

tr |D8TRX1|D8TRX1_VOLCA 1 MAATVGSISCAGASLLSSASGKYSSNQACFRKLGKFAALSLSIDSVAGSKSSAASRL 15RGLRVVCAATAVPKQKAVKPGVDRVLVAVDKK-EAKSVGVVLPAS
gi |66806699|ref XP_3637072.1| 1 -----MSSSTKSFPLPDRILVQRNRSIDIKGGGNYTHDKV
gi |66806193|ref XP_3636819.1| 1 -----MSKRFPLPDRILVQRNRSIDIKGGGNYTHDKV
YOR020C 1 0 -----MSTLTKSSEVPLDRVLVQRNRSIDIKGGGNYTHDKV
gi |85079266|ref XP_956315.1| 1 0 -----MAATTVRSVKSPLPDRVLVQRVKA-EAKTASGIFLPESS
gi |17555568|ref NP_497428.1| 1 0 -----MFLTAVRRSSNVLPKPLPDRVLVQRVAA-EKTKGKGMILPEKS
gi |4504523|ref NP_002148.1| 1 0 -----MAQAPFKFPLPDRVLVQRVSA-EVTVKGGIMLPEKS
Esi0000_0403 1 0 -----MASLPKRFPLPDRVLVQRVAA-EKTKGKGMILPEKS
Phpat_008027000|Phpat_008027000.1 1 0 -----MSTVTKRPLPDRVLVQRVAA-EKTKGKGMILPEKS
Phpat_008026900|Phpat_008026900.1 1 0 -----MSVTAAKRVLPLDRVLVQRVAA-EKTKGKGMILPEKS
Phpat_004G011000|Phpat_004G011000.1 1 0 -----MAQLMSVNRRLKPLDRVLVQRVAA-EKTKGKGMILPEKS
Phpat_012G089700|Phpat_012G089700.1 1 0 -----MSOLSVNARRLKPLDRVLVQRVAA-EKTKGKGMILPEKS
CMF129C|CMF129C 1 0 -----MSALSRRLPDRVLVQRVAA-EKTKGKGMILPEKS
g3695|g3695.t1 1 0 -----MAKRLIPLDRVLVQRVAA-EKTKGKGMILPEKS
GRMZM2G073401|GRMZM2G073401.T01 1 0 -----MAKRLIPLDRVLVQRVAA-EKTKGKGMILPEKS
LOC_0803g25050|LOC_0803g25050.1 1 0 -----MAKRLIPLDRVLVQRVAA-EKTKGKGMILPEKS
GRMZM2G410812|GRMZM2G410812.T01 1 0 -----MAKRLIPLDRVLVQRVAA-EKTKGKGMILPEKS
LOC_0807g44740|LOC_0807g44740.1 1 0 -----MAKRLIPLDRVLVQRVAA-EKTKGKGMILPEKS
GRMZM2G013652|GRMZM2G013652.T01 1 0 -----MAKRLIPLDRVLVQRVAA-EKTKGKGMILPEKS
GRMZM2G035063|GRMZM2G035063.T01 1 0 -----MAKRLIPLDRVLVQRVAA-EKTKGKGMILPEKS
Bra026173|Bra026173 1 0 -----MAKRLIPLDRVLVQRVAA-EKTKGKGMILPEKS
Bra026789|Bra026789 1 0 -----MAKRLIPLDRVLVQRVAA-EKTKGKGMILPEKS
Carubv10010732m.g|Carubv10010732m 1 0 -----MAKRLIPLDRVLVQRVAA-EKTKGKGMILPEKS
Bra016677|Bra016677 1 0 -----MAKRLIPLDRVLVQRVAA-EKTKGKGMILPEKS
AT1G14980 1 0 -----MAKRLIPLDRVLVQRVAA-EKTKGKGMILPEKS
Glyma06g41830|Glyma06g41830.1 1 0 -----MAKRLIPLDRVLVQRVAA-EKTKGKGMILPEKS
Bra024563|Bra024563 1 0 -----MAKRLIPLDRVLVQRVAA-EKTKGKGMILPEKS
Carubv10010739m.g|Carubv10010739m 1 0 -----MAKRLIPLDRVLVQRVAA-EKTKGKGMILPEKS
AT1G23100 1 0 -----MAKRLIPLDRVLVQRVAA-EKTKGKGMILPEKS
Glyma03g28120|Glyma03g28120.1 1 0 -----MAKRLIPLDRVLVQRVAA-EKTKGKGMILPEKS
Glyma19g30860|Glyma19g30860.1 1 0 -----MAKRLIPLDRVLVQRVAA-EKTKGKGMILPEKS
