

Table S1. List of RT-qPCR primers used for evaluating expression of the Nitrogen assimilation genes in *S. polyrhiza* ecotype NB5548.

Gene	Primer name	Forward	Primer name	Reverse	PCR product, length in bp
<i>NR</i>	nr-f2	CTTCTGGTCCGTCGATCTC	nr-r3	CCAGCAGTTGTTTCATCATTC	136
<i>NiR</i>	nir-f4	GAGGGAGGATGACGATGAAG	nir-r4	GTGAAGCAGAAGCGACGAG	108
<i>GS2</i>	GS2-f1	CATCGCGGAGTACATTTGG	GS2-r1	CACCTCACTGTCTTCTCCTG	154
<i>GS1;1</i>	GS1-6-5	GAGCAAAATGGGAAAGGG	GS1-6-4	GCTGCTGGTGATGATATTGTG	134
<i>GS1;2</i>	GS1-F5	TTCTCGTCATGTGCGACTCC	GS1-R7	CTCCTGCTCCAGTCCATACC	131
<i>GS1;3</i>	GS1-5 qF11	GGCGTCCTCCTGTCGTTT	GS1-5 qR11	CTTCTGATCTCGTCCATGC	119
<i>Fd-GOGAT</i>	g8-f4	ATACATTGCAAGACTGAGG	g8-r5	TGGTGAAGGTCATAGATAAGC	114
<i>NADH-GOGAT</i>	ng-f3	CTTGAAGGACGATGGCAGC	ng-r4	TATGAGTTCTTCCACACTAGG C	131
<i>Histon3</i>	H3dwqF1	CGCAAGTACCAGAAGAGCAC	H3dwqR1	CGAAGAGACCCACGAGGTAG	160
<i>Actin</i>	ActindwF1	TGTTTTCCCAAGTATCGTC	ActinR5	TCCCAGTTGGTGACGATT	153

Table S2. Distribution of potential regulatory DNA *cis*-elements along 1kb promoter region upstream of the translation start of eight *S. polyrhiza* genes related to N assimilation. The numbers for NRE-like elements and (GA/CT)_n repeats indicate their position related to the first gene ATG. Numbers for GAATC/GATTC, TATA-like and 4G elements show frequencies of those elements.

Promoter / <i>cis</i> -element	NRE-like	GAATC/GATTC	TATA-like	(GA/CT) _n	4G
<i>NR</i>	-41 to -72 -234 to -259	1	1	-710 to -796	5
<i>NiR</i>	-54 to -83 -84 to -108 -184 to -209 -216 to -240	ND	1	-796 to -808	1
<i>GS1;1</i>	-134 to -159	4	2	ND	2
<i>1;2</i>	-189 to -217 -477 to -503	6	1	-1010 to -1068	4
<i>GS1;3</i>	-634 to -659	ND	1	-368 to -400	3
<i>GS2</i>	-89 to -117 -124 to -148 -860 to -888	2	1	-541 to -585 -700 to -728	2
<i>Fd-GOGAT</i>	-247 to -271 -351 to -376	1	3	-329 to -351 -559 to -864	1
<i>NADH-GOGAT</i>	-86 to -109 -113 to -140 -161 to -191	2	5	-658 to -714	6

Table S3. List of primer used for cloning selected Nitrogen assimilation genes of *S.polyrhiza* ecotype NB5548.

Gene	Primer name	Forward	Primer name	Reverse	PCR product length in bp
NR	SpNRcl F1	TGTTTCATCCATCTGTCGGG	NR-R3	CCAGCAGTTGTTTCATCATTC	1454
NR	NRF2	CTTCTGGTCCGTCGATCTC	SpNRcl R1	AATGGAAGGGAGGGACTGG	1450
NIR	SpNIRcl F1	ATCACCCGCCGACCTCGTA	SpNIRcl R2	GCCACCAGCCCTCTCATCA	1445
NIR	SpNIRcl F2	GTGACGACCAGCAAGCAGA	SpNIRcl R1	CACCGTGAAGCAGAAGCGAC	1395
GS2	GS2-7-1	GTTGCAGAGCGGAGGAGAAGA G	GS2-7-2	ATGAAATAACAGACTGGGCGGA G	1392
GS1;1	GS1-6-2	CGCCGACATCAACACCTTCC	GS1-6-3	AGGATAAACTGGAGATGGGG	718
GS1;1	GS1-6-1	CTGAATCTTCCTTCCCCTCTC	GS1-6-4	GCTGCTGGTGATGATATTGTG	1134
GS1;2	GS1-2-1	CTTCTGACTTTTGGGTGCGTCC	GS1-2-2	GAAGGGGGGAGGACTTACTAGA G	733
GS1;2	GS1-2-1	CTTCTGACTTTTGGGTGCGTCC	GS1-2-4	GGAATGAGAAGGAACCCAGGA GG	1360
GS1;3	GS1-5-4	CATGGCTCTTCTCAACGAC	GS1-5-2	CTTCTTCTTCTCTCTCTAGGG	1088
Fd-GOGAT	g8-23f	GGCTATCTGTCAATCTAGGG	g8-23r	ACTCCGCTCTTAAATCCACC	526
Fd-GOGAT	gogat8-f2	TCTCCTCCTCCTCCTCTTCC	gogat8-r1	ACTAGATGGTGAGAAGGAGG	5224
NADH-GOGAT	SpNADH-GOGAT F1	ACATACGCCTTCCAGTTT	SpNADH-GOGAT R1	ATGATATTAGAGCTGGTCC	1428
NADH-GOGAT	SpNADH-GOGAT F2	CCTGAAAGAAAGGCTCTATAC	SpNADH-GOGAT R2	CCCTAGCAAGAATCTCAAAA	1417
NADH-GOGAT	SpNADH-GOGAT F3	TTGGTCTTTCTTCTGAGGT	SpNADH-GOGAT R3	TATTGAGCTGCTTCTGGT	1459
NADH-GOGAT	SpNADH-GOGAT F4	GAACAAGTAGTCAACAGCA	SpNADH-GOGAT R4	GGAAGTTATTCGTCTCAAG	1357
NADH-GOGAT	SpNADH-GOGAT F5	CAAGATCCCAGAATTCAAC	SpNADH-GOGAT R5	GTCGCCATTCTCTTTATGA	1399

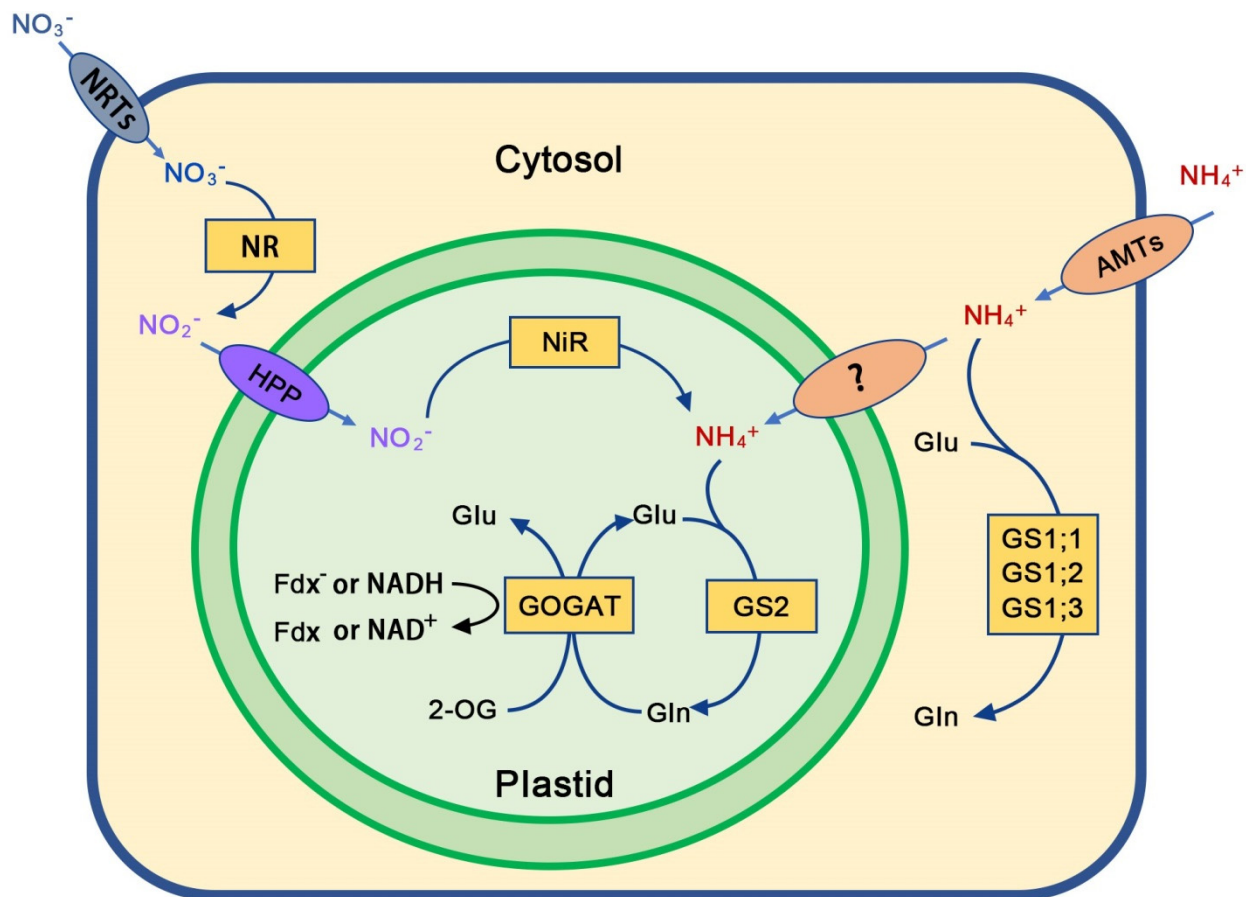


Figure S1. Simplified diagram of Nitrogen assimilation in plants. **NRTs**, nitrate transporters; **AMTs**, ammonium transporters; **HPP**, histidin-prolin-prolin containing protein; **NiR**, nitrite reductase; **NR**, nitrate reductase; **GS1;1**, **GS1;2**, **GS1;3**, tree isoforms of major cytosolic glutamine synthetases; **GS2**, chloroplast glutamine synthetase; **Fd-GOGAT**, ferredoxin-dependent glutamate-oxoglutarate-aminotransferase; **NADH-GOGAT**, NADH-dependent glutamate-oxoglutarate-aminotransferase; ? – unknown transporter; **2-OG**, 2-oxoglutarate; **Glu**, glutamate; **Gln**, glutamine;

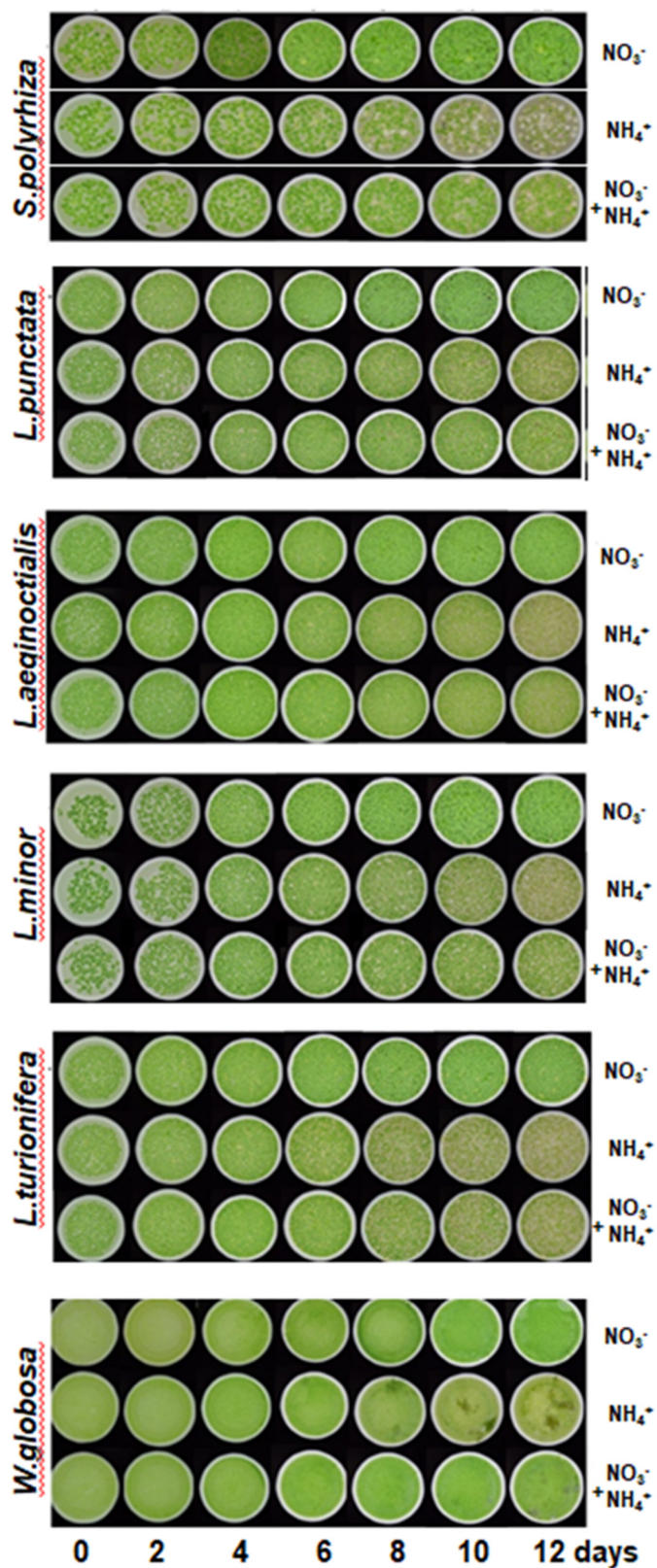


Figure S2. Photographic documentation of six duckweed species cultivated during 12 days on media supplied with 5 mM NO_3^- , 5 mM NH_4^+ as sole N source or 2.5 mM NO_3^- and 2.5 mM NH_4^+ .
0 – start point, 2, 4, 6, 8, 10, 12 days after inoculation.

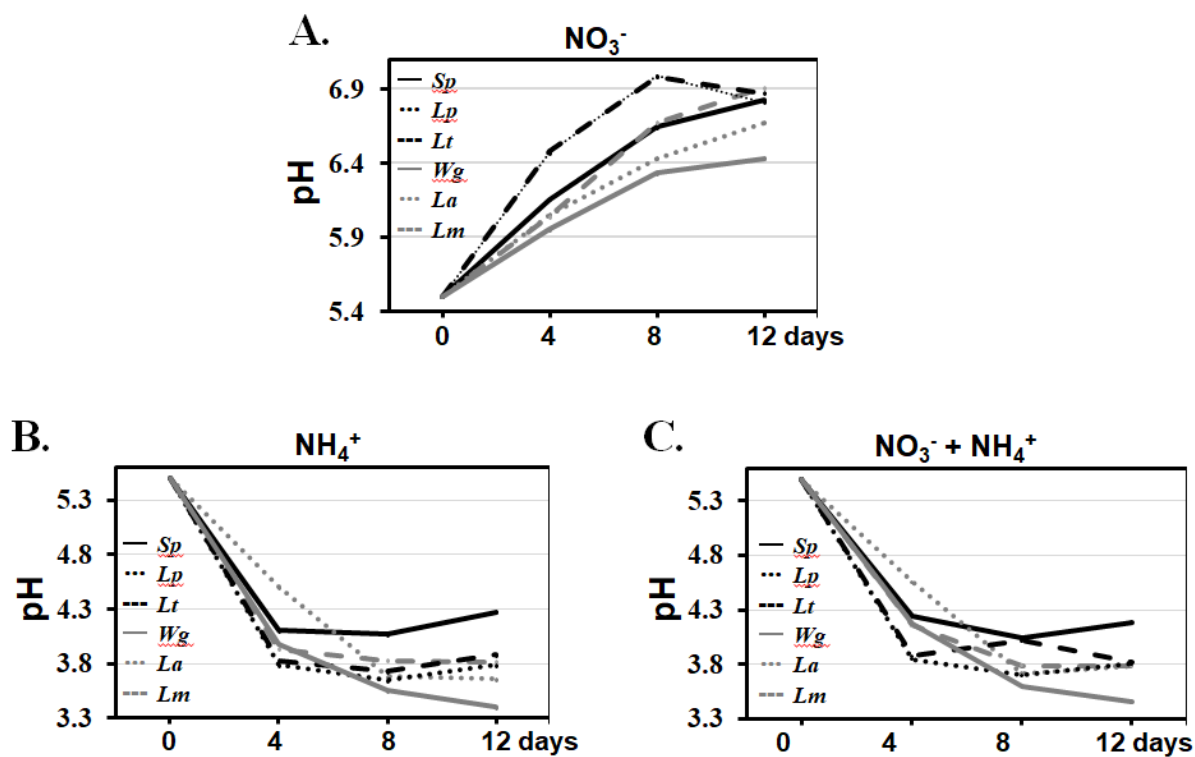


Figure S3. Comparative dynamics of pH changes during the course of duckweed cultivation over 12 days period in the medium supplied with different sources of Nitrogen. (A) medium supplied with 5 mM NO_3^- , (B) medium supplied with 5 mM NH_4^+ ; (C) medium supplied with 2.5 mM NO_3^- and 2.5 mM NH_4^+ (mix).

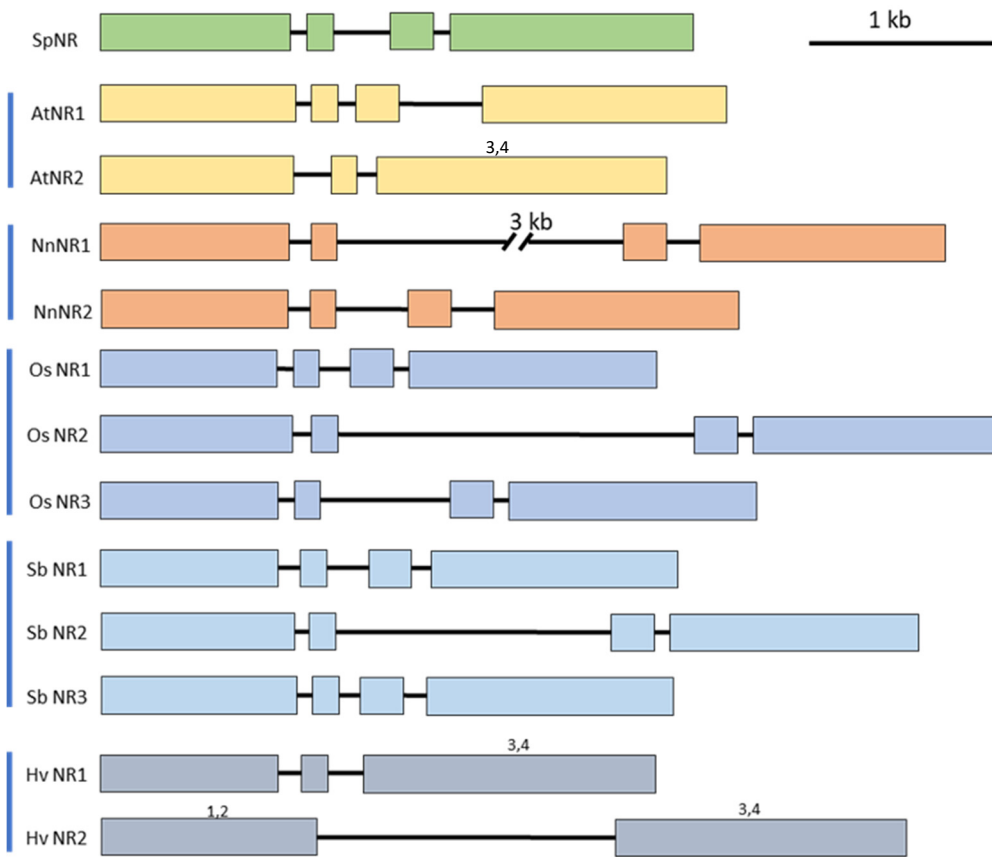


Figure S4. Comparison of the exon-intron structures between NR gene of *S. polyrhiza* and the homologues of some representative plant species: AtNR1 (*A. thaliana*, At1g77760); AtNR2 (*A. thaliana* At1g37130); NnNR1 (*N. nucifera*, LOC104589753); NnNR2 (*N. nucifera*, LOC104589330); OsNR1 (*O. sativa*, LOC4330867); OsNR2 (*O. sativa*, LOC4345795); OsNR3 (*O. sativa*, LOC4345798); SbNR1 (*S. bicolor*, LOC8078943); SbNR2 (*S. bicolor*, LOC8083522); SbNR3 (*S. bicolor*, LOC8055422), SpNR (*S. polyrhiza* CP019094, the 18th chromosome, position from 2346072 to 2349117). Coding sequences are colored boxes. Introns are black lines. The bar corresponds to 1kb of DNA sequence.

