	YLLQLCSGVD	ENVVGGCAQL	VFAPIDESFA	DDAPLLPSGF	RVIPLDQKT
Ara_thaATHB8	FLLQMC SGVD	ENAVESCAEL	IFAPIDASFS	DDAPIIPSGF	RIIPLDSKS
Ara_thaREVOLUTA	HLLQICTGID	ENAVGACSEL	IFAPINEMFP	DDAPLVPSGF	RVIIPVDAKT
Vit_vinHOX32-like	YLLQLCSGVD	ENAAGACAQL	VFAPIDESFA	DDAPLLPSGF	RVIPLDPKT
The_cacXP_007022870.1	YLLQLCSGID	ENAVGACAQL	VFAPIDESFA	DDAPLLPSGF	RVIPLDPKT
Ory_satHOX32	YLLQLCSGVD	ENAAGACAQL	VFAPIDESFA	DDAPLLPSGF	RVIPLDGKT
Pru_perppa001343mg	YLLQLCSGVD	ENAVGSCAQL	VFAPIDESFA	DDAPLLPSGF	HVIPLDPKT
Bra_disHOX32-like	YLLQLCSGVD	ENAAGACAQL	VFAPIDESFA	DDAPLLPSGF	RVIPLDAKT
Pop_triPHABULOSA	YLLQLCSGVD	ENAVGACAQL	VFAPIDESFA	DDAPLLSSGF	RVIPLDPKT
Pop_triPHABULOSAb	YLLQLCSGVD	ENALGACAQL	VFAPIDESFA	DDAPLLPSGF	RVIPLDPKT
Fra_vesHOX32-like	FLLQMC SGVD	ENAVGSCAQL	VFAPIDESFA	DDAPLLPSGF	HVIPLDAKT
Gly_maxATHB-14-like	YLLQLCSGVD	ESAVGACAQL	VFAPIDESFA	DDALLPSGF	RVIPLDPKS
Gly_maxREVOLUTA-like	HLLQICSGID	ENAVGACSEL	VFAPIDEMFP	DDAPLVPSGF	RIIPLDSKP
Gly_maxREVOLUTA-likeb	HLLQICSGID	ENAVGACSEL	VFAPIDEMFP	DDAPLIPSGF	RIIPLDSKP
Pru_perREV_IFL1	HLLQICSGVD	ENAVGACSEL	VFAPIDEMFP	DDAPLVPSGF	RIIPLDSKT
Ory_satHOX33	YLLQLCSGVD	ENATSASAQL	VFAPIDESFA	DDAPLLPSGF	RVIPLDTKM
Sol_tubATHB-14-like	YLLQLCSGVD	ENAAGACAQL	VFAPIDESFG	DDAPLIPSGF	RVIIPLEPKS
The_cacXP_007022872.1	YLLQLCSGID	ENAVGACAQL	VFAPIDESFA	DDAPLLPSGF	RVIPLDPKT
Ory_satHOX33-like	YLLQLCSGVD	ENATSASAQL	VFAPIDESFA	DDAPLLPSGF	RVIPLDTKM
Sol_lycREVOLUTA-like	HLLQMC SGTD	ENAVGACSEL	VFAPIDEMFP	DDAPLLPSGF	RIIPLDSKS
Sol_lycHOX32-like	YLLQLCSGVD	ENAAGACAQL	VFAPIDESFG	DDAPLLPSGF	RVIIPLEPKS
Gly_maxATHB-14-likeb	YLMQLCSGID	ENAIGACAQL	VFAPIDESFA	DDALLPSGF	RIIPLDPKT
Pop_triXP_006378973.1	HLLQICSGID	ENAVGACSEL	VFAPIDEMFP	DDAPLLPSGF	RVIIPLESKT
Ory_satACA64837.1	YLLQLCSGVD	ENATSASAQL	VFAPIDESFA	DDAPLLPSGF	RVIPLDTKM
Vit_vin013992	HLLQICSGVD	ENAVGACSEL	VFAPIDEMFP	DDAPLLPSGF	RIIPLDSKS
Ory_satOsJ_11861	YLLQLCSGVD	ENAAGACAQL	VFAPIDESFA	DDAPLLPSGF	RVIPLDGKT
Sol_tubREVOLUTA-like	HLLQMC SGTD	ENAVGACSEL	VFAPIDEMFP	DDAPLLPSGF	RIIPLDSKS
Gly_maxATHB-14-likec	YLMQLCSGID	ENAIGACAQL	VFAPIDESFA	DDALLPSGF	RIIPLDPKT
The_cacXP_007024277.1	FLLQLCSGMD	ENAVGTCAEL	IFAPIDASFA	DDAPLLPSGF	RIIPLDSGK
Vit_vinATHB-15-like	FLLQLCSGMD	ENAVGTCAEL	IFAPIDASFA	DDAPLLPSGF	RIIPLDSGK
Ric_comXP_002515977.1	FLLQLCSGMD	ENAVGTCAEL	IFAPIDASFA	DDAPLLPSGF	RIIPLDSAK
The_cacXP_007016751.1	HLLQICSGID	ENAVGACSEL	VFAPIDEMFP	DDAPLLPSGF	RIIPLDSKP
Sol_tubHOX32-like	YLLQLCSGVD	ENAAGACAQL	VFAPIDESFG	DDAPLLPSGF	RVIIPLEPKS
Sol_lycATHB-14-like	YLLQLCSGVE	ENATGACAQL	VFAHIDESFG	DDAPLLPSGF	SVIIPLEPKS
Sol_tubATHB-14-like_X1	YLLQLCSGVE	ENATGACAQL	VFAHIDESFG	DDAPLLPSGF	SVIIPLEPKS
Med_truATHB-14	YLLQLCSGID	ENSVGACAQL	VFAPIDESFA	DDALLPSGF	RVIPLDPKS
Zea_mayNP_001142394.1	FLLQLCSGVD	EDAPGACAQL	VFAPIDESFA	DDAPLLPSGF	RVIPLDAKT
Vit_vinREVOLUTA	HLLQICSGVD	ENAVGACSEL	VFAPIDEMFP	DDAPLLPSGF	RIIPLDSKS
Ory_braHOX32-like	YLLQLCSGVD	ENAAGACAQL	VFAPIDESFA	DDAPLLPSGF	RVIPLDAKA
Ric_comXP_002529946.1	HLLQICSGID	ENAVGACSEL	VFAPIDEMFP	DDAPLLPSGF	RIIPLDSKT
Tha_cacXP_007016749.1	HLLQICSGID	ENAVGACSEL	VFAPIDEMFP	DDAPLLPSGF	RIIPLDSKP
Fra_vesREVOLUTA-like	HLLQICSGVD	ENAVGACSEL	VFAPIDEMFP	DDAPLLPSGF	RIIIPLESKT
Zea_mayNP_001146215.1	FLLQLCSGID	EDAPGACAQL	VFAPIDESFA	DDAPLLPSGF	RVIPLDAKT
The_cacXP_007012152.1	FLLQLCSGVD	ENAVGTCAEL	IFAPIDASFS	DDAPIIPSGF	RIIPLDSGM
Pru_perppa001386mg	FLLQLCSGVD	ENSVGTCAEL	VFAPIDASFS	DDGPILPSGF	RIIPLDSRM
Pop_triAAX19057.1	FLLQLCSGVD	ENAVGTCAEL	IFAPIDASFS	DDAPIIPSGF	RIIPLDSGM
Pop_triXP_002309538.2	FLLQLCSGVD	ENAVGTCAEL	IFAPIDASFS	DDAPIIPSGF	RIIPLDSGM
Fra_vesATHB-8-like	FLLQLCSGVD	ENAVGTCAEL	VFAPIDASFS	DDAPILPSGF	RIIPLDSHM
Pop_triXP_002324794.1	FLLQLCSGVD	ENAVGTCAEL	IFAPIDASFS	DDAPIIPSGF	RIIPLDSGM
Vit_vin009744	FLLQLCSGVD	DNAVGTCSSEL	IFAPIDASFS	DDAPLLPSGF	RIIPLDSGV
Gly_maxATHB-8-like	FLLQLCSGVD	EHAVG TSAEL	VFAPIDASFS	DDAPILPSGF	RIIPLDSGT