Medtr7g089300|Medtr7g089300.1 1 0 -----MAKRLIPLDRVLVQRVAA-EKTKGKGMILPEKS
PGSC0003DMG40028744|PGSC0003DMT40006028 1 0 -----MAKRLIPLDRVLVQRVAA-EKTKGKGMILPEKS
PGSC0003DMG40028744|PGSC0003DMT40007396 1 0 -----MAKRLIPLDRVLVQRVAA-EKTKGKGMILPEKS
Medtr3g077350|Medtr3g077350.1 1 0 -----MAKRLIPLDRVLVQRVAA-EKTKGKGMILPEKS
29816.t000025|29816.m000688 1 0 -----MAKRLIPLDRVLVQRVAA-EKTKGKGMILPEKS
Potri_008G130500|Potri_008G130500.1 1 0 -----MAKRLIPLDRVLVQRVAA-EKTKGKGMILPEKS
Potri_010G116000|Potri_010G116000.1 1 0 -----MAKRLIPLDRVLVQRVAA-EKTKGKGMILPEKS
Cucsa_358500|Cucsa_358500.1 1 0 -----MAKRLIPLDRVLVQRVAA-EKTKGKGMILPEKS
Cucsa_280360|Cucsa_280360.1 1 0 -----MAKRLIPLDRVLVQRVAA-EKTKGKGMILPEKS
AC225518_12|AC225518_12.1 1 0 -----MAKRLIPLDRVLVQRVAA-EKTKGKGMILPEKS
Glyma07g34380|Glyma07g34380.1 1 0 -----MAKRLIPLDRVLVQRVAA-EKTKGKGMILPEKS
Glyma20g02110|Glyma20g02110.1 1 0 -----MAKRLIPLDRVLVQRVAA-EKTKGKGMILPEKS
GSVIVG01037354001|GSVIVT01037354001 1 0 -----MAKRLIPLDRVLVQRVAA-EKTKGKGMILPEKS
Eucgr_B02909|Eucgr_B02909.1 1 0 -----MAKRLIPLDRVLVQRVAA-EKTKGKGMILPEKS
Eucgr_B03754|Eucgr_B03754.1 1 0 -----MAKRLIPLDRVLVQRVAA-EKTKGKGMILPEKS
Potri_001G274300|Potri_001G274300.1 1 0 -----MAKRLIPLDRVLVQRVAA-EKTKGKGMILPEKS
Potri_009G068900|Potri_009G068900.1 1 0 -----MAKRLIPLDRVLVQRVAA-EKTKGKGMILPEKS
GSVIVG01011742001|GSVIVT01011742001 1 0 -----MAKRLIPLDRVLVQRVAA-EKTKGKGMILPEKS
GSVIVG01025759001|GSVIVT01025759001 1 0 -----MAKRLIPLDRVLVQRVAA-EKTKGKGMILPEKS

tr |D8TRX1|D8TRX1_VOLCA 62 VR-NKPTAGAVVA 73MGDVKA -----VKASKVLYSKFAG-TELELAGEBH----- 103-----VLLKEDDVIQVLPSPDKVAQLKP
gi |66806699|ref XP_3637072.1| 107 SQ-TKPSGGEVVE 118VGGGKMGGE-KSVPFCVTVGNITVYSKYG-TEQFNGADH----- 157-----ILLKEDDVIQVLPSPDKVAQLKP
YOR020C 1 0 -----YLLKEDDVIQVLPSPDKVAQLKP
gi |85079266|ref XP_956315.1| 37 A-NKTHEAVVVE 48VGGGRRITANG-FABLLKKGKRRILLNPSLGEKTVN-GVE 87-----CELLSNEVILFGMGN-----
gi |66806193|ref XP_3636819.1| 37 D-APTNNAKVVVA 47VGGGSLVLDGSEPHDIPVKEGDTVLLPEYGG-SMTVPWQPT 87-----VHLLSNEVDLGTIEN-----
YOR020C 1 0 -----VHLLSNEVDLGTIEN-----
gi |85079266|ref XP_956315.1| 40 V-KLNNSKVVVA 50VGGGALDDEGRILPVAVKEGDTVLLPEYGG-SFVKVGGSE-SE 89-----VHLLSNEVDLGTIEN-----
gi |17555568|ref NP_497428.1| 45 Q-GVVLQATVVA 55ACAGLNRKGEVAVITVVPKGDVLLPEYGG-HKVVVD-DKE 94-----VHLLSNEVDLGTIEN-----
