

# NODULATION COMPETITIVENESS AND DIVERSIFICATION OF SYMBIOSIS GENES IN COMMON BEANS FROM THE AMERICAN CENTERS OF DOMESTICATION

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## Supplementary Material

**SI. Fig. 1:** Protein alignment of *P. vulgaris* gene products Nfr1 (A), Nfr5 (B), Astray (C), RabA2 (D) and NIN (E), by using the Clustal-X v2.1 software [30]. Red color represents highly conserved residues; blue color represents variants in sequence.

### 1.A Nfr1 protein alignment

	1		60
Nfr1_Lotja	MKLTGILLF	FILLGHVCF HVESNLRGC	DLALASYIIL FGVFILGNIT
Nfr1_Medtr	MKLRGILLF	F-MFLKCVF VVESKVRGC	DVALASYVIM LP-FTYGNIT
Nfr1_Glyma	MELKGLLVF	F-LLEVCVY NVESKVRGC	DVAFASYVS PDL-LENIA
Nfr1_G1983	MELKGLLLF	F-LLEVCVY NVEAKLRGC	GAALASYVS FGISTLDDIT
Nfr1_BAT93	MELKGLLLF	F-LLEVCVY NVEAKLRGC	GAALASYVS FGISTLDDIT
Nfr1_G2358	MELKGLLLF	F-LLEVCVY NVEAKLRGC	GAALASYVS FGISTLDDIT
Nfr1_G2372	MELKGLLLF	F-LLEVCVY NVEAKLRGC	GAALASYVS FGISTLDDIT
Nfr1_G2124	MELKGLLLF	F-LLEVCVY NVEAKLRGC	GAALASYVS FGISTLDDIT
Nfr1_G2124	MELKGLLLF	F-LLEVCVY NVEAKLRGC	GAALASYVS FGISTLDDIT
Nfr1_Lotja	61	N--DAITSV NKDKLINDIN IQSFQRLNIP	FPDCDIGGEF LGHVFEYSAS
Nfr1_Medtr	SSLSVIVISY NKGKVSNGN	LFAPSRVNI	FPCECIGGDF LGHVFEYSAS
Nfr1_Glyma	---EVIISV NEDNINSNG-Y	PLSFYRLNIP	FPDCDIGGEF LGHVFEYSAS
Nfr1_G1983	S---DDIVSY NKDRIFNK-N	VLFFYRINIP	FPCECIRDEF LGHVFEYSAA
Nfr1_BAT93	S---DDIVSY NKDRIFNK-N	VLFFYRINIP	FPCECIRDEF LGHVFEYSAA
Nfr1_G2358	S---DDIVSY NKDRIFNK-N	VLFFYRINIP	FPCECIRDEF LGHVFEYSAA
Nfr1_G2372	S---DDIVSY NKDRIFNK-N	VLFFYRINIP	FPCECIRDEF LGHVFEYSAA
Nfr1_G2124	S---DDIVSY NKDRIFNK-N	VLFFYRINIP	FPCECIRDEF LGHVFEYSAA
Nfr1_G2124	S---DDIVSY NKDRIFNK-N	VLFFYRINIP	FPCECIRDEF LGHVFEYSAA
Nfr1_Lotja	121	LYANLTTVD LKRFNSYDP	KNIPNAKVN VTVNCSGNS
Nfr1_Medtr	SYASLTTVE LKRFNSYDQ	DHIPAKAKVN	VTVNCSGNS
Nfr1_Glyma	VYANLTTVE LKRFNSYDQ	NGIPNAKVN	VTVNCSGNS
Nfr1_G1983	VYANLTTVE LKRFNSYDQ	NDIPTNAKVN	VTVNCSGNS
Nfr1_BAT93	VYANLTTVE LKRFNSYDQ	NDIPTNAKVN	VTVNCSGNS
Nfr1_G2358	VYANLTTVE LKRFNSYDQ	NDIPTNAKVN	VTVNCSGNS
Nfr1_G2372	VYANLTTVE LKRFNSYDQ	NDIPTNAKVN	VTVNCSGNS
Nfr1_G2124	VYANLTTVE LKRFNSYDQ	NDIPTNAKVN	VTVNCSGNS
Nfr1_G2124	VYANLTTVE LKRFNSYDQ	NDIPTNAKVN	VTVNCSGNS
Nfr1_Lotja	181	QDIANQSSLD AGLIQSFNPS	VNFSKDSGIA FIPGRYKNGV
Nfr1_Medtr	QKIANQSNID EGLIQSYNSG	VNFSKDSGIV	FIPGRDQNGD
Nfr1_Glyma	HDIANETQLD AQLLNYNPG	VNFSQESGIV	FIPGR----
Nfr1_G1983	HDIANETQLD AQLLNYNPG	VNFSQESGIV	FIPGR-----
Nfr1_BAT93	HDIANETQLD AQLLNYNPG	VNFSQESGIV	FIPGR-----
Nfr1_G2358	HDIANETQLD AQLLNYNPG	VNFSQESGIV	FIPGR-----
Nfr1_G2372	HDIANETQLD AQLLNYNPG	VNFSQESGIV	FIPGR-----
Nfr1_G2124	HDIANETQLD AQLLNYNPG	VNFSQESGIV	FIPGR-----
Nfr1_G2124	HDIANETQLD AQLLNYNPG	VNFSQESGIV	FIPGR-----
Nfr1_Lotja	241	IAGTFVLLL AFCMVRYQK	KEE-EKAKLP TDISMALSTQ
Nfr1_Medtr	IAGIFGLLLL VVIYVRYFK	KKE-EK-EE-	TKLAEALSTQ
Nfr1_Glyma	IAGICGLLLL VICIYAKFFQ	KKEGKSKLP	T---MVFSSTQ
Nfr1_G1983	IAGICGLLLL VICIYAKFFQ	KKEGKSKLP	T---MVFSSTQ
Nfr1_BAT93	IAGICGLLLL VICIYAKFFQ	KKEGKSKLP	T---MVFSSTQ
Nfr1_G2358	IAGICGLLLL VICIYAKFFQ	KKEGKSKLP	T---MVFSSTQ