Sol_lycATHB-15-like	FLLQLCNGVD	ENAVGTCAEL	MFAPIDASFA	DDAPLLPSGF	RIIPLDSKA
Gly_maxATHB-8-likeb	FLLQLCSGVD	EHAVG TSAEL	VFAPIDASFS	DDAPILPSGF	RIIPLDSGT
Med_truXP_003603630.1	FLLQLCSGVD	EHAVG TSAEL	IFAPIDASFS	DDAPILPSGF	RIIIPLESKT

AmTr_v1.0_scaffold00148.15	---	NPODNT	AAA	IRTLDL	TSSLDIGSA	-	TNRASGDGG	GPNS	CNNLRS	
AmTr_v1.0_scaffold00056.60	-----	DG	SSP	NRTL DL	ASALEVGPA	-	GNRISGEFA	GGSGS	--LRS	
AmTr_v1.0_scaffold00155.45	-----	DG	PGT	NRTL DL	ASSIDVGST	-	GSRPSGESG	A-NGY	-TMRS	
Ara_thaPHABULOSA	-----	TPNG	ASA	NRTL DL	ASALE---	G-	STRQAGEAD	P-NGC	-NFRS	
Ara_thaATHB15	-----	EV	SSP	NRTL DL	ASALEIGSA	-	GTKASTDQS	GNSTC	--ARS	
Ara-thaPHAVOLUTA	-----	NPN	DH	QSA	SRTL DL	ASSLD---	G-	STKTDSET-	-----	NSRL
Ara_thaATHB8	-----	EG	LSP	NRTL DL	ASALDVG	-	-	SRTAGDSC	GSRGN	--SKS
Ara_thaREVOLUTA	-----	GDVQDL	LTAN	HRTL DL	TSSLEVGPS	-	PENASGNS	-	--	FSSSSSRC
Vit_vinHOX32-like	-----	DG	PAA	TRTL DL	ASTLEVGAG	-	GARPANESD	L-NNY	-NLRS	
The_cacXP_007022870.1	---	TLTCOSSADG	AGA	TRTL DL	ASALEVGP	-	SNRLAGDGD	P-SNY	-NLRS	
Ory_satHOX32	-----	DA	PSA	TRTL DL	ASTLEVGS	-	GTRASSDT	S-STC	-NTRS	
Pru_perppa001343mg	-----	DG	PTA	NRTL DL	ASTLEVGPS	-	GSRPVNEAD	G-NSY	-NLRS	
Bra_disHOX32-like	-----	DA	PSA	TRTL DL	ASTLEVGS	-	GTRAASDA-	-	--	PSTSNTRS
Pop_triPHABULOSA	-----	DA	PAT	TRTL DL	ASTLEVGP	-	GTRPASEAD	T-NSY	-NLRS	
Pop_triPHABULOSAb	-----	DA	PAA	TRTL DL	ASTLEVGP	-	GARPASEAD	T-NSY	-NLRS	
Fra_vesHOX32-like	-----	DG	PAT	NRTL DL	ASTLEVGAS	-	SARRVNEGD	A-NSY	-NLRS	
Gly_maxATHB-14-like	-----	DG	PAP	TRTL DL	ASTMEVGS	-	NARPAGEAD	L-NGY	-NLRS	
Gly_maxREVOLUTA-like	---	GDKKDA	VAT	NRTL DL	TSGFEVGPA	-	TTAGADA-	-	--	SSSQNTRS
Gly_maxREVOLUTA-likeb	---	GDKKEV	ATN	-	RTRL DL	TSGFEVGPA	-	TTAGTDA-	-	SSSQNTRS
Pru_perREV_IFL1	---	SDSKDT	LAT	HRTL DL	TSSLEVGST	-	TNNAAGEL-	-	--	SSFHNTRS
Ory_satHOX33	-----	DG	PSA	TRTL DL	ASALEVGP	-	GASRASVEA	S-GTC	--	NRS
Sol_tubATHB-14-like	-----	DV	PAA	TRTL DL	ASTLEAGTGG	SG	GTRPAGEIE	A-GNY	-NHRS	
The_cacXP_007022872.1	---	TLTCOSSADG	AGA	TRTL DL	ASALEVGP	-	SNRLAGDGD	P-SNY	-NLRS	
Ory_satHOX33-like	-----	DV	PSA	TRTL DL	ASALEVGP	-	GASRATDA	S-GVC	-NRS	
Sol_lycREVOLUTA-like	---	GDAQDT	LNA	HRTL DL	ASSLEVGPA	-	TNSTTGDA-	-	--	ASCYSARS
Sol_lycHOX32-like	-----	DV	PAA	TRTL DL	ASTLEAGTGG	SG	GTRPAGEIE	A-GNY	-NHRS	
Gly_maxATHB-14-likeb	-----	DG	PAS	TRTL DL	ASTLETGSG	-	NARSAGESD	L-NNY	-NLRS	
Pop_triXP_006378973.1	---	KDAQEA	LTT	NRTL DL	TSSLEVGPV	-	TNHASVDG-	-	--	SSC-HLRS
Ory_satACA64837.1	-----	DG	PSA	TRTL DL	ASALEVGP	-	GASRASVEA	S-GTC	--	NRS
Vit_vin013992	-----	DG	GDTQET	LTT	HRTL DL	TSSLEVGPA	-	TNQAAGDS-	-	SSCYNTRS
Ory_satOsJ_11861	-----	DA	PSA	TRTL DL	ASTLEVGS	-	GTRASSDT	S-STC	-NTRS	
Sol_tubREVOLUTA-like	---	GDAQDT	LNA	HRTL DL	ASSLEVGPA	-	RNSATGDM-	-	--	ASCYSARS
Gly_maxATHB-14-likec	-----	DG	LAS	TRTL DL	ASTLETGSG	-	NARSAGESD	S-NNY	-NLRS	
The_cacXP_007024277.1	-----	EA	SSP	NRTL DL	ASALEIGPT	-	GNKASNDYS	GNSGC	--	MRS
Vit_vinATHB-15-like	-----	EA	SSP	NRTL DL	ASALEIGPA	-	GNRSSNDYS	VNGGN	--	TRS
Ric_comXP_002515977.1	-----	EA	SSP	NRTL DL	ASALEIGPA	-	GNKSSTDYS	SNSGC	--	MRS
The_cacXP_007016751.1	---	SDTQDS	LTT	NRTL DL	TSSLEVGTA	-	TNHAAGDA-	-	--	PSCONSRS
Sol_tubHOX32-like	-----	DV	PAA	TRTL DL	ASTLEAGTGG	SG	GTRPAGEIE	A-GNY	-NHRS	
Sol_lycATHB-14-like	-----	DS	PSA	ARTL DL	ASTLEARTG	-	GTRPAGEVE	G-SSY	-NHRS	
Sol_tubATHB-14-like_X1	-----	DS	PSA	ARTL DL	ASTLEARTG	-	GTRLAGEVE	G-RSY	-NHRS	
Med_truATHB-14	-----	DG	PTT	SRTL DL	LE---	GSR	NARPSGEGA	GSNGY	-NLRS	
Zea_mayNP_001142394.1	-----	DV	PTAT	TRTL DL	ASALEVGS	-	GSGMRASCD	GSGTC	-	ATRS
Vit_vinREVOLUTA	---	GDTQET	LTT	HRTL DL	TSSLEVGPA	-	TNQAAGDS-	-	--	SSCYNTRS
Ory_braHOX32-like	-----	DA	PSA	TRTL DL	ASTLEVGS	-	GTRASSDT	S-GTC	-	NTRS
Ric_comXP_002529946.1	---	KDTQDA	LTT	SRTL DL	TSSLEVGPA	-	ANNTAGDA-	-	--	SSSQSTRS
Tha_cacXP_007016749.1	---	SDTQDS	LTT	NRTL DL	TSSLEVGTA	-	TNHAAGDA-	-	--	PSCONSRS
Fra_vesREVOLUTA-like	---	SDSKDA	LAT	HRTL DL	TSSLEVGST	-	TNHNAGDL-	-	--	NSFHNTRS