gi |4504523|ref NP_002148.1| 38 Q-GVVLQATVVA 48VGGGSRDDEGRILPVAVKEGDTVLLPEYGG-HKVVVD-DKE 94-----VHLLSNEVDLGTIEN-----
Esi0000_0403 37 L-GKLNNEGVVA 47VGGGRRITANG-FABLLKKGKRRILLNPSLGEKTVN-GVE 87-----CELLSNEVILFGMGN-----
Phpat_008027000|Phpat_008027000.1 39 -AKLNSGVVVE 48VGGGALDDEGRILPVAVKEGDTVLLPEYGG-SHRTLE--G 85-----REVVLNRDDELGTIEN-----
Phpat_008026900|Phpat_008026900.1 39 -AKLNSGVVVE 48VGGGALDDEGRILPVAVKEGDTVLLPEYGG-SHRTLE--G 85-----REVVLNRDDELGTIEN-----
Phpat_004G011000|Phpat_004G011000.1 40 -AKLNSGVVVA 49VGGGSRDDEGRILPVAVKEGDTVLLPEYGG-SFVKVGGSE-SE 89-----VHLLSNEVDLGTIEN-----
Phpat_012G089700|Phpat_012G089700.1 40 -AKLNSGVVVA 49VGGGSRDDEGRILPVAVKEGDTVLLPEYGG-SFVKVGGSE-SE 89-----VHLLSNEVDLGTIEN-----
CMF129C|CMF129C 37 TAKALNNEGVVA 48VGGGSRDDEGRILPVAVKEGDTVLLPEYGG-SHRTLE--G 85-----REVVLNRDDELGTIEN-----
g3695|g3695.t1 35 T-CKVNEGVVVA 45VGGGRRITANG-FABLLKKGKRRILLNPSLGEKTVN-GVE 87-----CELLSNEVILFGMGN-----
GRMZM2G073401|GRMZM2G073401.T01 34 -KQLNSKVVVA 43VGGGSRDDEGRILPVAVKEGDTVLLPEYGG-SEVKKLAADKE 83-----VHLLSNEVDLGTIEN-----
LOC_0803g25050|LOC_0803g25050.1 35 -KQLNSKVVVA 44VGGGSRDDEGRILPVAVKEGDTVLLPEYGG-SEVKKLAADKE 83-----VHLLSNEVDLGTIEN-----
GRMZM2G410812|GRMZM2G410812.T01 34 -KQLNSKVVVA 43VGGGSRDDEGRILPVAVKEGDTVLLPEYGG-SEVKKLAADKE 83-----VHLLSNEVDLGTIEN-----
LOC_0807g44740|LOC_0807g44740.1 34 -KQLNSKVVVA 43VGGGSRDDEGRILPVAVKEGDTVLLPEYGG-SEVKKLAADKE 83-----VHLLSNEVDLGTIEN-----
GRMZM2G013652|GRMZM2G013652.T01 34 -KQLNSKVVVA 43VGGGSRDDEGRILPVAVKEGDTVLLPEYGG-SEVKKLAADKE 83-----VHLLSNEVDLGTIEN-----
GRMZM2G035063|GRMZM2G035063.T01 34 -KQLNSKVVVA 43VGGGSRDDEGRILPVAVKEGDTVLLPEYGG-SEVKKLAADKE 83-----VHLLSNEVDLGTIEN-----
Bra026173|Bra026173 34 -SKLNSKVVVA 43VGGGSRDDEGRILPVAVKEGDTVLLPEYGG-TOVKLG-EKE 82-----VHLLSNEVDLGTIEN-----
Bra026789|Bra026789 34 -SKLNSKVVVA 43VGGGSRDDEGRILPVAVKEGDTVLLPEYGG-TOVKLG-EKE 82-----VHLLSNEVDLGTIEN-----
Carubv10010732m.g|Carubv10010732m 34 -SKLNSKVVVA 43VGGGSRDDEGRILPVAVKEGDTVLLPEYGG-TOVKLG-EKE 82-----VHLLSNEVDLGTIEN-----
Bra016677|Bra016677 34 -SKLNSKVVVA 43VGGGSRDDEGRILPVAVKEGDTVLLPEYGG-TOVKLG-EKE 82-----VHLLSNEVDLGTIEN-----
AT1G14980 27 -SKLNSKVVVA 36VGGGSRDDEGRILPVAVKEGDTVLLPEYGG-NKLFYTLIQFFNF I 87-LKF-----NMV-DIYN-----
Glyma06g41830|Glyma06g41830.1 34 -SKLNSKVVVA 43VGGGSRDDEGRILPVAVKEGDTVLLPEYGG-TOVKLG-EKE 82-----VHLLSNEVDLGTIEN-----