Nfr1_G2372	IAGICGLLLL VICIYAKFFQ	KKEGKSKLP	T---MVFSSTQ
Nfr1_G2124	IAGICGLLLL VICIYAKFFQ	KKEGKSKLP	T---MVFSSTQ
Nfr1_G2124	IAGICGLLLL VICIYAKFFQ	KKEGKSKLP	T---MVFSSTQ
Nfr1_Lotja	301	ATGLTSIMVA KMEFTYQEL	AKATNNSLD NKIQGGGFGA
Nfr1_Medtr	ATVFTGIMVA KMEFTYQEL	AKATNNSLD	NKIQGGGFGA
Nfr1_Glyma	ATGLGIMVA KMEFTYQEL	AKATNNSLE	NKIQGGGFGA
Nfr1_G1983	ATGLGIMVA KMEFTYQEL	AKATNNSLE	NKIQGGGFGA
Nfr1_BAT93	ATGLGIMVA KMEFTYQEL	AKATNNSLE	NKIQGGGFGA
Nfr1_G2358	ATGLGIMVA KMEFTYQEL	AKATNNSLE	NKIQGGGFGA
Nfr1_G2372	ATGLGIMVA KMEFTYQEL	AKATNNSLE	NKIQGGGFGA
Nfr1_G2124	ATGLGIMVA KMEFTYQEL	AKATNNSLE	NKIQGGGFGA
Nfr1_G2124	ATGLGIMVA KMEFTYQEL	AKATNNSLE	NKIQGGGFGA
Nfr1_Lotja	361	STEFCELVK LTHVHNLNV	RLIGYCVESG LFLVYEIDN
Nfr1_Medtr	SSEFCELVK LTHVHNLNV	RLIGYCVESG	LFLVYEIDN
Nfr1_Glyma	STEFCELVK LTHVHNLNV	RLIGYCVESG	LFLVYEIDN
Nfr1_G1983	STEFCELVK LTHVHNLNV	RLIGYCVESG	LFLVYEIDN
Nfr1_BAT93	STEFCELVK LTHVHNLNV	RLIGYCVESG	LFLVYEIDN
Nfr1_G2358	STEFCELVK LTHVHNLNV	RLIGYCVESG	LFLVYEIDN
Nfr1_G2372	STEFCELVK LTHVHNLNV	RLIGYCVESG	LFLVYEIDN
Nfr1_G2124	STEFCELVK LTHVHNLNV	RLIGYCVESG	LFLVYEIDN
Nfr1_G2124	STEFCELVK LTHVHNLNV	RLIGYCVESG	LFLVYEIDN
Nfr1_Lotja	421	VQIALDSARG LEYIHEHTVP	VYIHRDKSA NILIDNFRG
Nfr1_Medtr	VEIALDSARG LEYIHEHTVP	VYIHRDKSA	NILIDNFRG
Nfr1_Glyma	VQIALDSARG LEYIHEHTVP	VYIHRDKSA	NILIDNFRG
Nfr1_G1983	VQIALDSARG LEYIHEHTVP	VYIHRDKSA	NILIDNFRG
Nfr1_BAT93	VQIALDSARG LEYIHEHTVP	VYIHRDKSA	NILIDNFRG
Nfr1_G2358	VQIALDSARG LEYIHEHTVP	VYIHRDKSA	NILIDNFRG
Nfr1_G2372	VQIALDSARG LEYIHEHTVP	VYIHRDKSA	NILIDNFRG
Nfr1_G2124	VQIALDSARG LEYIHEHTVP	VYIHRDKSA	NILIDNFRG
Nfr1_G2124	VQIALDSARG LEYIHEHTVP	VYIHRDKSA	NILIDNFRG
Nfr1_Lotja	481	RLVGTFCYMP PEYAQGDVS	PKVDVYAFV VLYELISAKN
Nfr1_Medtr	RLVGTFCYMP PEYAQGDVS	PKVDVYAFV	VLYELISAKN
Nfr1_Glyma	RLVGTFCYMP PEYAQGDVS	PKVDVYAFV	VLYELISAKN
Nfr1_G1983	RLVGTFCYMP PEYAQGDVS	PKVDVYAFV	VLYELISAKN
Nfr1_BAT93	RLVGTFCYMP PEYAQGDVS	PKVDVYAFV	VLYELISAKN
Nfr1_G2358	RLVGTFCYMP PEYAQGDVS	PKVDVYAFV	VLYELISAKN
Nfr1_G2372	RLVGTFCYMP PEYAQGDVS	PKVDVYAFV	VLYELISAKN
Nfr1_G2124	RLVGTFCYMP PEYAQGDVS	PKVDVYAFV	VLYELISAKN
Nfr1_G2124	RLVGTFCYMP PEYAQGDVS	PKVDVYAFV	VLYELISAKN
Nfr1_Lotja	541	EALNKSDFCD ALRKLVDPRL	GENYPIDSVL KIAQLGRAC
Nfr1_Medtr	EALNQTDL SIKRLVDPRL	REDFYIDSVL	KIAQLGRAC
Nfr1_Glyma	EALNQNPFSE VIRKLVDPRL	GENYPIDSVL	KIAQLGRAC
Nfr1_G1983	EALNQNPFSE VIRKLVDPRL	GENYPIDSVL	KIAQLGRAC
Nfr1_BAT93	EALNQNPFSE VIRKLVDPRL	GENYPIDSVL	KIAQLGRAC
Nfr1_G2358	ETLQNPFSE VIRKLVDPRL	GENYPIDSVL	KIAQLGRAC
Nfr1_G2372	ETLQNPFSE VIRKLVDPRL	GENYPIDSVL	KIAQLGRAC
Nfr1_G2124	ETLQNPFSE VIRKLVDPRL	GENYPIDSVL	KIAQLGRAC
Nfr1_G2124	ETLQNPFSE VIRKLVDPRL	GENYPIDSVL	KIAQLGRAC
Nfr1_Lotja	601	SSPTEEDCD	SSYESTLIN LLSVR
Nfr1_Medtr	SSPTEEDCD	TSDENNTLIN	LLSVR
Nfr1_Glyma	SSPTEEDCD	-SYENNTLIN	LLSVR
Nfr1_G1983	SSPTEEDLD	-SYENNTLIN	LLSVR
Nfr1_BAT93	SSPTEEDLD	-SYENNTLIN	LLSVR
Nfr1_G2358	SSPTEEDLD	-SYENNTLIN	LLSVR
Nfr1_G2372	SSPTEEDLD	-SYENNTLIN	LLSVR
Nfr1_G2124	SSPTEEDLD	-SYENNTLIN	LLSVR
Nfr1_G2124	SSPTEEDLD	-SYENNTLIN	LLSVR

