

Supplementary Data Set 1. Sequence alignment used to construct the phylogenetic tree in Figure 1.

>PtGRXG4

-----MATITISLQTFPSLHSLSLN
SPQNTPTLSFYQSQKPFPSISLKSFNNTTLKSKPRSL SITAAFKTLSETELITVPLTADDEF
NSKMPSDCGVYAVYDKSNDLQFIGVTRNIGASVFSHLKSVPELCHSVKVGVVVEPKASL
TEAWKSWMEEYIKTTGKVPNETGNAT-----WIRQPSKKKADLRLTPGRHVQLTVPL
EELIDRLVK-----E-NKVVAFIK
GSRAPMCGFSQKVVGILESE-----GVDY-ESVDVLDE-EYNYGLRETL-----
K-KYS--NWPTFPQ-IFMNG----ELV-----GG-CDILTSMEKGEKELAGHFKK---

>PtGRXG3

-----MARLLSNTILKGISRASQSPRIVPASFNHVKLRFSSTTIPNDPDSHAD
FQPNNKAV-----NESGSCSGINI
KELVDKDVK-----E-HPIVIYMK
GYPDLPCGFSALAVRVLKQY-----NVPI-TARNILEY-P---DLRTGV-----
K-AYS--NWPTFPQ-IFIKG----EFI-----GG-SDIIMNMHQTGELKEKLQD---

-----IAGKEESE-----

>PtGRXG5

-----MGSQSLLVLSAPTTMIPSKIAASSLAPSRPGPLCFPRALTIITDSVVFVRVK
SNSARN-----KLASSIRCALTPAL
KTTLDKVVT-----S-HKVVLFMK
GTKDFPQCGFSQTVVQILKSL-----NVPF-ESVNILEN-E---LLRQGL-----
K-DYS--SWPTFPQ-LYIDG----EFF-----GG-CDITVEAYKSGELQEQVEK---

-----AMCS-----

>PtGRXG1

-----MSGSVKDVKSKAELDNI
TKSGEAVIIHFASWCDAKQMDQVFSHLSTDFPNTHFLTVEAEEQPEISEAFSVSSVPY
FVFKDGKTVDTLLEGADPSSLATKVARVAGSANPGEPAAPASLGMAAGPTVLETVKEFAK
ENGSSPQA-----NQAQPLSDDL
KNRLQQLID-----S-HPIMLFMK
GNPEAPRCGFSQKVIDILKDE-----NVKF-GTFDILSD-N---EVRDGL-----
K-LLS--NWPTFPQ-LYCKG----ELL-----GG-CDIAIAMHESGELKEVFRD---

-----HGIDAIGSVEAKVGGSENGKGGITQSTG

LSTTLTSRLES LINSSPVMLFMKGKPTPKCGFS GKVVAILQEEKVTFESFDILTDEEVR
QGLKVYSNWSSYPQLYIKGELIGGSDIVLEMQKSGEL-----

-----KRILVEKGIVQKETLEDHLKSLITSSPV
MLFMKGTPDAPRCGFSSKVVNALKEKGVSFSGFDILSDEEVRQGLKVFSNWPTFPQLYYK
GELIGGCDIILELRDNGELKSTLSE

>PtGRXG2

-----MGGSVKDVKSKAELDNI
TKSGEAVIIHFWATWCDASKQMDQVFSHLSTDFPKTHFLRVEAEEQPEISEAFVSSVVPY
FVFLKDGKTVDTLLEGADPSSLANKVAKVAGSANPGEPAAPASLGMAAGPTVLETVKEFTK
ENGSSQQA-----NQVQPLSDAL
KNQLQQLIG-----S-HPVMLFMK
GNAEAPKCGFSRKVV DILKGE-----NVKF-GTFDILSD----IEVREGL-----
K-LFS---NWPTFPQ-LYCKG-----ELL-----GG-CDIVIALHESGELKEVFRD---

-----HGIDTIGSNEAKVSGSENGKGGIAQSTG
LSMTLTSRLES LVNSSPVMLFMKGKPTPKCGFS GKVVAILREKVKFETFDILTDEEVR
QGLKVYSNWSSYPQLYIKGELIGGSDIVLEMQKSGEL-----