Zea_mayNP_001146215.1	-----	DV	PSA	TRTL DL	ASALEVGS	-	GGLCALSDS	G-SGT	RSTRS	
The_cacXP_007012152.1	-----	DA	SSP	NRTL DL	ASTLEVGAA	-	GNRATGDHS	GRCGS	--	TKS
Pru_perppa001386mg	-----	DA	PSP	NRTL DL	ASALEVGP	-	GSRASGDNA	GHSGN	--	TKS
Pop_triAAX19057.1	-----	DA	SSP	NRTL DL	ASALEVGP	-	GNRASGDLS	GRSGC	--	TKS
Pop_triXP_002309538.2	-----	DA	SSP	NRTL DL	ASALEVGP	-	GNRASGDLS	GRSGC	--	TKS
Fra_vesATHB-8-like	-----	DA	PSP	NRTL DL	ASALEVGP	-	GNRSSGDI	GHCGS	--	TKS
Pop_triXP_002324794.1	-----	DA	SSP	NRTL DL	ASALEVGP	-	GNRASGDLS	GRSGC	--	TKS
Vit_vin009744	-----	DG	SSP	NRTL DL	ASSLEVGPA	-	GNKASSDNS	GHTGS	--	AKS
Gly_maxATHB-8-like	-----	DA	ASP	NRTL DL	ASALEVGT	-	ANKAAGDNS	GHSGS	--	TKS
Sol_lycATHB-15-like	-----	DA	SSP	NRTL DL	ASTLEVGPA	-	GSRPTGDHS	KNSGS	--	AKS
Gly_maxATHB-8-likeb	-----	DA	ASP	NRTL DL	ASALEVGT	-	ANKAASDNS	AHSGS	--	TKS
Med_truXP_003603630.1	-----	DA	ASP	NRTL DL	ASALEVGT	-	GNKAGGDNS	GHSGI	--	TKS

AmTr_v1.0_scaffold00148.15	VLTIAFQFTF	EPH---	MRDN	VVAMARQYVR	GVVGSVQ RVA	MAISPSRLGA
AmTr_v1.0_scaffold00056.60	VLTIAFQFSY	ENNHEQ	IRDN	VATMARQYVR	SVISSVQ RVA	MALTPSRLNP
AmTr_v1.0_scaffold00155.45	VLTIAFQFTY	ETH---	LRDN	VVAMARQYVR	SVMASVQ RVA	MAISPSRMGP
Ara_thaPHABULOSA	VLTIAFQFTF	DNH---	SRDS	VASMARQYVR	SIVGSIQ RVA	LAIAP-RPGS
Ara_thaATHB15	VMTIAFEFGI	ESH---	MQEH	VASMARQYVR	GIISSVQ RVA	LALSPSHISS
Ara-thaPHAVOLUTA	VLTIAFQFTF	DNH---	SRDN	VATMARQYVR	NVVGSIQ RVA	LAITPRP---
Ara_thaATHB8	VMTIAFQLAF	EMH---	MQEN	VASMARQYVR	SVIASVQ RVA	LALSPSSH-Q
Ara_thaREVOLUTA	ILTIAFQFPF	ENN---	LQEN	VAGMACQYVR	SVISSVQ RVA	MAISPSGISP
Vit_vinHOX32-like	VLTIAFQFTF	ENH---	VRDN	VAAMARQYVR	SVMASVQ RVA	MAIAPSRLSS
The_cacXP_007022870.1	VLTIAFQFTF	ENH---	LRDN	VAAMARQYVR	SVVGSVQ RVA	MAIAPSRLSS
Ory_satHOX32	VLTIAFQFSY	ENH---	LRES	VAAMARQYVR	TVVASVQ RVA	MAIAPSRLGG
Pru_perppa001343mg	VLTIAFQFTF	ENH---	LRDN	VAAMARQYVR	SVVSSVQ RVA	MAIAPSRLSS
Bra_disHOX32-like	VLTIAFQFSY	ENH---	LRES	VASMARQYVR	TVVASVQ RVA	MAIAPSRLGG
Pop_triPHABULOSA	VLTIAFQFSF	ENH---	MRDN	VAAMARQYVR	GVVGSVQ RVA	MAIAPSRLSS
Pop_triPHABULOSAb	VLTIAFQFTF	ENH---	FRDN	VAAMARQYVR	GVVASVQ RVA	MAISPSRLSS
Fra_vesHOX32-like	VLTIAFQFTF	ENH---	MRDS	VAAMARQYVR	GVVSSVQ RVA	MAIAPSRLSS
Gly_maxATHB-14-like	VLTIAFQFTF	ENH---	TRDN	VAAMARQYVR	SVVGSVQ RVA	MAIAPSRLNT
Gly_maxREVOLUTA-like	VLTIAFQFPF	DSS---	LQDN	VAVMARQYVR	SVISSVQ RVA	MAISPSGINP
Gly_maxREVOLUTA-likeb	VLTIAFQFPF	DSS---	LQDN	VAVMARQYVR	SVISSVQ RVA	MAISPSGISP
Pru_perREV_IFL1	VLTIAFQFPF	ENS---	LQEN	VATMARQYVR	SVISSVQ RVA	MAISPSGLSP
Ory_satHOX33	VLTIAFQFSY	ENH---	LRES	VAAMARSYVR	AVMASVQ RVA	VAIAPSRLGP
Sol_tubATHB-14-like	VLTIAFQFTF	ESH---	YQDN	VAAAMARQYVR	SIVGSIQ RVA	MAIAPSRLSS
The_cacXP_007022872.1	VLTIAFQFTF	ENH---	LRDN	VAAMARQYVR	SVVGSVQ RVA	MAIAPSRLSS
Ory_satHOX33-like	VLTIAFQFSY	ENH---	LRDS	VAAMARNYVR	AVMASVQ RVA	VAIAPSRLGP
Sol_lycREVOLUTA-like	VLTIAFQFPF	EDN---	LQDN	VATMARQYVR	SVVSSVQ RVA	MAISPTGMNP
Sol_lycHOX32-like	VLTIASFQFTF	ESH---	YQDN	VAAMARQYVR	SIVGSIQ RVA	MAIAPSRLSS
Gly_maxATHB-14-likeb	VLTIAFQFTF	ENH---	LRDN	VAVMARQYVR	NVVRVSVQ RVA	MAIAPSRIST
Pop_triXP_006378973.1	VLTIAFQFPF	ESN---	LQDN	VATMARQYVR	SVISSVQ RVA	TAISPSGLNP
Ory_satACA64837.1	VLTIAFQFSY	ENH---	LRES	VAAAMARSYVR	AVMASVQ RVA	VAIAPSRLGP
Vit_vin013992	VLTIAFQFPF	ESN---	LQDN	VATMARQYVR	SVISSVQ RVA	MAISPSGLGP
Ory_satOsJ_11861	VLTIAFQFSY	ENH---	LRES	VAAMARQYVR	TVVASVQ RVA	MAIAPSRLGG
Sol_tubREVOLUTA-like	VLTIAFQFPF	EDN---	LQDN	VATMARQYVR	SVVSSVQ RVA	MAISPTGMNP
Gly_maxATHB-14-likec	VLTIAFQFTF	ENH---	LRDN	VAVMARQYVR	NVVRVSVQ RVA	MAIAPSRLST
The_cacXP_007024277.1	VMTIAFEFAP	ESH---	MQEH	VASMARQYVR	SIISSVQ RVA	LALSPSHLSS
Vit_vinATHB-15-like	VMTIAFEFAP	ESH---	LQEN	VASMARQYVR	SIISSVQ RVA	LALSPSHLSS
Ric_comXP_002515977.1	VMTIAFEFAP	ESH---	MQEH	VASMARQYVR	SIISSVQ RVA	LALSPSHSGS
The_cacXP_007016751.1	VLTIALQFPF	DSN---	LQDN	VAAMARQYVR	SVIASVQ RVA	MAISPSGLSP