A

SpNR	MVTSVDNRRF	GHLEKGGKGV	A-----	-----SPFV	SGAGDSFPNG	GAASFRRRHH	-----HHP-	48
OsNR3	MAASVQPRQ	FGHLE-PGSA	PVCGAASSNG	AKAYPP-ANG	IPRRADSPVR	GCGFP-----	--PLVSPPSR	--K-PPSDGS
OsNR2	MAASVQPRQ	FGHLE-PGSA	PVCGAASSNG	AKAYPP-ANG	IPRRADSPVR	GCGFP-----	--PLVSPPSR	--K-PPSDGS
SbNR2	MAA-VEPRQ	FGRLD-PGVA	-----TNG	AKAYPPASH	LPRRADSPVR	GCGFP-----	--PLVSPPSR	--SNKPPDDAS
HvNR2	MAASVEPRQ	FGRLDAPATA	PTARAPGSNG	-----	IRRRADSPVR	GCGFP-----	--SLISPP-R	--KGRVAEEE
BdNR2	MAASVEPRQ	FGRLDAPATA	-----GAGTNG	-----	IRRRADSPVR	GCGFS-----	--PLISPP-R	--KSCVHEEA
SbNR3	MAASVEPRQ	FGRLDAPATA	-----GAGTNG	-----	IRRRADSPVR	GCGFS-----	--PLISPP-R	--KSCVHEEA
OsNR1	MAASVEYK	LAPHWASNA	P-----	-----SSN	-----	-----	--DLF----	P SGGGKRRSGS
SbNR1	MAASVDRH	LAPHWPFGNA	P-----	-----PKS	-----	-----	--DMFRSGGP	GGGGKRRRAGS
HvNR1	MAASVEYNRQ	VSAPHPWPTNA	Q-----	-----	-----	-----	--DLFSS--	SGGGRRRSGA
BdNR1	MATTVDYNRQ	ASTHPWPSNA	Q-----	-----	-----	-----	--DLFSS--	NSGGNHREY-
AtNR2	MAASVDNRQY	ARLEP-----	-----GLNG	VVRSYKPP-V	PG-RSDSPKA	HQNQTNN--	-QTVFLKPAK	VH-----DDDE
AtNR1	MATSVDRNH	-----P-----	-----TMNG	VAHAFKPLV	PSPRSFDHR	HQNQTLVDIL	TETKIVKETE	VITTVDSYD
NnNR1	MEGSVENRHY	ICREP-----	-----CLSG	PVHGFKTAF-	NNLSDSPVR	SCNFSS--	A-PELSRPNQ	LAVM-----E
NnNR2	MAASVENRQF	SRLEP-----	-----GLSG	VVHGFKAAS-	NNRSDSPAR	VCFNFS--	ATPELSRPMK	PAPM-----D
Consensus	MAASVEPRQ	FGRLP-PGNA	-----NG	-----RR-DSPVR	GCGFP-----	--PLFSPP-R	--KG--XDG	
SpNR	-EDSDEDEDSD	YEEYIAALKA	SS-----GAG	EIEPSAL-DA	RDEATADAWV	ERNSSLIRLT	GKHPFNSEPP	LRRLMHGGFI
OsNR3	-DDEEEEEEQ-	-EDWR--ELY	GSHL---QLE	V-EPSV-RDA	RDEGTADAWI	ERNPLLIRLT	GKHPFNSEPP	LRRLMHGGFI
OsNR2	-DDEEEEEEQ-	-EDWR--ELY	GSHL---QLE	V-EPPV-RDA	RDEGTADAWI	ERNPLLIRLT	GKHPFNSEPP	LRRLMHGGFI
SbNR2	PSDDDDDDDD	-EDWR--ELY	GSHL---QLE	V-EPAV-HDA	RDEGTADAWI	ERNPSLVRLT	GKHPFNSEPP	LRRLMHGGFI
HvNR2	EDDDDDDEEG	HEDW--EAY	GSHL---QLE	V-EPT-RDP	RDEGTADAWI	ERNPSLVRLT	GKHPFNSEPP	LRRLMHGGFI
BdNR2	SSDEEEEEEQ-	-QDWR--ELY	GSHL---QLE	V-EPSV-RDP	RDEGTADAWI	DRNPSLVRLT	GKHPFNSEPP	LRRLMHGGFI
SbNR3	SSDDDDDEHQ	DDDDHRRHET	GSHYLRRLG	V-EPSVQHD	RDEGTADAWV	ERSASLIRLT	GKHPFNSEPP	LRRLMEHGFV
OsNR1	ETSDSDEDSI	PPDWR--SLY	-----HPRLE	VAEAPV-KDP	RDEATSDAWV	RRHPALVRLT	GKHPFNSEPP	LRRLMHGGFI
SbNR1	DSDEDEDSDI	PPDWR--SLY	-----LPRLE	V-EPPV-HDP	RDEATSDAWV	RRHPALVRLT	GKHPFNSEPP	LRRLMHGGFI
HvNR1	DSDEDEDSDV	PPDWR--SLY	-----SPRLD	V-EPSV-KDP	RDEATSDAWV	RRHPALVRLT	GKHPFNSEPP	LRRLMHGGFI
BdNR1	-DSDDDEDNI	PPDWR--SLY	-----RPRLE	V-DPPV-RDP	RDEATSDAWV	RRHPALVRLT	GKHPFNSEPP	LRRLMHGGFI
AtNR2	DVSSEDEEN	-ETHNSNAVY	YKEMIRKSNA	ELEPSVL-DP	RDEYTDADI	ERNPSMVRLT	GKHPFNSEPP	LRRLMHGGFI
AtNR1	DSSEDEDED	-ESHNRNVPY	YKELVKKSNS	DLEPSIL-DP	RDEYTDADI	ERNPSMVRLT	GKHPFNSEPP	LRRLMHGGFI
NnNR1	ESSSEDEG--	-DF-----D	WKDHLQATNR	ELEPSIL-DP	RDEYTDADI	ERNPSMVRLT	GKHPFNSEPP	LRRLMHGGFI
NnNR2	ESSSEDEG--	-DS-----Y	LKEQLQKANS	ELEPSIL-DP	RDEYTDADI	ERNPSMVRLT	GKHPFNSEPP	LRRLMHGGFI
Consensus	XSDSDEDED--	-EDWR--XLY	GSHL---XLE	V-EPSV-RDP	RDEGTADAWI	ERNPSLVRLT	GKHPFNSEPP	LRRLMHGGFI
SpNR	TPVPLHYVRN	HGAVPRGKWE	DWSVEVGLV	RRPRLTMD	IAGEFSAREL	PVTLACGGR	RKEQNMVQKS	IGFNWGAAGV
OsNR3	TPAALHFVRN	HGAVPRGDWS	TWTVEVTGLV	KRPMLTMD	LVNGFPAAVE	PVTLACGGR	RKEQNMVQQT	VGFNWGAAGV
OsNR2	TPAALHFVRN	HGAVPRGDWS	TWTVDVTGLV	KRPMLTMD	LVNGFPAAVE	PVTLACGGR	RKEQNMVQQT	VGFNWGAAGV
SbNR2	TPAPLHYVRN	HGAVPRGDWA	TWAVEVTGLV	KRPRLTMD	LARGFAEL	PVTLACGGR	RKEQNMVQQT	VGFNWGAAGV
HvNR2	TPAPLHYVRN	HGAVPRGDWA	TWTVEVTGLV	KRPRLTMD	LARGFAEL	PVTLACGGR	RKEQNMVQQT	VGFNWGAAGV
BdNR2	TPAPLHYVRN	HGAVPRADWA	TWTVEVTGLV	KRPRLTMD	LARGFAEL	PVTLACGGR	RKEQNMVQQT	VGFNWGAAGV
SbNR3	TPAPLHYVRN	HGAVPRGDWA	AWTVEVAGLV	KRPRLTMD	LARGFAEL	PVTLACGGR	RKEQNMVQQT	VGFNWGAAGV
OsNR1	TPAPLHYVRN	HGAVPKADWS	TWAVEVTGLV	KRPRLTMD	LARGFAEL	PVTLACGGR	RKEQNMVQQT	VGFNWGAAGV
SbNR1	TPAPLHYVRN	HGAVPRADWS	TWTVEVTGLV	KRPRLTMD	LARGFAEL	PVTLACGGR	RKEQNMVQQT	VGFNWGAAGV
HvNR1	TPVPLHYVRN	HGAVPKADWS	TWTVEVTGLV	KRPVKTMD	LARGFAEL	PVTLACGGR	RKEQNMVQQT	VGFNWGAAGV
BdNR1	TPAPLHYVRN	HGAVPKADWA	TWTVEVTGLV	KRPVKTMD	LARGFAEL	PVTLACGGR	RKEQNMVQQT	VGFNWGAAGV
AtNR2	TPVPLHYVRN	HGAVPKADWA	TWTVEVTGLV	KRPVKTMD	LARGFAEL	PVTLACGGR	RKEQNMVQQT	VGFNWGAAGV
AtNR1	TPVPLHYVRN	HGAVPKADWS	TWTVEVTGLV	KRPVKTMD	LARGFAEL	PVTLACGGR	RKEQNMVQQT	VGFNWGAAGV
NnNR1	TPVPLHYVRN	HGAVPKADWS	TWTVEVTGLV	KRPVKTMD	LARGFAEL	PVTLACGGR	RKEQNMVQQT	VGFNWGAAGV
NnNR2	TPVPLHYVRN	HGAVPKADWS	TWTVEVTGLV	KRPVKTMD	LARGFAEL	PVTLACGGR	RKEQNMVQQT	VGFNWGAAGV
Consensus	TPAPLHYVRN	HGAVPRADWA	TWTVEVTGLV	KRPRLTMD	LARGFAEL	PVTLACGGR	RKEQNMVQQT	VGFNWGAAGV
SpNR	STGVWRGRL	CDILRRCGIM	RRPPTGEAAG	GGAPPKMNV	FEGEDLPGG	GG-----SKY	GTSITREXAM	DPSRDIILAY
OsNR3	STSVWRGRL	RDVLRRCGIM	PSKG--GA--	-----LNVC	FEGEDLPGG	GG-----SKY	GTSITREXAM	DPSRDIILAY
OsNR2	STSVWRGRL	RDVLRRCGIM	PSKG--GA--	-----LNVC	FEGEDLPGG	GG-----SKY	GTSITREXAM	DPSRDIILAY
SbNR2	STSVWRGRL	RDVLRRCGIM	PRKGGGGA--	-----LNVC	FEGEDLPGG	GGGGGGSTKY	GTSITREXAM	DPSRDIILAY
HvNR2	STSVWRGRL	RDVLRRCGIM	-SKKGQ-A--	-----LNVC	FEGEDLPGG	GG-----SKY	GTSITREXAM	DPSRDIILAY
BdNR2	STSVWRGRL	RDVLRRCGIM	GARQGGGA--	-----LNVC	FEGEDLPGG	GG-----SKY	GTSITREXAM	DPSRDIILAY
SbNR3	STSVWRGRL	RDVLRRCGIM	VDDGGGGA--	-----LNVC	FEGEDLPGG	GG-----SKY	GTSITREXAM	DPSRDIILAY
OsNR1	STSVWRGVRL	RDVLRRCGIM	GASA--GA--	-----ANVC	FEGEDLPGG	GG-----SKY	GTSITREXAM	DPSRDIILAY
SbNR1	STSVWRGRL	RDVLRRCGIM	GAAD--GA--	-----ANVC	FEGEDLPGG	GG-----SKY	GTSITREXAM	DPSRDIILAY
HvNR1	STTVWRGVRL	RDVLRRCGIM	GAGA--A--	-----SNVC	FEGEDLPGG	GG-----SKY	GTSITREXAM	DPSRDIILAY
BdNR1	STSVWRGVRL	RDVLRRCGIM	GRSGDSGA--	-----SNVC	FEGEDLPGG	GG-----SKY	GTSITREXAM	DPSRDIILAY
AtNR2	STSVWRGVPL	CDVLRRCGIM	SRKG--GA--	-----LNVC	FEGEDLPGG	AGTAG--SKY	GTSITREXAM	DPSRDIILAY
AtNR1	STSLWKGIFL	SEILRRCGIF	SRRG--GA--	-----LNVC	FEGEDLPGG	GG-----SKY	GTSITREXAM	DPSRDIILAY
NnNR1	STSVWRGVRL	CDVLRRCGIM	SRRK--GA--	-----LNVC	FEGEDLPGG	GG-----SKY	GTSITREXAM	DPSRDIILAY
NnNR2	STSVWRGIRL	CKVLRRCGIM	SRRK--GA--	-----LNVC	FEGEDLPGG	GG-----SKY	GTSITREXAM	DPSRDIILAY
Consensus	STSVWRGRL	RDVLRRCGIM	GRKG--GA--	-----LNVC	FEGEDLPGG	GG-----SKY	GTSITREXAM	DPSRDIILAY
SpNR	MHNGELLSPD	HGFPVRMIP	GYIGGRMVKV	LKRIVTTAE	SDNYHYKDN	KVLPSPVDAE	LANAEAWWYK	PEYINELN
OsNR3	MQNGEPLLPD	HGFPVRMIP	GCTGGRMVKV	VKRIIVTTAE	SDNYHYKDN	KVLPSPVDAE	LANAEAWWYK	PEYINELN
OsNR2	MQNGEPLLPD	HGFPVRMIP	GCTGGRMVKV	VKRIIVTTAE	SDNYHYKDN	KVLPSPVDAE	LANAEAWWYK	PEYINELN
SbNR2	MQNGEPLLPD	HGFPVRMIP	GCTGGRMVKV	LKRIVTTAE	SDNYHYKDN	KVLPSPVDAE	LANAEAWWYK	PEYINELN
HvNR2	MQNGEPLLPD	HGFPVRMIP	GCTGGRMVKV	VKRIIVTTAE	SDNYHYKDN	KVLPSPVDAE	LANAEAWWYK	PEYINELN
BdNR2	MQNGEPLLPD	HGFPVRMIP	GCTGGRMVKV	VKRIIVTTAE	SDNYHYKDN	KVLPSPVDAE	LANAEAWWYK	PEYINELN
SbNR3	QQNGGFLLPD	HGFPVRMIP	GCTAGRMVKV	LKRIVTTAE	SDNYHYKDN	KVLPSPVDAE	LANAEAWWYK	PEYINELN
OsNR1	MQNGEPLLPD	HGFPVRMIP	GCTGGRMVKV	LKRIVTTAE	SDNYHYKDN	KVLPSPVDAE	LANAEAWWYK	PEYINELN
SbNR1	MQNGEPLLPD	HGFPVRMIP	GCTGGRMVKV	LKRIVTTAE	SDNYHYKDN	KVLPSPVDAE	LANAEAWWYK	PEYINELN
HvNR1	MQNGEPLLPD	HGFPVRMIP	GCTGGRMVKV	LKRIVTTAE	SDNYHYKDN	KVLPSPVDAE	LANAEAWWYK	PEYINELN
BdNR1	MQNGEPLLPD	HGFPVRMIP	GCTGGRMVKV	LKRIVTTAE	SDNYHYKDN	KVLPSPVDAE	LANAEAWWYK	PEYINELN
AtNR2	MQNGEPLLPD	HGFPVRMIP	GCTGGRMVKV	LKRIVTTAE	SDNYHYKDN	KVLPSPVDAE	LANAEAWWYK	PEYINELN
AtNR1	MQNGEPLLPD	HGFPVRMIP	GCTGGRMVKV	LKRIVTTAE	SDNYHYKDN	KVLPSPVDAE	LANAEAWWYK	PEYINELN
NnNR1	MQNGEPLLPD	HGFPVRMIP	GCTGGRMVKV	LKRIVTTAE	SDNYHYKDN	KVLPSPVDAE	LANAEAWWYK	PEYINELN
NnNR2	MQNGEPLLPD	HGFPVRMIP	GCTGGRMVKV	LKRIVTTAE	SDNYHYKDN	KVLPSPVDAE	LANAEAWWYK	PEYINELN
Consensus	MQNGEPLLPD	HGFPVRMIP	GCTGGRMVKV	LKRIVTTAE	SDNYHYKDN	KVLPSPVDAE	LANAEAWWYK	PEYINELN

SpNR	NSVITTPAHD	EILPINSVTS	QRFYTMKGYA	YAGGGKKVTR	VEVTLDDGET	WLQCELDLPE	RPNKYGYKWC	WCFWSVDLEV	436
OsNR3	NSVITAPGHD	EILPINGITT	QRGYTMKGYA	YSGGGKRI TR	VEVTLDDGET	WLCVLDLPE	KPTKYGKHWC	WCFWSVEVEV	441
OsNR2	NSVITTPGHD	EILPINGITT	QRGYTMKGYA	YSGGGKRI TR	VEVTLDDGET	WLCVLDLPE	KPTKYGKHWC	WCFWSVEVEV	441
SbNR2	NSVITTPGHD	EILPINAITT	QRGYTMKGYA	YSGGGKKVTR	VEVTLDDGET	WLVCVLDHPE	KPNKYGYKWC	WCFWSVEVEV	444
HwNR2	NSVITTPGHD	EILPINAFTT	QRAYTIKGYA	YSGGGKRI TR	VEVTLDDGES	WMLCTLDIPE	KPNKYGRYWC	WCFWSVEIEV	438
BdNR2	NSVITTPGHD	EILPINAFTT	QRAYTMKGYA	YSGGGKKI TR	VEVTLDDGET	WQVCTLDIPE	KPNKYGRYWC	WCFWSVEVEV	433
SbNR1	NSVITTPGHN	DFLPINAITT	QRTYTMKGFA	YSGGGKKVTR	VEVTLDDGGT	WLVCVLDHPE	KPTKYGRWC	WCFWSIDVEL	449
OsNR1	NSVITTPGHD	EVLPIALITT	QRPYTMKGYA	YSGGGKRVTR	VEVTLDDGET	WQVCNLDHPE	RPTKYGYKWC	WCFWSVDVEV	414
SbNR1	NSVITTPGHD	EVLPIALITT	QRPYTIKGYA	YSGGGKRVTR	VEVTLDDGET	WQVCNLDHPE	RPTKYGYKWC	WCFWSVDVEV	417
HwNR1	NSVITTPGHD	EVLPIALITT	QKPYTMKGYA	YSGGGKRVTR	VEVTLDDGET	WQVCLEHPE	RPTKYGYKWC	WCFWSVEVEV	416
BdNR1	NSVIATPGHD	EVLPIALITT	QKPYTMKGYA	YSGGGKRVTR	VEVTLDDGET	WQVCLEHPE	RPTKYGYKWC	WCFWSVEVEV	419
AtNR2	NSVITTPCHE	EILPINAFTT	QRPYTLKGYA	YSGGGKKVTR	VEVTLDDGET	WVNCALDHQE	KPNKYGKFWC	WCFWSLEVEV	443
AtNR1	NSVITTPGHA	EILPINAFTT	QKPYTLKGYA	YSGGGKKVTR	VEVTLDDGDT	WSVCELDHQE	KPNKYGKFWC	WCFWSLDVEV	446
NnNR1	NSVITTPCHE	EFLPINSTAN	QRPYTLRGYA	YSGGGKKVTR	VEVTLDDGES	WLVCALDHPE	KPNKYGYKWC	WCFWSLDVEM	432
NnNR2	NSVITTPCHQ	EILPINSTTT	QRSYTLRGYA	YSGGGKKVTR	VEVTLDDGDS	WLVCALDHPE	KPNRYGYKWC	WCFWSVEVEV	433
Consensus	NSVITTPGHD	EILPINAXTT	QRPYTMKGYA	YSGGGKKVTR	VEVTLDDGET	WLVCALDHPE	KPNKYGYKWC	WCFWSVEVEV	
SpNR	LDLLGAKEIA	VRAWDQALNT	QPEKL IWNVL	GMMNNCWFRV	KVNVCPRPHG	EIGLVFEHPT	KPGNQTGGWM	AREKHLEITE	516
OsNR3	LDLLGAKEIA	VRAWDQSHNT	QPEKL IWNLM	GMMNNCWFKV	KVNVCPRPHG	EIGLVFEHPT	QPGNQTGGWM	ARQKHLETA	521
OsNR2	LDLLGAKEIA	VRAWDQSHNT	QPEKL IWNLM	GMMNNCWFKV	KVNVCPRPHG	EIGLVFEHPT	QPGNQTGGWM	ARQKHLETA	521
SbNR2	LDLLGAKEIA	VRAWDQSLNT	QPEKL IWNLM	GMMNNCWFKV	KVNVCPRPHG	EIGLVFEHPT	QPGNQSGGWM	ARQKHLETA	524
HwNR2	LDLLGAKEVA	VRAWDQTHNT	QPEKL IWNLM	GMMNNCWFKI	KVNVCPRPHG	EIGLVFEHPT	QPGNQTGGWM	ARQKHLETA	518
BdNR2	LDLLGAKEVA	VRAWDQTHNT	QPEKL IWNLM	GMMNNCWFKV	KVNVCPRPHG	EIGLVFEHPT	QPGNQTGGWM	ARQKHLETA	513
SbNR3	ADLLACKEIA	VRAWDQSLNT	QPEFLTWLNL	GMMTNCWFRV	KVNVCPRPSNG	EIGLAFEHPV	QPGNQPGGWM	AQKKHIESAE	529
OsNR1	LELLAAKEIA	VRAWDESLNT	QPEKL IWNLM	GMMNNCWFRV	KTKTCRPHKG	EIGLVFEHPT	QPGNQAGGWM	ARQKHLETS	493
SbNR1	LDVLGAKEIA	VRAWDEAMNT	QPEKL IWNLM	GMMNNCWFRV	KINACRPHKG	EIGMVFEHPA	QPGNQPGGWM	ARQKHLETS	496
HwNR1	LELLGAKEMA	VRAWDEALNT	QPEKL IWNLM	GMMNNCWFRV	KINVCPRPHG	EIGLVFDHPT	QPGNQSGGWM	ARQKHLETS	495
BdNR1	LELLGAKEMA	VRAWDEAMNT	QPEKL IWNLM	GMMNNCWFRV	KINVCPRPHG	EIGLVFEHPT	QPGNQPGGWM	ARQKHMDTST	499
AtNR2	LDLLSAKEIA	VRAWDETLNT	QPEKMIWNLM	GMMNNCWFRV	KTNVCKPHKG	EIGLVFEHPT	LPGNESGGWM	AKERHLEKSA	523
AtNR1	LDLLSAKDVIA	VRAWDESFNT	QPDKL IWNLM	GMMNNCWFRV	RTNVCKPHKG	EIGLVFEHPT	RPGNQSGGWM	AKERQLEISS	526
NnNR1	LDLLGANEIA	VRAWDESLNT	QPEEL IWNLM	GMMNNCWFRV	KMNVCPRHKG	EIGLVFEHPT	QPGNQPGGWM	DRQKHLDS	511
NnNR2	MYLLGAKEIA	VRAWDETLNT	QPEKL IWNLM	GMMNNCWFRV	KMNVCPRHKG	EIGLVFEHPT	QPGNQPGGWM	ARQKHLETS	512
Consensus	LDLLGAKEIA	VRAWDESLNT	QPEKL IWNLM	GMMNNCWFRV	KVNVCPRPHG	EIGLVFEHPT	QPGNQXGGWM	ARQKHLETS	
SpNR	GQ-----S-	LKKSISPPFM	NTAA---KHY	SMSEVRRHST	RDSAWIVVHG	HVYDCTSLFK	DHPGGADSL	INAGTDCTED	586
OsNR3	AAA-----PGL	K-RSTSTPFM	NT-T-DGKQF	TMSEVRKHSS	QDSAWIVVHG	HVYDCTAFLK	DHPGGADSL	INAGTDCTEE	594
OsNR2	AAA-----PGL	K-RSTSTPFM	NT-T-DGKQF	TMSEVRKHSS	QDSAWIVVHG	HVYDCTAFLK	DHPGGADSL	INAGTDCTEE	594
SbNR2	AAA-----PGL	K-RSTSTPFM	STIS-DGKQF	TMSEVRRHAS	QESAWIVVHG	HVYDCTKFLK	DHPGGADSL	INAGTDCTEE	598
HwNR2	AAA-----PGL	K-RSTSTPFM	NTAG-D-KQF	TMSEVRKHGS	KESAWIVVHG	HVYDCTAFLK	DHPGGADSL	INAGSDCTEE	591
BdNR2	AAA-----PGL	K-RSTSTPFM	NTTG-D-KQF	TMSEVRKHGS	QESAWIVVHG	HVYDCTAFLK	DHPGGADSL	INAGTDCTEE	586
SbNR3	AAGAASPPAL	PPRSTSAATS	TTNT-ASNQF	TMSEVRRHAS	KDSAWIVVHG	HVYDCTEYK	DHPGGADSL	INAGTDCTEE	608
OsNR1	-ESAV---ST	LKRSTSTPFL	NTATTQ---Y	TMSEVRRHTT	PESAWIVVHG	HVYDCTGFLK	DHPGGADSIM	INAGTDCTEE	566
SbNR1	-ESAQ---GT	LKKSTSTPFL	NTATTQ---Y	TMSEVRRHTS	PDSAWIVVHG	HIYDCTGFLK	DHPGGADSL	INAGTDCTEE	569
HwNR1	-ETQO---GT	LKRSTSTPFL	STASAQ---F	TMSEVRRHAS	KDSAWIVVHG	HVYDCTAFLK	DHPGGADSL	INAGSDCTEE	568
BdNR1	SETSQ---GT	LKRSTSTPFL	AVAAANSRY	AMSEVRRHAS	RESAWIVVHG	HVYDCTGFLK	DHPGGADSL	INAGTDCTEE	576
AtNR2	DA-----PPS	LKKSSTSTPFL	NTTA---KMY	SMSEVKKHNS	ADSCWIVVHG	HIYDCTRFLM	DHPGGSDSL	INAGTDCTEE	595
AtNR1	ES-----NNT	LKKSSTSTPFL	NTAS---KMY	SISEVRKHNT	ADSCWIVVHG	HIYDCTRFLK	DHPGGSDSL	INAGTDCTEE	598
NnNR1	ES-----NPI	MKKSSTSTPFL	NISS---KTF	SMSEVKKHNS	AESAWIVVHG	KVYDCTPFLK	DHPGGADSL	INAGSDCTEE	583
NnNR2	ES-----NQT	MKKSSTSTPFL	NTSS---KTF	SMPEVKNHNS	AESAWIVVHG	HVYDCTGFLK	DHPGGVDSL	INAGSDCTEE	584
Consensus	AAA-----PGX	LKRSTSTPFL	NTAX-D-KQF	TMSEVRKHXS	XDSAWIVVHG	HVYDCTAFLK	DHPGGADSL	INAGTDCTEE	
SpNR	FDAlHSEKAK	SMLETYRVGE	LITTTG--YLS	DA-----S	NHGANNLAL-	--LSSIAEA-	---APSPRR	VALVPRE-KI	649
OsNR3	FDAlHSDKAK	ALLDTRYIGE	LITTTGAGYSS	D-----NS	VHGASN-LSQ	--LAPIREAI	K-APAP---V	ALSSPRD-KV	659
OsNR2	FDAlHSDKAK	ALLDTRYIGE	LITTTGAGYSS	D-----NS	VHGASN-LSQ	--LAPIREAI	K-APAP---V	ALSSPRD-KV	659
SbNR2	FDAlHSDKAK	ALLDTRYIGE	LITTTGTGYSS	D-----NS	VHGSSAVLSN	--LAPIREAV	R-APAP---V	ALSNPRE-KI	664
HwNR2	FDAlHSDKAK	ALLDTRYIGE	LITTTGTGYNS	D-----NS	VHGSS-LSH	--LAPIREAT	KVAGAP---I	ALSSPRE-KV	657
BdNR2	FDAlHSDKAK	ALLDTRYIGE	LITTTGTGYNS	D-----NS	VHGSSN-LSH	--LAPIREAT	K-ALAP---I	ALSSPRE-KV	651
SbNR3	FDAlHSDKAK	DLGAYRIGD	LLVTAAGTEQ	A-----SH	SH-----LEH	---API----	-GGPAPPVVV	ALSNPREKKV	668
OsNR1	FDAlHSDKAR	GLLEMYRIGE	LIVTGSDYS-	P-----QS	SSADLTISVE	SPTAAAPAV	-----PVSTV	ALSNPRE-KV	632
SbNR1	FDAlHSDKAR	GLLDLYRVGE	LIVTGSDYS-	P-----QN	SHADLRAIDE	APAAAAPAAQ	-----SVSTV	ALSNPRE-KV	635
HwNR1	FDAlHSAKAR	GLLEMYRVGE	LIVTGNDYS-	P-----QS	SHADLAAIVE	APAVVVPRL-	-----PASAV	ALANPRE-KV	633
BdNR1	FDAlHSAKAR	GLLEMYRVGE	LIVTGADYS-	P-----QS	SHADLNAIAE	PPPTVVPPQV	ISSSSSSAV	ALANPRE-KV	648
AtNR2	FEAlHSDKAK	KMLLEDYRIGE	LITTTG--YSS	DSSS--PNNS	VHGSSAVFSL	--LAPIGEA-	---TPVRNL	ALVNPRE-KV	663
AtNR1	FEAlHSDKAK	KMLLEDYRIGE	LITTTG--YDS	---S--PNVS	VHGASNFGSL	--LAPIKEL-	---TPQRNI	ALVNPRE-KI	663
NnNR1	FDAlHSDKAR	KMLLEDYRIGE	LITTTG--YTS	DSSSS--PNNS	VHGASN-LSQ	--LAPIKEV-	---STVTINV	ALI-PRE-KI	651
NnNR2	FDAlHSDKAK	KMLLEDYRLGQ	LIVTAAGTEQ	DSSSS--PNNS	VHGASDL-TH	--LDPIKEV-	---TVTRNV	ALI-PRE-KI	652
Consensus	FDAlHSDKAK	ALLETRYIGE	LITTTG-GYSS	D-----NS	VHGASN-LSX	--LAPIREA-	---AP---V	ALSNPRE-KV	
SpNR	QCRLVSKTSL	SHDVRFRFA	LPAADQVLGL	PVGKHI FLCA	LVDGKPCMR	YTPSTDEEI	GHFELLVKVY	FKDVHPKFP	729
OsNR3	PCQLVDKKEL	SRDVRFRFA	LPSSDQVLGL	PVGKHI FLCA	SIEGKLCMR	YTPSTMVDEV	GHFDLLIKVY	FKNEHPKFP	739
OsNR2	PCQLVDKKEL	SRDVRFRFA	LPSSDQVLGL	PVGKHI FLCA	SIEGKLCMR	YTPSTMVDEV	GHFDLLIKVY	FKNEHPKFP	739
SbNR2	HCRLVGKKEL	SRDVRFRFA	LPSSDQVLGL	PVGKHI FLCA	TIDGKLCMR	YTPSTMVDEI	GHFDLLIKVY	FKNEHPKFP	744
HwNR2	PCRLVDKKEL	SHDVRFRFA	LPSSDQVLGL	PVGKHI FLCA	TIDGKLCMR	YTPSTMVDEI	GHFDLLIKVY	FKNEHPKFP	737
BdNR2	PCRLVDKKEL	SHDVRFRFA	LPSSDQVLGL	PVGKHI FLCA	NIEGKLCMR	YTPSTMVDEI	GHFDLLIKVY	FKDEHPKFP	731
SbNR3	PCRLVAKTVL	SRDVRFRFA	LPSSGQVLGL	PVGKHI FLCA	SIDGKLCMR	YTPTSSVDEV	GHFDLLIKVY	FKNEHPKFP	748
OsNR1	KCRLMDKKSL	SYNVRFRFA	LPSPDQKLGL	PVGKHI FLCA	SIDGKLCMR	YTPTSSVDEV	GYIELLIKVI	FKGEDPKFP	712
SbNR1	RCRLVDKKSL	SYNVRFRFA	LPSPDQKLGL	PVGKHI FLCA	SIDGKLCMR	YTPTSPVDEV	GHIELLIKVI	FKDEDPKYPN	715
HwNR1	RCRLVDKKSL	SHNVRFRFA	LPSPHQKLGL	PVGKHI FLCA	STGGKLCMR	YTPTSSVEEV	GHVELLIKVI	FKDEDPKFP	713
BdNR1	RCRLVGKKSV	SRNVRFRFA	LPSPDQKLGL	PVGKHI FLCA	TTGGKLCMR	YTPTSSPEES	GHVELLIKVI	FKGEDPKFP	728
AtNR2	PVQLVEKTSI	SHDVRFRFA	LPVEDMVGL	PVGKHI FLCA	TIDNKLCLRA	YTPSTVDVV	GHFELLVKVI	FGGVHPRFPN	743
AtNR1	PVRLIEKTSI	SHDVRFRFA	LPSEDQKLGL	PVGKHI FLCA	NINDKLCLRA	YTPSTAIDAV	GHIDLVLKVI	FKDVHPRFPN	743
NnNR1	PCKLICKTSI	SHDVRFRFA	LPSPDQVLGL	PVGKHI FLCA	TIDNKLCLRA	YTPTSSVDDV	GYFDLVKVIY	FKGMNPKFPN	731
NnNR2	ACKLVSKTSI	SHDVRFRFA	LPSPDQVLGL	PVGKHI FLCA	TIDGKLCMR	YTPTSSVDEV	GYFDLVKVIY	FKGMNPKFPN	732
Consensus	PCRLVDKKSL	SHDVRFRFA	LPSSDQVLGL	PVGKHI FLCA	XIDGKLCMR	YTPTSSVDEV	GHFELLVKVIY	FKDEHPKFPN	