-----KKVLEIEKGIVQKETIEDRIKSLITSSPV
MLFMKGTPDAPRCGFSSKVVNALKEEGVSVFESFDILSDEEVRQGLKVFSNWPTFPQLYYK
GELIGGCDIIMELRDNGELKSTLSE

>PtGRXD3

-----MEKAAVSEKDITNSPTSEKHEEDAI I AEGDNQMRVSEEVNSLDTRK
DNPKLDKDNAESDAGES IDESSGLEFKCPVDNVVKHDDLKGE CENMGMEPKSVGAKLNND
TQRVVSGDKMDEVGDLEPKAEENKQTPEEILGEQKEPEPVFDGTEVPGMEANRSTSFHS
SDADHEAEGSAWPEKAVALKNFVKEKGA VAVT SVLRVLSVKRDEVEWVTGDEK EASDSA
KDKEVTEVSQKPADRS AWNPLSYIMYSHDDAENKFEQGVGSE EPPQPIAMKGR I ILYT-
-----RLGCQDCKEVRFLHRK-----RLRY-VEINIDVYPSRKLELEKFT-----
-----GSSTVPK-VFFNE-----IVI-----GG-LTELNGLDESGKLGKIDYLIT
EAPASEAPLPLSGEDDASTSGSIDELALIVRKMESILVKDRFYKMRRFTNCF LGSEAV
DFLSEDQYL EREEATEFGRKLVSKLFFRHILDENIFEDGNHLYRFLDNDPVSSQCYNIP
RGIVEAKPKPITEIAARLRF LSCAIFEAFTSVDGKHVDYRSIHGSEEFARYLR I IQELQR
VELLDMPREEKLAFFINLYNMMAIHA I LVLGFPKGALERRKLF GDFQYVIGGCTYSLSAI
QNGILLRGNQRPPY NLTKPFVVKDKRSKVTLPYAEPLIHFALVCGRSGPALRCFSPGDID
KELMEAARDFLRGGGLIIDLNAKTAFASKILKWF-----SVDFGKNEMEVLKHASNFLE
PTYSETLMELLDGAQLKVTYQPYDWGLNN-----

>PtGRXD1

-----MEVINGEL
LKPAGEEKLGIKVTE SNGVVDKEI IKTRYENENLSSSVHLS PSSNSNVNQDDPAGDTTKP
EDI IAVTPKINGYKQTIQPDFHLPKPEAPPGLSPSPSPQPYENGN AVVRSKSLSESFTAV
DMP SIGFKIKDRSNSLSETISKRFSS LKFDDGDDYMNKVKSFDSGVTEFKISGLKVVV
MLKNNEKEE-----QIKGRVSFFS
-----RSNCRDCTAVRSFFRER-----GLKF-VEINIDVYRQREKELIERT-----
-----GSSQVPQ-IFFND-----KLF-----GG-LVALNSLRN SGGFEERLKEMLG
KKCSGDAPAPPVYGFDD-HEEESTDEMVGIVKVLQRQLPIQDR LMKMKIVKNCFAGKEMV
EVLIIHFD CGRKKAVEIGKQLARKHFIHVFGENDFEDGNHYRFL EHEPFI-PKCYNFR
GSTNDSEPKPAVVVGQR LNKIMSAIL ESYASDDRRHV DYAGISKSEEFRRYVNLVQDLHR
VDLLMLSQDEKLAFFLN LHNAMVIHAIIRVGYPEGAIERRSFSSNFQYIVGGSSYSLNTI
TNGILRSNRRSPYSLVKPFGTGDKRLEVALPKVNPLIHFGLCIGTTSSPPVRF FT SQIE
AELRCAARKFFQRSGMEVDLEKRTVYLR I IKWF-----SGDFGQEKEILRCI INYLDA
TKAGLLTHLLGDGGPVNI VYQDYDWSINS-----