Bra024563|Bra024563 34 -SKLNSKVVVA 43VGGGSRDDEGRILPVAVKEGDTVLLPEYGG-TOVKLG-EKE 82-----VHLLSNEVDLGTIEN-----
Carubv10010739m.g|Carubv10010739m 34 -SKLNSKVVVA 43VGGGSRDDEGRILPVAVKEGDTVLLPEYGG-TOVKLG-EKE 82-----VHLLSNEVDLGTIEN-----
AT1G23100 34 -SKLNSKVVVA 43VGGGSRDDEGRILPVAVKEGDTVLLPEYGG-TOVKLG-EKE 82-----VHLLSNEVDLGTIEN-----
Glyma03g28120|Glyma03g28120.1 34 -SKLNSKVVVA 43VGGGSRDDEGRILPVAVKEGDTVLLPEYGG-TOVKLG-EKE 82-----VHLLSNEVDLGTIEN-----
Glyma19g30860|Glyma19g30860.1 34 -SKLNSKVVVA 43VGGGSRDDEGRILPVAVKEGDTVLLPEYGG-TOVKLG-EKE 82-----VHLLSNEVDLGTIEN-----
Medtr7g089300|Medtr7g089300.1 34 -SKLNSKVVVA 43VGGGSRDDEGRILPVAVKEGDTVLLPEYGG-TOVKLG-EKE 82-----VHLLSNEVDLGTIEN-----
PGSC0003DMG40028744|PGSC0003DMT40006028 34 -SKLNSKVVVA 43VGGGSRDDEGRILPVAVKEGDTVLLPEYGG-TOVKLG-EKE 82-----VHLLSNEVDLGTIEN-----
PGSC0003DMG40028744|PGSC0003DMT40007396 34 -SKLNSKVVVA 43VGGGSRDDEGRILPVAVKEGDTVLLPEYGG-TOVKLG-EKE 82-----VHLLSNEVDLGTIEN-----
Medtr3g077350|Medtr3g077350.1 34 -SKLNSKVVVA 43VGGGSRDDEGRILPVAVKEGDTVLLPEYGG-TOVKLG-EKE 82-----VHLLSNEVDLGTIEN-----
29816.t000025|29816.m000688 34 -SKLNSKVVVA 43VGGGSRDDEGRILPVAVKEGDTVLLPEYGG-TOVKLG-EKE 82-----VHLLSNEVDLGTIEN-----
Potri_008G130500|Potri_008G130500.1 34 -SKLNSKVVVA 43VGGGSRDDEGRILPVAVKEGDTVLLPEYGG-TOVKLG-EKE 82-----VHLLSNEVDLGTIEN-----
Potri_010G116000|Potri_010G116000.1 34 -SKLNSKVVVA 43VGGGSRDDEGRILPVAVKEGDTVLLPEYGG-TOVKLG-EKE 82-----VHLLSNEVDLGTIEN-----
Cucsa_358500|Cucsa_358500.1 34 -SKLNSKVVVA 43VGGGSRDDEGRILPVAVKEGDTVLLPEYGG-TOVKLG-EKE 82-----VHLLSNEVDLGTIEN-----
Cucsa_280360|Cucsa_280360.1 34 -SKLNSKVVVA 43VGGGSRDDEGRILPVAVKEGDTVLLPEYGG-TOVKLG-EKE 82-----VHLLSNEVDLGTIEN-----
AC225518_12|AC225518_12.1 34 -SKLNSKVVVA 43VGGGSRDDEGRILPVAVKEGDTVLLPEYGG-TOVKLG-EKE 82-----VHLLSNEVDLGTIEN-----
Glyma07g34380|Glyma07g34380.1 34 -SKLNSKVVVA 43VGGGSRDDEGRILPVAVKEGDTVLLPEYGG-TOVKLG-EKE 82-----VHLLSNEVDLGTIEN-----
Glyma20g02110|Glyma20g02110.1 34 -SKLNSKVVVA 43VGGGSRDDEGRILPVAVKEGDTVLLPEYGG-TOVKLG-EKE 82-----VHLLSNEVDLGTIEN-----
GSVIVG01037354001|GSVIVT01037354001 34 -SKLNSKVVVA 43VGGGSRDDEGRILPVAVKEGDTVLLPEYGG-TOVKLG-EKE 82-----VHLLSNEVDLGTIEN-----
Eucgr_B02909|Eucgr_B02909.1 34 -SKLNSKVVVA 43VGGGSRDDEGRILPVAVKEGDTVLLPEYGG-TOVKLG-EKE 82-----VHLLSNEVDLGTIEN-----