		820		840		860		880	
SpNR	GGLMSQHLD	SLPLGAA-VDV	KGPLGHI EYT	GGGNFSVNGE	RKRATKLAMI	AGGTGITPIY	QVMQAVLRD-	PEDDTEIHLV	807
OsNR3	GGLMTQYLD	LPVGA-YIDV	KGPLGHI EYT	GRGEFVINGK	PRNARRLAMI	AGGSGITPMY	QVIQSVLRDQ	PEDTTEMHLV	818
OsNR2	GGLMTQYLD	LPVGA-YIDV	KGPLGHI EYT	GRGEFVINGK	PRNARRLAMI	AGGSGITPMY	QVIQSVLRDQ	PEDTTEMHLV	818
SbNR2	GGLMTQYLD	LPVGS-YIDV	KGPLGHI EYT	GRGSFVINGK	QRHASRLAMI	CGGSGITPMY	QVIQAVLRDQ	PEDDTEMHV	823
HvNR2	GGLMTQYLD	LQVGSYIDV	KGPLGHI EYT	GRGNFVINGK	QRRARRLAMI	CGGSGITPMY	QVIQAVLRDQ	PEDETEMHV	817
BdNR2	GGLMTQHLE	LQIGAS-IDV	KGPLGHI EYT	GRGNFTINGK	ARHARRLAMI	CGGSGITPMY	QVIQAVLRDQ	PEDETEMHV	810
SbNR3	GGRMTQYLD	LPIGAR-VDV	KGPVGHIEY	GRGGLVIDGE	PRRAGRLVMV	AGGSGITPIY	QVIQAVLRDQ	PEDDTEMHV	827
OsNR1	GGLMSQYLDY	LPLGAT-IDI	KGPIGHIEYA	GRGAFTVNGE	RRFARRLAMI	AGGTGITPVY	QVIQAVLRDQ	PDDGTEMHV	791
SbNR1	GGLMSQYLD	LPLGAT-IDI	KGPIGHIEYA	GRGGFVNGE	RRFARRLAMI	AGGTGITPVY	QVIQAVLRDQ	PDDTEMHV	794
HvNR1	GGLMSQYLD	LPLGAP-VDI	KGPVGHIEYA	GRGAFTVNGE	RRFARRLAMI	AGGTGITPVY	QVIQAVLRDQ	PDDTTEMHLV	792
BdNR1	GGLMSQYLD	LPLGAC-VDI	KGPVGHIEY	GRGEFVNGE	RRVARRLAMI	AGGTGITPVY	QVIQAVLRDQ	-EDGTEMHV	806
ANR2	GGLMSQYLD	LPIGST-LEI	KGPLGHI EYT	GKGSFTVHGK	PKFADKLAML	AGGTGITPVY	QIIQAILKD-	PEDETEMYVI	821
ANR1	GGLMSQHLD	LPIGSM-IDI	KGPLGHI EYT	GKGNFLVSGK	PKFAKKLAML	AGGTGITPIY	QIIQSILSD-	PEDETEMYVV	821
NnNR1	GGLMSQYLD	LSLGST-VNV	KGPLGHI EYT	GKGSFTVHGK	PKFAKKLAML	AGGTGITPIY	QVIQAILRD-	PEDDTEMYVV	809
NnNR2	GGLMSQYLD	LPLEST-LDV	KGPLGYIEY	GRGNFTVHGK	AKFAKKLAMI	AGGTGITPIY	QVIQAILKD-	PEDDTEMYVV	810
Consensus	GGLMSQYLD	LPLGAT-IDV	KGPLGHI EYT	GRGNFVNGK	PRFARRLAMI	AGGTGITPXV	QVIQAVLRDQ	PEDETEMHV	
		900		920		940		960	
SpNR	YANRTEDDIL	LREELDGWAK	ERSEQVQVWY	VVGETK--DP	GWSYSGVFVT	EEILRQRVPA	AAA-DVLALA	CGPPPMQLQFA	884
OsNR3	YANRTEDDIL	LRDELDRWAA	EYDRLKQWY	VIDQVKRPEE	GWKYSGVFVT	EEVLRHVPE	GGD-DTLALA	CGPPPMIKFA	897
OsNR2	YANRTEDDIL	LRDELDRWAA	EYDRLKQWY	VIDQVKRPEE	GWKYSGVFVT	EEVLRHVPE	GGD-DTLALA	CGPPPMIKFA	897
SbNR2	YANRTEDDIL	LRDELDRWAA	EYDRLKQWY	VIDQVKRPEE	GWKYSGVFVT	EAVLRHVPE	GGD-DTLALA	CGPPPMIQFA	902
HvNR2	YANRSEDDIL	LRDELDRWAA	EYDRLKQWY	VIDQVKRPEE	GWKFSVGFVT	EDILRAHVPE	GGD-DTLALA	CGPPPMIKFA	896
BdNR2	YANRTEDDIL	LRDELDRWAA	EYDRLKQWY	VIDQVKRPEE	GWKFSVGFVT	EAILREHVPE	GGD-DTLALA	CGPPPMIKFA	889
SbNR3	YANRTEDDIL	LRGELDRWAA	EYDRLKQWY	VISQVKRPEE	-WKYSVGVVT	EAILREHVPE	GGD-GTLALV	CGPPMLIQFA	905
OsNR1	YANRTEDDML	LREEIDRWAA	AHPARLKQWY	VVSKVARPED	GWEYGVGRVD	ERTLREHLP	G-DGETLALV	CGPPAMVECT	870
SbNR1	YANRTEDDML	LREEIDRWAA	AHPARLKQWY	VVSKVARPED	GWAYGVGRVD	EQVLRHLP	G-DSETLALV	CGPPAMIECT	873
HvNR1	YANRTEDDML	LREEIDRWAA	ANPARLKQWY	VVSKVGRPED	AWEYGVGRVD	EQVLRHLP	GGDGETLALV	CGPPAMLECT	872
BdNR1	YANRTEDDML	LREEIDRWAA	EHPGRLKQWY	VVSNVARPED	SWEYGVGRVD	ERVLRHLP	GGDGETLALV	CGPPAMIECT	886
ANR2	YANRTEEDIL	LREELDGWAE	QYPDRLKQWY	VV-ESAK--E	GWAYSTGFIS	EAIMREHLP	GLDGSALAMA	CGPPPMIQFA	898
ANR1	YANRTEDDIL	LREELDGWAE	KHKERLKIWY	VV-EIAK--E	GWSYSTGFIT	EAVLRHLP	GLEGSALAMA	CGPPPMIQFA	898
NnNR1	YANRTEDDIL	LREELDGWAE	KH-ERLKQWY	VVGKALR--E	GWKYSEGLIT	ESVLRHLP	G-SSDTLALA	CGPPPMIQFA	885
NnNR2	YANRTEDDIL	LREELDGWAE	KN-ERLKQWY	VVGESLR--E	GWKYSGVFIT	ENILREHLP	G-SSDTLALA	CGPPPMIQFA	886
Consensus	YANRTEDDIL	LREELDRWAA	EYDRLKQWY	VVXQVKRPEE	GWKYSGVFVT	EAVLRHVPE	GGD-DTLALA	CGPPPMIQFA	
SpNR	VVPNLEKMGY	DVKNALQF	903						
OsNR3	VSPNLEKMKY	DMANSFIVF	916						
OsNR2	VSPNLEKMKY	DMANSFIVF	916						
SbNR2	VSPNLEKMNY	DMANSFVVF	921						
HvNR2	ISP NLEKMKY	DMANSFISF	915						
BdNR2	ISP NLEKMKY	DMANSFISF	908						
SbNR3	VSPNLEKMKH	HVD-SVIVF	923						
OsNR1	VRPGLEKMGY	DLDKSCLVF	889						
SbNR1	VRPGLEKMGY	DLDKACLVF	892						
HvNR1	VRPGLEKMGY	DLDKDCLVF	891						
BdNR1	VRPALEKMGY	DLDKSCLVF	905						
ANR2	VQPNLEKMQY	NIKEDFLIF	917						
ANR1	LQPNLEKMGY	NVKEDLLIF	917						
NnNR1	VVPNLEKMKY	DVKESLLVF	904						
NnNR2	VVPNLEKMNY	DVKESLLVF	905						
Consensus	VSPNLEKMXV	DXXNSFLVF							

B

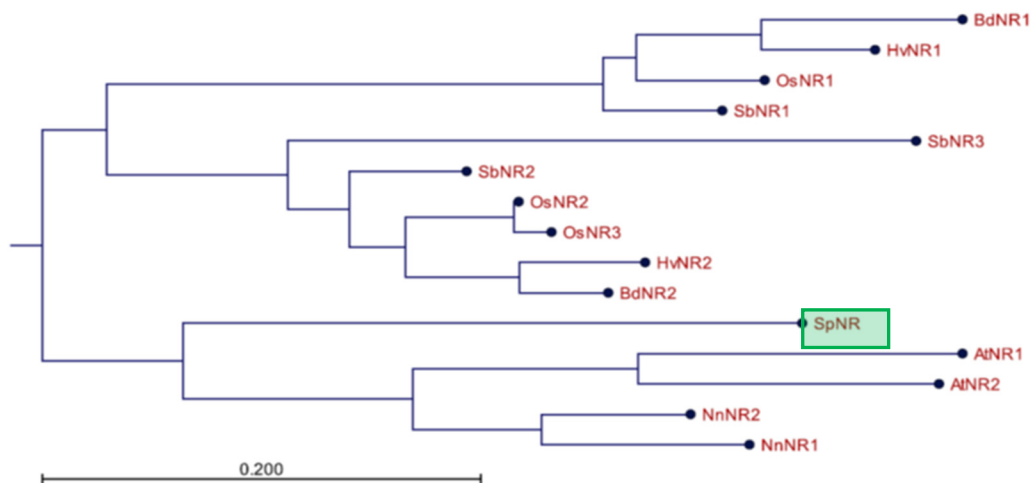


Figure S5. Sequence alignment of NR protein from *S. polyrhiza* with other representative species (A) and the resulting proteins phylogenetic tree (B). AtNR1 – *A. thaliana*, NP_177899.1; AtNR2 – *A. thaliana*, NP_174901.1; BdNR1 – *B. distachyon*, XP_003570548.1; BdNR2 – *B. distachyon*, XP_003574607.1; HvNR1 – *H. vulgare*, KAE8814139; HvNR2 – *H. vulgare*, KAE8794287; NnNR1 – *N. nucifera*, XP_010246478; NnNR2 – *N. nucifera*, XP_010245911; OsNR1 – *O. sativa*, XP_015622710.1; OsNR2 – *O. sativa*, XP_015650300.1; OsNR3 – *O. sativa*, XP_015650643.1; SbNR1 – *S. bicolor*, XP_002454625.1; SbNR2 – *S. bicolor*, XP_002444490.1; SbNR3 – *S. bicolor*, XP_002454083.1; SpNR – *S. polyrhiza* (sequence translated from Acc. OL421561)

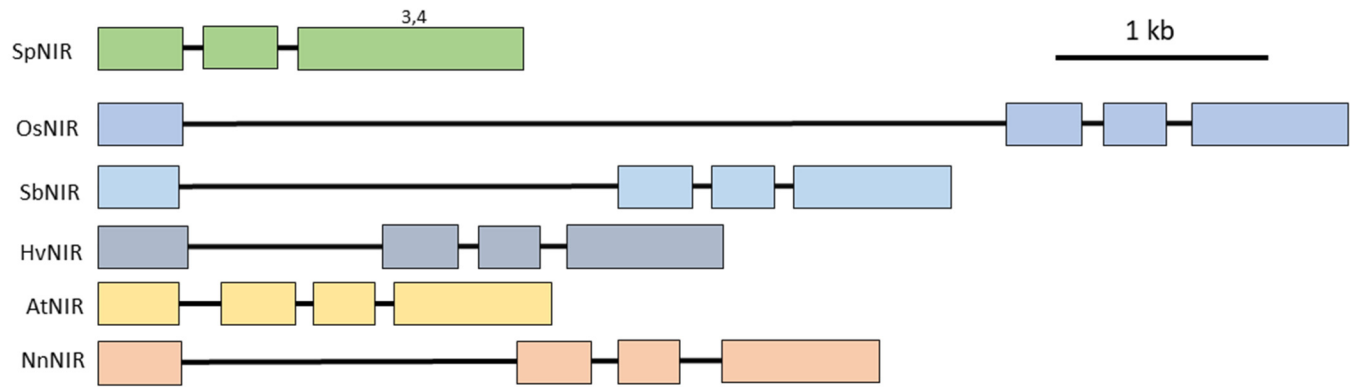


Figure S6. Comparison of the exon-intron structures between *NIR* genes of *S. polyrhiza* and other representative plant species. *AtNIR* – *A. thaliana*, At2g15620; *NnNIR* – *N. nucifera*, LOC104601782; *OsNIR* – *O. sativa*, LOC4326014; *SbNIR* – *S. bicolor*, LOC8075200, *SpNIR* – *S. polyrhiza* CP019094, the 18th chromosome, position from 2760613 to 2758617. Coding sequences are colored boxes. Introns are black lines. The bar corresponds to 1kb of DNA sequence.

A

		20		40		60		80	
SpNIR	-MSSSAVH--	LSMPSWQAVR	RQRR----RG	PAVLATATPT	AAPAAPQPPA	PPEDGA-EVS	RLEPRVEQRE	GGYWVLKEKF	72
OsNIR	MASSASLQRF	L--PPYPHAA	ASRC----RP	PGVRARPVQS	STVSAPSSST	PAADEAVSAE	RLEPRVEQRE	GRYWVLKEKY	74
SbNIR	MASSASLQRF	LPSSSHAATA	SSSR----RR	TG-RARAAYS	MPPSSP----	-PATGEVPAE	RLEPRVEERE	GGYWVLKEKY	70
HvNIR	MASSASLQSF	LP-PSAHAAT	SSSRLRPSRA	RPVQCAAV--	SAPSSSSSSA	SPSASAVPSE	RLEPRVEQRE	GGYWVLKEKY	77
BdNIR	MASSASLQRF	LPSSAHSTPS	SSQRGRRARR	PVLQCSAVSA	PSSSSPAPAA	---GAVAAE	RLEPRVEQRE	GGYWVLKEKY	76
AtNIR	-MTSFSLTF-	-TSPLLPSSS	TKPK----R-	-SVLVAQAQT	TAPAE-----	-STASVDAD	RLEPRVELKD	G-FFILKEKF	63
NnNIR	-MSSSFRFL	APSVPSSSSM	RRTR----RG	ARAPAAATPS	QAEA-----	PSVAKEVDGS	RLEPRVEERE	G-YWVLKEKF	68
Consensus	MASSASLQRF	LPXPSHXAXX	SSXR----RX	PGVXAAAVXS	SAPSSP----A	PPXXGAVXAE	RLEPRVEQRE	GGYWVLKEKY	
		100		120		140		160	
SpNIR	RPGINPQEKV	KLEKEPMALF	MEGGIRDLAA	TPLEDIEASK	LSKDDIDVRL	KWLGLFHRRK	HQYGRFMMRL	KLPNGVTTSE	152
OsNIR	RTGLNPQEKV	KLGEKPMSLF	MEGGIKELAK	MPMEEIEADK	LSKEDIDVRL	KWLGLFHRRK	HQYGRFMMRL	KLPNGVTTSE	154
SbNIR	RTGLNPQEKV	KLEKEPMGLF	MEDGIKDLAK	IPMEEIDAK	LTKDDVDVRL	KWLGLFHRRK	HQYGRFMMRL	KLPNGVTTSE	150
HvNIR	RTSLNPQEKV	KLGEKPMALF	TEGGINDLAK	LPMEQIDADK	LTKEVDVRL	KWLGLFHRRK	QQYGRFMMRL	KLPNGVTTSE	157
BdNIR	RTGLNPQEKV	KLGEKPMALF	TESGIRDLAK	IPMAEIDADK	LAKEDVDVRL	KWLGLFHRRK	QQYGRFMMRL	KLPNGVTTSE	156
AtNIR	RKGINPQEKV	KIEREPMKLF	MENGEELAK	KSMEEIDSEK	SSKDDIDVRL	KWLGLFHRRK	HQYGRFMMRL	KLPNGVTTSE	143
NnNIR	RQGINPQEKV	KLEREPMKLF	MEGGINELAK	TPLQEI EKSK	LTKDDIDVRL	KWLGLFHRRK	HQYGRFMMRL	KLPNGVTTSE	148
Consensus	RTGLNPQEKV	KLEKEPMALF	MEGGIXDLAK	XPMEEIDADK	LXKDDIDVRL	KWLGLFHRRK	HQYGRFMMRL	KLPNGVTTSE	
		180		200		220		240	
SpNIR	QIRYLAGVIE	AYGEDGCADV	TTRQNWQIRG	VRLPDVPAIL	DGLAGVGLSS	LQSGMDNVNR	PVGNPFLAGD	PHEIVDTRPY	232
OsNIR	QTRYLASVIE	AYGKEGCADV	TTRQNWQIRG	VTLPDVPAIL	DGLNAVGLTS	LQSGMDNVNR	PVGNPFLAGD	PDEIVDTRSY	234
SbNIR	QTRYLASVIE	AYGADGCADV	TTRQNWQIRG	VTLPDVPAIL	DGLRAVGLTS	LQSGMDNVNR	PVGNPFLAGD	PHEIVDTRPY	230
HvNIR	QTRYLASVID	KYGEEGCADV	TTRQNWQIRG	VTLPDVPEIL	DGLRSVGLTS	LQSGMDNVNR	PVGSPFLAGD	PDEIVDTRPY	237
BdNIR	QTRYLASVID	KYGEEGCADV	TTRQNWQIRG	VTLPDVPEIL	DGLHSVGLTS	LQSGMDNVNR	PVGNPFLAGD	PDEIVDTRPY	236
AtNIR	QTRYLASVIR	KYGEDGCADV	TTRQNWQIRG	VTLPDVPEIL	KGLASVGLTS	LQSGMDNVNR	PVGNPFLAGD	PHEIVDTRPY	223
NnNIR	QTRCLASVIR	KYGEKGCADV	TTRQNWQIRG	VELPDVPEIM	EDLVRVGLTS	LQSGMDNVNR	PVGNPFLAGD	PHEIVDTRPY	228
Consensus	QTRYLASVIE	KYGEEGCADV	TTRQNWQIRG	VTLPDVPXIL	DGLXSVGLTS	LQSGMDNVNR	PVGNPFLAGD	PHEIVDTRPY	
		260		280		300		320	
SpNIR	ANLLSQFITG	NDRGNPAVTN	LPRKWNACVV	GSHDLYEHPH	INDLAYMPAT	KEGRFGFNLL	VGGFISPKRW	AEAVPLDAWV	312
OsNIR	TNLLSSYITS	NFGQNTITN	LPRKWNVCVI	GSHDLYEHPH	INDLAYMPAV	KGKFGFNLL	VGGFISPKRW	EEALPLDAWV	314
SbNIR	TNLLSSYITN	NSQGNNTITN	LPRKWNVCVI	GSHDLYEHPH	INDLAYMPAV	KDGKFGFNLL	VGGFISPKRW	AEALPLDAWV	310
HvNIR	TNLLSSYITN	NSEGNLAITN	LPRKWNVCVI	GTHDLYEHPH	INDLAYMPAE	KDGKFGFNLL	VGGFISPKRW	GEALPLDAWV	317
BdNIR	TNLLSSYITN	NSQGNLAVTN	LPRKWNVCVI	GSHDLYEHPH	INDLAYMPAE	KDGKFGFNLL	VGGFISPKRW	GEALPLDAWV	316
AtNIR	TNLLSQFITA	NSQGNPDFTN	LPRKWNVCVV	GTHDLYEHPH	INDLAYMPAN	KDGRFGFNLL	VGGFFSPKRC	EEAIPLDWV	303
NnNIR	TNLLSHFITG	NSGGNPAVTN	LPRKWNVCVV	GSHDLFEHPP	INDLAYMPAT	KDGRFGFNLL	VGGFFSPKRC	AEAVPLDAWV	308
Consensus	TNLLSSYITN	NSQGNPAXTN	LPRKWNVCVI	GSHDLYEHPH	INDLAYMPAX	KDGKFGFNLL	VGGFISPKRW	AEALPLDAWV	
		340		360		380		400	
SpNIR	PGEDVVPVCR	AVLEAYRDLG	TRGNRQKTRM	MWLIDELGIE	AFRAEVERRM	PQGVLPRGAS	PAEELVKKDW	LRRDYLGVHP	392
OsNIR	PGDDIIPVCK	AVLEAYRDLG	TRGNRQKTRM	MWLIDELGME	AFRSEVEKRM	PNGVLERAAP	--EDLIDKKW	QRRDYLGVHP	392
SbNIR	AGDDVVPVCR	AILEAYRDLG	FRGNRQKTRM	MWLIDELGME	VFRSEVEKRM	PNGVLERAAP	--AEDLVDKTW	ERRDYLGVHP	388
HvNIR	PGDDIIPVCK	AVLEAYRDLG	TRGNRQKTRM	MWLIDELGME	AFRSEIEKRM	PNGVLERAAP	--EDLIDKKW	ERRDYLGVHP	395
BdNIR	PGDDIIPVCK	AILEAYRDLG	TRGNRQKTRM	MWLIDELGME	VFRSEIEKRM	PQGVLERAA-	--AEDMIDKAW	ERRDYLGVHP	394
AtNIR	PADDVLPCK	AVLEAYRDLG	TRGNRQKTRM	MWLIDELGVE	GFRTEVEKRM	PNGKLERGS-	--SEDLVNKKW	ERRDYFGVHP	381
NnNIR	PADDVVPVCK	AVLEAYRDLG	TRGNRQKTRM	MWLIDELGVE	GFRAEVVKRM	PQGLERSS-	--EEDLVQKQW	ERRDYLGVHP	386
Consensus	PGDDVXPVCK	AVLEAYRDLG	TRGNRQKTRM	MWLIDELGME	AFRSEVEKRM	PNGVLERAAP	--AEDLVDKXW	ERRDYLGVHP	
		420		440		460		480	
SpNIR	QKQQLCFVVG	LHVPVGRVQA	SDMFELARLA	DEYGTGELRL	TVEQNVVIPN	VPEGRVAALL	EEPLLQERFL	PEPSALMRGL	472
OsNIR	QKQEGMSYVG	LHVPVGRVQA	ADMFELARLA	DEYSGELRL	TVEQNIIVIPN	VKNEKVEALL	SEPLLQ-KFS	PQPSLLMKGL	471
SbNIR	QKQEGLSYVG	LHVPVGRVQA	ADMFELARLA	DEYGTGELRL	TVEQNIIVLPN	VSNERVEDALL	AEPLLQRQFS	PEPSLLMKGL	468
HvNIR	QKQEGLSFVG	LHVPVGRVQA	ADMFELARLA	DEYSGELRL	TVEQNIIVLPN	VKNEKVDALL	AEPLLQ-KHFS	AHPSLLMKGL	474
BdNIR	QKQQLSFGV	LHVPVGRVQA	ADMYSLARLA	DEYSGELRL	TVEQNIIVLPN	VPNDKIPSL	AEPLLQ-KFS	AQPSLLMKGL	473
AtNIR	QKQEGLSFVG	LHVPVGRVQA	DDMDLARLA	DTYSGELRL	TVEQNIIVIPN	VETSKTEALL	QEPFLKNRFS	PEPSILMKGL	461
NnNIR	QKQEGFSFVG	LHVPVGRVQA	EEMDELARLA	DEYSGELRL	TVEQNVVIPN	VENSKLEALL	KEPLLNRNFS	PEPSLLMKGL	466
Consensus	QKQEGLSFVG	LHVPVGRVQA	ADMFELARLA	DEYSGELRL	TVEQNIIVIPN	VXNEKVEALL	AEPLLQNRFS	PEPSLLMKGL	
		500		520		540		560	
SpNIR	VACTGNQFCG	QAI IETKARA	VRVAEETERR	VALPAGKSVR	MHWTGCPNSC	AQVQVADIGF	MGCMDARDAAG	KVCEAVDIYLV	552
OsNIR	VACTGNQFCG	QAI IETKQRA	LLVTSQVEKL	VSVP--RAVR	MHWTGCPNSC	GQVQVADIGF	MGCLTKDSAG	KIVEAADIFV	549
SbNIR	VACTGNQFCG	QAI IETKARA	LQVTRVEKR	VSVP--RPVR	MHWTGCPNSC	GQVQVADIGF	MGCLTKDSDG	KIVEAADIFV	546
HvNIR	VACTGNQFCG	QAI IETKARA	LQVTRDVEAR	VSVP--KAVR	MHWTGCPNSC	AQVQVADIGF	MGCLTKNSSG	KIVEAADIFV	552
BdNIR	VACTGNQFCG	QAI IETKARA	LRVTRDVERR	VSVP--RAVR	MHWTGCPNSC	AQVQVADIGF	MGCLTKNGSG	KIVEAADIFV	551
AtNIR	VACTGSQFCG	QAI IETKLRA	LKVTEEVERL	VSVP--RPVR	MHWTGCPNTC	GQVQVADIGF	MGCLTRGEEG	KPVEGADVYV	539
NnNIR	VACTGNQFCG	QAI IETKARA	LKVTEEVERR	VAVT--RPVR	MHWTGCPNSC	GQVQVADIGF	MGCMTRDENG	KACEGVDVFL	544
Consensus	VACTGNQFCG	QAI IETKARA	LXVTXEVERR	VSVP--RXVR	MHWTGCPNSC	GQVQVADIGF	MGCLTKDSXG	KIVEAADIFV	
		580		600					
SpNIR	GGRVGSDSHL	GSVYKKGVPC	KDLVPVLVDI	LVERFGAVPR	QREDDDEEEE	ER			604
OsNIR	GGRVGSDSHL	AGAYKKSVPC	DELAPIVADI	LVERFGAVRR	EREDEEE---	--			596
SbNIR	GGRVGSDSHL	ADVYKKSVPC	KDLVPIVADL	LVERFGAVPR	EREDEEE---	--			593
HvNIR	GGRIGSDSHL	TGVYKKAVPC	EDLVPIVADL	LVERFGAVPR	EREDEEE---	--			599
BdNIR	GGRVGSDSHL	TGVWKKAVPC	EDLVPIVADL	LVERFGAVPR	EREDEEE---	--			598
AtNIR	GGRIGSDSHI	GEIYKKGVRV	TELVPVVAEI	LIFKFGAVPR	EREENED---	--			586
NnNIR	GGRIGSDSHL	GDVYKKSVPC	KDLVPLVVDI	LINHFGAVPR	DREEEGED---	--			592
Consensus	GGRVGSDSHL	GGVYKKSVPC	KDLVPIVADI	LVERFGAVPR	EREDEEE---	--			