>PtGRXD2

MELTNGELIKADAQEKLGINVAEANGSVADGNLVKGI IQTGLAKENLSKSVHPS PNSSND
FNYDDPAGDIKPAQKQ QEDGFCEIEME EEEKQDSATEIFSSDDAVERITSTGNHVEKEEN
DDI IAVSPKVN GYIQVIQPD IHLPKPEAPPGLSPSSTPSPQND DVVTRSKSLPNSFTV
DMP SIGFKIKDRSNSLSASISKRF SFFKSDDGDDYMNHKVNSFDSGVTRFNISGLKVTV
KLKKDDEEE-----QIK-GRISFFS-
-----RSNCRDCTAVRSFFRER-----GLKF-VEINIDVYRQREKELIERT-----

-----GNSQVPQ-IFNE-----KLF-----GG-LVALNSLRNSGGFEQRLKEMLA
KKCSGNAPAPPVYGFDD-HEEESTDEMWWIVKVLKLP IQDRMLMKKIVRNCFAGNEMV
EVI IHHFDCGRKKAVEIGKQLARKHFIHHVFGENDFEDGNHYRFFIEHEPFI-PKCYNFR
GSTNDSEPKPAVVVGQRLNKIMSAILESHASDDRCLVDYAGISKSEEFRRYDNLAQDLHR
VDVLKLSQDEKLAFFLNLHNAMVIHAVIRVGCPEGAIDRRSFYSDFQYIVGGSPYSLNTI
KNGILRSNRRSPYSLVKPFGTGDKRLEVVLPKVNPLIHFGLCNGTRSSPTVRFFTPQIE
AELRCATREFFQRNGIEVDLEKRTVYLTRIIKWF-----SGDFGQEKEILRWIINYLDA
TKAGLLTHLLGDGGPVNIVYQDYDWSINA-----

>PtGRXA7

-----MQQAIPYKSWPLYTNNKPLISPFQLIARHNNG-----
-----GVVATQEVKLG
SGNMSKMQ-----E-NAIIVFA-
---RRGCCMSLVAKRLLLGL-----GVNP-AVYEIDEA-DEISVLEELEMICND-
G-GKG-SKKKVQFPA-LFIGG-----KLF-----GG-LDKLMAAHISGELVPILKE---

-----AGAL-----

-----WL-----

>PtGRXA8

-----MQQAIPYKSWLPLYTNNKPLISPSQLISHHSNG-----
-----GVVAAQEVKLG
SRNISEMQ-----E-NAIIVFA-
---RRGCCMSHVAKRLLLGL-----GVNP-AVYEIDEA-DEISVLEELEMIGNDI
G-GKGNKKKVQFPA-LVIGG-----KLF-----GG-LDTLMATHISGELVPILKE---

-----AGAL-----

-----WL-----

>PtGRXA9

-----MQEAIPFRAYSPATTSGNRRLPARDHGGANTS-----
-----SGHVLVVTNGH
ENHVQKLV-----E-NSVIVFG-
---KRGCCMCHVVKRLLLGL-----GVNP-PVFEVEEK-EEDDVIKELSMIDSDR
G-GEG--VDQVQFPV-VFVGG-----KLF-----GG-LERVMATHITGELVPILKD---

-----AGAL-----

-----WL-----

>PtGRXA11

-----MQEAIPFRAYSPATTAGNRRLPGRDSCDHGGANSTS-----

-----AGHVLIIVTNGQ
ESHVQKLVS-----E-NSIAIFG-
---KRGCCMCHVVKLLGL-----GVNP-PVFEVEEK-EEDYVIKALS-----
MIKGGKDADQVQFPV-VFVGG---KLF-----GG-LERIIASHITGELVPILKD---

-----AGAL-----
-----WL-----

>PtGRXA1

-----MQRLRRRCSNDVVRLDLTTPPNS-----SSLSIDGAEST
ETRIQRLIS-----E-HPVIIFS-
---RSSCCMCHVMKLLATI-----GVHP-TVIELDDH-EISALPPAAE-----
DGSPS---PSSLAPA-VFIGG---TCV-----GG-LESLVALHLSGHLVPKLVE---

-----VGVL-----

---AFSPGYDNNNNPIISS-----

>PtGRXA2

-----MQGLRQRCSDDVDLLDLSSPLNSSSS-----SSLSIDEAEST
ETRIQRLIS-----E-HPVIIFS-
---RSSCCMCHVMKLLATI-----GVHPTKIYALPPAAEDG-----
-----IGG-----TCV-----GG-LESLVALHLSGHLVPKLVE---