Eucgr_B03754|Eucgr_B03754.1 34 -SKLNSKVVVA 43VGGGSRDDEGRILPVAVKEGDTVLLPEYGG-TOVKLG-EKE 82-----VHLLSNEVDLGTIEN-----
Potri_001G274300|Potri_001G274300.1 34 -SKLNSKVVVA 43VGGGSRDDEGRILPVAVKEGDTVLLPEYGG-TOVKLG-EKE 82-----VHLLSNEVDLGTIEN-----
Potri_009G068900|Potri_009G068900.1 34 -SKLNSKVVVA 43VGGGSRDDEGRILPVAVKEGDTVLLPEYGG-TOVKLG-EKE 82-----VHLLSNEVDLGTIEN-----
GSVIVG01011742001|GSVIVT01011742001 34 -SKLNSKVVVA 43VGGGSRDDEGRILPVAVKEGDTVLLPEYGG-TOVKLG-EKE 82-----VHLLSNEVDLGTIEN-----
GSVIVG01025759001|GSVIVT01025759001 34 -SKLNSKVVVA 43VGGGSRDDEGRILPVAVKEGDTVLLPEYGG-TOVKLG-EKE 82-----VHLLSNEVDLGTIEN-----

tr |D8TRX1|D8TRX1_VOLCA 127 LGDRILIKGAK-AEDKTAGGVLATDSGK 155PTFGTVVAVGEGKEDEETKQMKPN-----VEVGA-----TVMYS 190KYSGETEFEE-DG
tr |D8RAQ5|D8RAQ5_SELML 179 PVNDRVLKVAE-AEDKTAGGVLATDSVKEK 208PVGIVVAVGPGSYGEDGTR-KPLE-----VSGID-----NVLYS 242KYAGNEFKND
gi |66806699|ref XP_637072.1| 103 ----- 102----- 102-----
gi |66806193|ref XP_636819.1| 103 ----- 102----- 102-----
YOR020C 107 ----- 106----- 106-----
gi |85079266|ref XP_956315.1| 105 ----- 104----- 104-----
gi |17555568|ref NP_497428.1| 109 ----- 108----- 108-----
gi |4504523|ref NP_002148.1| 103 ----- 102----- 102-----
Esi0000_0403 102 ----- 101----- 101-----
Phpat.008G027000|Phpat.008G027000.1 103 ----- 102----- 102-----
Phpat.008G026900|Phpat.008G026900.1 105 ----- 105----- 105-----
Phpat.004G011000|Phpat.004G011000.1 107 ----- 106----- 106-----
Phpat.012G089700|Phpat.012G089700.1 107 ----- 106----- 106-----
CMF129C|CMF129CT 102 ----- 101----- 101-----
g3695|g3695.t1 100 ----- 99----- 99-----
GRMZM2G073401|GRMZM2G073401_T01 98 ----- 97----- 97-----
LOC_Os03g25050|LOC_Os03g25050.1 98 ----- 98----- 98-----
GRMZM2G410812|GRMZM2G410812_T01 106 DEVPDKNEIIRLRKVASVGV--GDKHD 131AEVHSLTDAAGANDNSWILLFYLCAAFMVSNIWNGAVYDVNIIGLSSNNLHCLARCUSA 191VIEGSEYTRVVEREQ
LOC_Os07g44740|LOC_Os07g44740.1 99 ----- 98----- 98-----
GRMZM2G013652|GRMZM2G013652_T01 99 ----- 98----- 98-----
GRMZM2G035063|GRMZM2G035063_T01 99 ----- 98----- 98-----
Bra026173|Bra026173 105 IELKIV--VSLGMDAGTI--SSGMR 125TSWGRCTKIEKG* 137
Bra026789|Bra026789 99 ----- 98----- 98-----
Carubv10010732m.g|Carubv10010732m 99 ----- 98----- 98-----
Bra016677|Bra016677 99 ----- 98----- 98-----
AT1G14980 99 ----- 98----- 98-----