B

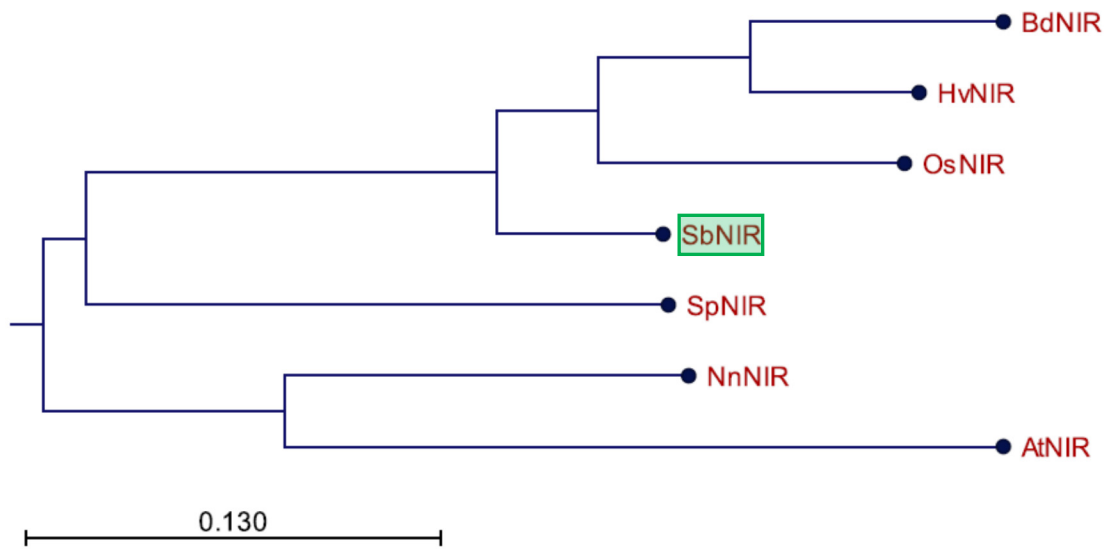


Figure S7. Sequence alignment of NIR protein from *S. polyrhiza* with other representative species (A) and the resulted phylogenetic tree (B).; AtNIR – *A. thaliana*, NP_179164; BdNIR - *B. distachyon*, XP_003570568; HvNIR - *H. vulgare*, BAW00383; NnNIR - *N. nucifera*, XP_010263547; OsNIR - *O. sativa*, XP_015641702.1; Sb NIR - *S. bicolor*, XP_002454602; SpNIR - *S. polyrhiza* (sequence translated from Acc. OL421562)

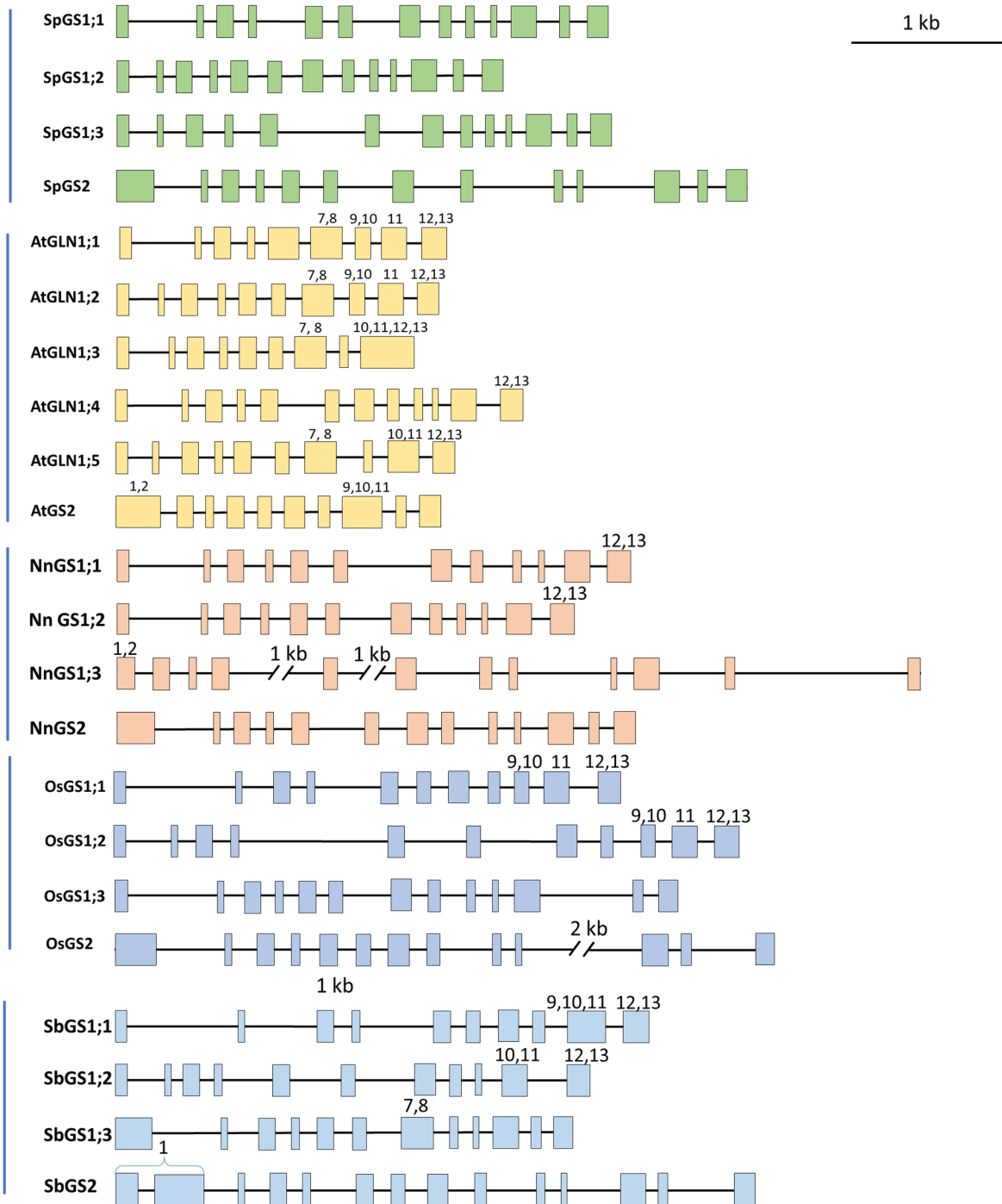


Figure S8. Comparison of the exon-intron structures between GS genes of *S. polyrhiza* and other representative plant species. *AtGln1;1* – *A. thaliana*, At5g37600); *AtGln1;2* – *A. thaliana*, At1G66200; *AtGln1;3* – *A. thaliana*, At3g17820; *AtGln1;4* – *A. thaliana*, At5g16570; *AtGln1;5* – *A. thaliana*, At1g48470; *AtGS2* – *A. thaliana*, At5g35630; *NnGS1;1* – *N. nucifera*, LOC104607411; *NnGS1;2* – *N. nucifera*, LOC104607404; *NnGS1;3* – *N. nucifera*, LOC104592454; *NnGS2* – *N. nucifera*, LOC104596403, *OsGS1;1* – *O. sativa*, LOC4330649, *OsGS1;2* – *O. sativa*, LOC4332108, *OsGS1;3* – *O. sativa*, LOC4333896, *OsGS2* – *O. sativa*, LOC4337272, *SbGS1;1* – *S. bicolor*, LOC110434374, *SbGS1;2* – *S. bicolor*, LOC8056868, *SbGS1;3* – *S. bicolor*, LOC110431761, *SbGS2* – *S. bicolor*, LOC110436381, *SpGS1;1* – *S. polyrhiza* CP019094, the 7th chromosome, position from 6306673 to 6309664, *SpGS1;2* – *S. polyrhiza* CP019094, the 18th chromosome, position from 1351512 to 1353850, *SpGS1;3* – *S. polyrhiza* CP019094, the 14th chromosome, position from 1601445 to 1604468, *SpGS2* – *S. polyrhiza* CP019094, the 1st chromosome, position from 4942769 to 4946754. Coding sequences are represented by colored boxes, introns are black lines. The bar corresponds to 1kb of DNA sequence.

A

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		180		200		220		240	
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OsGS1;1	GGSGMDLRSK	ARTLSGPVTD	PSKLPKWNVD	GSSTGQAPGE	DSEVILYPQA	IFKDPFRKGN	NILVMDCYT	PAGEPIPTNK	106
SbGS1;1	GGSGMDLRSK	ARTLSGPVTD	PSKLPKWNVD	GSSTGQAPGE	DSEVILYPQA	IFKDPFRFGN	NILVMDCYT	PAGEPIPTNK	106
HvGS1;1	GGSGMDLRSK	ARTLSGPVTD	PSKLPKWNVD	GSSTGQAPGE	DSEVILYPQA	IFKDPFRFGN	NILVMDCYT	PAGEPIPTNK	106
BdGS1;1	GGSGMDLRSK	ARTLSGPVTD	PSKLPKWNVD	GSSTGQAPGE	DSEVILYPQA	IFKDPFRFGN	NILVMDCYT	PAGEPIPTNK	106
NnGLN1;1	GGSGLDMRSK	ARTLSGPVSD	PSKLPKWNVD	GSSTGQAPGE	DSEVILYPQA	IFRDPFRFGN	NILVMCDTYT	PSGEPIPTNK	106
NnGLN1;2	GGSGMDMRSK	AKTLSGPVSD	PSKLPKWNVD	GSSTGQAPGE	DSEVILYPQA	IFRDPFRFGN	NILVMCDTYT	PAGEPIPTNK	106
NnGLN1;3	GGSGMDLRSK	ARTLSGPVTD	PQKLPKWNVD	GSSTGQAPGE	DSEVILYPQA	IFRDPFRFGN	NILVMCDYT	PAGEPIPTNK	106
OsGS1;2	GGSGIDLRSK	ARTVKGPITD	VSQLPKWNVD	GSSTGQAPGE	DSEVILYPQA	IFKDPFRFGD	NILVMDCYT	PQGEPIPTNK	106
SbGS1;2	GGSGIDLRSK	ARTVKGPITD	PSQLPKWNVD	GSSTGQAPGE	DSEVILYPQA	IFKDPFRFGD	NILVMDCYT	PQGEPIPTNK	106
BdGS1;2	GGSGIDLRSK	ARTVNGPITD	ASQLPKWNVD	GSSTGQAPGE	DSEVILYPQA	IFKDPFRFGD	NILVMDCYT	PQGVPIPTNK	106
HvGS1;2	GGSGIDIRSK	ARTVNGPITD	ASQLPKWNVD	GSSTGQAPGE	DSEVILYPQA	IFKDPFRFGD	NILVMDCYT	PQGVPIPTNK	106
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AtGLN1;2	GGSGMDMRSK	ARTLPGPVTD	PSKLPKWNVD	GSSTGQAPGQ	DSEVILYPQA	IFKDPFRFGN	NILVMCDAYT	PAGEPIPTNK	106
AtGLN1;4	GGSGLDMRSK	ARTLPGPVTD	PSQLPKWNVD	GSSTGQAPGD	DSEVILYPQA	IFKDPFRFGN	NILVMCDAYT	PAGEPIPTNK	106
AtGLN1;3	GGSGMDIRSK	ARTLPGPVTD	PSKLPKWNVD	GSSTGQAAGE	DSEVILYPQA	IFKDPFRFGN	NILVMCDAYT	PAGDPIPTNK	106
SpGS1;2	GGSGLDMRSK	ARTLSGPVDD	PSKLPKWNVD	GSSTGQAPGE	DSEVILYPQA	IFKDPFRFGN	NILVMCDAYT	PAGEPIPTNK	106
OsGS1;3	GGTGMDVRSK	ARTLSGPVDD	PSKLPKWNFD	GSSTGQATGD	DSEVILHPQA	IFRDPFRKGN	NILVMCDYA	PNGEPIPTNN	108
SbGS1;3	GGSGMDVRSK	ARTLSGPVDD	PSKLPKWNFD	GSSTGQAPGD	DSEVILCPRA	IFRDPFRKGN	NILVMCDYE	PNGKPIPSNK	106
HvGS1;3	GGTGMDVRSK	ARTLPGPVDD	PSKLPKWNFD	GSSTGQATGD	DSEVILHPQA	IFRDPFRKGN	NILVMCDYA	PTGEPIPSNK	106
BdGS1;3	GGTGMDMRSK	ARTLPGPVDD	PSKLPKWNFD	GSSTGQATGD	DSEVILCPQA	IFRDPFRKGN	NILVMCDYA	PTGEPIPSNK	106
SpGS1;3	GGSGMDMRSK	ARTLPGSVSD	PKELPKWNVD	GSSTGQAPGE	NSEVILHPQA	IFKDPFRFGN	NILVMCDAYT	PAGEPIPTNK	106
AtGS1;5	GGSGMDIRSK	ARTLPGPVSN	PTKLPKWNVD	GSSTGQAPGE	DSEVILYPQA	IFKDPFRFGN	NILVMCDAYR	PAGDPIPTNN	106
SpGS2	GGSGIDVRSK	SRTISKAVEH	PSLEPKWNVD	GSSTGQAPGE	DSEVILYPQA	IFKDPFRFGN	NILVMCDYT	PNGEPIPTNK	160
NnGS2	GGSGIDLRSK	SRTISKPVED	PSLEPKWNVD	GSSTGQAPGE	DSEVILYPQA	IFKDPFRFGN	NILVICDSYT	PAGEPIPTNK	166
AtGS2	GGSGIDLRSK	SRTIEKPVED	PSLEPKWNVD	GSSTGQAPGE	DSEVILYPQA	IFRDPFRFGN	NILVICDTWT	PAGEPIPTNK	164
OsGS2	GGTGIDLRSK	SRTISKPVED	PSLEPKWNVD	GSSTGQAPGE	DSEVILYPQA	IFKDPFRFGN	NILVMCDTYT	PAGEPIPTNK	162
SbGS2	GGSGIDIRSK	SRTISKPVED	PSLEPKWNVD	GSSTGQAPGE	DSEVILYPQA	IFKDPFRFGN	NILVICDTYT	PQGEPLPTNK	231
HvGS2	GGSGIDLRSK	SRTISKPVED	PSLEPKWNVD	GSSTGQAPGE	DSEVILYPQA	IFKDPFRFGN	NILVICDTYT	PQGEPIPTNK	168
BdGS2	GGSGIDIRSK	SRTISKPVAD	PSLEPKWNVD	GSSTGQAPGE	DSEVILYPQA	IFKDPFRFGN	NILLVCDTYT	PAGEPIPTNK	164
Consensus	GGSGMDLRSK	ARTLSGPVTD	PSKLPKWNVD	GSSTGQAPGE	DSEVILYPQA	IFKDPFRFGN	NILVMDCYT	PAGEPIPTNK	
		260		280		300		320	
SpGS1;1	RFNAAKFVSN	PDVIAEVPWY	GIEQEYTLQ	KDINWPLGWP	VGGFPGPQGP	YYCGTGADKA	FGRDIVDAH	KACLYAGINI	186
OsGS1;1	RHNAAKIFSS	PEVASEEPWY	GIEQEYTLQ	KDINWPLGWP	VGGFPGPQGP	YYCGIGADKS	FGRDIVDSHY	KACLYAGINI	186
SbGS1;1	RHNAAKIFSN	PEVAAEPPWY	GIEQEYTLQ	KDINWPLGWP	LGGFPGPQGP	YYCGIGADKS	FGRDIVDAH	KACLYAGINI	186
HvGS1;1	RYNAAKIFSN	PDVAAEPPWY	GIEQEYTLQ	KDINWPLGWP	VGGFPGPQGP	YYCGIGADKS	FGRDIVDSHY	KACLYAGINI	186
BdGS1;1	RHNAAKIFSN	PAVAAEPPWY	GIEQEYTLQ	KDINWPLGWP	VGGFPGPQGP	YYCSIGADKS	FGRDIVDSHY	KACLYAGINI	186
NnGLN1;1	RCNAAKIFNH	PDVLAEEWLF	GIEQEYTLQ	KDVKWPVGWP	VGGFPGPQGP	YYCGVGADKA	WGRDIVDSHY	KACLYAGINI	186
NnGLN1;2	RCNAAKIFSH	PDVLAEEWLF	GIEQEYTLQ	KDVKWPVGWP	VGGFPGPQGP	YYCGVGADKA	WGRDIVDSHY	KACLYAGINI	186
NnGLN1;3	RYNAAKIFSH	PDVLAEEWLF	GIEQEYTLQ	KDVWPLGWP	VGGFPGPQGP	YYCGAGADKA	FGRDIVDSHY	KACLYAGINI	186
OsGS1;2	RHSAAKIFSH	PDVVAEVPWY	GIEQEYTLQ	KDVNWPVGWP	VGGFPGPQGP	YYCAAGAEKA	FGRDIVDAH	KACLYAGINI	186
SbGS1;2	RYNAAKFVSH	PDVAAEVPWY	GIEQEYTLQ	KDVNWPVGWP	VGGYPPGPQGP	YYCAAGADKA	FGRDIVDAH	KACLYAGINI	186
BdGS1;2	RHNAAKIFNN	PKVAAEVTWY	GIEQEYTLQ	KDVNWPVGWP	VGGYPPGPQGP	YYCAAGADKA	FGRDIVDAH	KACLYAGINI	186
HvGS1;2	RHNAAKIFNS	AKVAAEETWY	GIEQEYTLQ	KDVNWPVGWP	IGGYPPGPQGP	YYCAAGADKA	FGRDIVDAH	KACLYAGINI	186
AtGLN1;1	RHAAAKVFSS	PDVAAEVPWY	GIEQEYTLQ	KDVKWPVGWP	IGGYPPGPQGP	YYCGIGADKS	FGRDIVDSHY	KACLYAGINI	186
AtGLN1;2	RHAAAKIFAN	PDVIAEVPWY	GIEQEYTLQ	KDVNWPVGWP	IGGYPPGPQGP	YYCSIGADKS	FGRDIVDAH	KACLYAGINI	186
AtGLN1;4	RHAAAKIFED	PSVVAEETWY	GIEQEYTLQ	KDINWPLGWP	VGGFPGPQGP	YYCGVGADKA	FGRDIVDSHY	KACLYAGINV	186
AtGLN1;3	RHNAAKIFSH	PDVAAEPPWY	GIEQEYTLQ	KDVNWPVGWP	VGGYPPGPQGP	YYCGVGADKA	IGRDIVDAH	KACLYAGIGI	186
SpGS1;2	RYKAAQIFSD	PAVVAEVPWY	GLEQEYTLQ	KDVKWPVGWP	LGGFPAPQGP	YYCGTGVDKA	FGRDIVDAH	KACLYAGINI	186
OsGS1;3	RYNAAKIFSH	PDVKAEEPPWY	GIEQEYTLQ	KHINWPLGWP	LGGYPPGPQGP	YYCAAGADKS	YGRDIVDAH	KACLYAGINI	188
SbGS1;3	RHGAATIFSH	PDVKAEEPPWY	GIEQEYTLQ	KDINWPLGWP	LGGYPPGPQGP	YYCAAGADKS	YGREIVDAH	KACLYAGIDI	186
HvGS1;3	RYNAAKIFGH	PDVKEEPPWY	GIEQEYTLQ	KDINWPLGWP	LGGYPPGPQGP	YYCAAGAEKS	YGRDIVDAH	KACLYAGINI	186
BdGS1;3	RSSAANIFSH	PDVKAEEPPWY	GIEQEYTLQ	KDINWPLGWP	LGGYPPGAQGP	YYCATGAES	YGRDIVDAH	KACLYAGVNI	186
SpGS1;3	RFLAEKIFSH	PDVIAEPPWY	GIEQEYTLQ	RDVHWPVGWP	VGGFPRPQGP	YYCGVGADKA	FGRDIVDSHY	KACLYAGINV	186
AtGS1;5	RHKAVKIFDH	PNVKAEEPPWY	GIEQEYTLQ	KDVKWPVGWP	LGGFPGPQGP	YYCAVGADKA	FGRDIVDAH	KACLYAGSLI	186
SpGS2	RYRAAQIFSD	PKVVAEVPWF	GIEQEYTLQ	SNVWPLGWP	IGGYPPGPQGP	YYCSAGADKS	FGRDIVDAH	KACLYAGINI	240
NnGS2	RYRAAQIFSD	PKVVQEVWY	GIEQEYTLQ	TNVKWPVGWP	IGAYPPGPQGP	YYCGVGADKS	FGRDIVDAH	KACLYAGINI	246
AtGS2	RAKAAEIFSN	KKVSGEVPWF	GIEQEYTLQ	QNVKWPVGWP	VGAFFPGPQGP	YYCGVGADKI	WGRDIVDAH	KACLYAGINI	244
OsGS2	RNRAAQVFS	PKVVSQVPWF	GIEQEYTLQ	RDVWPLGWP	VGGYPPGPQGP	YYCAVGSCKS	FGRDIVDAH	KACLYAGINI	242
SbGS2	RHRAAQIFSD	PKVVEQVPWF	GIEQEYTLQ	KDVNWPVGWP	VGGYPPGPQGP	YYCAVGADKS	FGRDIVDAH	KACLYAGINI	311
HvGS2	RHMAAQIFSD	PKVTSQVPWF	GIEQEYTLQ	RDVWPLGWP	VGGYPPGPQGP	YYCAVGSCKS	FGRDIVDAH	KACLYAGIEI	248
BdGS2	RHRAAQIFSD	PKVASQVPWF	GIEQEYTLQ	RDVWPLGWP	VGGYPPGPQGP	YYCAVGSCKS	FGRDIVDAH	KACLYAGIEI	244
Consensus	RHNAAKIFSH	PDVAAEPPWY	GIEQEYTLQ	KDVNWPVGWP	VGGXPPGPQGP	YYCGVGADKS	FGRDIVDAH	KACLYAGINI	