Sol_tubHOX32-like	VLTIASFQFTF	ESH---	YQDN	VAAMARQYVR	SIVGSIQ RVA	MAIAPSRLSS
Sol_lycATHB-14-like	VLTIAFQFAF	ENH---	YREN	VAAMARQYVR	SIVGSIQ RVA	MAIAPSRLCS
Sol_tubATHB-14-like_X1	VLTIAFQFAF	ENH---	YREN	VAAMARQYVR	SIVGSIQ RVA	MAIAPSRLCS
Med_truATHB-14	VLTIAFQFTF	ENH---	LRDN	VASMARQYVR	SVVASVQ RVA	MAIAPSRPGT
Zea_mayNP_001142394.1	VLTIAFQFSF	ENH---	LRES	VAAAMAKQYVR	GVMASVQ RVA	MAIAPSRLGS
Vit_vinREVOLUTA	VLTIAFQFPF	ESN---	LQDN	VATMARQYVR	SVISSVQ RVA	MAISPSGLGP
Ory_braHOX32-like	VLTIAFQFSY	ENH---	LRES	VAAMARQYVR	TVVASVQ RVA	MAIAPSRLGG
Ric_comXP_002529946.1	VLTIAFQFPF	ESN---	LQEN	VATMARQYVR	SVISSVQ RVA	MAISPSGLGP
Tha_cacXP_007016749.1	VLTIALQFPF	DSN---	LQDN	VAAMARQYVR	SVIASVQ RVA	MAISPSGLSP
Fra_vesREVOLUTA-like	VLTIAFQFPF	ESS---	LQDN	VASMARQYVR	NVISSVQ RVA	MAISPSGLSP
Zea_mayNP_001146215.1	VLTIAFQFSF	ENH---	LRES	VAAMARQYVR	AVMAIVQ RVA	MAISPSRLGP
The_cacXP_007012152.1	VMTIAFQFVY	EIH---	LQEN	VATMARQYVR	SIIASVQ RVA	LALSPSRFGS
Pru_perppa001386mg	VMTIAFQFAF	EIH---	LQDN	VASMARQYVR	SIIASVQ RVA	LALSPSRFGS
Pop_triAAX19057.1	VMTIAFQFAF	EMH---	LQEN	VASMARQYVR	SIIASVQ RVA	LALSPSHFGS
Pop_triXP_002309538.2	VMTIAFQFAF	EMH---	LQEN	VTSMARQYVR	SIIASVQ RVA	LALSPSHFGS
Fra_vesATHB-8-like	VMTIAFQFAF	EIH---	LQDN	VASMARQYVR	SIIASVQ RVA	LALSPSRFGS
Pop_triXP_002324794.1	VMTIAFQFAF	EMH---	LQEN	VASMARQYVR	SIIASVQ RVA	LALSPSHFGS
Vit_vin009744	VMTISFQFAF	EMH---	LQEN	VASMARQYVR	SIISSVQ RVA	LALSPSRFGP
Gly_maxATHB-8-like	VMTIAFQFAF	EVH---	LQEN	IATMARQYVR	SIIASVQ RV	LALSPSRFGS
Sol_lycATHB-15-like	VMTIAFQFAF	EIH---	LQES	IAAMARQYVR	SIISSVQ RVA	LALSPSRIGS
Gly_maxATHB-8-likeb	VMTIAFQFAF	EVH---	LQEN	IATMARQYVR	SIIASVQ RV	LALSPSRFGS
Med_truXP_003603630.1	VMTIAFQFAF	EAH---	LQDN	IAAMARQYVR	SIVASVQ RV	LALSPSRFGS

AmTr_v1.0_scaffold00148.15	QM-GPRLP	PPG	SPEAVTLTRW	ITHSY	----	----	RFHLGV	DLLRADCH	-A
AmTr_v1.0_scaffold00056.60	HN-GLRPP	PPG	TPEALTLARW	ICHSY	----	----	RFHLGV	ELLRPNGE	-G
AmTr_v1.0_scaffold00155.45	GL-GPRPP	PPG	TPEAVTLARW	ICQSY	----	----	RFHSGV	ELLRVDSQ	-A
Ara_thaPHABULOSA	NI-SPISV	P	SPEALTLVRW	ISRSY	----	----	SLHTGA	DLFGSDSQT	S
Ara_thaATHB15	QV-GLRTP	PLG	TPEAQTARW	ICQSY	----	----	RGYMGV	ELLKNSD	-G
Ara_thaPHAVOLUTA	---	GSMQLPT	SPEALTLVRW	ITRSY	----	----	SIHTGA	DLFGADSQ	S
Ara_thaATHB8	LS-GLRPP	PPA	SPEAHTLARW	ISHSY	----	----	RCYLG	DLLK--	-PH-G
Ara_thaREVOLUTA	SL-GSKL	SPG	SPEAVTLAQW	ISQSY	----	----	SHHLGS	ELLTIDSL	-G
Vit_vinHOX32-like	HM-GLKPL	PLG	SPEALTLARW	ICRSY	----	----	RIHTGG	ELLRVDSQ	-G
The_cacXP_007022870.1	NM-EPKAL	PLG	SPEALTLARW	ICRSY	----	----	RIHTGE	ELLRVDSQ	-A
Ory_sathOX32	QI-ETKN	NPPG	SPEAHTLARW	IGRSY	----	----	RFHTGA	DLLRTDSQ	-S
Pru_perppa001343mg	QM-VPKLP	PLG	SPEAHTLARW	ICRSY	----	----	RIHTGA	ELFRVDSQ	-S
Bra_disHOX32-like	QI-EMKN	NPPG	SPEAHTLARW	IGKSY	----	----	RFHTGA	ELLECTDSQ	-S
Pop_tripHABULOSA	NV-GPKTL	PLG	SPEALTLAQW	ICRSY	----	----	RIHTGG	ELFRVESQ	-A
Pop_tripHABULOSAb	NM-GPKSL	PLV	SPEALTLARW	IYRSY	----	----	RIHTGG	ELFRVDSQ	-A
Fra_vesHOX32-like	QI-GPKAL	PLG	SPEAQTARW	IFQSY	----	----	RIHTGA	EIFRLESP	-S
Gly_maxATHB-14-like	QL-APKSL	PLG	SPEALTLARW	IFRSY	----	----	RMHTGT	ELFKAEST	-A
Gly_maxREVOLUTA-like	SI-GAKLS	SPG	SPEAVTLAHW	ICQSY	----	----	SYLGS	DLLRSDSL	-V
Gly_maxREVOLUTA-likeb	SV-GAKLS	SPG	SPEAVTLAHW	ICQSY	----	----	SYIGS	DLLRSDSL	-V
Pru_perREV_IFL1	SLGGPKL	SPG	SPEALTLAHW	ICQSY	----	----	SFHVGA	ELLRPDSL	-G
Ory_sathOX33	QI-GMKHP	PPA	SPEALTLASW	IGRSY	----	----	RAHTGA	DIRWSDTE	-D
Sol_tubATHB-14-like	QL-TPKSF	PLG	SPEAVTLARW	ISRSY	----	----	RVHTGG	DLFOVDSQ	-A
The_cacXP_007022872.1	NM-EPKAL	PLG	SPEALTLARW	ICRSY	----	----	RIHTGE	ELLRVDSQ	-A
Ory_sathOX33-like	QI-GMKHP	PPA	SPEALTLASW	IGRSY	----	----	RVHTGA	DIRWSDTE	-D
Sol_lycREVOLUTA-like	TL-GAKLS	SPG	SPEAVTLASHW	ICQSY	----	----	SYHMTG	ELLRADSS	-G
Sol_lycHOX32-like	QL-TPKSF	PLV	SPEAVTLARW	ISRSY	----	----	RVNTGG	DLFOVDSQ	-A
Gly_maxATHB-14-likeb	QL-GPKSL	PLG	PPEALTLARW	ICKSY	----	----	SLHTCT	ELFSVEST	-S