Glyma06g41830|Glyma06g41830.1 98 ----- 97----- 97-----
Bra024563|Bra024563 88 ----- 87----- 87-----
Carubv10010739m.g|Carubv10010739m 98 ----- 97----- 97-----
AT1G23100 98 ----- 97----- 97-----
Glyma03g28120|Glyma03g28120.1 98 ----- 97----- 97-----
Glyma19g30860|Glyma19g30860.1 98 ----- 97----- 97-----
Medtr7g089300|Medtr7g089300.1 106 ----- 105----- 105-----
PGSC0003DMG402023448|PGSC0003DMT40006028 104 ----- 103----- 103-----
PGSC0003DMG400028744|PGSC0003DMT40007396 98 ----- 97----- 97-----
Medtr3g077350|Medtr3g077350.1 90 ----- 89----- 89-----
29816.t000025|29816.m000688 98 ----- 97----- 97-----
Potri.008G130500|Potri.008G130500.1 98 ----- 97----- 97-----
Potri.010G111600|Potri.010G111600.1 98 ----- 97----- 97-----
Cucsa.358500|Cucsa.358500.1 98 ----- 97----- 97-----
Cucsa.280360|Cucsa.280360.1 98 ----- 97----- 97-----
AC225518_12|AC225518_12.1 98 ----- 97----- 97-----
Glyma07g34380|Glyma07g34380.1 98 ----- 97----- 97-----
Glyma20g02110|Glyma20g02110.1 123 ----- 122----- 122-----
GSVIVG01037354001|GSVIVT01037354001 98 ----- 97----- 97-----
Eucgr.B02909|Eucgr.B02909.1 98 ----- 97----- 97-----
Eucgr.B03754|Eucgr.B03754.1 98 ----- 97----- 97-----
Potri.001G274300|Potri.001G274300.1 98 ----- 97----- 97-----
Potri.009G068900|Potri.009G068900.1 98 ----- 97----- 97-----
GSVIVG01011742001|GSVIVT01011742001 98 ----- 97----- 97-----
GSVIVG01025759001|GSVIVT01025759001 98 ----- 97----- 97-----

tr |D8TRX1|D8TRX1_VOLCA 202 EQYIVV-----RESDILAOLA----- 217-----
tr |D8RAQ5|D8RAQ5_SELML 254 NSQYVVM-----RVSDLLAILS----- 270-----
gi |66806699|ref XP_637072.1| 103 ----- 102----- 102-----
gi |66806193|ref XP_636819.1| 103 ----- 102----- 102-----
YOR020C 107 ----- 106----- 106-----
gi |85079266|ref XP_956315.1| 105 ----- 104----- 104-----
gi |17555568|ref NP_497428.1| 109 ----- 108----- 108-----
gi |4504523|ref NP_002148.1| 103 ----- 102----- 102-----
Esi0000_0403 102 ----- 101----- 101-----
Phpat.008G027000|Phpat.008G027000.1 103 ----- 102----- 102-----
Phpat.008G026900|Phpat.008G026900.1 106 ----- 105----- 105-----
Phpat.004G011000|Phpat.004G011000.1 107 ----- 106----- 106-----
Phpat.012G089700|Phpat.012G089700.1 107 ----- 106----- 106-----
CMF129C|CMF129CT 102 ----- 101----- 101-----
g3695|g3695.t1 100 ----- 99----- 99-----