			340		360		380		400
SpGS1;1	SGINGEVMPG	QWEFQVGPVV	GISAGDQVWV	ARYILERITE	IAGVVVSFDP	KPIKGDWNGA	GAHTNYSTQS	MRNDGGYEV	266
OsGS1;1	SGINGEVMPG	QWEFQVGPVS	GISAGDQVWV	ARYILERITE	IAGVVVSFDP	KPIPGDWNGA	GAHTNYSTKS	MRNDGGYEV	266
SbGS1;1	SGINGEVMPG	QWEFQVGPVS	GISAGDQVWV	ARYILERITE	IAGVVLTFDP	KPIPGDWNGA	GAHTNYSTKS	MRNEGGYEV	266
HvGS1;1	SGINGEVMPG	QWEFQVGPTV	GISAGDQVWV	ARYILERITE	IAGVVVTFDP	KPIPGDWNGA	GAHTNYSTES	MRNDGGFKV	266
BdGS1;1	SGINGEVMPG	QWEFQVGPVS	GISAGDQVWV	ARYLLERITE	IAGVVVSFDP	KPIPGDWNGA	GAHTNYSTES	MRNDGGFQV	266
NnGLN1;1	SGINGEVMPG	QWEFQVGPVS	GISAGDELWI	ARYILERITE	IAGVVLTFDP	KPIQGDWNGA	GAHTNYSTKS	MRSEGGYEV	266
NnGLN1;2	SGINGEVMPG	QWEFQVGPVS	GISAGDELWI	ARYILERITE	IAGVVLTFDP	KPIQGDWNGA	GAHTNFSTKS	TRNEGGYEV	266
NnGLN1;3	SGINGEVMPG	QWEFQVGPVS	GISAGDELWI	ARYILERITE	IAGVVLTFDP	KPIKGDWNGA	GAHTNYSTKS	MRNDGGIDV	266
OsGS1;2	SGINGEVMPG	QWEFQVGPVS	GI AADQVWV	ARYILERVTE	VAGVVLSDP	KPIPGDWNGA	GAHTNFSTKS	MREPGGYEV	266
SbGS1;2	SGINGEVMPG	QWEFQVGPVS	GISAGDEI WV	ARYILERITE	IAGI VLSLDP	KPIQGDWNGA	GAHTNYSTKS	MREAGGYEV	266
BdGS1;2	SGINGEVMPG	QWEFQVGPVS	GI AASDQLWV	ARYILERITE	VAGVVLSDP	KPIPGDWNGA	GAHTNYSTKS	MREAGGFV	266
HvGS1;2	SGINGEVMPG	QWEFQVGPVS	GI AASDQLWV	ARYILERITE	VAGVVLSDP	KPIPGDWNGA	GAHTNYSTKS	MRQAGGYEV	266
AtGLN1;1	SGINGEVMPG	QWEFQVGPVS	GI SAAD EIWV	ARYILERITE	IAGVVVSFDP	KPIPGDWNGA	GAHCNYSTKS	MREEGGYE	266
AtGLN1;2	SGINGEVMPG	QWEFQVGPVS	GI SAAD EIW	ARYILERITE	IAGVVVSFDP	KPIPGDWNGA	GAHTNYSTKS	MREEGGYE	266
AtGLN1;4	SGTNGEVMPG	QWEFQVGPTV	GI AADQVWV	ARYILERITE	LAGVVLSDP	KPIPGDWNGA	GAHTNYSTKS	MREDGGYEV	266
AtGLN1;3	SGINGEVMPG	QWEFQVGPVE	GISAGDQVWV	ARYLLERITE	ISGV IVSFDP	KPVPGDWNGA	GAHCNYSTKT	MRNDGGLEV	266
SpGS1;2	SGINGEVMPG	QWEFQVGPVS	GI AADDELWV	ARYILERITE	VAGVVLSDP	KPIKGDWNGA	GCHTNYSTKT	MREEGGFV	266
OsGS1;3	SGINAEVMPG	QWEFQIGPVV	GV SAGDHVWV	ARYILERITE	IAGVVVSFDP	KPIPGDWNGA	GAHTNYSTKS	MRSDGGYEV	268
SbGS1;3	SGINAEVMPG	QWEFQVGPVS	GV SAGDQLWV	ARYILERITE	IAGVVVSFDP	KPIPGDWNGA	GAHTNYSTKS	MRSDGGYEV	266
HvGS1;3	GGINAEVMPG	QWEFQVGPVS	GISAGDELWA	ARYILERITE	IAGVVVSFDP	KPIPGEWNGA	GAHTNYSTKS	MRSEGGYEV	266
BdGS1;3	GGINAEVMPG	QWEFQVGPVS	GISAGDELWV	ARYILERITE	IAGVVVSFDP	KPVPGEWNGA	GAHTNYSTKS	MRSEGGYEV	266
SpGS1;3	SGVNGEVMPG	QWEFQVGPVS	GISAGDQIWA	ARYILERITE	IAGVLLSFDP	KPIKGDWNGA	GAHTNYSTNS	MRNNGGMD	266
AtGS1;5	GGANGEVMPG	QWEFQISPTV	GI GAGDQLWV	ARYILERITE	ICGV IVSFDP	KPIQGDWNGA	AAHTNFSTKS	MRKDGGDL	266
SpGS2	SGTNGEVMPG	QWEYQVGPVS	GI DAGDH I WV	SRYILERITE	QAGVVLSDP	KPIEGDWNGA	GCHTNYSTKT	MREDGGFE	320
NnGS2	SGTNGEVMPG	QWEYQVGPVS	GI EAGDH IWC	SRYILERITE	QAGVVLTLDP	KPIEGDWNGA	GCHTNYSTKS	MREEGGFV	326
AtGS2	SGTNGEVMPG	QWEFQVGPVS	GI DAGDHVWC	ARYLLERITE	QAGVVLTLDP	KPIEGDWNGA	GCHTNYSTKS	MREEGGFV	324
OsGS2	SGTNGEVMPG	QWEYQVGPVS	GI EAGDH IWI	SRYILERITE	QAGVVLTLDP	KPIQGDWNGA	GCHTNYSTKS	MREDGGFE	322
SbGS2	SGTNGEVMPG	QWEYQVGPVS	GI EAGDH IWI	SRYILERITE	QAGVVLTLDP	KPIQGDWNGA	GCHTNYSTKT	MREDGGFD	391
HvGS2	SGTNGEVMPG	QWEYQVGPVS	GI DAGDH IWA	SRYILERITE	QAGVVLTLDP	KPIQGDWNGA	GCHTNYSTLS	MREDGGFDV	328
BdGS2	SGTNGEVMPG	QWEYQVGPVS	GI DAGDH IWA	SRYILERITE	QAGVVLTLDP	KPIQGDWNGA	GCHTNYSTKA	MREDGGFEV	324
Consensus	SGINGEVMPG	QWEFQVGPVS	GISAGDQXWV	ARYILERITE	IAGVVLSDP	KPIPGDWNGA	GAHTNYSTKS	MREDGGYEV	
		420		440		460		480	
SpGS1;1	KKAI EKLGLR	HKEHIAAYGE	GNERRLTGRH	ETADINTFLW	GVANRGASIR	VGRETEQNGK	GYFEDRRPAS	NMDPYVVTAM	346
OsGS1;1	KSAI EKLKLR	HKEHISAYGE	GNERRLTGRH	ETADINTFSW	GVANRGASVR	VGRETEQNGK	GYFEDRRPAS	NMDPYIVTSM	346
SbGS1;1	KAAI EKLKLR	HKEHIAAYGE	GNERRLTGRH	ETADINTFSW	GVANRGASVR	VGRETEQNGK	GYFEDRRPAS	NMDPYVVTSM	346
HvGS1;1	VDAVEKLKLR	HKEHIAAYGE	GNERRLTGKH	ETADINTFSW	GVANRGASVR	VGRETEQNGK	GYFEDRRPAS	NMDPYVVTSM	346
BdGS1;1	VAAVEKLKLR	HKEHIAAYGE	GNERRLTGKH	ETADINTFSW	GVANRGASVR	VGRETEQNGK	GYFEDRRPAS	NMDPYVVTAM	346
NnGLN1;1	KKAI EKLGLR	HKEHISAYGE	GNERRLTGRH	ETADINTFVW	GVANRGASIR	VGRDTERAGK	GYFEDRRPAS	NMDPYVVTSM	346
NnGLN1;2	KKAI EKLGLR	HKEHIAAYGE	GNERRLTGRH	ETADINTFAW	GVANRGASIR	VGRDTERAGK	GYFEDRRPAS	NMDPYVVTSM	346
NnGLN1;3	KKAI EKLGLR	HKEHISAYGE	GNERRLTGRH	ETADINTFSW	GVANRGASIR	VGRDTEKAGK	GYFEDRRPAS	NMDPYVVTSM	346
OsGS1;2	KKAI EKLGLR	HKEHIAAYGE	GNERRLTGRH	ETADINTFKW	GVANRGASIR	VGRDTEKAGK	GYFEDRRPAS	NMDPYVVTGM	346
SbGS1;2	KKAI EKLGLR	HTEHIAAYGE	GNERRLTGRH	ETADINTFKW	GVANRGASIR	VGRDTEREGK	GYFEDRRPAS	NMDPYVVTGM	346
BdGS1;2	KKAI EKLGLR	HTEHIAAYGE	GNERRLTGHH	ETADINTFKW	GVANRGASIR	VGRDTEKD GK	GYFEDRRPAS	NMDPYVVTSM	346
HvGS1;2	KKAI EKLGLR	HMQHIAAYGE	GNERRLTGHH	ETADINTFKW	GVADRGASIR	VGRDTEKD GK	GYFEDRRPAS	NMDPYVVTSM	346
AtGLN1;1	KKAI EKLGLR	HKEHIAAYGE	GNERRLTGHH	ETADINTFLW	GVANRGASIR	VGRDTEKEGK	GYFEDRRPAS	NMDPYIVTSM	346
AtGLN1;2	KKAI EKLGLR	HKEHISAYGE	GNERRLTGHH	ETADINTFLW	GVANRGASIR	VGRDTEKEGK	GYFEDRRPAS	NMDPYVVTSM	346
AtGLN1;4	KKAI EKLGLR	HKEHIAAYGE	GNERRLTGKH	ETADINTFLW	GVANRGASIR	VGRDTEQAGK	GYFEDRRPAS	NMDPYVTSM	346
AtGLN1;3	KKAI EKLGLR	HKEHIAAYGE	GNERRLTGKH	ETADINTFSW	GVANRGASVR	VGRDTEKEGK	GYFEDRRPAS	NMDPYVVTSM	346
SpGS1;2	KKAI EKLGLR	HKEHISAYGE	GNERRLTGHH	ETADINTFKW	GVANRGASIR	VGRDTEKEGK	GYFEDRRPAS	NMDPYVVTSM	346
OsGS1;3	KKAI EKLGLR	HREHIAAYGD	GNERRLTGRH	ETADINNFVW	GVANRGASVR	VGRDTEKD GK	GYFEDRRPAS	NMDPYLV TAM	348
SbGS1;3	KKAI EKLGLR	HREHIAAYGD	GNERRLTGRH	ETADINTFIW	GVANRGASVR	VGRDTEKEGK	GYFEDRRPAS	NMDPYVVTSL	346
HvGS1;3	KRAI EKLGLR	HTEHIAAYGE	GNERRLTGRH	ETADINTFVW	GVANRGASVR	VGRDTEKEGR	GYFEDRRPAS	NMDPYVVTSM	346
BdGS1;3	KKAI EKLGLR	HGEHIAAYGE	GNERRLTGRH	ETADINTFVW	GVANRGASVR	VGRDTEKEGK	GYFEDRRPGS	NMDPYVVTSK	346
SpGS1;3	RRAI EKLGLR	HMEHIAAYGD	GNERRLTGRH	ETADINTFSW	GIADRGASVR	VGRETEMAGN	GYFEDRRPAS	NMDPYVVTSM	346
AtGS1;5	KEAI EKLGLR	HKEHIAAYGE	GNERRLTGKH	ETADINTFSW	GVADRGASVR	VGRDTEKEGK	GYFEDRRPSS	NMDPYLV TAM	346
SpGS2	KKAVGNLALR	HKEHISAYGE	GNERRLTGKH	ETADINTFSW	GVANRGCSVR	VGRETERQ GK	GYLEDRRPAS	NMDPYVVTSL	400
NnGS2	KKAI EKLGLR	HKEHISAYGE	GNERRLTGKH	ETADINTFSW	GVANRGCSIR	VGRDTEKQ GK	GYLEDRRPAS	NMDPYVVTSL	406
AtGS2	KKAI EKLGLR	HKEHISAYGE	GNERRLTGKH	ETASIDQFSW	GVANRGCSIR	VGRDTEAK GK	GYLEDRRPAS	NMDPYIVTSL	404
OsGS2	KKAI EKLGLR	HDLHISAYGE	GNERRLTGLH	ETASIDNF SW	GVANRGCSIR	VGRDTEAK GK	GYLEDRRPAS	NMDPYVVTAL	402
SbGS2	KRAI EKLGLR	HDLHISAYGE	GNERRLTGKH	ETASIDTFSW	GVANRGCSVR	VGRDTEAK GK	GYLEDRRPAS	NMDPYIVTGL	471
HvGS2	KKAI EKLGLR	HDLHIAAYGE	GNERRLTGLH	ETASIDFSW	GVANRGCSIR	VGRDTEAK GK	GYLEDRRPAS	NMDPYVTAL	408
BdGS2	KKAI EKLGLR	HDLHISAYGE	GNERRLTGLH	ETASIDFSW	GVANRGCSIR	VGRDTEANGK	GYLEDRRPAS	NMDPYVTAL	404
Consensus	KKAI EKLGLR	HKEHIAAYGE	GNERRLTGRH	ETADINTFSW	GVANRGASIR	VGRDTEKEGK	GYFEDRRPAS	NMDPYVVTSM	

500				
SpGS1;1	I A E T T I L W K P	-----	-----	356
OsGS1;1	I A E T T I I W K P	-----	-----	356
SbGS1;1	I A D T T I L W K P	-----	-----	356
HvGS1;1	I A E T T I L W K P	-----	-----	356
BdGS1;1	I A D T T I L W K P	-----	-----	356
NnGLN1;1	I A E T T I L W K P	-----	-----	356
NnGLN1;2	I A E T T I L W K P	-----	-----	356
NnGLN1;3	I A E T T I L W N P	-----	-----	356
OsGS1;2	I A E T T L L W K Q	N-----	-----	357
SbGS1;2	I A E T T I L W N G	N-----	-----	357
BdGS1;2	I A E T T L L L - -	-----	-----	354
HvGS1;2	I A E T T L L L - -	-----	-----	354
AtGLN1;1	I A E T T I L W N P	-----	-----	356
AtGLN1;2	I A E T T L L W N P	-----	-----	356
AtGLN1;4	I A E S T I L W K P	-----	-----	356
AtGLN1;3	I A E T T I L G - -	-----	-----	354
SpGS1;2	I A E T T I L W K P	T-----	-----	357
OsGS1;3	I A E T T I L W E P	S H G H G H G Q S N	G K-----	370
SbGS1;3	I A E T T I L W E P	S H S N G K G A A A	P-----	367
HvGS1;3	I A E T T I L W K A	G L S N G K - - - -	-----	362
BdGS1;3	I A E T T I L W E P	N L S N G E - - - -	-----	362
SpGS1;3	I A E T T I L W K P	-----	-----	356
AtGS1;5	I A E T T I L - - -	-----	-----	353
SpGS2	L A E T T I L W E P	T V E S - - A A A Q	K V Q L E V	424
NnGS2	L A E T T I L W E P	T L E A E A L A A Q	K L S L K V	432
AtGS2	L A E T T L L W E P	T L E A E A L A A Q	K L S L N V	430
OsGS2	L A E T T I L W E P	T L E A E V L A A K	K L A L K V	428
SbGS2	L A E T T I L W Q P	T L E A E V L A A K	K L A L K V	497
HvGS2	L A E T T I L W E P	T L E A E A L A A K	K L A L K V	434
BdGS2	L A E T T L L W E P	T L E A E V L A A K	K L A L K V	430
Consensus	I A E T T I L W K P	-----	-----	

B

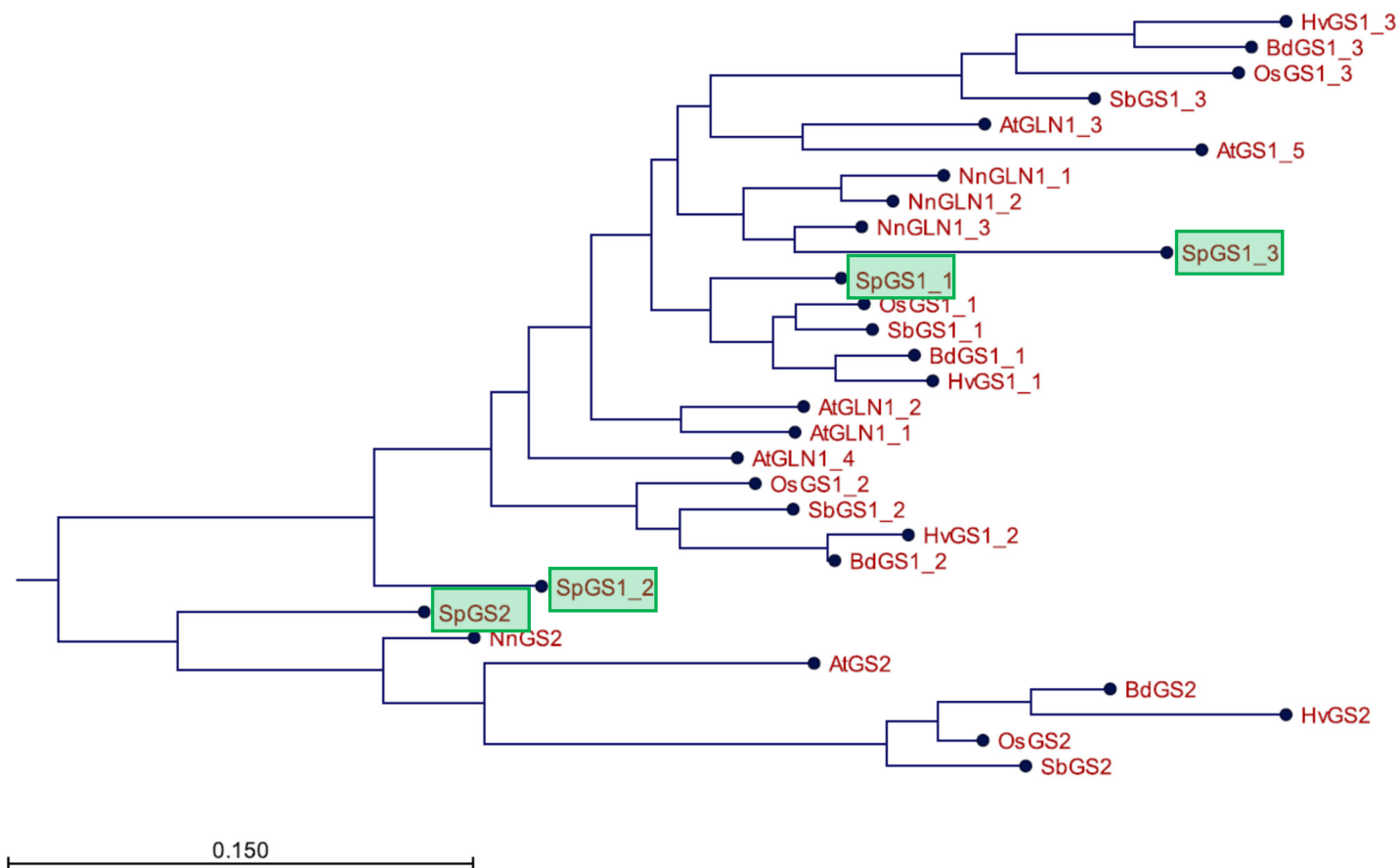


Figure S9. Sequence alignment of GS proteins from *S. polyrhiza* with other representative species (A) and the resulted phylogenetic tree (B). AtGln1;1 – *A. thaliana*, NP_198576.1, AtGln1;2 – *A. thaliana*, NP_176794.1, AtGln1;3 – *A. thaliana*, NP_188409.1; AtGln1;4 – *A. thaliana*, NP_001331815.1; AtGln1;5 – *A. thaliana*, NP_175280.1; AtGS2 – *A. thaliana*, NP_001031969.1; BdGS1;1 – *B. distachyon*, XP_010236151.1, BdGS1;2 – *B. distachyon*, XP_003558466.1, BdGS1;3 – *B. distachyon*, XP_003560727.2, BdGS2 – *B. distachyon*, XP_003580719.1, HvGS1;1 – *H. vulgare*, AFX60875.1; HvGS1;2 – *H. vulgare*, AFX60876.1, HvGS1;3 – *H. vulgare*, AFX60877.1, HvGS2 – *H. vulgare*, P13564.2, NnGS1;1 – *N. nucifera*, XP_010271383.1, NnGS1;2 – *N. nucifera*, XP_010271347.1; NnGS1;3 – *N. nucifera*, XP_010250142.1, NnGS2 – *N. nucifera*, XP_010255852.1, OsGS1;1 – *O. sativa*, XP_015626102.1, OsGS1;2 – *O. sativa*, XP_015631679.1, OsGS1;3 – *O. sativa*, XP_015628694.1, OsGS2 – *O. sativa*, XP_015635322.1, SbGS1;1 – *S. bicolor*, XP_021313946.1, SbGS1;2 – *S. bicolor*, XP_002465624.1, SbGS1;3 – *S. bicolor*, XP_021306978.1,

SbGS2 - *S. bicolor*, XP_021319069.1, SpGS1;1 - *S. polyrhiza* (sequence translated from Acc. ID MZ605906) , SpGS1;2 - *S. polyrhiza* (sequence translated from Acc. ID MZ605907); SpGS1;3 - *S. polyrhiza* (sequence translated from Acc. ID MZ605908), SpGS2 - *S. polyrhiza* (sequence translated from Acc. MZ605909)

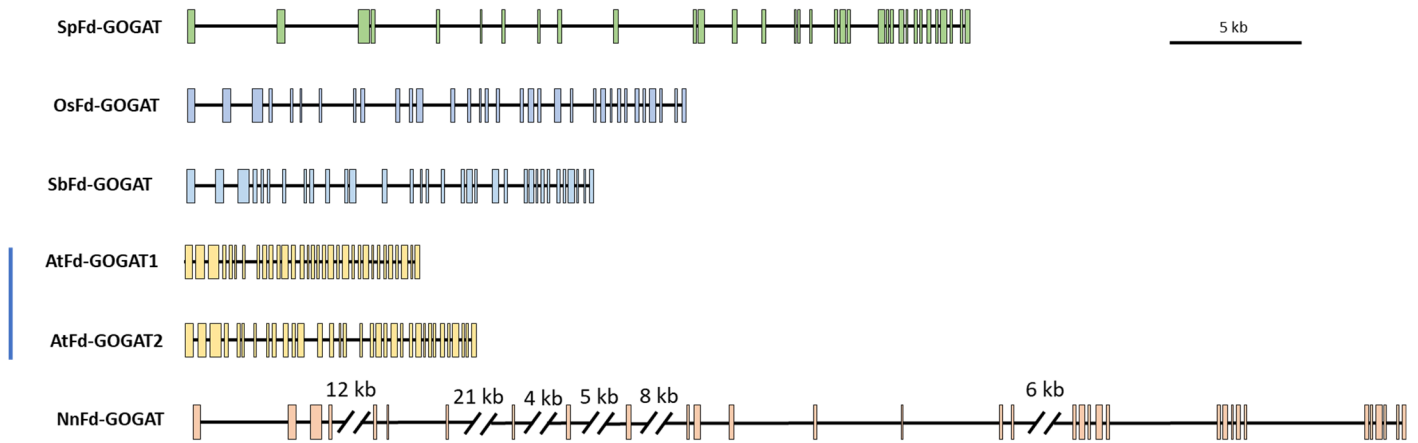


Figure S10. Diagrammatic representation of the structure of *Fd-GOGAT* genes.

At Fd-GOGAT1 - *A. thaliana*, At5g04140, *AtFd-GOGAT2* - *A. thaliana*, At2g41220, *NnFd-GOGAT* - *N. nucifera*, LOC104611350, *OsFd-GOGAT* - *O. sativa*, LOC4344164, *SbFd-GOGAT* - *S. bicolor*, LOC8073135, *SpFd-GOGAT* - *S. polyrhiza* CP019094, the 1st chromosome, position from 4454784 to 4484474. Coding sequences are colored boxes. Introns are black lines. The bar is 5 kb.