Pop_triXP_006378973.1	AL-GPKLS	SAG	SPEALTLAHW	ICQSYWQVLP	QVSS	CYHLGA	ELLRSDSV	-G	
Ory_satAC64837.1	QI-GMKHP	PPA	SPEALTLASW	IGRSY	----	----	RAHTGA	DIRWSDTE	-D
Vit_vin013992	AV-GPKLS	SAG	SPEALTLAHW	ICQSY	----	----	SYHVGA	ELLRSDSV	-G
Ory_satOsJ_11861	QI-ETKN	NPPG	SPEAHTLARW	IGRSY	----	----	RFHTGA	DLLRTDSQ	-S
Sol_tubREVOLUTA-like	TL-GAKLS	SPG	SPEAVTLASHW	ICQSY	----	----	SYHMTG	ELLRADSS	-G
Gly_maxATHB-14-likec	QL-TPKSF	PLG	PPEALTLARW	ICRSY	----	----	RLHTCT	ELFSVEST	-S
The_cacXP_007024277.1	HA-GLRTP	PLG	TPEAQTARW	ICQSY	----	----	RLYMGV	ELLKSGSE	-G
Vit_vinATHB-15-like	HA-GLRPP	PLG	TPEAHTLARW	ISHSY	----	----	RCYLG	ELLKSSGE	-G
Ric_comXP_002515977.1	HA-GLRTP	PLG	TPEAQTARW	ICQSY	----	----	RCYLG	ELLKSSSE	-G
The_cacXP_007016751.1	TV-GPKLS	SPG	SPEALTLAHW	ICQSY	----	----	SYHLGA	ELLRAESL	-G
Sol_tubHOX32-like	QL-TPKSF	PLV	SPEAVTLARW	ISRSY	----	----	RVNTGG	DLFOVDSQ	-A
Sol_lycATHB-14-like	QL-TPKSF	PLG	SPEAVTLARW	ICRSY	----	----	KNHTGG	ELLQVDSQ	-A
Sol_tubATHB-14-like_X1	QL-TPKSF	PLG	SPEAVTLARW	ICRSY	----	----	KNHTGG	ELLQVESQAA	-G
Med_truATHB-14	QL-GPKSL	PLG	SPEAHALARW	ISRSY	----	----	RMHTGA	ELFRVESA	-A
Zea_mayNP_001142394.1	RI-ELKH	PPG	SPEALALATW	IGRSY	----	----	RAHTGT	EIRWSDTE	-G
Vit_vinREVOLUTA	AV-GPKLS	SAG	SPEALTLAHW	ICQSY	----	----	SYHVGA	ELLRSDSV	-G
Ory_braHOX32-like	QI-ETKH	PPG	SPEAHTLARW	IGRSY	----	----	RFHTGA	DLLRTDSQ	-S
Ric_comXP_002529946.1	AV-GPKLS	SPG	SPEALTLAHW	ICQSY	----	----	SYLGA	ELLRSDSL	-A
Tha_cacXP_007016749.1	TV-GPKLS	SPG	SPEALTLAHW	ICQSY	----	----	SYHLGA	ELLRAESL	-G
Fra_vesREVOLUTA-like	SM-GPKLS	SPG	SPEALTLANW	ICQSY	----	----	SYHLGA	ELLQPDSL	-G
Zea_mayNP_001146215.1	HV-ELKH	PPG	SPEALALASW	IGRSY	----	----	RAHTGT	EIRWSDTEDA	-G
The_cacXP_007012152.1	LA-DFRTP	PPG	TPEAQTLAGW	ICDSY	----	----	RCYLG	ELLK--	-NE-G
Pru_perppa001386mg	NS-GFRPP	PPG	TPEAQTLAGW	ICQSY	----	----	RCYLG	DLLK--	-SE-G
Pop_triAAX19057.1	HA-GFRPP	PPG	TPEAHTLARW	ICESY	----	----	RCYLG	ELLK--	-NE-G
Pop_triXP_002309538.2	HA-GFRPP	PPG	TPEAHTLARW	ICESY	----	----	RCYLG	ELLK--	-NE-G
Fra_vesATHB-8-like	HA-GFRPP	PPG	TPEAQTLAGW	ICQSY	----	----	RCYLG	ELLK--	-SE-G
Pop_triXP_002324794.1	HA-GFWPP	PHG	TPEAHTLARW	ICESY	----	----	RIYLG	KLLK--	-NE-G
Vit_vin009744	QM-GFRPL	PLG	TPEAHTLARW	ICQSY	----	----	RCYLG	ELLKPSNE	-G
Gly_maxATHB-8-like	HN-AFHL	PPG	TPEAQTARW	ICNSY	----	----	RFYLG	ELLK--	-CE-G
Sol_lycATHB-15-like	LP-GLRSP	PPG	TPEAQTARW	ICQSY	----	----	RFFLG	ELLKSASG	-G
Gly_maxATHB-8-likeb	HN-AFHL	PPG	TPEAQTARW	ICNSY	----	----	RFYLG	ELLK--	-CE-G
Med_truXP_003603630.1	QN-AFPL	PPG	TPEAQTTRW	ICNSY	----	----	RFYLG	ELLK--	-CE-G

AmTr_v1.0_scaffold00148.15	-GDSVMKLLW	HYSDAIMCCS	LK	---	AL	P	VFT	--	FANQA	GLDMLETTLV
AmTr_v1.0_scaffold00056.60	-GESLLKMLW	HHADAIMCCS	LK	---	AL	P	VFT	--	FANQA	GLDMLETTLV
AmTr_v1.0_scaffold00155.45	-GDSLLKLLW	HHSDAIMCCS	LK	---	AS	P	IFS	--	FSNQA	GLDMLETTLV
Ara_thaPHABULOSA	-GDTLLHQLW	NHSDAILCCS	LK	TN	--	AS	P	VFT	--	FANQT
Ara_thaATHB15	-NESILKNLW	HHTDAI ICCS	MK	---	AL	P	VFT	--	FANQA	GLDMLETTLV
Ara-thaPHAVOLUTA	GGDTLLKQLW	DHSDAILCCS	LK	TN	--	AS	P	VFT	--	FANQA
Ara_thaATHB8	-TD-LLKSLW	HHPDVAVMCCS	LK	---	AL	SP	VFT	--	FANQA	GLDMLETTLV
Ara_thaREVOLUTA	SDDSVLKLLW	DHQDAILCCS	LK	---	PQ	P	VFM	--	FANQA	GLDMLETTLV
Vit_vinHOX32-like	-GDAVLKLLW	NHSDAIMCCS	LK	TN	--	AS	P	VFT	--	FANQA
The_cacXP_007022870.1	-GDALLKQLW	HHSDAIMCCS	LK	TN	--	AS	P	VFT	--	FANQA
Ory_sathOX32	-TDSSLKAMW	QHSDSIMCCS	LK	---	AA	P	VFT	--	FANQA	GLDMLETTLI
Pru_perppa001343mg	-GDAVLKQLW	HHSDAIMCCS	VK	TN	--	AS	P	VFT	--	FANQA
Bra_disHOX32-like	-ADALKALW	QHSDSIMCCS	LK	---	AA	P	VFT	--	FANQA	GLDMLETTLI
Pop_tripHABULOSA	-GDALLKQLW	HHSDAIMCCS	LK	TN	--	AS	P	VFT	--	FANQA
Pop_tripHABULOSAb	-GDALLKRLW	HHSDAIMCCS	LK	TN	--	AS	P	VFT	--	FANQA
Fra_vesHOX32-like	-GDAVLKQLW	NHPDAIMCCS	VK	TN	--	AS	P	VFT	--	FANQA
Gly_maxATHB-14-like	-GDAILKQLW	HHPDAILCCS	VK	TN	--	AS	P	VFT	--	FANQA