GRMZM2G073401|GRMZM2G073401_T01 98 ----- 97----- 97-----
LOC_Os03g25050|LOC_Os03g25050.1 98 ----- 98----- 98-----
GRMZM2G410812|GRMZM2G410812_T01 206 RINLSNVHTDELQEAELPSRVSABEANIKSSMQIVVKL8AGVVLDS 251WNDSRYLVHCIFRIRVWQRFPTTPRSHTFEPGYSSSSGSQHDDGYDADRRAGLRLS
LOC_Os07g44740|LOC_Os07g44740.1 99 ----- 98----- 98-----
GRMZM2G013652|GRMZM2G013652_T01 99 ----- 98----- 98-----
GRMZM2G035063|GRMZM2G035063_T01 99 ----- 98----- 98-----
Bra026173|Bra026173 138 ----- 137----- 137-----
Bra026789|Bra026789 99 ----- 98----- 98-----
Carubv10010732m.g|Carubv10010732m 99 ----- 98----- 98-----
Bra016677|Bra016677 99 ----- 98----- 98-----
AT1G14980 99 ----- 98----- 98-----
Glyma06g41830|Glyma06g41830.1 98 ----- 97----- 97-----
Bra024563|Bra024563 88 ----- 87----- 87-----
Carubv10010739m.g|Carubv10010739m 98 ----- 97----- 97-----
AT1G23100 98 ----- 97----- 97-----
Glyma03g28120|Glyma03g28120.1 98 ----- 97----- 97-----
Glyma19g30860|Glyma19g30860.1 98 ----- 97----- 97-----
Medtr7g089300|Medtr7g089300.1 106 ----- 105----- 105-----
PGSC0003DMG402023448|PGSC0003DMT40006028 104 ----- 103----- 103-----
PGSC0003DMG400028744|PGSC0003DMT40007396 98 ----- 97----- 97-----
Medtr3g077350|Medtr3g077350.1 90 ----- 89----- 89-----
29816.t000025|29816.m000688 98 ----- 97----- 97-----
Potri.008G130500|Potri.008G130500.1 98 ----- 97----- 97-----
Potri.010G111600|Potri.010G111600.1 98 ----- 97----- 97-----
Cucsa.358500|Cucsa.358500.1 98 ----- 97----- 97-----
Cucsa.280360|Cucsa.280360.1 98 ----- 97----- 97-----
AC225518_12|AC225518_12.1 98 ----- 97----- 97-----
Glyma07g34380|Glyma07g34380.1 98 ----- 97----- 97-----
Glyma20g02110|Glyma20g02110.1 123 ----- 122----- 122-----
GSVIVG01037354001|GSVIVT01037354001 98 ----- 97----- 97-----
Eucgr.B02909|Eucgr.B02909.1 98 ----- 97----- 97-----
Eucgr.B03754|Eucgr.B03754.1 98 ----- 97----- 97-----
Potri.001G274300|Potri.001G274300.1 98 ----- 97----- 97-----
Potri.009G068900|Potri.009G068900.1 98 ----- 97----- 97-----
GSVIVG01011742001|GSVIVT01011742001 98 ----- 97----- 97-----
GSVIVG01025759001|GSVIVT01025759001 98 ----- 97----- 97-----

tr D8TRX1 D8TRX1_VOLCA	218	--	217	-----	217
tr D8RAQ5 D8RAQ5_SELML	271	---	270	-----	270
gi 66806699 ref XP_637072.1	103	102	-----	102	
gi 66806193 ref XP_636819.1	103	102	-----	102	
FOR020C	107	106	-----	106	