## 1.B Nfr5 protein alignment

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1
Nfr5_Lotja MAVFF--LTS GSLSLFLALT LLF-TNIAAR SEKISGPDFS CPVDSPPSCE YVVTYTAQSP
Nfr5_Glyma MAVFFPFLPL HSQILCLVIM LFS-TNIVAQ SQQDNRTNFS CPSDSPSCE YVVTYTAQSP
Nfr5_G1983 MAVFFVSLTL GAQILYVVLM --FF-TCIEAQ SQQTNGTNFS CPNSPSPSCE YVVTYISQSP
Nfr5_BAT93 MAVFFVSLTL GAQILYVVLM --FF-TCIEAQ SQQTNGTNFS CPNSPSPSCE YVVTYISQSP
Nfr5_G2358 MAVFFVSLTL GAQILYVVLM --FS-TCIEAQ SQQTNGTNFS CPNSPSPSCE YVVTYITQSP
Nfr5_G2372 MAVFFVSLTL GAQILYVVLM --FS-TCIEAQ SQQTNGTNFS CPNSPSPSCE YVVTYITQSP
Nfr5_G2124 MAVFFVSLTL GAQILYVVLM --FS-TCIEAQ SQQTNGTNFS CPNSPSPSCE YVVTYITQSP
Nfr5_G2124 MAVFFVSLTL GAQILYVVLM --FS-TCIEAQ SQQTNGTNFS CPNSPSPSCE YVVTYITQSP
Nfr5_Medtr MSAFF--LPS SSHALFLVLM LFFLTNISAQ PLYISETNFT CPVDSPPSCE YVAVYRAQSP

61
Nfr5_Lotja NLSLSTNISD IFDTSPLSIA RASNIDAGKD KLVPGQVLLV PVTCCGAGNH SSANTSYQIQ
Nfr5_Glyma NLSLSTNISN IFDTSPLSIA RASNLEPMDK KLVKQVLLV PVTCCGCTGNR SFANISYEIN
Nfr5_G1983 NLSLSTSVSN IFDTSPLSIA RASNQHEED KLIPGQVLLI PVTCCGCTGNR SFANISYEIN
Nfr5_BAT93 NLSLSTSVSN IFDTSPLSIA RASNQHEED KLIPGQVLLI PVTCCGCTGNR SFANISYEIN
Nfr5_G2358 NLSLSTSVSN IFDTSPLSIA RASNQHEED KLIPGQVLLI PVTCCGCTGNR SFANISYEIN
Nfr5_G2372 NLSLSTSVSN IFDTSPLSIA RASNQHEED KLIPGQVLLI PVTCCGCTGNR SFANISYEIN
Nfr5_G2124 NLSLSTSVSN IFDTSPLSIA RASNQHEED KLIPGQVLLI PVTCCGCTGNR SFANISYEIN
Nfr5_G2124 NLSLSTSVSN IFDTSPLSIA RASNQHEED KLIPGQVLLI PVTCCGCTGNR SFANISYEIN
Nfr5_Medtr NLSLSTNISD IFNLSPLRIA KASNIEADK KLIPDQLLLV PVTCCGCTGMR SFANITYS1K

121
Nfr5_Lotja LQDSYDFVAT TLYENLTNWH IVQASNPGVN FYLLPERVKV VFPLFCRCPS KNQLNRG1QY
Nfr5_Glyma QGDSFYFVAT TSYENLTNWR AVMDLNPVLS FNKLPIGIQV VFPLFCCKPS KNQLDRG1KY
Nfr5_G1983 QGDSFYFVAT TLYQNLTNWH AVMDLNPGLS PFTLPIGIQV VIPLFCCKPS KNQLDRG1KY
Nfr5_BAT93 QGDSFYFVAT TLYQNLTNWH AVMDLNPGLS OFTLPIGIQV VIPLFCCKPS KNQLDRG1KY
Nfr5_G2358 QGDSFYFVAT TLYQNLTNWH AVMDLNPGLS PFTLPIGIQV VIPLFCCKPS KNQLDRG1KY
Nfr5_G2372 QGDSFYFVAT TLYQNLTNWH AVMDLNPGLS PFTLPIGIQV VIPLFCCKPS KNQLDRG1KY
Nfr5_G2124 QGDSFYFVAT TLYQNLTNWH AVMDLNPGLS PFTLPIGIQV VIPLFCCKPS KNQLDRG1KY
Nfr5_G2124 QGDSFYFVAT TLYQNLTNWH AVMDLNPGLS PFTLPIGIQV VIPLFCCKPS KNQLDRG1KY
Nfr5_Medtr QGNFFILSI TSYQNLTNYL EFKNFNPLS PTLPLDITKV SVPLFCCKPS KNQLNRG1KY