-----LGVL-----

---AFSSGYGNNNHIIIS-----

>PtGRXA15

MDMVNRLVA-----D-RPVVVS-
---RSTCCMSHSIKTLISSF-----GANP-TVYELDQI-PNGKQIEKAL-----
VQQLG---CQPSVPA-VFIGQ---EFV-----GG-DKQVMSLQVRNELAPLLRK---

-----AGAI-----

-----WI-----

>PtGRXA21

>PtGRXA23

MDVLNVMIQ-----E-KPVVIFS-
---KSSCCMSHSIKSLIRGF-----GANP-TVYELDRI-PNGQQIERAL-----
V-QLG--FGQSVPA-VFIGQ----RLV-----GN-ERQVMSLHVQNQLVPLLIQ----

-----AGAI-----

-----WI-----

>PtGRXA18

MDVVNAMIQ-----E-KPVVIFS-
---KSSCCMSHSIESLIRGF-----GANP-TIYQLDQL-PNGHQIERAL-----
V-QLG--FRQSVPV-VFIGQ----KLV-----GN-ERQVMGLHVRNQLVPLLIQ----

-----AGAI-----

-----WI-----

>PtGRXA16

MDVVNVMIQ-----E-KPVVIFS-
---KSSCCMSHSIESLMRGF-----GANP-TIYQLDQI-PNGQQIERAL-----
M-QLG--FRQSVPA-VFIGQ----QLI-----GN-ERQVMSLHIQNQLVPLLIQ----

-----AGAI-----

-----WI-----

>PtGRXA17

MDVVNVLIQ-----D-KPVVIFS-
---KSSCCMSHSVETLIRGF-----GANP-TVYDLDRIPNGQQIERAL-----
M-QLG--FRQSVPA-VFIGQ----QLV-----GN-ERNVMSLHIQNQLVPLLIQ----

-----AGAI-----

-----WI-----

>PtGRXA19

MDKVLRLAS-----E-QGVVIFI-
---KSTCCCLCYAVKILFQEI-----GVDP-LVHEIDQD-PEGREMEKAL-----
T-RMG---CSAPVPA-VFVGG---KLL-----GS-TNEVMSLHLSGSLNQLMKP---

-----YQSQ-----

-----T-----

>PtGRXA25

MDKVMGLAS-----E-KGVVIFS-
---KSSCCCLCYAVKILFQEI-----GVDP-LVYEIDQD-PEGREMEKAL-----
T-RLG---CNAPVPA-VFIGG---KLM-----GS-TNEVMSLHLSGSLIPMLKP---

-----YQN-----

>PtGRXA10

MERVTKLAS-----E-RPVVIFS-
---KTTCCMCHTIKTLFCDF-----GVNP-AVHELDEM-PRGREIEQAL-----
T-R-A---GCPTLPA-VFIGG---EIV-----GG-ANEVMSLHLSRSLIPMLKH---

-----AGAL-----

-----WV-----

>PtGRXA12

MERVTNLAS-----E-RPVVIFS-
---KSSCCMCHTIKTLFNEF-----GVNV-AVHELDEM-PRGREIEQAL-----
S-R-F---GCPTLPA-VFIGG---ELV-----GG-ANEVMSLHLNRSRSLIPMLKR---

MDQVRDLAS-----K-NAAVIFT-
---KSSCCMCHSIKTLFYEL-----GASP-AIHELDRE-ANGREMEWAL-----
R-GLG---CNPTVPA-VFIGG---KWV-----GS-AKDVLSLHLDGSLKQMLME---

-----AKAI-----

-----WF-----

>PtGRXA14

MDRVAKLAS-----Q-KAVVIFS-
---KSSCCMCHAIRLFYDQ-----GVSP-AIYELDED-SRGKEMEWAL-----
M-RLG---CNPSVPA-VFIGG---KFV-----GS-ANTVMTLQLNGSLKLLKE---