Gly_maxREVOLUTA-like	-GDMMLKQLW	HHQDAILCCS	LK	---	SL	P	VFI	--	FANQA	GLDMLETTLV
Gly_maxREVOLUTA-likeb	-GDMMLKQLW	HHQDAILCCS	LK	---	PL	P	VFI	--	FANQA	GLDMLETTLV
Pru_perREV_ IFL1	-GDSMLKHLW	HHQDAILCCS	LK	---	SL	P	VFI	--	FANQA	GLDMLETTLV
Ory_sathOX33	-ADSPLALLW	KHSDAILCCS	LK	---	PA	P	MFT	--	FANNA	GLDILETTLV
Sol_tubATHB-14-like	-GDAVLKQLW	HHSDAIMCCS	VK	MN	--	AS	A	VFT	--	FANQA
The_cacXP_007022872.1	-GDALLKQLW	HHSDAIMCCS	LK	TN	--	AS	P	VFT	--	FANQA
Ory_sathOX33-like	-ADSPLALLW	KHNDAILCCS	LK	---	PA	P	MFT	--	FANNA	GLDILETTLV
Sol_lycREVOLUTA-like	-DESVLKNLW	QHQDAILCCS	LK	---	SL	P	VFI	--	FANKA	GLDMLETTLV
Sol_lycHOX32-like	-GDAVLKQLW	HHSDAIMCCS	VK	MN	VS	AS	A	VFT	--	FANQA
Gly_maxATHB-14-likeb	-GDAILKQLW	HHPDAILCCS	VK	TN	--	AS	P	VFT	--	FANQA
Pop_triXP_006378973.1	-GDSVLKHLW	HHPDAILCCS	LE	---	AL	P	VFI	--	FANQA	GLDMLETTLV
Ory_satACA64837.1	-ADSPLALLW	KHSDAILCCS	LK	---	PA	P	MFT	--	FANNA	GLDILETTLV
Vit_vin013992	-GDSVLKNLW	HHQDAILCCS	LK	---	SL	P	VLI	--	FANQA	GLDMLETTLV
Ory_satOsJ_11861	-TDSSLKAMW	QHSDSIMCCS	LK	---	AA	P	VFT	--	FANQA	GLDMLETTLI
Sol_tubREVOLUTA-like	-DESVLKNLW	QHQDAILCCS	LK	---	SL	P	VFI	--	FANKA	GLDMLETTLV
Gly_maxATHB-14-likec	-GDAILKQLW	HHPDAILCCS	VK	TD	--	AS	P	VFT	--	FANQA
The_cacXP_007024277.1	-SETILKTLW	HHSDAILCCS	LK	---	AL	P	VFT	--	FANQA	GLDMLETTLV
Vit_vinATHB-15-like	-SETILKTLW	HLSDAIMCCS	LK	---	AL	P	VFT	--	FANQA	GLDMLETTLV
Ric_comXP_002515977.1	-GESILKTLW	HHSDAIMCCS	LK	---	AL	P	VFT	--	FANQA	GLDMLETTLV
The_cacXP_007016751.1	-GDAVLKNLW	QHQDAILCCS	LK	---	SL	P	VFI	--	FANQA	GLDMLETTLV
Sol_tubHOX32-like	-GDAVLKQLW	HHSDAIMCCS	VK	MN	VS	AS	A	VFT	--	FANQA
Sol_lycATHB-14-like	-GDAVLKQLW	HHTDSIMCCS	VK	MN	--	DS	A	FFS	--	FANQA
Sol_tubATHB-14-like_X1	-GDAVLKQLW	HHTDSIMCCS	VK	MN	--	DS	A	VFS	--	FSNQA
Med_truATHB-14	-SDAILKQLW	HHSDAIMCCS	VK	TN	--	AS	P	IFT	--	FSNQA
Zea_mayNP_001142394.1	-ADSPLMLFW	KHSDAILCCS	LK	---	P	--	P	AFTL	K	FANSA
Vit_vinREVOLUTA	-GDSVLKNLW	HHQDAILCCS	LK	---	SL	P	VLI	--	FANQA	GLDMLETTLV
Ory_braHOX32-like	-TDSSLKAMW	QHSDSIMCCS	LK	---	AA	P	VFT	--	FANQA	GLDMLETTLI
Ric_comXP_002529946.1	-GDSVLKQLW	HHQDAILCCS	LK	---	SL	P	VFI	--	FANQA	GLDMLETTLV
Tha_cacXP_007016749.1	-GDAVLKNLW	QHQDAILCCS	LK	---	SL	P	VFI	--	FANQA	GLDMLETTLV
Fra_vesREVOLUTA-like	-GDSMLKHLW	HHQDAILCCS	LK	---	SV	P	VFI	--	FANQA	GLDMLETTLV
Zea_mayNP_001146215.1	-AGSPLTLFW	KHSDAI ICCS	LK	---	--	--	P	AFTL	K	FANSA
The_cacXP_007012152.1	-SESILKMLW	HHTDAVLCCS	LK	---	AL	P	VFT	--	FANQA	GLDMLETTLV
Pru_perppa001386mg	-SESILKSLW	HHSDAILCCS	LK	---	AL	P	VFT	--	FANQA	GLDMLETTLV
Pop_triAAX19057.1	-SESILKTLW	HHSDALMCCS	LK	---	TL	P	VFT	--	FANQA	GLDMLETTLV
Pop_triXP_002309538.2	-SESILKTLW	HHSDALMCCS	LK	---	TL	P	VFT	--	FANQA	GLDMLETTLV
Fra_vesATHB-8-like	-SESILKTLW	HHSDAILCCS	LK	---	AL	P	VFT	--	FANQA	GLDMLETTLV
Pop_triXP_002324794.1	-SDSILKTLW	HHSDALVCCS	LK	---	TL	P	VFT	--	FSNQA	GLDMLETTLV
Vit_vin009744	-NESILKTLW	HHSDAVMCCS	LK	---	AL	P	VFT	--	FANQA	GLDMLETTLV
Gly_maxATHB-8-like	-SESILKSLW	HHSDAVLCCS	LK	---	AL	P	VFT	--	FANQA	GLDMLETTLV
Sol_lycATHB-15-like	-SESILKEIW	DHSDALMCCS	MK	---	AL	P	VFT	--	FANEA	GLDMLETTLV
Gly_maxATHB-8-likeb	-SESILKSLW	HHSDAVLCCS	LK	---	AL	P	VFT	--	FANQA	GLDMLETTLV
Med_truXP_003603630.1	-SESILKSLW	HHSDAVLCCS	LK	---	AL	P	VFT	--	FANQA	GLDMLETTLV

AmTr_v1.0_scaffold00148.15	ALQDISLDKI	LD-EGGRKSL	CSDFTKIMQQ	---	GTYLPA	GICVSSMGRP
AmTr_v1.0_scaffold00056.60	ALQDITLEKI	FD-ENGRKTL	CADFAQIMQQ	---	GFAYLQG	GLCVSSMGRP
AmTr_v1.0_scaffold00155.45	ALQDITLDDKI	LD-ENGRKVL	YSEFPKIMQQ	---	GFAYLPA	GICVSSMGRP
Ara_thaPHABULOSA	ALQDIMLDDKI	LD-EPGRKAL	CSEFPKIMQQ	---	GYAHLPA	GVCASSMGRM
Ara_thaATHB15	ALQDISLEKI	FD-DNGRKTLL	CSEFPQIMQQ	---	GFACLOG	GICLSSMGRP
Ara-thaPHAVOLUTA	ALQDIMLDDKI	LD-DSGRRAL	CSEFAKIMQQ	---	GYANLPA	GICVSSMGRP
Ara_thaATHB8	ALQDITLDDKI	FDNNNGKKTLL	SSEFPQIMQQ	---	GFMCMDG	GICMSSMGRA
Ara_thaREVOLUTA	ALQDITLEKI	FD-ESGRKAI	CSDFAKLMQQ	---	GFACLPS	GICVSTMGRH