181
Nfr5_Lotja LITYVWKPNL NVSLVSAKFG ASPADILTEN RYQDFTAAT NLPILIPVTO LPBLTQPSND
Nfr5_Glyma LITYVWKPGD NVSLVSDKFG ASPEDIMSEN NYQNFATAAN NLPVLPVTR LPVLARSPPD
Nfr5_G1983 LITHWQPNL NVSFVSNKLG ASPQDILSEN NYQNFATAAS NLPVLPVTL LPDLIQSPSD
Nfr5_BAT93 LITHWQPNL NVSFVSNKLG ASPQDILSEN NYQNFATAAS NLPVLPVTL LPDLIQSPSD
Nfr5_G2358 LITHWQPNL NVSFVSNKLG ASPQDILSEN NYQNFATAAS NLPVLPVTL LPDLIQSPSD
Nfr5_G2372 LITHWQPNL NVSFVSNKLG ASPQDILSEN NYQNFATAAS NLPVLPVTL LPDLIQSPSD
Nfr5_G2124 LITHWQPNL NVSFVSNKLG ASPQDILSEN NYQNFATAAS NLPVLPVTL LPDLIQSPSD
Nfr5_G2124 LITHWQPNL NVSFVSNKLG ASPQDILSEN NYQNFATAAS NLPVLPVTL LPDLIQSPSD
Nfr5_Medtr LITYWQDND NVTLVSSKFG ASQVEMLAEN NH--NFTAAT NRSVLPVTS LPKLDQPSND

241
Nfr5_Lotja GRKSSI-HLL VILGITLQCT LLTAVLTGTL VYVYCRKKA LNRASSAET ADKLLSGVSG
Nfr5_Glyma GRKGI-RLP VIIGISLQCT LLVVLAVLL VYVYCLMKT LNRASSAET ADKLLSGVSG
Nfr5_G1983 GRKHRI-GLP VIIGISLQCT LLVVSAIILL CVVCLMKMS LNRASSAET ADKLLSGVSG
Nfr5_BAT93 GRKHRI-GLP VIIGISLQCT LLVVSAIILL CVVCLMKMS LNRASSAET ADKLLSGVSG
Nfr5_G2358 GRKHRI-GLP VIIGISLQCT LLVVSAIILL CVVCLMKMS LNRASSAET ADKLLSGVSG
Nfr5_G2372 GRKHRI-GLP VIIGISLQCT LLVVSAIILL CVVCLMKMS LNRASSAET ADKLLSGVSG
Nfr5_G2124 GRKHRI-GLP VIIGISLQCT LLVVSAIILL CVVCLMKMS LNRASSAET ADKLLSGVSG
Nfr5_G2124 GRKHRI-GLP VIIGISLQCT LLVVSAIILL CVVCLMKMS LNRASSAET ADKLLSGVSG
Nfr5_Medtr GRKSSQNLA LIIGISLQSA FFLVLTLSL VYVYCLMKR LNRSSSET ADKLLSGVSG

301
Nfr5_Lotja YVSKFNVEI DEIMEATKDF SDECKVGEV YKANIEGRV AVKIKIEGGA NEELKIQKV
Nfr5_Glyma YVSKPTMYET DAIMEATMNL SEQCKIGESV YKANIEGKVL AVKRFKED-V TELKILQKV
Nfr5_G1983 YVSKPTMYET GAILEATMNL SEQCKIGESV YKANIEGKVL AVKRFKED-V TELKILQKV
Nfr5_BAT93 YVSKPTMYET GAILEATMNL SEQCKIGESV YKANIEGKVL AVKRFKED-V TELKILQKV
Nfr5_G2358 YVSKPTMYET GAILEATMNL SEQCKIGESV YKANIEGKVL AVKRFKED-V TELKILQKV
Nfr5_G2372 YVSKPTMYET GAILEATMNL SEQCKIGESV YKANIEGKVL AVKRFKED-V TELKILQKV
Nfr5_G2124 YVSKPTMYET GAILEATMNL SEQCKIGESV YKANIEGKVL AVKRFKED-V TELKILQKV
Nfr5_G2124 YVSKPTMYET GAILEATMNL SEQCKIGESV YKANIEGKVL AVKRFKED-V TELKILQKV
Nfr5_Medtr YVSKPTMYEI DAIMEGTNL SDNCKIGESV YKANIDGRVL AVKIKIKD-A SEELKILQKV

361
Nfr5_Lotja NHGNLVKLMG VSSDNDGNCF LVVEYAENGSLAEWLFSSK- ---SGTFPNSL TWSQRISIAV
Nfr5_Glyma NHGNLVKLMG VSSDNDGNCF VVVEYAENGSLDEWLFSSK SDTSNSRASL TWCQRISIAV
Nfr5_G1983 NHGNLVKLMG VSSDNDGNCF VVVEYAENGSLQEWLFAKSC SETLNSRSTSL TWCQRISIAV
Nfr5_BAT93 NHGNLVKLMG VSSDNDGNCF VVVEYAENGSLQEWLFAKSC SETLNSRSTSL TWCQRISIAV
Nfr5_G2358 NHGNLVKLMG VSSDNDGNCF VVVEYAENGSLQEWLFAKSC SETLNSRSTSL TWCQRISIAV
Nfr5_G2372 NHGNLVKLMG VSSDNDGNCF VVVEYAENGSLQEWLFAKSC SETLNSRSTSL TWCQRISIAV
Nfr5_G2124 NHGNLVKLMG VSSDNDGNCF VVVEYAENGSLQEWLFAKSC SETLNSRSTSL TWCQRISIAV
Nfr5_G2124 NHGNLVKLMG VSSDNDGNCF VVVEYAENGSLQEWLFAKSC SETLNSRSTSL TWCQRISIAV
Nfr5_Medtr NHGNLVKLMG VSSDNDGNCF LVVEYAENGSLAEWLFSES- SKTSNSVSVL TWSQRITIAM