-----AGAL-----

-----WL-----

>PtGRXA4

-----MYQTESWGSYMPARTNLGDP-----

LERIGRLAS-----E-NAVVIFS-
---ISSCCMCHAIRLFCGM-----GVNP-TVYELDED-PRGKEMEKAL-----
MRLLG---SSSAVPV-VFIGG---KLV-----GA-MDRVMAHINGSLSVPLLKE---

-----AGAL-----

-----WL-----

>PtGRXA5

-----MQYHQAESWGY-----

-----VPMRTSMVSDP-----

LEKVARLAS-----G-SAVVIFS-
---ISSCCMCHAVKRLFCGM-----GVNP-TVYELDHD-PRGKEIEKAL-----
MRLLG---SSTSVPV-VFIGG---KLI-----GA-MDRVMAHISGTLVPLLKE---

-----AGAL-----

-----WL-----

>PtGRXA6

-----MQYHQAESWGYH-----
-----VPTRTCMASDP
LEKVARLAS-----E-SAVVVS-
---ISSCCMCHAVKRLFCEM-----GVNP-TVYELDHD-PRGEEIEKAL-----
MRLLG---NSTSVPV-VFIGG---KLI-----GA-MERVMASHISGTLVPLLKE---

-----AGAL-----
-----WL-----

>PtGRXB5

-----MATRIRLPSILATAVTLTVLA-----
-----ASLWAAGSPE
ATFVKKTIS-----S-HQIVIFS-
---KSYCPYCKKAKGVFKEL-----NQTP-HVVELDQR-EDGHDIQDAM-----
S-EIV---GRRTVPQ-VFIGG---KHI-----GG-SDDTVEAYESGELAKLLGV---

-----ASEQKDDL-----

>PtGRXB6

-----MKRIQCSIALNRTTIGLLLLLVALAN-----
-----ELKVTEASNSA
SAFVQNVIIY-----S-NKIVIFS-
---KSYCPYCLRAKRVFSEL-----YEKP-FAVELDLR-DDGGEIQDYI-----
L-DLV---GKRTVPQ-IFVNG---KHI-----GG-SDDLRAAVESGELQKLL-----

-----GTE-----

>PtGRXB4

-----MADTLTNLTPLPLKSSRTLSSLRGLPICSTPLSNSSSSLKTTSTCSRILSINGPKR
YRPMASARA-----TDSSSPSSSFGSRL
EDAVKKTVA-----E-NPVVVYS-
---KTWCYSYSSEVKSLFKRL-----NVDP-LVVELDELGAQGPQIQKVL-----
E-RLT---GQHTVPN-VFIGG---KHI-----GG-CTDTVKLYRKGELEPLLSE---

-----ANAKKSQG-----

>Potri.001G159000

-----MRGNNKALL
VRALIFGSHRSSMNSFSRHLHENLISNPSKTSHPKSLSNFTTKFHFSTPYLQPFORTLC
SSSSSGAS-----NIVLVKSDEEL
NSGLKNVQE-----KSSPAVFYFT
---ATWCGPCKFISPVIEEL-----SKKY-PHATIIYKVDIDTEGLQNAL-----
A-SLN---IAAVPTLDFYKNGKKETTIV-----GA-DVAKLKNTMESLYRED-----

>Potri.007G074000

-----MDKIILSSTSTPLSTSSLPLRRTVTSTASLSSPKKLFLLRSTQS
QRKLSSSSRRSTSFCKVHKSTTITCG-----
-----AITEIN
ESEFQNVVL-----NSD-RPVLVEFV
---ATWCGPCRLISPAMESV---AQEYGDRL-TVVKIDHD-ANPKLIKEYK-----
V-----YGLPALV-LFKDG---KEVPESRREGAITKAKLKEYVDALLESISVA---

>Potri.013G132200

-----MVSSMVLSSYPS
SRLKCSLSNPQSVIMMSSPQPTVALLFPVRLGGAASFAEFGGLRIQMGSKLSPSLVSINT
RRNPKVFCRIV-----SEAQETVVDIPTVTDET
WQSLVIEAD-----GPVMIEFW
---APWCGPCRIIHPVIAEL---STEYGGKL-KCFMLNTDESPSTVTKYGI-----
-----RSIPTIIIFKKGEKKDAII-----GAVPKTTLISNIKKFL-----