Vit_vinHOX32-like	ALQDIMLDDKI	LD-EAGRKIL	CSEFSKIMQQ	---	GFAYLPA	GICTSSMGRP
The_cacXP_007022870.1	ALQDIMLDDKI	LD-EAGRKIL	CSEFSKIMQQ	---	GFAYLPA	GICVSSMGRP
Ory_sathOX32	ALQDISLEKI	LD-DDGRKAL	CTEFPKIMQQ	---	GFAYLPG	GVCVSSMGRP
Pru_perppa001343mg	ALQDIMLDDKI	LD-EAGRKIL	CSEFSKIMQQ	---	GFAYLPA	GLCASSMGRP
Bra_disHOX32-like	ALQDISLEKI	LD-DDGRKAL	CSEFPKIMQQ	---	GFAYLPG	GVCVSSMGRP
Pop_tripHABULOSA	ALQDIMLDDKI	LD-EAGRKIL	CSEFSKITQQ	---	GFAYLPA	GICVSSMGRP
Pop_tripHABULOSAb	ALQDIMLDDKI	LD-EAGRKIL	CSEFSKIMQQ	---	GYAYLPA	GICVSSMGRP
Fra_vesHOX32-like	ALQDIMLDDKI	LD-EAGRKVL	CSEFSKIMLQ	---	GFAYLPA	GMCASSMGRP
Gly_maxATHB-14-like	ALQDIMLDDKI	LD-ESSRKIL	CSEFSKIMQQ	---	GFAYLPA	GICASSMNRP
Gly_maxREVOLUTA-like	ALQDITLDDKI	FD-EAGRKAL	CTDFAKLMQQ	---	GFAYLPA	GICMSTMGRH
Gly_maxREVOLUTA-likeb	ALQDITLDDKI	FD-EAGRKAL	CTDFAKLMQQ	---	GFAYLPA	GICMSTMGRH
Pru_perREV IFL1	ALQDISLDDKI	FD-ECGRKTL	CADFAKLMNQ	---	GFAYLPA	GICMSTMGRH
Ory_sathOX33	NLQDISLEMI	LD-DEGRKAL	CSEFPKIMQQ	---	GFAYLPG	GVCVSSMGRP
Sol_tubATHB-14-like	ALQDIMLDDKI	LD-EAGRKVL	LSEFSKIMQQ	---	GFAYLPA	GICVSSMGRP
The_cacXP_007022872.1	ALQDIMLDDKI	LD-EAGRKIL	CSEFSKIMQQ	---	VKFSVS	GLCSSD----
Ory_sathOX33-like	NLQDISLEMI	LD-DEGRKAL	CSEFPKIMQQ	---	GFAYLPG	GVCVSSMGRP
Sol_lycREVOLUTA-like	ALQDISLDDKI	FD-ESGRKVL	LSEFAKIMEQ	---	GFAYLPG	GICMSTMGRH
Sol_lycHOX32-like	ALQDIMLDDKI	LD-EAGRKVL	LSEFSKIMQQ	---	GFAYLPA	GICVSSMGRP
Gly_maxATHB-14-likeb	ALQDIMLDDKI	LD-EAGRKFL	CIEFSKIMQQ	---	GFAYLPA	GICVSSMNRP
Pop_tripXP_006378973.1	ALQDITLDDKI	FD-ESGRKAL	FTDFAKLMQQ	ANN	GFAYLPA	GICMSTMGRN
Ory_satAC64837.1	NLQDISLEMI	LD-DEGRKAL	CSEFPKIMQQ	---	GFAYLPG	GVCVSSMGRP
Vit_vin013992	ALQDISLDDKI	FD-ESGRKGL	CADFAKIMQQ	---	GFAYLPA	GICMSTMGRH
Ory_satOsJ_11861	ALQDISLEKI	LD-DDGRKAL	CTEFPKIMQQ	---	GFAYLPG	GVCVSSMGRP
Sol_tubREVOLUTA-like	ALQDISLDDKI	FD-EPGREVL	LSEFAKIMEQ	---	GFAYLPG	GICMSTMGRH
Gly_maxATHB-14-likec	ALQDIMLDDKI	LD-EAGRKVL	CIEFSKIMQQ	---	GFAYLPA	GICVSSMNRP
The_cacXP_007024277.1	ALQDITLDDKI	FD-DHGRKTL	CTEFPQIMQQ	---	GFACLOG	GICLSSMGRP
Vit_vinATHB-15-like	ALQDITLDDKI	FD-DHGRKTL	CSEFPQIMQQ	---	GFACLOG	GICLSSMGRP
Ric_comXP_002515977.1	ALQDITLDDKI	FD-DHGRKTL	CSEFPQIMQQ	---	GFACLOG	GICLSSMGRP
The_cacXP_007016751.1	ALQDITLDDKI	FD-ESGRKAL	CSDFAKLMQQ	---	---	---
Sol_tubHOX32-like	ALQDIMLDDKI	LD-EAGRKVL	LSEFSKIMQQ	---	GFAYLPA	GICVSSMGRP
Sol_lycATHB-14-like	ALQDIMLDDKI	LD-EAGRKVL	LSEFPKIMQQ	---	GFAYLPA	GLCVSSMGRP
Sol_tubATHB-14-like_X1	ALQDIMLDDKI	LD-EAGRKVL	LSEFPKIMQQ	---	GFAYLPA	GLCVSSMGRP
Med_truATHB-14	ALQDIMLDDKI	LD-EAGRKIL	CSEFSKIMQQ	---	GYASLPG	GICVSSMNRP
Zea_mayNP_001142394.1	NIQDLPLEAV	LD-EEGQKAL	SAQLPAIMQQ	---	GLAYLPG	GVCRSSMGRP
Vit_vinREVOLUTA	ALQDISLDDKI	FD-ESGRKGL	CADFAKIMQQ	---	GFAYLPA	GICMSTMGRH
Ory_braHOX32-like	ALQDISLEKI	LD-DDGRKAL	CSEFPKIMQQ	---	GLAYLPG	GVCVSSMGRP
Ric_comXP_002529946.1	ALQDITLDDKI	FD-ESGRKAL	CADFAKLMQQ	---	GFAGLPG	GICMSTMGRH
Tha_cacXP_007016749.1	ALQDITLDDKI	FD-ESGRKAL	CSDFAKLMQQ	---	GFAYLPA	GICMSTMGRN
Fra_vesREVOLUTA-like	ALQDISLDDKI	FD-ESGRKTL	CTDFAKLMQQ	---	GFAYLPA	GICMSTMGRH
Zea_mayNP_001146215.1	NVQDLQLEAV	LD-DGGQKAL	VAQLPKIMLQ	---	GLAYLPG	GVCRSSMGRP
The_cacXP_007012152.1	ALQDISLEKI	FD-ENGRKAL	FAEFPQVMQQ	---	GFMCLOG	GICLSSMGRP
Pru_perppa001386mg	ALQDITLEKI	FD-DNGRKTLL	FSEFPQIMQQ	---	GFMCLOG	GICMSSMGRP
Pop_tripAAX19057.1	ALQDITLEKI	FD-DNGRKTLL	YSEFPQIMQQ	---	GFMCLOG	GICLSSMGRP
Pop_tripXP_002309538.2	ALQDITLEKI	FD-DNGRKTLL	YSEFPQIMQQ	---	GFMCLOG	GICLSSMGRP
Fra_vesATHB-8-like	ALQDITLEKI	FD-DNGRKTLL	FTEFPQIMQQ	---	GFMCLOG	GICMSSMGRP
Pop_tripXP_002324794.1	ALQDITLEKI	FD-DNGRKTLL	CSEFPQIMQQ	---	GFMCLOG	GICLSSMGRP
Vit_vin009744	ALQDITLEKT	FD-DNGRKTLL	CSEFPQIMQQ	---	GFVCLQG	GVCLSSMGRP
Gly_maxATHB-8-like	ALQDITLEKI	FD-DNGKKTLL	CTEFPQIMQQ	---	GFMCLOG	GICLSSMGRP
Sol_lycATHB-15-like	ALQDISLEKI	FD-DNGRKTLL	YSELQIMQQ	---	GFACLOG	GICLSSMGRP