421
Nfr5_Lotja DVAVGLQYMH ERTYPRIIHR DITTSNILLD SNFKAKIANF AMARTSTNPM MPKIDVFAFG
Nfr5_Glyma DVAMGLQYMH EHAYPRIVHR DITTSNILLD SNFKAKIANF SMARTFTNPM MPKIDVFAFG
Nfr5_G1983 DVSMGLQYMH EHAYPRIVHR DITTSNILLD SNFKAKIANF SMARTFTNPM MSKIDVFAFG
Nfr5_BAT93 DVSMGLQYMH EHAYPRIVHR DITTSNILLD SNFKAKIANF SMARTFTNPM MSKIDVFAFG
Nfr5_G2358 DVSMGLQYMH EHAYPRIVHR DITTSNILLD SNFKAKIANF SMARTFTNPM MSKIDVFAFG
Nfr5_G2372 DVSMGLQYMH EHAYPRIVHR DITTSNILLD SNFKAKIANF SMARTFTNPM MSKIDVFAFG
Nfr5_G2124 DVSMGLQYMH EHAYPRIVHR DITTSNILLD SNFKAKIANF SMARTFTNPM MSKIDVFAFG
Nfr5_G2124 DVSMGLQYMH EHAYPRIVHR DITTSNILLD SNFKAKIANF SMARTFTNPM MSKIDVFAFG
Nfr5_Medtr DVAVGLQYMH ERTYPRIIHR DITTSNILLG SNFKAKIANF GMARTSTNSM MPKIDVFAFG

481
Nfr5_Lotja VVLIELLTGR KAMTTRENKE VVMLNKDIME IFDIEENREE RLRKWMDFNL ESFYHIDNAL
Nfr5_Glyma VVLIELLTGR KAMTTRENKE VVMLNKDIWK IFDQENREE RLRKWMDFKL ESYPIDYAL
Nfr5_G1983 VVLIELLTGR KAMTTRENKE VVMLATDIWK IFDQENREE RLRKWMDFKL DNYYPIDYAL
Nfr5_BAT93 VVLIELLTGR KAMTTRENKE VVMLNKDIWK IFDQENREE RLRKWMDFKL DNYYPIDYAL
Nfr5_G2358 VVLIELLTGR KAMTTRENKE VVMLNKDIWK IFDQENREE RLRKWMDFKL DNYYPIDYAL
Nfr5_G2372 VVLIELLTGR KAMTTRENKE VVMLNKDIWK IFDQENREE RLRKWMDFKL DNYYPIDYAL
Nfr5_G2124 VVLIELLTGR KAMTTRENKE VVMLATDIWK IFDQENREE RLRKWMDFKL DNYYPIDYAL
Nfr5_G2124 VVLIELLTGR KAMTTRENKE VVMLATDIWK IFDQENREE RLRKWMDFKL DNYYPIDYAL
Nfr5_Medtr VVLIELLTGR KAMTTRENKE VVILNKDFWK IFDLEGNREE RLRKWMDFKL ESFYHIDNAL

541
Nfr5_Lotja SLASLAVNCT ADKLSRPSM AEIVLSLSFL TQSSNPTLE RSLTSSGLDV EDDAHIVTSI
Nfr5_Glyma SLASLAVNCT ADKLSRPTI AEIVLSLSLL TQSP-ATLE RSLTSSGLDV EA-TQIVTSI
Nfr5_G1983 SLASLAVNCT ADKLSRPTI AEIVLSLSLL TQSP-ATLE RSLTSSGLDV EA-TQIVTSI
Nfr5_BAT93 SLASLAVNCT ADKLSRPTI AEIVLSLSLL TQSP-ATLE RSLTSSGLDV EA-TQIVTSI
Nfr5_G2358 SLASLAVNCT ADKLSRPTI AEIVLSLSLL TQSP-GTLE RSLTSSGLDV EA-TQIVTSI
Nfr5_G2372 SLASLAVNCT ADKLSRPTI AEIVLSLSLL TQSP-GTLE RSLTSSGLDV EA-TQIVTSI
Nfr5_G2124 SLASLAVNCT ADKLSRPTI AEIVLSLSLL TQSP-GTLE RSLTSSGLDV EA-TQIVTSI
Nfr5_G2124 SLASLAVNCT ADKLSRPTI AEIVLSLSLL TQSP-GTLE RSLTSSGLDV EA-TQIVTSI
Nfr5_Medtr SLASLAVNCT ADKLSRPTI AEIVLSLSLL TQSP-ATLE RSLTSSGLDV EA-TQIVTSI

601
Nfr5_Lotja TAR
Nfr5_Glyma AAR
Nfr5_G1983 SAR
Nfr5_BAT93 SAR
Nfr5_G2358 SAR
Nfr5_G2372 SAR
Nfr5_G2124 SAR
Nfr5_G2124 SAR
Nfr5_Medtr IAR

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## 1.C Astry protein alignment

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1
ASTR_Lotja MDQHGGVATG SHERNELVRV RHG-SDHGSK PVKNLNGQIC QICGETVGLT ANGDIFVACH 60
ASTR_Medtru ME---GVETG SHERNELVRA RHDVSETGSK PLKNLNGQIC QICGDTVGLT ATGEVFFVACH
ASTR_Glymax MERSGGMVTG SHERNELVRV RHG-SDSGSK PLKNLNGQIC QICGDTIGLT ATGDLFVACH
ASTR_G19833 MERSGGMVTG SHERNELVTV RHG-SDSGSK PVKNLNGQIC QICGDTIGLT ATGDVFFVACH
ASTR_BAT93 MERSGGMVTG SHERNELVTV RHG-SDSGSK PVKNLNGQIC QICGDTIGLT ATGDVFFVACH
ASTR_G23587 MERSGGMVTG SHERNELVTV RHG-SDSGSK PVKNLNGQIC QICGDTIGLT ATGDVFFVACH
ASTR_G23724 MERSGGMVTG SHERNELVTV RHG-SDSGSK PVKNLNGQIC QICGDTIGLT ATGDVFFVACH
ASTR_G21244 MERSGGMVTG SHERNELVTV RHG-SDSGSK PVKNLNGQIC QICGDTIGLT ATGDVFFVACH
ASTR_G21245 MERSGGMVTG SHERNELVTV RHG-SDSGSK PVKNLNGQIC QICGDTIGLT ATGDVFFVACH