A

SpFd-GOGAT	MAQSAAA--A	AAVSAAPRAL	LPSPTANSDS	-----A	FFSRNRSLLL	RQ-----RS	IVVHRRLL-CG	A---GRG-SR	58
OsFd-GOGAT	MATLPRAAAA	AAPSPA--AL	LPLPRAAP--	LLAGR--AA	ARSAARRLRA	R---GTRAPP	LAAARRGW--	-----GGV-S-	63
BdFd-GOGAT	-----MAAT	LPRVAPPSL	LPLPRAAP--	-----LLLA	GRAAARRLRA	R---GARAPA	LAAARRSWAV	-----S-	54
SbFd-GOGAT	MATLPRAAP-	--PTPAA--L	LPLPRAAPPL	LLAGR--AA	AARRSR-LRA	R---G---P	SAAARRSWVV	ASSSSSS-S-	62
AtFd-GOGAT1	-----MAM	QSLSPVPKLL	STTPSS--	-----	VLSSDKNFFF	VDFVGLYCKS	KRTRRRLRGD	SSSSSR-S-	58
AtFd-GOGAT2	-----MA	LQSPGATGAS	SSVSRLLSA	-----	KLSSSTKTIFS	VDFVRSYCIS	KGTKR--N	ELSGFRGYSP	59
NnFdGOGAT	-----MAL	QSVPMPLQL	YSNGFSSTTS	LSATK--SS	IFDANRGLLF	ADFI GLCCKS	KRTRQRIGIG	AVRRGRG-S-	68
Consensus	-----AAAA	XXPSPAP-XL	LPLPRAAP-S	L-A-R--XA	AXSAXRRLRA	RD--GLXCXS	KAXARRXW-X	A-S-GRG-S-	
SpFd-GOGAT	LLPSMPRSVR	VGAHQREGTC	SVGNSKQTVS	S-----	-----RARRS	K-----	-VADLNDILS	ERGACGVGF I	114
OsFd-GOGAT	-----PRAVL	DLPRRREAA-	--EKPAQKA-	-----	-----	-----	--ADLNEILS	ERGACGVGF V	102
BdFd-GOGAT	-----TRAVL	DVPRHRAPP	A-QKPQVEA-	-----	-----	-----	--ADLNDILA	ERGACGVGF V	95
SbFd-GOGAT	-----SRAVL	GGVARREAPP	APQKPTQQA-	-----	-----	-----	--ADLNHILS	ERGACGVGF V	104
AtFd-GOGAT1	SLSRLS-SVR	AVIDLERVHG	VSEKDLSSPS	ALRPQVRFFT	DINFTNTQRA	KFHPWLWGSFK	QVANLEDI LS	ERGACGVGF I	137
AtFd-GOGAT2	LLKSSLRSPF	SVKAILNSDR	AAGDASSSPS	DLKP--	-----	-----	QVAYLEDI LS	ERGACGVGF I	113
NnFdGOGAT	-LGRSWSSVK	AVLDVNRVDF	A-----SKES	D-----	-----TVRRA	E-----N	EVANLNDI LS	ERGACGVGF I	120
Consensus	-L--XRSVL	XVPXRREXP	A-XKPQXAS	-----	-----	-----	-VADLNDILS	ERGACGVGF I	
SpFd-GOGAT	ANLKNEASHK	IVEDALVALG	CMEHRGGCGA	DNDSDGAGL	MTSPVWDLYN	NWADKQGLPF	LDTRYKTGVM	VFLPQSDAM	194
OsFd-GOGAT	ANLKNEPSFN	IVRDALVALG	CMEHRGGCGA	DNDSDGSGSL	MSGIPWDLFN	DWANKQGLAP	LDRTNTGVM	VFLPQDENSM	182
BdFd-GOGAT	ANLKNEPSFN	IVRDALTALG	CMEHRGGCGA	DNDSDGAGL	MSGIPWDLFN	DWASKQGLPP	FERTNTGVM	VFLPQNEESM	175
SbFd-GOGAT	ANLKNVPSFN	IVRDALMALG	CMEHRGGCGA	DNDSDGAGL	MSAIPWDLFD	DWANKQGLAP	FDRRTNTGVM	VFLPQDEKSM	184
AtFd-GOGAT1	ANLDNIPSHG	VVKDALIALG	CMEHRGGCGA	DNDSDGSGSL	MSSIPWDFFN	VWAKEQSLAP	FDKLHTGVM	IFLPQDDTFM	217
AtFd-GOGAT2	ANLENKATHK	IVNDALIALG	CMEHRGGCGS	DNTSDGSGSL	MTSIPWDLFN	EWAEKQGIAS	FDRTHTGVM	LFLPRDDNIR	193
NnFdGOGAT	ANLENNASHE	IKDALTALG	CMEHRGGCGA	DNDSDGSGSL	MTSIPWDLFN	NWANKQGIAS	LDKLHTGVM	VFLPKDDDSM	200
Consensus	ANLKNEPSHN	IVRDALXALG	CMEHRGGCGA	DNDSDGSGSL	MSSIPWDLFN	DWANKQGLAP	FDRTXTGVM	VFLPQDDXSM	
SpFd-GOGAT	EEAKKIVINT	CLKEGLEIVG	WRPVPVNESV	VGYAKETLP	NIQQLFVKVY	KEDNVDDLER	ELYICRKLIE	RAVQSEKWSN	274
OsFd-GOGAT	EEAKAVYAKV	FTDEGLEVLG	WRTPVPNVSF	VGRYAKETMP	NIQQIFVKVA	KEDNADDIER	ELYICRKLIE	RATKSASWAD	262
BdFd-GOGAT	EEAKAAVAKV	FTDEGLEVLG	WRPVPFNLSV	VGRFAKETMP	NIQQIFVKVA	KEDDADDIER	ELYICRKLIE	RAAKSASWAD	255
SbFd-GOGAT	EEAKAATEKV	FTDEGLEVLG	WRPVPFNVSF	VGRNAKETMP	NIQQIFVKVA	KEDNADDIER	ELYISRKLIE	RATKSFSWAD	264
AtFd-GOGAT1	QEAKQVNIENI	FEKEGLQVLG	WRPVPVNPVI	VGKNARETMP	NIQQVFVKIA	KEDSTDDIER	ELYICRKLIE	RAVATESWGT	297
AtFd-GOGAT2	KEAKKVITSI	FEKEGLEVLG	WRDVPVEASI	VGHNAKQTMP	NTEQVFVRIV	KDDKVDDVER	ELYICRKLIE	RAVASESWAS	273
NnFdGOGAT	KEAKSVIENT	FKQEGLDVLG	WRPVPINVAV	VGYAKETMP	NIQQVFVKIS	NEENIDDIER	ELYICRKLIE	RVSKLEKWGD	280
Consensus	EEAKAVIEXV	FXXEGLEVLG	WRPVPXNVSV	VGRXAKETMP	NIQQXFVKVA	KEDNADDIER	ELYICRKLIE	RAVKSESAD	
SpFd-GOGAT	DLYFCSFSNQ	TVVYKGMRLS	EVLGQFYLDL	QSDLYKSPFA	IYHRRYSTNT	SPRWPLAQPM	RLLGHNGEIN	TIQGNLNMWQ	354
OsFd-GOGAT	ELYFCSLSSR	TIVYKGMRLS	EILGQFYLDL	QNELYKSPFA	IYHRRYSTNT	SPRWPLAQPM	RLLGHNGEIN	TIQGNLNMWR	342
BdFd-GOGAT	ELYFCSLSSR	TIIYKGMRLS	EVLGQFYLDL	QNELYKSPFA	IYHRRYSTNT	SPRWPLAQPM	RLLGHNGEIN	TIQGNLNMWR	335
SbFd-GOGAT	ELYFCSLSNR	TIVYKGMRLS	EVLGQFYLDL	QNELYKSPFA	IYHRRYSTNT	SPRWPLAQPM	RLLGHNGEIN	TIQGNLNMWR	344
AtFd-GOGAT1	ELYFCSLSNQ	TIVYKGMRLS	EALGLFYLDL	QNELYKSPFA	IYHRRYSTNT	SPRWPLAQPM	RFLGHNGEIN	TIQGNLNMWQ	377
AtFd-GOGAT2	ELYFSSLSNQ	TIVYKGMRLS	EVLGLFYDPDL	QNELYKSPFA	IYHRRYSTNT	SPRWHLAQPM	RFLGHNGEIN	TIQGNLNMWT	353
NnFdGOGAT	ELYFCSLSNQ	TIVYKGMRLS	EVLGQFYSDL	QSDLYKSPFA	IYHRRYSTNT	SPRWPLAQPM	RLLGHNGEIN	TIQGNLNMWQ	360
Consensus	ELYFCSLSNQ	TIVYKGMRLS	EVLGQFYLDL	QNELYKSPFA	IYHRRYSTNT	SPRWPLAQPM	RLLGHNGEIN	TIQGNLNMWQ	
SpFd-GOGAT	SRETTIKSPV	WRGRENEIRP	YGNPKGSDSA	NLDSAAELL	RSGRSPAEL	MILVPEAYKK	HPTLSIKYPE	VIDFYDYKYG	434
OsFd-GOGAT	SREATLQSPV	WRGREHEIRP	FGDPKASDSA	NLDSTAELL	RSGRSPAEL	MILVPEAYKN	HPTLSIKYPE	VIDFYDYKYG	422
BdFd-GOGAT	SREATIQSPV	WRGRENEIRP	FGDPKASDSA	NLDNAELL	RSGRSPAEL	MMLVPEAYKN	HPTLSIKYPE	VIDFYDYKYG	415
SbFd-GOGAT	SRETTLQSPV	WRGREHEICP	FGDPKASDSA	NLDSTAELL	RSGRSPAEL	MILVPEAYKN	HPTLSIKYPE	VIDFYDYKYG	424
AtFd-GOGAT1	SREASLKAAV	WNGRENEIRP	FGNPRGSDSA	NLDSAAELMI	RSGRTPAEL	MILVPEAYKN	HPTLSVKYPE	VDFDYDYKYG	457
AtFd-GOGAT2	SREASLRSPV	WHGRENDIRP	ISNPKASDSA	NLDSAAELL	RSGRTPAEL	MILVPEAYKN	HPTLMIKYPE	AVDFDYDYKYG	433
NnFdGOGAT	SRETSLKSPV	WRGREDEICP	YGNPKASDSA	NLDSAAELL	RSGRSPAEL	MILVPEAYKN	HPTLMIKYPE	VDFDYDYKYG	440
Consensus	SREATLXSPV	WRGRENEIRP	FGNPKASDSA	NLDSAAELL	RSGRSPAEL	MILVPEAYKN	HPTLSIKYPE	VIDFYDYKYG	
SpFd-GOGAT	QMEAWDGPAL	LLFSDGKTVG	ACLDNRGLRP	ARYWRTVDV	VYVASEVGV	PMDESKITMK	GRLGPGMMIT	VDLQNGQVYE	514
OsFd-GOGAT	QMEAWDGPAL	LLFSDGRTVG	ACLDNRGLRP	ARYWRTSDV	VYVASEVGV	PMDESKVVMK	GRLGPGMMIT	VDLQTGQVLE	502
BdFd-GOGAT	QMEAWDGPAL	LLFSDGRTVG	ACLDNRGLRP	ARYWRTSDG	VYVASEVGV	PMDESKVVMK	GRLGPGMMIT	VDLQTGQVLE	495
SbFd-GOGAT	QMEAWDGPAL	LLFSDGRTVG	ATLDNRGLRP	ARYWRTSDV	VYVASEVGV	PMDESKVVMK	GRLGPGMMIT	VDLQTGQVLE	504
AtFd-GOGAT1	QMEAWDGPAL	LLFSDGKTVG	ACLDNRGLRP	ARYWRTSDNF	VYVASEVGV	PVDEAKVTMK	GRLGPGMMIA	VDLVNGQVYE	537
AtFd-GOGAT2	QMEPWDGPAL	VLFSDGKTVG	ACLDNRGLRP	ARYWRTSDNV	VYVASEVGV	PMDESKVTMK	GRLGPGMMIS	VDELNGQVYE	513
NnFdGOGAT	QMEAWDGPAL	LLFSDGKTVG	ACLDNRGLRP	ARYWRTVDNV	VYVASEVGV	PMDESRVTMK	GRLGPGMMIT	ADLLTGQVYE	520
Consensus	QMEAWDGPAL	LLFSDGKTVG	ACLDNRGLRP	ARYWRTSDXF	VYVASEVGVX	PMDESKVTMK	GRLGPGMMIT	VDLQTGQVYE	
SpFd-GOGAT	NTDVKKKVAS	AHPYQWLNE	NMRSMKPVNF	LSSPVMDEL	VLRHQQAQFY	SSDEVQMVE	TMASQGKEPT	FCMGDDIPLA	594
OsFd-GOGAT	NTEVKKKVAS	ANPYGSWLQ	STRSIKPVNF	QSSVAMDNET	VLRHQQAQFY	SSDEVQMVE	TMASQGKEPT	FCMGDDIPLA	582
BdFd-GOGAT	NTEVKKKVAS	AKPYGTWLQ	STRSIKPVNF	QSSPVMDET	VLRHQQAQFY	SSDEVQMVE	TMASQGKEPT	FCMGDDIPLA	575
SbFd-GOGAT	NTEVKKTVAL	ASPYGTWLQ	RTRSIKPVNF	LSTTIMDNET	VLRHQQAQFY	SSDEVQMVE	SMASQGKEPT	FCMGDDIPLA	584
AtFd-GOGAT1	NTEVKKRIS	FNYPGKWIKE	NSRFLKPVNF	KSSTVMNEE	ILRSQQAQFY	SSDEVQMVE	SMASQGKEPT	FCMGDDIPLA	617
AtFd-GOGAT2	NTEVKKRVAS	YNYPGKVVSE	NLRNLKPSNY	LSSAILETDE	TLRRQQAQFY	SSDEVQMVE	SMAAQGKEPT	FCMGDDTPVA	593
NnFdGOGAT	NTDVKKRVAL	SNYPGKWLSE	NMRTLKPVNF	LSASVMDKEI	ILRHQQAQFY	SSDEVQMVE	TMAAQGKEPT	FCMGDDIPLA	600
Consensus	NTEVKKRVAS	ANPYGKWLQ	NTRSXKPVNF	LSSXVMDNET	VLRHQQAQFY	SSDEVQMVE	TMASQGKEPT	FCMGDDIPLA	
SpFd-GOGAT	XLSQXPHMIY	DYFKQRFQAV	TNPAIDPLRE	GLVMSLEVN	GKRGNILEVG	PQNAQVILS	SPVLNEGELE	TLMKDTALTP	674
OsFd-GOGAT	VLSQKPHMLF	DYFKQRFQAV	TNPAIDPLRE	GLVMSLEVN	GKRGNILEVG	PENADQVTL	SPVLNEGELE	SLLNDSKLKP	662
BdFd-GOGAT	VLSQKPHMLF	DYFKQRFQAV	TNPAIDPLRE	GLVMSLEVN	GKRGNILEVG	PENADQVALS	SPVLNEGELE	SLLDKTKLP	655
SbFd-GOGAT	VLSQRPHELLY	DYFKQRFQAV	TNPAIDPLRE	GLVMSLEVN	GKRGNILEVG	PENADLVALS	SPVLNEGELE	TLLKDKPKLP	664
AtFd-GOGAT1	GLSQRPHELLY	DYFKQRFQAV	TNPAIDPLRE	GLVMSLEVN	GKRGNILEVG	PENASQVILS	NPVLNEGALE	ELMKDQYLKP	697
AtFd-GOGAT2	VLSQKPHMLY	DYFKQRFQAV	TNPAIDPLRE	GLVMSLEVN	GKRGNILEVG	PQNVSQVLS	GPVLNERELE	GLLGDPLLS	673
NnFdGOGAT	ALSQKPHMLF	DYFKQRFQAV	TNPAIDPLRE	GLVMSLEVN	GKRGNILEVG	PENASQVILS	SPVLNEGELE	LLMEDPYLKP	680
Consensus	VLSQKPHMLY	DYFKQRFQAV	TNPAIDPLRE	GLVMSLEVN	GKRGNILEVG	PENAXQVILS	SPVLNEGELE	XLLKDKPKLP	

		740		760		780		800	
SpFd-GOGAT	QVLPTFFD I G	KGIDGSLQKA	LEELCEAADE	AVRNGSQLL I	LSDRSEEL I EP	TRPAIPILLA	VGAVHQHL I Q	NGLRMSAS I V	754
OsFd-GOGAT	KVLSTYFD I R	KGLDGS LDKA	IKVLCD EADA	AVRNGSQLLV	LSDRSEALEP	TRPAIPILLA	VGAIHQHL I Q	NGLRMSAS I V	742
BdFd-GOGAT	TVLSTYFS I R	KGLDGS LDKA	IKALCEEADA	AVRSGSQLLV	LSDRSEALEP	TRPAIPILLA	VGAIHQHL I Q	NGLRMSAS I V	735
SbFd-GOGAT	KVLSTYFD I R	KGLDGS LDKT	IQALCEEADA	AVRSGSQLLV	LSDRSEALEP	TRPAIPILLA	VGAIHQHL I Q	NGLRMSAS I V	744
AtFd-GOGAT1	KVLSTYFD I R	KGVEGSLQKA	LYYLCEAA DD	AVRSGSQLLV	LSDRSDRL EP	TRPSIPIMLA	VGAVHQHL I Q	NGLRMSAS I V	777
AtFd-GOGAT2	QILPTFFD I R	RGIEGSLKKG	LLKLCEAADE	AVRNGSQLLV	LSDRSDNPEP	TRPAIPMLLA	VGAVHQHL I Q	NGLRMSAS I I	753
NnFdGOGAT	QVLPTFFD I R	KGLDGSLEKT	IKKLCEADA E	AVRNGSQLL I	LSDRSEEL EP	TRPAIPILLA	VGSVHQHL I Q	NGLRMSAS I V	760
Consensus	XVLSTYFD I R	KGLDGS LDKA	IKXLCEXAD X	AVRNGSQLLV	LSDRSEALEP	TRPAIPILLA	VGAVHQHL I Q	NGLRMSAS I V	
		820		840		860		880	
SpFd-GOGAT	ADTAQCFSTH	QFACL IGYGA	SAICPYLA FE	TCRQWRLSTK	TVNLMKNGKM	PTVTMEQCQR	NFSKAVK SGL	LKILSKMG I S	834
OsFd-GOGAT	ADTAQCFSTH	QFACL IGYGA	SAICPYLA FE	TCRQWRLSNK	TVNLMRNGKM	PTVTIEQAQR	NFIKAVK SGL	LKILSKMG I S	822
BdFd-GOGAT	ADTAQCFSTH	QFACL IGYGA	SAICPYLA FE	TCRQWRLSNK	TVNLMRNGKM	PTVTIEQAQR	NFIKAVK SGL	LKILSKMG I S	815
SbFd-GOGAT	ADTAQCFSTH	HFACL IGYGA	SAVCPYLA FE	TCRQWRLSNK	TVNLMRNGKM	PTVTIEQAQR	NFTKAVK LGL	LKILSKMG I S	824
AtFd-GOGAT1	ADTAQCFSTH	HFACL VGYGA	SAVCPYLA FE	TCRQWRLSNK	TVAFMRNGK I	PTVTIEQAQK	NYTKAVNAGL	LKILSKMG I S	857
AtFd-GOGAT2	ADTAQCFSTH	HFACL IGYGA	SAICPHLA FE	TCRQWRLSNK	TVNMMRNGKM	PTVTMEQAQK	NYRKAVNTGL	LKVL SKMG I S	833
NnFdGOGAT	ADTAQCFSTH	QFACL IGYGA	SAVCPYLA FE	TCRQWRLSTK	TVNLMRNGKM	PTVTMEQAQR	NFKAVK SGL	LKILSKMG I S	840
Consensus	ADTAQCFSTH	QFACL IGYGA	SAICPYLA FE	TCRQWRLSNK	TVNLMRNGKM	PTVTIEQAQR	NFXKAVK SGL	LKILSKMG I S	
		900		920		940		960	
SpFd-GOGAT	LLSSYCGAQ I	FEIYGLGHD I	VDAFCGSVS	KIGGLNFDEL	ARETLSFWVK	AFSEDTAKRL	ENFGFIQFRP	GGEYHGNPQ	914
OsFd-GOGAT	LLSSYCGAQ I	FEIYGLGQEV	VDAFCGSVS	KIGGLTLDEL	GRETLSFWVK	AFSEDTAKRL	ENFGFIQSRP	GGEYHANNPE	902
BdFd-GOGAT	LLSSYCGAQ I	FEIYGLGQEV	VDAFCGSVS	KIGGLTLDEL	GRETLSFWVK	AFSEDTAKRL	ENFGFIQSRP	GGEFHANNPE	895
SbFd-GOGAT	LLSSYCGAQ I	FEIYGLGQEV	VDAFCGSVS	KIGGLTLDEL	GRETLSFWVK	AFSEDTAKRL	ENFGFIQSRP	GGEYHANNPE	904
AtFd-GOGAT1	LLSSYCGAQ I	FEIYGLGQDV	VDAFTGGSVS	KISGLTFDEL	ARETLSFWVK	AFSEDTTKRL	ENFGFIQFRP	GGEYHNNPPE	937
AtFd-GOGAT2	LFSSYCGAQ I	FEIYGLGNEV	VEFSFRGSAS	KIGGLTLDEL	ARETLTFWVR	AFSEDTAKRL	ENFGFIQFRP	GGEYHGNPPE	913
NnFdGOGAT	LLSSYCGAQ I	FEIYGLGKDI	VDAFCGSVS	NIGGLTLDEL	ARETLSFWVK	AFSEDTAKRL	ENFGFIQFRP	GGEYHGNPPE	920
Consensus	LLSSYCGAQ I	FEIYGLGQEV	VDAFCGSVS	KIGGLTLDEL	ARETLSFWVK	AFSEDTAKRL	ENFGFIQFRP	GGEYHNNPPE	
		980		1,000		1,020		1,040	
SpFd-GOGAT	MSKLLHKA VR	QKSESA YAVY	QQHLASRPVS	VLRDLLEFKS	DRAPIPVGKV	EPASSIVORF	CTGGMSLGA I	SRETHEA I A I	994
OsFd-GOGAT	MSKLLHKA VR	EKSDNAYTVY	QQHLASRPVN	VLRDLLELKS	DRAPIPIGKV	EPATSI VERF	CTGGMSLGA I	SRETHEA I A I	982
BdFd-GOGAT	MSKLLHKA I R	EKSDNAYTIY	QQHLASRPVN	VLRDLVELKS	DRAPIPIGKV	EPATSI VERF	CTGGMSLGA I	SRETHEA I A I	975
SbFd-GOGAT	MTKLLHKA I R	EKRDNAYTVY	QQHLASRPVN	VLRDLLELKS	DRAPIPIGKV	EPATSI VERF	CTGGMSLGA I	SRETHEA I A I	984
AtFd-GOGAT1	MSKLLHKA VR	EKSETAYAVY	QQHLASRPVN	VLRDLLEFKS	DRAPIPVGKV	EPAVAI VORF	CTGGMSLGA I	SRETHEA I A I	1017
AtFd-GOGAT2	MSKLLHKA VR	EKSETAYAVY	QQHLANRPIT	VFRDLLEFKS	DRNP IPVGKV	EPASSI VERF	CTGGMSLGA I	SRETHEA I A I	993
NnFdGOGAT	MSKLLHKA VR	QKNESVYSIY	QQHLANRPVN	VLRDLLEFKS	DRPPIPVGKV	ESAA SI VORF	CTGGMSLGA I	SRETHEA I A I	1000
Consensus	MSKLLHKA VR	EKSENAYXVY	QQHLASRPVN	VLRDLLEFKS	DRAPIPVGKV	EPATSI VERF	CTGGMSLGA I	SRETHEA I A I	
		1,060		1,080		1,100		1,120	
SpFd-GOGAT	AMNRLGGKSN	SGEGGEDP I R	WNPLTDVTDG	YSPTLPHLKG	LQNGDTATSA	IKQVASGRFG	VTPTFLVNAD	QLEIK I AQGA	1074
OsFd-GOGAT	AMNR IGGKSN	SGEGGEDP I R	WSPLADVEDG	YSPTLPHLKG	LQNGDTATSA	IKQVASGRFG	VTPTFLVNAE	QIEIK I AQGA	1062
BdFd-GOGAT	AMNR IGGKSN	SGEGGEDP I R	WSPLADVDDG	YSPTLPHLKG	LQNGDTATSA	IKQVASGRFG	VTPTFLVNAE	QIEIK I AQGA	1055
SbFd-GOGAT	AMNR IGGKSN	SGEGGEDP I R	WNPLTDVVDDG	YSPTLPHLKG	LQNGDTATSA	IKQVASGRFG	VTPTFLVNAN	QIEIK I AQGA	1064
AtFd-GOGAT1	AMNR IGGKSN	SGEGGEDP I R	WKPLTDVVDDG	YSPTLPHLKG	LQNGDIATSA	IKQVASGRFG	VTPTFLVNAD	QLEIKVAQGA	1097
AtFd-GOGAT2	AMNRLGGKSN	SGEGGEDP I R	WKPLTDVVDDG	YSSTLPHLKG	LQNGDTATSA	IKQVASGRFG	VTPTFLVNAD	QLEIKVAQGA	1073
NnFdGOGAT	AMNRLGGKSN	SGEGGEDP I R	WSPLTDVVDDG	YSPTLPHLKG	LQNGDTATSA	IKQVASGRFG	VTPTFLVNAD	QLEIK I AQGA	1080
Consensus	AMNR IGGKSN	SGEGGEDP I R	WSPLTDVVDDG	YSPTLPHLKG	LQNGDTATSA	IKQVASGRFG	VTPTFLVNAD	QLEIK I AQGA	
		1,140		1,160		1,180		1,200	
SpFd-GOGAT	KPGEGGQLPG	KKVSAYIARL	RNSKPGVPLI	SPPPHHDIYS	IEDLAQLIYD	LHQVNP KAKV	SVKLVAEAGI	GTVASGVAKG	1154
OsFd-GOGAT	KPGEGGQLPG	KKVSAYIARL	RNSKPGVPLI	SPPPHHDIYS	IEDLAQLIYD	LHQINPKAKV	SVKLVAEAGI	GTVASGVSKG	1142
BdFd-GOGAT	KPGEGGQLPG	KKVSAYIARL	RNSKPGVPLI	SPPPHHDIYS	IEDLAQLIYD	LHQINPKAKV	SVKLVAEAGI	GTVASGVSKA	1135
SbFd-GOGAT	KPGEGGQLPG	KKVSAYIARL	RNSKPGVPLI	SPPPHHDIYS	IEDLAQLIYD	LHQINPKAKV	SVKLVSEAGI	GTVASGVSKG	1144
AtFd-GOGAT1	KPGEGGQLPG	KKVSAYIARL	RSSKPGVPLI	SPPPHHDIYS	IEDLAQLIYD	LHQINPNKAV	SVKLVAEAGI	GTVASGVAKG	1177
AtFd-GOGAT2	KPGEGGQLPG	KKVSAYIARL	RNSKPGVPLI	SPPPHHDIYS	IEDLAQLIYD	LHQVNP KAKV	SVKLVSETGI	GTVASGVAKG	1153
NnFdGOGAT	KPGEGGQLPG	KKVSAYIARL	RNSKPGVPLI	SPPPHHDIYS	IEDLAQLIYD	LHQVNP KAKV	SVKLVAEAGI	GTVASGVAKG	1160
Consensus	KPGEGGQLPG	KKVSAYIARL	RNSKPGVPLI	SPPPHHDIYS	IEDLAQLIYD	LHQINPKAKV	SVKLVAEAGI	GTVASGVAKG	
		1,220		1,240		1,260		1,280	
SpFd-GOGAT	NADI I Q I SGH	DGGTGASPI S	SIKHAGGPWE	LGLAETHQTL	IANGLRERV I	LRVDGGFKSG	VDVLMAA SMG	ADEYGFGSVA	1234
OsFd-GOGAT	NADI I Q I SGH	DGGTGASPI S	SIKHAGGPWE	LGLSETHQTL	IQNGLRERVV	LRVDGGFRSG	LDVLMAAAMG	ADEYGFGSVA	1222
BdFd-GOGAT	NADVIQ I SGH	DGGTGASPI S	SIKHAGGPWE	LGLTETHQTL	IQNGLRERVV	LRVDGGFRSG	LDVLLAAAMG	ADEYGFGSVA	1215
SbFd-GOGAT	NADI I Q I SGH	DGGTGASPI S	SIKHAGGPWE	LGLTETHQTL	IQNGLRERVV	LRVDGGFRSG	RDVLMAAAMG	ADEYGFGSVA	1224
AtFd-GOGAT1	NADI I Q I SGH	DGGTGASPI S	SIKHAGGPWE	LGLTETHQTL	IANGLRERV I	LRVDGGGLKSG	VDVLMAAAMG	ADEYGFGLSA	1257
AtFd-GOGAT2	NADI I Q I SGY	DGGTGASPI S	SIKHAGGPWE	LGLAETQKTL	IANGLRERV I	LRVDGGFKSG	VDVLI AAAMG	ADEYGFGLTA	1233
NnFdGOGAT	NADI I Q I SGH	DGGTGASPI S	SIKHAGGPWE	LGLTETHQTL	IENGLRERV I	LRVDGGFKSG	VDVLMAAAMG	ADEYGFGSVA	1240
Consensus	NADI I Q I SGH	DGGTGASPI S	SIKHAGGPWE	LGLTETHQTL	IQNGLRERV I	LRVDGGFKSG	VDVLMAAAMG	ADEYGFGSVA	
		1,300		1,320		1,340		1,360	
SpFd-GOGAT	MIATGCVMAR	ICHTNNCPVG	VASQREELRA	RFPGVPGDLV	NYFLYVAEEV	RGILAQLGYE	KMDDVI GRTD	LLRPRHVS L M	1314
OsFd-GOGAT	MIATGCVMAR	ICHTNNCPVG	VASQREELRA	RFPGVPGDLV	NYFLFVAEEV	RATLAQLGFE	KLDDI I GRTD	ILKAKHVS L A	1302
BdFd-GOGAT	MIATGCVMAR	ICHTNNCPVG	VASQREELRA	RFPGVPGDLV	NYFLFVAEEV	RATLAQLGYE	KLDDI TGRD	LLKPKHVS L V	1295
SbFd-GOGAT	MIATGCVMAR	ICHTNNCPVG	VASQREELRA	RFPGVPGDLV	NYFLFVAEEV	RATLAQLGYE	KLDDVI GRTD	LLKPKHVS L V	1304
AtFd-GOGAT1	MIATGCVMAR	ICHTNNCPVG	VASQREELRA	RFPGVPGDLV	NYFLYVAEEV	RGILAQLGYN	SLDDI I GRTE	LLRPDI S L V	1337
AtFd-GOGAT2	MIATGCI MAR	ICHTNNCPVG	VASQREELRA	RFPGLPGDLV	NFFLYIAEEV	RGILAQLGYE	KLDDI I GRTD	LLKARDI S L V	1313
NnFdGOGAT	MIATGCVMAR	ICHTNNCPVG	VASQREELRA	RFPGVPGDLV	NYFMFVAEEV	RGILAQLGYE	KMDDI I GRTD	ILRPNI S L V	1320
Consensus	MIATGCVMAR	ICHTNNCPVG	VASQREELRA	RFPGVPGDLV	NYFLYVAEEV	RGILAQLGYE	KLDDI I GRTD	LLKPRHVS L V	
		1,380		1,400		1,420		1,440	
SpFd-GOGAT	KTQQIDL SYL	LSSVGLPKWS	STEIRNQPVH	TNGPVLD DVL	LSDPEI TEA I	EKEKVVNKTI	KIYNVDRAVC	GR IAGV IAKK	1394
OsFd-GOGAT	KTQHIDL KYL	LSSAGLPKWS	SSQIRSQDVH	SNGPVLD ETL	LADPD I SDAI	ENEKEVSKTF	KIYNVDRAVC	GRVAGV IAKK	1382
BdFd-GOGAT	KTQHIDL GYL	LMNSGLPKWS	SSQIRSQDVH	SNGPVLD ETL	LADPEVSDAI	ENEKEVSKTF	KIYNVDRAVC	GRVAGV IAKK	1375
SbFd-GOGAT	KTQHIDL GYL	LSNAGLPKWS	SSQIRSQDVH	TNGPVLD ETL	LADPEI ADI A	ENEKEVSKTF	KIYNVDRAVC	GRVAGV IAKK	1384
AtFd-GOGAT1	KTQHL DLSYL	LSSVGTSPLS	STEIRKQEVH	TNGPVLDDDI	LADPLV IDAI	ENEKVVEKTV	KIYNVDRAVC	GRVAGV IAKK	1417
AtFd-GOGAT2	KT - HLDLSYL	LSSVGLPKRS	STSIRKQEVH	SNGPVLD DTL	LQDPEI MDAI	ENEKTVHKTM	KIYNVDRSVC	GR IAGV IAKK	1392
NnFdGOGAT	KTQHL DLSYI	LSSVGLPKLS	STKIRNQDVH	TNGPVLD DVI	LSDPEI SDAI	ENEKVVNKTI	KIYNVDRAVC	GR IAGV VAKK	1400
Consensus	KTQHIDL SYL	LSSVGLPKWS	STQIRSQDVH	TNGPVLD DTL	LADPEI SDAI	ENEKXVSKTF	KIYNVDRAVC	GRVAGV IAKK	