Gly_maxATHB-8-likeb	ALQDITLEKI	FD-DNGKKTLL	CTEFPQIMQQ	---	GFMCLOG	GICLSSMGRP
Med_truXP_003603630.1	ALQDITLEKI	FD-DNGKKTLL	CSEFPQIMQQ	---	GFMCLOG	GICLSSMGRP

AmTr_v1.0_scaffold00148.15	VS Y DQAI A AWK	VL--TEEEAT	--HCLAFMFI	NWSFV
AmTr_v1.0_scaffold00056.60	VS Y ERAVAWK	VL--NEEEST	--HCICFMFM	NWSFV
AmTr_v1.0_scaffold00155.45	VS Y EQAVAWK	VL--NEDDCT	--HCLAFMFL	NWSFV
Ara_thaPHABULOSA	VS Y EQATVVK	VL--EDDES N	--HCLAFMFV	NWSFV
Ara_thaATHB15	VS Y ERAVAWK	VL--NEEENA	--HCICFVFI	NWSFV
Ara_thaPHAVOLUTA	VS Y EQATVVK	VV--DDNES N	--HCLAF T LV	SWSFV
Ara_thaATHB8	VT Y EKAVG W K	VL--NDEDEP	--HCICFMFL	NWSFI
Ara_thaREVOLUTA	VS Y EQAVAWK	VFAASEENNN	NLHCLAFS F V	NWSFV
Vit_vinHOX32-like	VS Y EQAI A AWK	VL--NDEDS N	--HCLAFMFI	NWSFV
The_cacXP_007022870.1	VS Y EQAI A AWK	VL--NDNDAN	--HCL T FMFV	NWSFV
Ory_satHOX32	VS Y EQAVAWK	VL--SDDDT P	--HCLAFMFV	NWSFV
Pru_perppa001343mg	VS Y DQAVAWK	VV--NDDDS N	--HCLAFMFM	SWSFV
Bra_disHOX32-like	VS Y EQAVAWK	VL--SEDDT P	--HCLAFMFV	NWSFV
Pop_triPHABULOSA	VS Y EQAVAWK	VL--NDDDS N	--HCLAFMFM	NWSFV
Pop_triPHABULOSA b	VS Y EQAI A AWK	VL--NDDNS N	--HCLAFMFI	NWSFV
Fra_vesHOX32-like	VS Y EQAVAWK	VV--NDEDS N	--HCLALMFT	NWSFV
Gly_maxATHB-14-like	VS Y EQAVAWK	VL--NDDDS N	--HCLAFMFI	NWSFV
Gly_maxREVOLUTA-like	VS Y DQAI A AWK	VL T -GEDNTV	--HCLAFSFI	NWSFV
Gly_maxREVOLUTA-like b	VS Y DQAI A AWK	VL T -GEDNTV	--HCLAFSFI	NWSFV
Pru_perREV_IFL1	VS Y EQAVAWK	VLA-AEENS V	--HCLAFSFM	NWSFV
Ory_satHOX33	AS Y EQAVAWK	VL--SDDDA P	--HCLAFMLV	NWTFM
Sol_tubATHB-14-like	IS Y EQAI A AWK	VL--NDDDS N	--HCLAFMFI	NWSFV
The_cacXP_007022872.1		-----IEFFPS	N-----	
Ory_satHOX33-like	AS Y EQAVAWK	VL--SDDDA P	--HCLAFMLV	NWTFM
Sol_lycREVOLUTA-like	IS Y EQAI A AWK	VFAASSEENAV	--HCLAFSFI	NWSFV
Sol_lycHOX32-like	IS Y EQAI A AWK	VL--NDDDS N	--HCLAFMFI	NWSFV
Gly_maxATHB-14-like b	VS Y EQAI A AWK	VL--DDDS N	--HCLAFVFM	NWSFV
Pop_triXP_006378973.1	VS Y EQAV S WK	VLA-AEENTV	--HCIAFSFV	NWSFL
Ory_satACA64837.1	AS Y EQAVAWK	VL--SDDDA P	--HCLAFMLV	NWTFM
Vit_vin013992	VS Y EQAI A AWK	VLA-AEENTV	--HCLAFSFI	NWSFV
Ory_satOsJ_11861	VS Y EQAVAWK	VL--SDDDT P	--HCLAFMFV	NWSFV
Sol_tubREVOLUTA-like	IS Y EQAI A AWK	VFAASSEENAV	--HCLAFSFI	NWSFV
Gly_maxATHB-14-like c	VS Y EQAI A AWK	VL--DDDS N	--HCLAFVFM	NWSFV
The_cacXP_007024277.1	VS Y ERAVAWK	VL--NEEENA	--HCICFMFI	NWSFV
Vit_vinATHB-15-like	VS Y ERAVAWK	VL--NEEENA	--HCICFMFM	NWSFV
Ric_comXP_002515977.1	VS Y ERAVAWK	VL--NEEENA	--HCICFMFI	NWSFV
The_cacXP_007016751.1		-----VSP	N-----	
Sol_tubHOX32-like	IS Y EQAI A AWK	VL--NDDDS N	--HCLAFMFI	NWSFV
Sol_lycATHB-14-like	VS Y EQAVAWK	VL--NDDNS N	--HCLAFMFT	NWSFI
Sol_tubATHB-14-like_X1	VS Y EQAVAWK	VL--NDDNSS	--HCLAFMFT	NWSFI
Med_truATHB-14	VS Y EQAI A AWK	VL--NDDAN	--HCLAFMFI	NWSFV
Zea_mayNP_001142394.1	AS Y EQAVAWK	VV--GDDGAP	--QCLALMLA	NWTFI
Vit_vinREVOLUTA	VS Y EQAI A AWK	VLA-AEENTV	--HCLAFSFI	NWSFV
Ory_braHOX32-like	VS Y EQAVAWK	VL--SDDDT P	--HCLAFMFV	NWSFV
Ric_comXP_002529946.1	VS Y EQAVAWK	VLA-ADESTV	--HCLAFS F V	NWSFV
Tha_cacXP_007016749.1	VS Y EQAVAWK	VLA-ADESTV	--HCLAFS F V	NWSFV
Fra_vesREVOLUTA-like	VS Y EQAI G WK	VLS-GEDNSV	--HCLAFS F V	NWSFV
Zea_mayNP_001146215.1	AS Y EQAVAWK	VV--GDDGAP	--QCLALMFV	NWTFI
The_cacXP_007012152.1	VS Y ERAVAWK	VV--NDEENA	--HCICFMFI	NWSFV
Pru_perppa001386mg	IS Y ERAVAWK	VL--NEEETA	--HCICFMFI	NWSFV
Pop_triAAX19057.1	VS Y ERAVAWK	VL--NEEESA	--HCICFMFI	NWSFV
Pop_triXP_002309538.2	VS Y ERAVAWK	VL--NEEESA	--HCICFMFI	NWSFV
Fra_vesATHB-8-like	IS Y ERAVAWK	VL--NEEETA	--HCICFMFI	NWSFV
Pop_triXP_002324794.1	VS Y ERAVAWK	VL--NEEESA	--HCICFMFM	NWSFV
Vit_vin009744	VS Y ERAVAWK	VL--TEEDNA	--HCICFMFI	NWSFV
Gly_maxATHB-8-like	VS Y ERAVAWK	VL--NEEESA	--HCICFMFI	NWSFV
Sol_lycATHB-15-like	IS Y ERAVAWK	VL--NEEEDA	--HCICFMFI	NWSFV
Gly_maxATHB-8-like b	VS Y ERAVAWK	VL--NEEESA	--HCICFMFI	NWSFV
Med_truXP_003603630.1	IT Y ERAVAWK	VL--NEEESA	--HCICFMFI	NWSFV