61
ASTR_Lotja ECAFQLCHPC YEYERNVSP YCPQCKTRYE SHKSSQMEG DDDDDDDDED VDDLENEVKY 120
ASTR_Medtru ECSFPLCYPC YEYEWKNVIQ SCPQCKTRFK SHKDDPRVKG GDD----EDD VDDLRLNEVKY
ASTR_Glymax ECGFPLCHSC YEYELKNVSQ SCPQCKTFT SRQEGAEVEG DDDD---EDD ADDLDNGINY
ASTR_G19833 ECGLPLCHSC YEYELKNVSQ SCPQCKTRFT SHQEGAGVEG DDDD---DED ADDLDNEINY
ASTR_BAT93 ECGFPLCHSC YEYELKNVSQ SCPQCKTRFT SHQEGAGVEG DDDD---DED ADDLDNEINY
ASTR_G23587 ECGFPLCHSC YEYELKNVSQ SCPQCKTRFT SHQEGAGVEG DDDD---DED ADDLDNEINY
ASTR_G23724 ECGFPLCHSC YEYELKNVSQ SCPQCKTRFT SHQEGAGVEG DDDD---DED ADDLDNEINY
ASTR_G21244 ECGFPLCHSC YEYELKNVSQ SCPQCKTRFT SHQEGAGVEG DDDD---DED ADDLDNEINY
ASTR_G21245 ECGFPLCHSC YEYELKNVSQ SCPQCKTRFT SHQEGAGVEG DDDD---DED ADDLDNEINY

121
ASTR_Lotja GQGNRMKARL QWEEDADLSS SSGHDSQMQN PHLTNGQLMS GENLCAT--- -----TSGPM 180
ASTR_Medtru GQGNNAKAGW QWDEDADLSS SSGHDSQLQN PHLTNGQLMS GDIPCATSDT QSVQTTSGPL
ASTR_Glymax GQGNNSKSGM LWEEADLSS SSGHDSHIPN PHLVNGQPMS GEFPCATSDA QSMQTTSDPM
ASTR_G19833 GQGNNSKAGM QWEEDADFSS SSGHDSQIPN PHLANGQPMS GDIPCATSDA QSMQTTSGLM
ASTR_BAT93 GQGNNSKAGM QWEEDADFSS SSGHDSQIPN PHLANGQPMS GDIPCATSDA QSMQTTSGLM
ASTR_G23587 GQGNNSKAGM QWEEDADFSS SSGHDSQIPN PHLANGQPMS GDIPCATSDA QSMQTTSGLM
ASTR_G23724 GQGNNSKAGM QWEEDADFSS SSGHDSQIPN PHLANGQPMS GDIPCATSDA QSMQTTSGLM
ASTR_G21244 GQGNNSKAGM QWEEDADFSS SSGHDSQIPN PHLANGQPMS GDIPCATSDA QSMQTTSGLM
ASTR_G21245 GQGNNSKAGM QWEEDADFSS SSGHDSQIPN PHLANGQPMS GDIPCATSDA QSMQTTSGLM

181
ASTR_Lotja GQSKKQVSLP YVDPKQPGLE SDEEIRRVEP FGGESAATSA SRPDTGSNPG PERVQGAGEG 240
ASTR_Medtru GQSENVHSRA YVDPKQPGLE SDEEIRRVDP MGGESAGTSA SRKGTGSTAG PERVQGAGEG
ASTR_Glymax GQSEKQVSLP YADPKQPGPE SDEEIRRVEP IGGESAGTSA SRPDAGSNAG TERAQGTGDS
ASTR_G19833 ----- -AAAKQPGPE SDEEIRRVEP IGGESAGTVA SRPDARSNAG AERVQGTGEG
ASTR_BAT93 ----- -AAAKQPGPE SDEEIRRVEP IGGESAGTVA SRPDARSNAG AERVQGTGEG
ASTR_G23587 ----- -AAAKQPGPE SDEEIRRVEP IGGESAGTVA SRPDARSNAG AERVQGTGEG
ASTR_G23724 ----- -AAAKQPGPE SDEEIRRVEP IGGESAGTVA SRPDARSNAG AERVQGTGEG
ASTR_G21244 ----- -AAAKQPGPE SDEEIRRVEP IGGESAGTVA SRPDARSNAG AERVQGTGEG
ASTR_G21245 ----- -AAAKQPGPE SDEEIRRVEP IGGESAGTVA SRPDARSNAG AERVQGTGEG

241
ASTR_Lotja QKKRGRSSAD KESKRLKRLR RNRVSAQQAR ERKKAYLTDL ETKVKDLETN NSELKERLST 300
ASTR_Medtru QKKRGRSPAD KESKRLKRLR RNRVSAQQAR ERKKAYLSDL ETRVNDLEKK NSELKEKLST
ASTR_Glymax QKKRGRSPAD KESKRLKRLR RNRVSAQQAR ERKKAYLIDL ETRVKDLEKK NSELKERLST
ASTR_G19833 QKKRGRSPAD KESKRLKRLR RNRVSAQQAR ERKKAYLIDL ETRVKDLEKK NSELKERLST
ASTR_BAT93 QKKRGRSPAD KESKRLKRLR RNRVSAQQAR ERKKAYLIDL ETRVKDLEKK NSELKERLST
ASTR_G23587 QKKRGRSPAD KESKRLKRLR RNRVSAQQAR ERKKAYLIDL ETRVKDLEKK NSELKERLST
ASTR_G23724 QKKRGRSPAD KESKRLKRLR RNRVSAQQAR ERKKAYLIDL ETRVKDLEKK NSELKERLST
ASTR_G21244 QKKRGRSPAD KESKRLKRLR RNRVSAQQAR ERKKAYLIDL ETRVKDLEKK NSELKERLST
ASTR_G21245 QKKRGRSPAD KESKRLKRLR RNRVSAQQAR ERKKAYLIDL ETRVKDLEKK NSELKERLST