		1,460		1,480		1,500		1,520	
SpFd-GOGAT	YGD	TGFAGQL	NITFMGSAGQ	SFGCFLTPGM	NIRLVGEAND	YVGKGMAGGE	LVLTPPENFG	FCPEEATIVG	NTCLYGATGG 1474
OsFd-GOGAT	YGD	TGFAGQL	NITFTGSAGQ	SFGCFLTPGM	NIRLVGEAND	YVGKGMAGGE	LVVVPVEKTG	FVPEDAAIVG	NTCLYGATGG 1462
BdFd-GOGAT	YGD	TGFAGQL	NITFTGSAGQ	SFGCFLTPGM	NVRLVGEAND	YVGKGMAGGE	LVVVPVDDTG	FVPEEAAIVG	NTCLYGATGG 1455
SbFd-GOGAT	YGD	TGFAGQL	NITFNGSAGQ	SFGCFLTPGM	NIRLVGEAND	YVGKGMAGGE	LVVVPVDKTG	FVPEDATIVG	NTCLYGATGG 1464
AtFd-GOGAT1	YGD	TGFAGQV	NLTFLGSAGQ	SFGCFLIPGM	NIRLIGESND	YVGKGMAGGE	IVVTPVEKIG	FVPEEATIVG	NTCLYGATGG 1497
AtFd-GOGAT2	YGD	TGFAGQL	NLTFTGSAGQ	SFACFLTPGM	NIRLVGEAND	YVGKGMAGGE	VVILPVESTG	FRPEDATIVG	NTCLYGATGG 1472
NnFdGOGAT	YGD	TGFAGQL	NITFTGSAGQ	SFACFLTPGM	NIRLIGEAND	YVGKSMAGGE	LVVTPVENTG	FCPEDATIVG	NTCLYGATGG 1480
Consensus	YGD	TGFAGQL	NITFTGSAGQ	SFGCFLTPGM	NIRLVGEAND	YVGKGMAGGE	LVVXPVEKTG	FVPEDATIVG	NTCLYGATGG
		1,540		1,560		1,580		1,600	
SpFd-GOGAT	QLF	VRGKAGE	RFAVRNSLTE	AVVEGTGDHC	CEYMTGGCVV	VLGKVGRNVA	AGMTGGLAYI	LDEDDTL LPK	VNREIVRMQR 1554
OsFd-GOGAT	QVF	VRGKTGE	RFAVRNSLQ	AVVEGTGDHC	CEYMTGGCVV	VLGKVGRNVA	AGMTGGLAYI	LDEDDTL LPK	VNKEIVKMQR 1542
BdFd-GOGAT	QVF	VRGKTGE	RFAVRNSLQ	AVVEGTGDHC	CEYMTGGCVV	VLGKVGRNVA	AGMTGGLAYI	LDEDDTL LPK	VNKEIVKMQR 1535
SbFd-GOGAT	QVF	VRGKAGE	RFAVRNSLCQ	AVVEGTGDHC	CEYMTGGCVV	VLGKAGR NVA	AGMTGGLAYI	LDEDDTL LPK	VNKEIVKMQR 1544
AtFd-GOGAT1	QIF	ARGKAGE	RFAVRNSLA	AVVEGTGDHC	CEYMTGGCVV	VLGKVGRNVA	AGMTGGLAYL	LDEDDTL LPK	INREIVKIQR 1577
AtFd-GOGAT2	LLF	VRGKAGE	RFAVRNSLAQ	AVVEGTGDHC	CEYMTGGCVV	ILGKVGRNVA	AGMTGGLAYI	LDEDDTL LPK	MNKEIVKIQR 1552
NnFdGOGAT	QVF	VRGKAGE	RFAVRNSLAQ	AVVEGTGDHC	CEYMTGGCVV	VLGKVGRNVA	AGMTGGLAYI	LDEDDTL LPK	VNKEIVKIQR 1560
Consensus	QVF	VRGKAGE	RFAVRNSLAQ	AVVEGTGDHC	CEYMTGGCVV	VLGKVGRNVA	AGMTGGLAYI	LDEDDTL LPK	VNKEIVKMQR
		1,620		1,640		1,660			
SpFd-GOGAT	VNAPV	GQMQL	KSLIEAHVEK	TGSTKGATIL	REWEAYLPLF	WQIVPPSEED	TPEASAEIQR	V-PT-K----	EMQSA---- 1623
OsFd-GOGAT	VNAPAGQMQL	KGLIEAYVEK	TGSEKGATIL	REWEAYLPLF	WQLVPPSEED	SPEACAEFER	VLAKQA---T	TVQSAK---	1615
BdFd-GOGAT	VNAPAGQMQL	KGLIEAYVEK	TGSVKGAKIL	SEWEAYLPLF	WQLVPPSEED	SPEACAEFER	VLARQA---T	AVQSAK---	1608
SbFd-GOGAT	VNAPAGQMQL	KSLIESYVEK	TGSEKGATIL	REWEAYLPLF	WQLVPPSEED	SPEACAEFER	VLAKQAKQAT	TQLSAK---	1620
AtFd-GOGAT1	VTAPAGELQL	KSLIEAHVEK	TGSSKGATIL	NEWKEYLPLF	WQLVPPSEED	TPEASAAAYVR	TSTGEV----	TFQSA----	1648
AtFd-GOGAT2	VTSPVGTQL	KSLIEAHVEK	TGSSKGAMIV	EEWDKYLAMF	WQLVPPSEED	TPEANSD--H	ILKTTTGDEE	QVSSTLAEK	1629
NnFdGOGAT	VNAPAGQIQL	KSLIEAHVEK	TGSNKGSAIL	KDWEAYLPLF	WQLVPPSEED	TPEACADFER	ISPGQV----	TLQKA----	1631
Consensus	VNAPAGQMQL	KSLIEAHVEK	TGSXKGATIL	REWEAYLPLF	WQLVPPSEED	TPEACAEFER	VLAXQA---T	TVQSAK---	

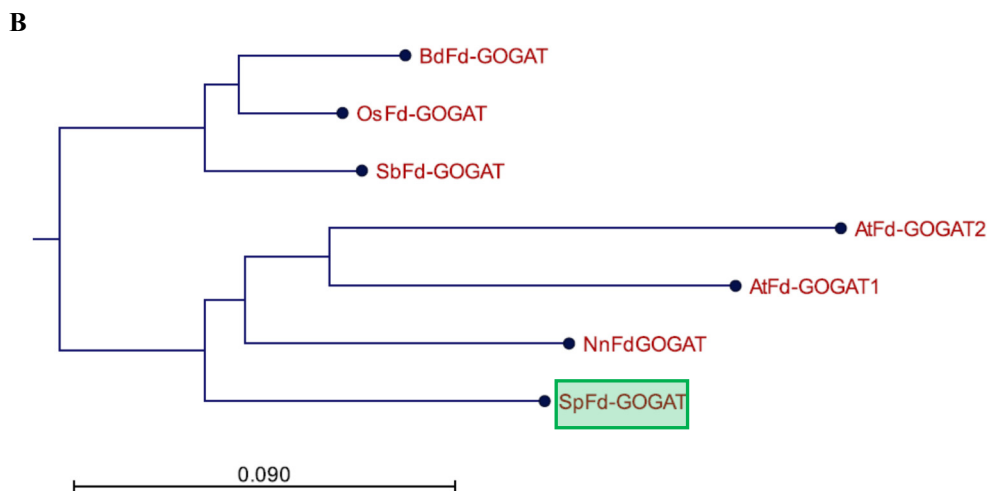


Figure S11. Sequence alignment of Fd-GOGAT protein from *S. polyrhiza* with other representative species **(A)** and the resulted phylogenetic tree **(B)**. AtFd-GOGAT1 - *A. thaliana*, NP_850763.1, AtFd-GOGAT2 - *A. thaliana*, NP_181655.1, BdFd-GOGAT - *B. distachyon*, XP_003559858.1, NnFd-GOGAT - *N. nucifera*, XP_010276670, OsFd-GOGAT - *O. sativa*, XP_015646712.1, SbFd-GOGAT - *S. bicolor*, XP_002463318.2, SpFdGOGAT - *S. polyrhiza* (sequence translated from Acc. ID MZ605910)

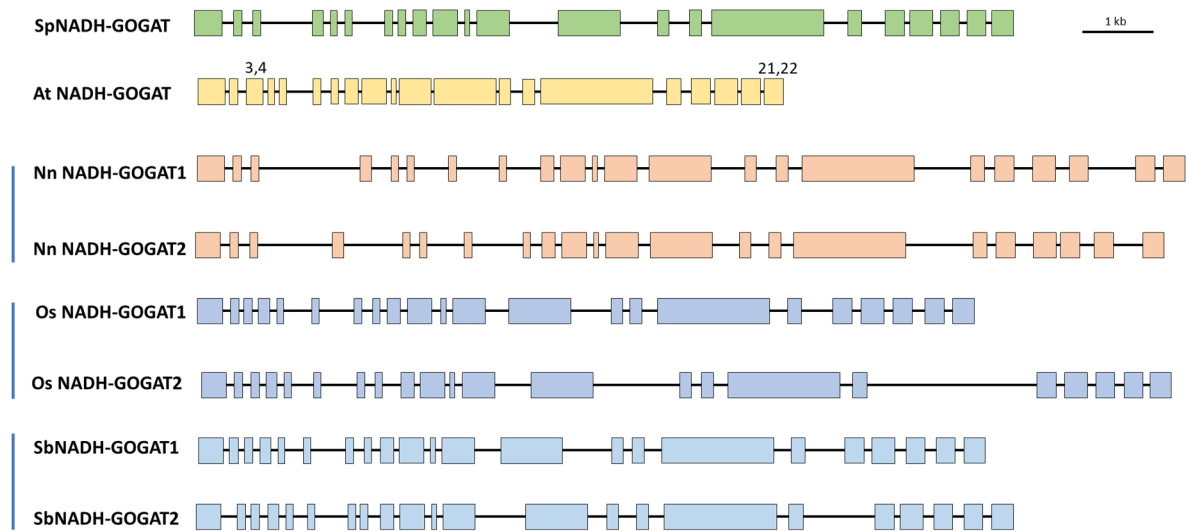


Figure S12. Diagrammatic representation of the structure of *NADH-GOGAT* genes. Coding sequences are colored boxes. Introns are black lines. The bar is 1 kb. *At NADH-GOGAT* - *A. thaliana*, At5g53460, *NnNADH-GOGAT1* - *N. nucifera*, LOC104600364, *NnNADH-GOGAT2* - *N. nucifera*, LOC104604004, *OsNADH-GOGAT1* - *O. sativa*, LOC4324398, *OsNADH-GOGAT2* - *O. sativa*, LOC4339561, *SbNADH-GOGAT1* - *S. bicolor*, LOC8068026, *SbNADH-GOGAT* - *S. bicolor*, LOC8074568, *SpNADH-GOGAT* - *S. polyrhiza* CP019094, the 8th chromosome, position from 4978991 to 4990379.

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				580				600					620					640	
SpNADH-GOGAT	CLEDVLSVSP	ETDRLSPPI	S	GVVQADSHDD	SMENVGVRL	LQPLKAFGYT	VEALEMLLP	MVKDATEALG	SMGNDTPLAV	633									
AINADH-GOGAT	ELKDIIESVP	EAEIRAPSI	S	GVVPAASND	SMESMGIHGL	LSPLKAFGYT	VEALEMLLP	MAKDGEALG	SMGNDTPLAV	630									
NnNADH-GOGAT1	ELKDIVDSVH	EADRVPPAIS	S	GSVPASSHDD	NMENMGIHGL	VAPLKAFGYT	VEALEMLLP	MAKDGEALG	SMGNDTPLAV	625									
NnNADH-GOGAT2	ELKDIVSVH	ESDRVPPAIS	S	GAVPASSHDD	NMENMGIHGL	LAPLKSFGYT	VEALEMLLP	MAKDGEALG	SMGNDTPLAV	625									
OsNADH-GOGAT1	YLKDIIVESVP	ETERVAPGIS	S	GSLTQKN--E	KKEHAGVNGI	VTPLKAFGYT	VEALEMLLP	MAKDGEALG	SMGNDTPLAV	611									
SbNADH-GOGAT1	HLKDIIVESVP	ETDRVAPIS	S	SSLPQKN--E	NKDDVGVNGI	LTPLKAFGYT	VEALEMLLP	MAKDGEALG	SMGNDTPLAV	607									
BdNADH-GOGAT1	YLKDIIVESVP	ETDRVAPIS	A	GSIPQMN--D	NKECKGVNGI	VTPLKAFGYT	VEALEMLLP	MAKDGEALG	SMGNDAPLAV	607									
OsNADH-GOGAT2	QLTDIIIESVN	EAEIRAPSI	S	GALPI TK--E	NKADMGICGI	LTPLKAFGYT	REALEMLLP	MAKDGEALG	SMGNDTPLAV	618									
SbNADH-GOGAT2	QLADIIIESVP	ETERGAPRID	S	-MLPQKN--E	NKEAFCIHGI	LAPLKAFGYT	VTETLEMLLP	MAKNGVEALG	SMGNDTPLAV	628									
BdNADH-GOGAT2	ELRDIIESVS	ATERIAPMIS	S	GAL-----	-REPVGVNGI	LAPLKAFGYT	LETLDMLLP	MAKDGEALG	SMGNDTPLAV	611									
Consensus	ELKDIIVESVP	ETXRVAPIS	S	GSLPXXN--E	NKENMGI XGI	LXPLKAFGYT	VEALEMLLP	MAKDGEALG	SMGNDTPLAV										
				660															
SpNADH-GOGAT	MSDRAKIPSE	YFKQMFQVNT	NPPIDPIREK	IVTSMCEMIG	PEGDLTETTE	EQCHRLALKG	PLLSIGEMEA	IKKMNFGQWR	710										
AINADH-GOGAT	MSNREKLCFE	YFKQMFQVNT	NPPIDPIREK	IVTSMCEMIG	PEGDLTETTE	EQCHRLSLKG	PLLLIEEMEA	IKKMNVRGWR	710										
NnNADH-GOGAT1	MSNREKLTFE	YFKQMFQVNT	NPPIDPIREK	IVTSMCEMIG	PEGDLTETTE	QQCHRLSLKG	PLLSIEEMEA	IKKMNVRGWR	705										
NnNADH-GOGAT2	MSNREKLTFE	YFKQMFQVNT	NPPIDPIREK	IVTSMCEMIG	PEGDLTETTE	EQCHRLSLKG	PLLSMDEMEA	IKKMNVRGWR	705										
OsNADH-GOGAT1	MSNREKLTFE	YFKQMFQVNT	NPPIDPIREK	IVTSMCEMIG	PEGDLTETTE	KQCNRALLEG	PLVSIDEMEA	IKKMNVRGWR	691										
SbNADH-GOGAT1	MSNREKLTFE	YFKQMFQVNT	NPPIDPIREK	IVTSMCEMIG	PEGDLTETTE	KQCNRALLEG	PLVSIDEMEA	IKKMDVRGWR	687										
BdNADH-GOGAT1	MSNREKLTFE	YFKQMFQVNT	NPPIDPIREK	IVTSMCEMIG	PEGDLLEITE	KQCNRALIKG	PLVSIDEMEA	IKKMDVRGWR	687										
OsNADH-GOGAT2	MSNREKLTFE	YFKQMFQVNT	NPPIDPIREK	IVTSMCEMIG	PEGDLSETTE	RQCNRLLTKS	PLLNTNEMEA	IKKMNVRGWR	698										
SbNADH-GOGAT2	MSNREKMPFD	YFKQMFQVNT	NPPIDPIREK	IVTSMCEMIG	PEGDLSETTE	HQCNRLLKLG	PLLIIDEMEA	IKKMNVRGWR	708										
BdNADH-GOGAT2	MSNREKLTAE	YFKQMFQVNT	NPPIDPIREK	IVTSMCEMIG	PEGDLSETTE	RQCNRLLTKS	PLLIIDEMEA	IKKMNVRGWR	691										
Consensus	MSNREKLTFE	YFKQMFQVNT	NPPIDPIREK	IVTSMCEMIG	PEGDLTETTE	EQCHRLALKG	PLLSIDEMEA	IKKMNVRGWR											
				740															
SpNADH-GOGAT	SKVLDITYSK	NRGRKGLEET	LDRICSEARA	AIREGYTLLV	LSDRGFSSER	VGVSLLAVG	AVHQHLSVKL	ERTRIGLIVE	793										
AINADH-GOGAT	TKVLDITYAK	ERGTRKLEET	LDRICSEANE	AIKEGYTLLV	LSDRAFSPNR	VAVSSLLAVG	AVHHHLVKLT	ARTQVGLVVE	790										
NnNADH-GOGAT1	SKVLDITYLK	SGRGRKLEEM	LDRICSEAEH	AIKEGTILLV	LSDRAFSPNR	VAVSSLLAVG	AVHHHLVKEL	ERTRIGLIVE	785										
NnNADH-GOGAT2	SKVLDITYPK	SRGMKGLEET	LDRICSEARD	ALKEGYTLLV	LSDRAFSPNR	VAVSSLLAVG	AVHHHLVKL	ERTRIGLIVE	785										
OsNADH-GOGAT1	SKVLDITYPK	KSGRKGLEET	LDRICTEARG	AIKKGTYTLV	LSDRGFSSDR	VAVSSLLAVG	AVHQHLSVANL	ERTRVGLLVE	771										
SbNADH-GOGAT1	SKVLDITYPK	KSGRKGLEEA	LDRICAEARE	AISKGYTILLV	LSDRGFSSDR	VAVSSLLAVG	AVHQHLSVANH	ERTRIGLIVE	767										
BdNADH-GOGAT1	SKVLDITYPK	KSGRKGLEET	LDRICAEARE	AIRNGYKILV	LSDRGFSSDR	VAVSSLLAVG	AVHQHLSVANL	ERTRVGLLVE	767										
OsNADH-GOGAT2	SKVLDITYPK	KNGRMGLQET	LDKICAQARE	AIHEGYTILLV	LSDRGFSSER	VAVSSLLAVG	AVHQHLSVSHL	ERTRIGLIVE	778										
SbNADH-GOGAT2	SKVLDITYPK	VYGRKGLEQT	LDKLCAQARE	AIHGYTILLI	LSDRGFSPDR	VPVSSLLAVG	AVHQHLSVNL	DRTRIGLLVD	788										
BdNADH-GOGAT2	SKVLDITYPK	KYGRKGLEQT	LDKVCAQARE	AIQEGYKILV	ISDRGFSPDH	VAVSSLLAVG	AVHQHLSVNH	ERTHVGLLVE	771										
Consensus	SKVLDITYPK	KRGRKGLEET	LDRICAEARE	AIKEGYTILLV	LSDRGFSSDR	VAVSSLLAVG	AVHQHLSVNL	ERTRIGLIVE											
				820															
SpNADH-GOGAT	SAEPREVHNF	CTLVGYGADA	ICPYLAIEAI	WRLQIDGKIP	PKASGELHSR	DELVORYFKA	SNDGMMKVLA	KMGISTLAS	873										
AINADH-GOGAT	SAEPREVHNF	CTLVGFGADA	ICPYLAVEAV	YRLQVDGKIP	PKSNGEFHSK	EELVKKYFKA	SNYGMKVLA	KMGISTLAS	870										
NnNADH-GOGAT1	SAEPREVHNF	CTLVGFGADA	ICPYLAIEAI	WRLQIDGKIP	PKASGELHSR	EELVKKYFKA	SNYGMKVLA	KMGISTLAS	865										
NnNADH-GOGAT2	SAEPREVHNF	CTLVGYGADA	ICPYLAIEAI	WRLQVDGKIP	PKASGEFHSK	EELVKKYFKA	STYGMKVLA	KMGISTLAS	865										
OsNADH-GOGAT1	SAEPREVHNF	CTLVGFGADA	VCPYLAIEAI	WCLQNDGKIP	PNGDGKPYSK	EELVKKYFYA	SNYGMKVLA	KMGISTLAS	851										
SbNADH-GOGAT1	SAEPREVHNF	CTLVGFGADA	ICPYLAIEAI	WCLQNDGKIP	PNGDGQLYSK	EELVKKYFYA	SNYGMKVLA	KMGISTLAS	847										
BdNADH-GOGAT1	SAEPREVHNF	CTLVGFGADA	ICPYLAIEAI	WCLQIDGKIP	PNGDGQPDSC	EELVKKYFYA	SIYGMKVLA	KMGISTLAS	847										
OsNADH-GOGAT2	SAEPREVHNF	STLIGFGADA	ICPYLAIEAI	WRLQIDGRIP	P-NDGKPYTQ	EQLIEKYFYA	SNYGMKVLA	KMGISTLAS	857										
SbNADH-GOGAT2	SAEPREVHNF	CTLLGFGADA	ICPYLAIEAI	WRLQIDEXIP	PKDDGQLYPK	E-LIDKYFYA	SNNGIMKVLA	KMGISTLAS	867										
BdNADH-GOGAT2	SAEPHEVHNF	CTLIGYGADA	ICPYLAIEVI	CRLQIDGRIP	CTDGEQYTTQ	EQXLAQKYFNA	SNYGMKVLA	KMGISTLAS	851										
Consensus	SAEPREVHNF	CTLVGFGADA	ICPYLAIEAI	WRLQIDGKIP	PKXDGXPYSK	EELVKKYFYA	SNYGMKVLA	KMGISTLAS											
				900															
SpNADH-GOGAT	KGAQIFEALG	LSSEVIKCF	NGTPSRVEGA	NFEILARDAL	RLHESAFPSR	ALPPGSAEAV	ALPNPGDYHW	RKGGEVHLND	953										
AINADH-GOGAT	KGAQIFEALG	LSSEVIKCF	AGTPSRVEGA	TFEMLARDGL	QLHELAFPT	GYAPGSAEAS	ALTNPNGYHW	RKNGEIHLND	950										
NnNADH-GOGAT1	KGAQIFEALG	LSSEVIKCF	AGTPSRVEGA	TFEMLARDAL	RLHESAFPT	ALPPGSAEAV	ALPNPGDYHW	RKGGEIHLND	945										
NnNADH-GOGAT2	KGAQIFEALG	LSSEVIKCF	KGTSPSRVEGA	TFEMLALDAL	QLHEMAFPTR	AMPPGSAEAV	ALPNPGDYHW	RKGGEIHLND	945										
OsNADH-GOGAT1	KGAQIFEALG	LSSEVIKCF	DGTSPRIEGA	TFEMLARDAL	RLHELAFPSR	APPPGSAEAD	ALPNPGDYHW	RKNGEVHLND	931										
SbNADH-GOGAT1	KGAQIFEALG	LSSEVIKCF	EGTPSRIEGA	TFEMLARDAL	RLHELAFPSR	TPPAGSADAK	ALPNPGDYHW	RKNGEIHLND	927										
BdNADH-GOGAT1	KGAQIFEALG	LSSEVIKCF	EGTPSRIEGA	TFEMLARDAL	RLHELAFPSR	LPPAGSADAK	ALPNPGDYHW	RKNGEIHLND	927										
OsNADH-GOGAT2	KGAQIFEALG	LASEVVSCKF	EGTPSRVEGA	TFEMLAQDAL	RLHEIAFPSS	TLPPGSAEAD	ALPNPGDYHW	RKNGEVHLND	937										
SbNADH-GOGAT2	KGAQIFEALG	LASEVVSCKF	EGTPSRVEGS	TFEMLAQDAL	HLLKLAFPSR	TLPPGSAEAD	SLPNPGDHHW	RKNGEVHLND	947										
BdNADH-GOGAT2	KGAQIFEALG	LASEVIKCF	EGTPSKVEGA	KFDMLANDAL	RLHDLAFPSR	SWPHGSAEAD	ALPNPGDYHW	RKNGEVHLND	931										
Consensus	KGAQIFEALG	LSSEVIKCF	EGTPSRVEGA	TFEMLARDAL	RLHELAFPSR	ALPPGSAEAX	ALPNPGDYHW	RKNGEIHLND											
				980															
SpNADH-GOGAT	PLAIAKLQEA	ARANSVAAYK	EYSRRVQELN	KECNLRGMLK	FKDVPKINL	DEVEPASEIV	KRFCTGAMS	GSISLEAHTT	103										
AINADH-GOGAT	PLAIAKLQEA	ARTNSVAAYK	EYSKRINELN	KQSNLRGLMK	FKDADVKIPL	DEVEPASEIV	KRFCTGAMS	GSISLEAHTT	103										
NnNADH-GOGAT1	PLAMAKLQEA	ARNSVAAYR	EYSKRINELN	KQSNLRGLMK	FKEAKGVPL	DEVEPASEIV	KRFCTGAMS	GSISLEAHTT	102										
NnNADH-GOGAT2	PLAIAKLQEA	ARNSVAAYR	EYSKRINELN	KQSNLRGLMK	FKEAEVKVPL	DEVEPASEIV	KRFCTGAMS	GSISLEAHTT	102										
OsNADH-GOGAT1	PLAMAKLQEA	ARVNSRAAYK	EYSRRVQELN	KTCNLRGLMK	FKDADIMSV	DEVEPASEIV	KRFVTGAMS	GSISLEAHTT	101										
SbNADH-GOGAT1	PLAMGKLQEA	ARVNSRAAYK	EYSKRINELN	KACNLRGLMK	FKDISDKISL	DEVEPASEIV	KRFCTGAMS	GSISLEAHTT	100										
BdNADH-GOGAT1	PLAMAKLQEA	AKVNSRAAYK	EYSKRINELN	KACNLRGLMK	FKDISNKISL	DEVEPASEIV	KRFCTGAMS	GSISLEAHTT	100										
OsNADH-GOGAT2	PFSIAKLQEA	ARINSREAYK	EYSRRVQELN	KACTLRGLMK	FREIPNOISL	DEVEPASEIV	KRFCTGAMS	GSISLEAHTT	101										
SbNADH-GOGAT2	PFSIAKLQEA	ARLDSREAYK	EYSRRTEELS	KQCTLRGLMK	FREIPVIRISL	DEVEPASEIV	KRFCTGAMS	GSISLEAHTT	102										
BdNADH-GOGAT2	PLSIAKLQEA	ARINSKEAYK	EYSRLIQDNN	KACTLRGLMK	FRETDRIRISL	DEVEPASEIM	KRFCTGAMS	GSISLEAHTT	101										
Consensus	PLAIAKLQEA	ARVNSRAAYK	EYSXRIQELN	KACNLRGLMK	FKXIPVKISL	DEVEPASEIV	KRFCTGAMS	GSISLEAHTT											
				1,060															
SpNADH-GOGAT	LAIAMNKLGG	KSNTGEGGEL	PSRLVPLPDG	SMNPKRSAIK	QVASGRFGVT	SYLITNADEL	QIKMAQGA	GEGGELPGHK	111										
AINADH-GOGAT	LAMAMNKLGG	KSNTGEGGEL	PSRMEPLADG	SRNPKRSSIK	QIASGRFGVS	SYLITNADEL	QIKMAQGA	GEGGELPGHK	111										
NnNADH-GOGAT1	LAIAMNKLGG	KSNTGEGGEL	PSRMQPLPDG	SMNPKRSAIK	QVASGRFGVS	SYLITNADEL	QIKMAQGA	GEGGELPGHK	110										
NnNADH-GOGAT2	LAIAMNKLGG	KSNTGEGGEL	PSRMQPLPDG	SRNPKRSAIK	QVASGRFGVS	SYLITNADEL	QIKMAQGA	GEGGELPGHK	110										
OsNADH-GOGAT1	LAMAMNKLGG	KSNTGEGGEL	PSRMEPLADG	SMNPKRSAIK	QVASGRFGVS	SYLITNADEL	QIKMAQGA	GEGGELPGHK	109										
SbNADH-GOGAT1	LAIAMNKLGG	KSNTGEGGEL	PSRMEPLPDG	SMNPKRSAIK	QVASGRFGVS	SYLITNADEL	QIKMAQGA	GEGGELPGHK	108										
BdNADH-GOGAT1	LAVAMNKLGG	KSNTGEGGEL	PSRMEPLPDG	SMNPKRSAIK	QVASGRFGVS	SYLITNADEL	QIKMAQGA	GEGGELPGHK	108										
OsNADH-GOGAT2	LAEAMNKLGG	KSNTGEGGEL	PCRMVPLPDG	SKNPRISAIK	QVASGRFGVS	IYYLTNAVEV	QIKMAQGA	GEGGELPGHK	109										
SbNADH-GOGAT2	MARAQNIKRA	KSNTGEGGEL	PSRMEPLPDG	SMNPLSSAIK	QVASGRFGVS	IYYLTNAIEL	QIKMAQGA	GEGGELPGHK	110										
BdNADH-GOGAT2	LAEAMNKLGG	KSNTGEGGEL	PSRMELLADG	SMNPRISAIK	QVASGRFGVS	IYYLTNAIEI	QIKMAQGA	GEGGELPGHK	109										
Consensus	LAIAMNKLGG	KSNTGEGGEL	PSRMEPLPDG	SMNPKRSAIK	QVASGRFGVS	SYLITNADEL	QIKMAQGA	GEGGELPGHK											