gi 85079266 ref XP_956315.1	105	104	-----	104	
gi 17555568 ref NP_497428.1	109	108	-----	108	
gi 4504523 ref NP_002148.1	103	102	-----	102	
Esi0000_0403	102	101	-----	101	
Phpat_008G027000 Phpat_008G027000.1	103	102	-----	102	
Phpat_008G026900 Phpat_008G026900.1	106	105	-----	105	
Phpat_004G011000 Phpat_004G011000.1	107	106	-----	106	
Phpat_012G089700 Phpat_012G089700.1	107	106	-----	106	
CMF129C CMF129CT	102	101	-----	101	
g3695 g3695.t1	100	-----	99	-----	
GRMZM2G073401 GRMZM2G073401_T01	98	-----	97	-----	
LOC_Os03g25050 LOC_Os03g25050.1	99	-----	98	-----	
GRMZM2G410812 GRMZM2G410812_T01	312	311	RGGLDFGASRKKKFEVGGSSGSHGAGSLQRFVAVSRSGPLSYR*	356	
LOC_Os07g44740 LOC_Os07g44740.1	99	-----	98	-----	
GRMZM2G013652 GRMZM2G013652_T01	99	-----	98	-----	
GRMZM2G035063 GRMZM2G035063_T01	99	-----	98	-----	
Bra026173 Bra026173	138	137	-----	137	
Bra026789 Bra026789	99	-----	98	-----	
Carubv10010732m.g Carubv10010732m	99	-----	98	-----	
Bra016677 Bra016677	99	-----	98	-----	
AT1G14980	99	-----	98	-----	
Glyma06g41830 Glyma06g41830.1	98	-----	97	-----	
Bra024563 Bra024563	88	-----	87	-----	
Carubv10010739m.g Carubv10010739m	98	-----	97	-----	
AT1G23100	98	-----	97	-----	
Glyma03g28120 Glyma03g28120.1	98	-----	97	-----	
Glyma19g30860 Glyma19g30860.1	98	-----	97	-----	
Medtr7g089300 Medtr7g089300.1	106	105	-----	105	
PGSC0003DMG402023448 PGSC0003DMT40006028	104	103	-----	103	
PGSC0003DMG400028744 PGSC0003DMT40007396	98	-----	97	-----	
Medtr3g077950 Medtr3g077950.1	90	-----	89	-----	
29816.t000025 29816.m000688	98	-----	97	-----	
Potri_008G130500 Potri_008G130500.1	98	-----	97	-----	
Potri_010G111600 Potri_010G111600.1	98	-----	97	-----	
Cucsa_358500 Cucsa_358500.1	98	-----	97	-----	
Cucsa_280360 Cucsa_280360.1	99	-----	98	-----	
AC225518_12 AC225518_12.1	98	-----	97	-----	
Glyma07g34380 Glyma07g34380.1	98	-----	97	-----	
Glyma20g02110 Glyma20g02110.1	123	122	-----	122	
GSVIVG01037354001 GSVIVT01037354001	98	-----	97	-----	
Eucgr_B02909 Eucgr_B02909.1	98	-----	97	-----	
Eucgr_B03754 Eucgr_B03754.1	98	-----	97	-----	
Potri_001G274300 Potri_001G274300.1	98	-----	97	-----	
Potri_009G068900 Potri_009G068900.1	98	-----	97	-----	
GSVIVG01011742001 GSVIVT01011742001	98	-----	97	-----	
GSVIVG01025759001 GSVIVT01025759001	98	-----	97	-----	