301
ASTR_Lotja LQENQMLRQ ILKNTTASRR GNSGTTNAE 330
ASTR_Medtru LQENQMLRQ ILKNTTASRR GNSGNTAE
ASTR_Glymax LQENQMLRQ ILKNTTASRR GNSGTTNAE
ASTR_G19833 LQENQMLRQ ILKNTTASRR GNSGTTNAE
ASTR_BAT93 LQENQMLRQ ILKNTTASRR GNSGTTNAE
ASTR_G23587 LQENQMLRQ ILKNTTASRR GNSGTTNAE
ASTR_G23724 LQENQMLRQ ILKNTTASRR GNSGTTNAE
ASTR_G21244 LQENQMLRQ ILKNTTASRR GNSGTTNAE
ASTR_G21245 LQENQMLRQ ILKNTTASRR GNSGTTNAE
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## 1.D Rab protein alignment

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1                                     60
Rab_Glyma MAHRVDHEYD YLFKIVLIGD SGVGKSNILS RFRNEFCLE SKSTIGVEFA TRTLQVEGKT
Rab_19833 MTHRVDHEYD YLFKIVLIGD SGVGKSNILS RFRNEFCLE SKSTIGVEFA TRTLQVEGKT
Rab_BAT93  MTHRVDHEYD YLFKIVLIGD SGVGKSNILS RFRNEFCLE SKSTIGVEFA TRTLQVEGKT
Rab_21244 MTHRVDHEYD YLFKIVLIGD SGVGKSNILS RFRNEFCLE SKSTIGVEFA TRTLQVEGKT
Rab_23724 MTHRVDHEYD YLFKIVLIGD SGVGKSNILS RFRNEFCLE SKSTIGVEFA TRTLQVEGKT
Rab_23587 MTHRVDHEYD YLFKIVLIGD SGVGKSNILS RFRNEFCLE SKSTIGVEFA TRTLQVEGKT
Rab_21245 MTHRVDHEYD YLFKIVLIGD SGVGKSNILS RFRNEFCLE SKSTIGVEFA TRTLQVEGKT
Rab_Lotja  MAHRVDHEYD YLFKIVLIGD SGVGKSNILS RFRNEFCLE SKSTIGVEFA TRTLQVEGKT
Rab_Medtr MAHRVDHEYD YLFKIVLIGD SGVGKSNILS RFRNEFCLE SKSTIGVEFA TRTLQVEGKT

61                                     120
Rab_Glyma VKAQIWDTAG QERYRAITSA YYRGAVGALL VYDITKRQTF DNVQRWLREL RDHADSNIVI
Rab_19833 VKAQIWDTAG QERYRAITSA YYRGAVGALL VYDITKRQTF DNVQRWLREL RDHADSNIVI
Rab_BAT93  VKAQIWDTAG QERYRAITSA YYRGAVGALL VYDITKRQTF DNVQRWLREL RDHADSNIVI
Rab_21244 VKAQIWDTAG QERYRAITSA YYRGAVGALL VYDITKRQTF DNVQRWLREL RDHADSNIVI
Rab_23724 VKAQIWDTAG QERYRAITSA YYRGAVGALL VYDITKRQTF DNVQRWLREL RDHADSNIVI
Rab_23587 VKAQIWDTAG QERYRAITSA YYRGAVGALL VYDITKRQTF DNVQRWLREL RDHADSNIVI
Rab_21245 VKAQIWDTAG QERYRAITSA YYRGAVGALL VYDITKRQTF DNVQRWLREL RDHADSNIVI
Rab_Lotja  VKAQIWDTAG QERYRAITSA YYRGAVGALL VYDITKRQTF DNVQRWLREL RDHADSNIVI
Rab_Medtr VKAQIWDTAG QERYRAITSA YYRGAVGALL VYDITKRQTF DNVQRWLREL RDHADSNIVI

121                                    180
Rab_Glyma MMAGNKSCLS HLRVSEDDG QALAREGLS FLETSALEAT NIEKAFQITL TEIYHIVSKK
Rab_19833 MMAGNKSCLS HLRVYEDDG QNLAEREGLS FLETSALEAT NIEKAFQITL TEIYHIVSKK
Rab_BAT93  MMAGNKSCLS HLRVYEDDG QNLAEREGLS FLETSALEAT NIEKAFQITL TEIYHIVSKK
Rab_21244 MMAGNKSCLS HLRVYEDDG QNLAEREGLS FLETSALEAT NIEKAFQITL TEIYHIVSKK
Rab_23724 MMAGNKSCLS HLRVYEDDG QNLAEREGLS FLETSALEAT NIEKAFQITL TEIYHIVSKK
Rab_23587 MMAGNKSCLS HLRVYEDDG QNLAEREGLS FLETSALEAT NIEKAFQITL TEIYHIVSKK
Rab_21245 MMAGNKSCLS HLRVYEDDG QNLAEREGLS FLETSALEAT NIEKAFQITL TEIYHIVSKK
Rab_Lotja  MMAGNKSCLN HLRVSEDDG GALSEKEGLS FLETSALEAT NIEKAFQITL TEIYHIVSKK
Rab_Medtr MMAGNKSCLN HLRVSEDDG QALAEKEGLS FLETSALEAT NIEKAFQITL TEIYHIVSKK

181                                    216
Rab_Glyma ALAAQEAVG TTLPGQGTI NVGDASGNTK RGCST
Rab_19833 ALAAQEAVG TTLPGQGTI NVGDASGNTK RGCST
Rab_BAT93  ALAAQEAVG TTLPGQGTI NVGDASGNTK RGCST
Rab_21244 ALAAQEAVG TTLPGQGTI NVGDASGNTK RGCST
Rab_23724 ALAAQEAVG TTLPGQGTI NVGDASGNTK RGCST
Rab_23587 ALAAQEAVG TTLPGQGTI NVGDASGNTK RGCST
Rab_21245 ALAAQEAVG TTLPGQGTI NVGDASGNTK RGCST
Rab_Lotja  ALAAQEATAG ASVPGQGTI NVADTSNTK KGCST
Rab_Medtr ALAAQEAG TSLPGQGTI NVADSSANTK RGCST
```



**SI. Table 1:** Accession number of sequences retrieved from data bases described in Methods that were used for the protein alignment and phylogenetic analysis

	<b>NFR1</b>	<b>NFR5</b>	<b>ASTRAY</b>	<b>NIN</b>	<b>RAB</b>
<b><i>P. vul. G19833</i></b>	XP_007141617	XP_007156886	XP_007146305	XP_007137300	ACV82919
<b><i>P. vul. BAT93*</i></b>	GCA_001517995	GCA_001517995	GCA_001517995	GCA_001517995	GCA_001517995
<b><i>P. vul. G23587**</i></b>	SRX2537723	SRX2537723	SRX2537723	SRX2537723	SRX2537723
<b><i>P. vul. G23724**</i></b>	SRX2537724	SRX2537724	SRX2537724	SRX2537724	SRX2537724
<b><i>P. vul. G21245**</i></b>	SRX2537725	SRX2537725	SRX2537725	SRX2537725	SRX2537725
<b><i>P. vul. G21244**</i></b>	SRX540119	SRX540119	SRX540119	SRX540119	SRX540119
<b><i>Glycine max</i></b>	XP_006575588	NP_001341125	NP_001237272	XP_003523488	XP_003537971
<b><i>Lotus japonicus</i></b>	CAE02591	CAE02598	BAC20318	CAB61243	CAA98179
<b><i>Medicago trunc.</i></b>	XP_024640165	XP_003611889	XP_013459310	XP_003618108	XP_013456161

\*Identifier has not been assigned for BAT93 proteins and therefore they were inferred from its assembly accession.

\*\*Idem for *P. vulgaris* genomes G23587, G23724, G21244 and G21245, identifier has not been yet assigned for proteins and therefore these were inferred from its SRAs accessions.

**SI. Table 2:** Analysis of model topology of proteins Nfr1 and Nfr5. PyMOL (Molecular Graphics System v2.4, Schrödinger, LLC) and VMD were used to assess topology and calculate values of root-mean-square deviation, RMSD [32, 33]

GENOME	PROTEIN	PDB ID	METHOD	RANGE	SEQUENCE IDENTITY	SEQUENCE SIMILARITY	COVERAGE	RESOLUTION	TEMPLATE	DESCRIPTION	RMSD
BAT93	nfr1	6CTH	Ray-X	289-580	36.71	0.38	0.48	1.70Å	Crystal Structure of Pathogenesis-related Protein 1G (PR-1G) Kinase Domain from Cacao	Concanavalin A-like lectin protein kinase family protein	0.000
G19833	nfr1	6CTH	Ray-X	289-580	36.71	0.38	0.48	1.70Å	Crystal Structure of Pathogenesis-related Protein 1G (PR-1G) Kinase Domain from Cacao	Concanavalin A-like lectin protein kinase family protein	0.000
G21244	nfr1	6CTH	Ray-X	289-580	37.06	0.38	0.48	1.70Å	Crystal Structure of Pathogenesis-related Protein 1G (PR-1G) Kinase Domain from Cacao	Concanavalin A-like lectin protein kinase family protein	1.104
G21245	nfr1	6CTH	Ray-X	289-580	37.06	0.38	0.48	1.70Å	Crystal Structure of Pathogenesis-related Protein 1G (PR-1G) Kinase Domain from Cacao	Concanavalin A-like lectin protein kinase family protein	1.104
G23587	nfr1	6CTH	Ray-X	289-580	37.06	0.38	0.48	1.70Å	Crystal Structure of Pathogenesis-related Protein 1G (PR-1G) Kinase Domain from Cacao	Concanavalin A-like lectin protein kinase family protein	1.104
G23724	nfr1	6CTH	Ray-X	289-580	37.06	0.38	0.48	1.70Å	Crystal Structure of Pathogenesis-related Protein 1G (PR-1G) Kinase Domain from Cacao	Concanavalin A-like lectin protein kinase family protein	1.104
BAT93	nfr5	6BFN	Ray-X	300-570	31.92	0.36	0.44	2.26Å	Crystal structure of human IRAK1	Interleukin-1 receptor-associated kinase 1 Crystal structure of human IRAK1	0.000
G19833	nfr5	6BFN	Ray-X	300-570	31.03	0.36	0.44	2.26Å	Crystal structure of human IRAK1	Interleukin-1 receptor-associated kinase 1 Crystal structure of human IRAK1	0.015
G21244	nfr5	6BFN	Ray-X	300-570	31.03	0.36	0.44	2.26Å	Crystal structure of human IRAK1	Interleukin-1 receptor-associated kinase 1 Crystal structure of human IRAK1	0.762
G21245	nfr5	6BFN	Ray-X	300-570	31.03	0.36	0.44	2.26Å	Crystal structure of human IRAK1	Interleukin-1 receptor-associated kinase 1 Crystal structure of human IRAK1	0.791
G23587	nfr5	6BFN	Ray-X	300-570	31.54	0.36	0.44	2.26Å	Crystal structure of human IRAK1	Interleukin-1 receptor-associated kinase 1 Crystal structure of human IRAK1	0.761
G23724	nfr5	6BFN	Ray-X	300-570	31.42	0.36	0.44	2.26Å	Crystal structure of human IRAK1	Interleukin-1 receptor-associated kinase 1 Crystal structure of human IRAK1	0.820