			1,140		1,160		1,180		1,200	
SpNADH-GOGAT	VIGDIAVTRN	STAGVGLISP	PPHHDYSISIE	DLAQLIHDLK	NSNPGARISV	KLVSEAGVGV	IASGVVKGHA	DHVLISGHDG	1193	
AINADH-GOGAT	VIGDIAITRN	STAGVGLISP	PPHHDYSISIE	DLAQLIHDLK	NANPGARISV	KLVSEAGVGV	IASGVVKGHA	DHVLISGHDG	1190	
NnNADH-GOGAT1	VIGDIAVTRN	STAGVGLISP	PPHHDYSISIE	DLAQLIHDLK	NANPGARISV	KLVSVAGVGV	IASGVVKGHA	EHVLSGHDG	1185	
NnNADH-GOGAT2	VIGDIAVTRN	STAGVGLISP	PPHHDYSISIE	DLAQLIHDLK	NSNPGARISV	KLVSEAGVGV	IASGVVKGHA	DHVLISGHDG	1185	
OsNADH-GOGAT1	VIGDIAVTRH	STAGVGLISP	PPHHDYSISIE	DLAQLIHDLK	NSNPRARISV	KLVSEAGVGV	VASGVVKGHA	DHVLISGHDG	1171	
SbNADH-GOGAT1	VIGDIAVTRH	STAGVGLISP	PPHHDYSISIE	DLAQLIHDLK	NSNPGARISV	KLVSEAGVGV	VASGVVKGHA	DHVLISGHDG	1167	
BdNADH-GOGAT1	VIGDIAVTRH	STAGVGLISP	PPHHDYSISIE	DLAQLIHDLK	NSNPGARISV	KLVSEAGVGV	VASGVVKGHA	DHVLISGHDG	1167	
OsNADH-GOGAT2	VIGDIAVTRH	STAGVGLISP	PPHHDYSISIE	DLAQLIHDLK	NANPGARISV	KLVSEAGVGV	VASGVVKGHA	DHVLISGHDG	1177	
SbNADH-GOGAT2	VIGDIAVTRH	STAGVGLISP	PPHHDYSISIE	DLAQLIYDLK	SNPGARISV	KLVSEAGVGV	VASGVVKGHA	DHVLISGHDG	1187	
BdNADH-GOGAT2	VIGDIAVTRH	STAGVGLISP	PPHHDYSISIE	DLSQLIHDLK	NANPGARISV	KLVSEAGVGV	VASGVVKAHA	DHVLISGHDG	1171	
Consensus	VIGDIAVTRX	STAGVGLISP	PPHHDYSISIE	DLAQLIHDLK	NSNPGARISV	KLVSEAGVGV	VASGVVKGHA	DHVLISGHDG		
		1,220		1,240		1,260		1,280		
SpNADH-GOGAT	GTGASRWTGI	KNAGLPWELG	LAETHQTLVA	NDLRGRTVLQ	TDGQLKTGKD	VAAIALLGAE	EFGFSTAPLI	TLGCIIMMRKC	1273	
AINADH-GOGAT	GTGASRWTGI	KNAGLPWELG	LAETHQTLVA	NDLRGRTVLQ	TDGQLKTGRD	VAAIALLGAE	EFGFSTAPLI	TLGCIIMMRKC	1270	
NnNADH-GOGAT1	GTGASRWTGI	KNAGLPWELG	LAETHQTLVA	NDLRGRITLQ	TDGQLKTGRD	VVAIALLGAE	EFGFSTAPLI	TLGCIIMMRKC	1265	
NnNADH-GOGAT2	GTGASRWTGI	KNAGLPWELG	LAETHQTLVA	NDLRGRITLQ	TDGQLKTGRD	VVAIALLGAE	EFGFSTAPLI	TMGCIIMMRKC	1265	
OsNADH-GOGAT1	GTGASRWTGI	KNAGLPWELG	LAETHQTLVA	NGLRGRAILQ	TDGQLKTGKD	VAVACLLGAE	EFGFSTAPLI	TLGCIIMMRKC	1251	
SbNADH-GOGAT1	GTGASRWTGI	KNAGLPWELG	LAETHQTLVA	NGLRGRAVLQ	TDGQLKTGRD	VAVACLLGAE	EFGFSTAPLI	TLGCIIMMRKC	1247	
BdNADH-GOGAT1	GTGASRWTGI	KNAGLPWELG	LAETHQTLVA	NGLRGRAVLQ	TDGQLKTGRD	VAVACLLGAE	EFGFSTAPLI	TLGCIIMMRKC	1247	
OsNADH-GOGAT2	GTGASRWTGI	KNAGLPWELG	LAETHQTLVA	NGLRGRAVLQ	TDGQMKTGKD	VAVACLLGAE	EFGFSTAPLI	TLGCIIMMRKC	1257	
SbNADH-GOGAT2	GTGASRWTGI	KNAGLPWELG	LAETHQTLVA	NGLRGRAVLQ	TDGQMKTGKD	VVAIACLLGAE	EFGFSTAPLI	ALGCIIMMRKC	1267	
BdNADH-GOGAT2	GTGASRWTGI	KNAGLPWELG	LAETHQTLVA	NGLRGRAVLQ	TDGQLKTGRD	VVAIACLLGAE	EFGFSTAPLI	TLGCIIMMRKC	1251	
Consensus	GTGASRWTGI	KNAGLPWELG	LAETHQTLVA	NGLRGRAVLQ	TDGQLKTGRD	VAXACLLGAE	EFGFSTAPLI	TLGCIIMMRKC		
		1,300		1,320		1,340		1,360		
SpNADH-GOGAT	HKNTCPVGIA	TQDPVLRKFF	AGEPEHVINF	FFMLAEVRE	IMAQLGFRTL	LEMVGRSDML	EIDQVNVNSN	EKLENDLSL	1353	
AINADH-GOGAT	HKNTCPVGIA	TQDPVLRKFF	AGEPEHVINF	FFMLAEVRE	IMSGLGFRTV	TEMIGRADML	ELDRVVKNN	EKLENDLSL	1350	
NnNADH-GOGAT1	HKNTCPVGIA	TQDPVLRKFF	AGEPEHVINF	FFMLAEVRE	IMSGLGFRTI	NEMVGRSDML	EVDKEVVNSN	EKLENDLSL	1345	
NnNADH-GOGAT2	HKNTCPVGIA	TQDPVLRKFF	AGEPEHVINF	FFMLAEVRE	IMSGLGFRTI	NEMVGRSDML	EVDKEVKNK	EKLENDLSL	1345	
OsNADH-GOGAT1	HTNTCPVGIA	TQDPVLRKFF	AGEPEHVINF	FFMLAEELRE	IMSGLGFRTI	TEMVGRSDML	EVDPEVVKSN	EKLENDLSL	1331	
SbNADH-GOGAT1	HMNTCPVGIA	TQDPVLRKFF	AGEPEHVINF	FFMLAEELRE	IMANLGFRTI	TEMVGRSDML	EVDPEVVKSN	EKLENDLSL	1327	
BdNADH-GOGAT1	HTNTCPVGIA	TQDPVLRKFF	AGEPEHVINF	FFMLAEELRE	IMAQLGLRSI	NEMVGRSDML	EVDPEVVKSN	EKLENDLSL	1327	
OsNADH-GOGAT2	HTNTCPAGIA	TQDPVLRKFF	AGKPEHVINY	FFMLAEVRE	IMAQLGFRTV	NEMVGRSDML	EIDPKVLEGN	EKLENDLSR	1337	
SbNADH-GOGAT2	HTNTCPVGIA	TQDPVLRKFF	SGKPEHLINF	FFMLAEVRE	IMSGLGFRTI	NEMVGRSDML	EVDPEVLKGN	EKLQNDLSL	1347	
BdNADH-GOGAT2	HTNTCPVGIA	TQDPVLRKFF	SGKPEHVINY	FFMVAEVRE	IMSRLGFRTV	NEMVGRSDML	EVDPEVLKGN	EKLENDLSQ	1331	
Consensus	HTNTCPVGIA	TQDPVLRKFF	AGEPEHVINF	FFMLAEVRE	IMSGLGFRTI	NEMVGRSDML	EVDPEVVKSN	EKLENDLSL		
		1,380		1,400		1,420		1,440		
SpNADH-GOGAT	LLKPAAEIRP	EAAQYCIQKQ	DHGLDMALDN	KLIVLSKAAL	EKGLPVYIDL	PVQNVNRAVG	TMLSHEVTKR	YRMDGLPSDC	1433	
AINADH-GOGAT	LLRPAAEIRP	EAAQYCVQKQ	DHGLDMALDQ	ELIALSKAAL	EKSLPVYIET	PICNVNRAVG	TMLSHEVTKR	YHGLTLPKDT	1430	
NnNADH-GOGAT1	LLRPAADIRP	EAAQYCIQKQ	DHGLDMALDN	KLIALSTPAL	EKGLPVYIEV	PIRNVNRAVG	TMLSHEVTKR	YHMAGLPADT	1425	
NnNADH-GOGAT2	LLRPAADIRP	EAAQYCIQKQ	DHGLDMALDQ	KLIALSKAAL	EKALPVYIEL	PIRNVNRAVG	TMLSHEVTKR	YHIALGLPADT	1425	
OsNADH-GOGAT1	LLKPAAEIRP	EAAQYCVQKQ	DHGLDMALDN	KLIALSKAAL	EKEVRFVLET	PIQNTNRAVG	TMLSHEVTKR	YHMKGLPAGT	1411	
SbNADH-GOGAT1	LLKPAASEIRP	GVAQYCVQKQ	DHGLDMALDN	KLIDLSRTAI	EKQVRVFIET	PIQNTNRAVG	TMLSHEVTKR	YHMSGLPAGT	1407	
BdNADH-GOGAT1	LLKPAAEIRP	GAAQYCVQKQ	DHGLDMALDN	KLIALSKAAL	EKQVRVFIET	PIKNTNRAVG	TMLSHEVTKR	YHMKGLDSDT	1407	
OsNADH-GOGAT2	LLKPAAEISP	GAVQYCVQKQ	DHGLDMALDN	KLIASSTAAL	EKGVRVFIET	PVRNINRAVG	TMLSHEVTKR	YHIGHLPSDT	1417	
SbNADH-GOGAT2	LLKPAAEISP	EAVQYCVQKQ	DHGLDKALDN	KLIASSRAAL	EKRFRVFIET	LKNTDRAVG	TMLSHEVTKL	FRMPGLPDDT	1427	
BdNADH-GOGAT2	LLKPAASKISP	GAAQYCVQKQ	DHGLHRAALDN	KLIALSRVAL	EKGSRVFIET	SVRNTNRTVG	AMLSHEVTKR	YHIGHLPSDT	1411	
Consensus	XLKPAAEIRP	GAAQYCVQKQ	DHGLDMALDN	KLIALSKAAL	EKGXRVFIET	PIRNTNRAVG	TMLSHEVTKR	YHMXGLPXD		
		1,460		1,480		1,500		1,520		
SpNADH-GOGAT	IHIKLGSGSAG	QSLGAFLCPG	ITLELEGDSN	DYVGKGLSGG	KVIVYPPRKS	NFDPKENIVI	GNVALYGATK	GEAYFNGMAA	1513	
AINADH-GOGAT	IHIKFTGSAG	QSLGAFLCPG	IMLELEGDSN	DYVGKGLSGG	KVVYPPKGS	SFDPKENIVI	GNVALYGATS	GEAYFNGMAA	1510	
NnNADH-GOGAT1	IHIKLGGSAG	QSLGAFLCPG	ITLELEGDSN	DYVGKGLSGG	KIVVYPPRES	QFDPKENIVI	GNVALYGATS	GEAYFNGMAA	1505	
NnNADH-GOGAT2	IHIKLTGSAG	QSFGAFLCPG	IMLELEGDSN	DYVGKGLSGG	KIVVYPPRKS	QFDPKENIVI	GNVALYGATS	GEAYFNGMAA	1505	
OsNADH-GOGAT1	IHVKL TGSAG	QSLGAFLCPG	ITLELEGDSN	DYVGKGLSGG	KIVVYPPRDS	TFIPEDNIVI	GNVALYGATI	GEAYFNGMAA	1491	
SbNADH-GOGAT1	IHVYKFTGSAG	QSFGAFLCPG	ITLELEGDSN	DYVGKGLSGG	KIVVYPPRNS	SFVPEDNIVI	GNVALYGATK	GEAYFNGMAA	1487	
BdNADH-GOGAT1	IHVKL TGSAG	QSFGAFICPG	ITLELEGDSN	DYVGKGLSGG	KIVVYPPRNS	TFIPEDNIVI	GNVALYGATK	GEAYFNGMAA	1487	
OsNADH-GOGAT2	IHIKLGSGSAG	QSFGAFLCPG	ITLELEGDSN	DYVGKGLSGG	KIVVYPPRNS	RFNPDQDNIVI	GNVALYGATK	GEAYFNGMAA	1497	
SbNADH-GOGAT2	IHVKLNGSAG	QSFGAFLCPG	ITLELEGDSN	DYVGKGLSGG	KIVVYPPRNS	RFIPQDNIVI	GNVALYGSTK	GEAYFNGMAA	1507	
BdNADH-GOGAT2	IHVKLNGSAG	QSFGAFLCPG	ITLKLEGDSN	DYVGKGLSGG	KIVVYPPRNS	RFNPDQDNIVI	GNVALYGSTK	GEAYFNGMAA	1491	
Consensus	IHXKLTGSAG	QSFGAFLCPG	ITLELEGDSN	DYVGKGLSGG	KIVVYPPRNS	RFDPKDNIVI	GNVALYGATK	GEAYFNGMAA		
		1,540		1,560		1,580		1,600		
SpNADH-GOGAT	ERFCVRNSGA	KAVVEGVGDH	GCEYMTGGTV	VVLGKTGRNF	AAGMSGGVIAY	VLDADSTFKT	RCNLELVOLD	KVEEEDDITT	1593	
AINADH-GOGAT	ERFSVRNSGA	KAVVEGLGDH	GCEYMTGGTV	VVLGKTGRNF	AAGMSGGIAY	VLDVDGKFNT	RCNLELVOLD	KVEEEDDKMT	1590	
NnNADH-GOGAT1	ERFCVRNSGA	KAVVEGVGDH	GCEYMTGGTV	VVLGKTGRNF	AAGMSGGIAY	VLDVDGKFQS	RCNLELVOLD	KVEEEDIMT	1585	
NnNADH-GOGAT2	ERFCVRNSGA	KAVVEGVGDH	GCEYMTGGTV	VVLGKTGRNF	AAGMSGGIAY	VLDVDEKFQS	RCNLELVOLD	KVEEEDIMT	1585	
OsNADH-GOGAT1	ERFCVRNSGA	QAVVEGIGDH	GCEYMTGGTV	VILGKTGRNF	AAGMSGGIAY	VYDIDGKFSV	RCNHELVDLY	HVEEEDDITT	1571	
SbNADH-GOGAT1	ERFCVRNSGA	QAVVEGIGDH	GCEYMTGGTV	VILGKTGRNF	AAGMSGGIAY	VYDVGKFSV	RCNHELVDLY	HVEEEDDITT	1567	
BdNADH-GOGAT1	ERFCVRNSGA	ITVVEGIGDH	GCEYMTGGTV	VILGKTGRNF	AAGMSGGIAY	VYDVGTFSA	RCNHELVDLY	HVEEEDDITT	1567	
OsNADH-GOGAT2	ERFCVRNSGA	QAVVEGIGDH	GCEYMTGGTV	VILGKTGRNF	AAGMSGGIAY	VYDVGKFSV	RCNYELVDLY	AVVEEDDITT	1577	
SbNADH-GOGAT2	ERFCVRNSGA	QAVVEGIGDH	GCEYMTGGTV	VILGKTGRNF	AAGMSGGIAY	VYDVGMFST	RCNHELVDLY	NVDEEDDITT	1587	
BdNADH-GOGAT2	ERFCVRNSGA	EAVVEGIGDH	GCEYMTGGTV	VILGKTGRNF	AAGMSGGIAY	VYDVGKFSV	RCNHELVELY	RVVEEDDIT	1571	
Consensus	ERFCVRNSGA	XAVVEGIGDH	GCEYMTGGTV	VILGKTGRNF	AAGMSGGIAY	VYDVGKFSV	RCNXELVDLY	KVEEEXDITT		
		1,620		1,640		1,660		1,680		
SpNADH-GOGAT	LRVMIQQHQR	HTNSELAKEV	LANFDELLPK	FVKVFPDYK	RVLQNMKAEE	AAKEAQ----	---QREE-AE	LMKKDAFQEL	1665	
AINADH-GOGAT	LKMMIQQHQR	HTNSQLAQEV	LADFENLLPK	FIKVFPDYK	RVLSAMKHEE	VSKQATIRAS	EEADETEEKE	LEEKDAFAEL	1670	
NnNADH-GOGAT1	LRMMIQQHQR	HTNSELAREV	LANFENLLPK	FIKVFPDYK	RVLANLRAEQ	AAKDAKERRA	KEAEEQEEAE	LMEKDAFEEL	1665	
NnNADH-GOGAT2	LRMMIQQHQR	HTNSELAREV	LADFENLLPK	FIKVFPDYK	RVLANMKAEQ	AAK-----KVV	REAQEEQEEAE	LMKKDAFEEL	1661	
OsNADH-GOGAT1	LKMMIEQHRL	NTGSVARDI	LSNFDNLLPK	FVKVFPDYK	RVLQNMKAEE	AA-----A	LKAKEP----	-----	1630	
SbNADH-GOGAT1	LKMMIEQHRL	NTESVLARDI	LSDFDNLLPK	FVKVFPDYK	RVLQNMKAEE	AV-----A	KAKEP-----	-----	1626	
BdNADH-GOGAT1	LKMMIEQHRL	HTGSVLAKDI	LKSFSSLLPK	FVKVFPDYK	RVLQNMKAEE	AA-----A	SHAKEP----	-----	1626	
OsNADH-GOGAT2	LRMMIQQHRL	HTQSDLRDI	LSNFDNLLPK	FIKVFPDYK	RVLQNMKAEE	AA-----A	KEAEQKAREV	V-DKKPVEVI	1648	
SbNADH-GOGAT2	LRVMIQQHRL	NTESVLAKDI	LSNFDNLLPK	FVKVFPDYK	RVLQNMKAEE	V-----A	KEAEQKMRKK	GWKKKAGEMI	1659	
BdNADH-GOGAT2	LRMMIEQHRL	NTESHLAKYI	LSSFEDQLPK	FVKVFPDYK	RVLQNMKAEE	VAKA-----	---AEEKTRKM	LMDKKAGEET	1643	
Consensus	LRMMIQQHRL	HTXSVLARDI	LSNFDNLLPK	FVKVFPDYK	RVLQNMKAEE	AAK-----A	KEAEEEXE-XE	LMDKDAFEEL		

SpNADH-GOGAT	KKLASASINE	KAN-GRIEEP	QPLKRPTRVA	NAVKHGRGFVN	YEREGVSYRD	PNARIQDWKE	-VSEESKPGP	LLKTQSARCM	1743
AINADH-GOGAT	KNMMAASSKE	EMSGNGVAAE	A---RPSKVD	NAVKNGGFIA	YEREGVKYRD	PNVRLNDWNE	-VMEESKPGP	LLTQSARCM	1746
NnNADH-GOGAT1	KKLAAASLND	KAS-QKVEKA	VQLKRPTKVD	NAIKNGGFIA	YERESISYRD	PSNRISDWKE	-VMEEPKPGP	LLNTQSARCM	1743
NnNADH-GOGAT2	KKLALASSND	RDKVNKEQV	VASKRPTKVD	NAVKNGGFIA	YERESISYRD	PTVRVNDWKE	-VMEESKLG	LLKTQSARCM	1740
OsNADH-GOGAT1	KISNGVSVTT	K-----KVQPE	QSTNRPTRSV	NAKKYRGFIS	YERESISYRD	PNERVKDWKE	-VAIESVPGP	LLNTQSARCM	1705
SbNADH-GOGAT1	KVANGISVTT	K-----KVQPD	QSASRPTRVA	NAKKYRGFIT	YERESISYRD	PKERVKDWKE	-VAIESTPGP	LLNTQSARCM	1701
BdNADH-GOGAT1	KVPNGVSVTT	K-----KIQTE	QSTSRPTRVA	NAKKYRGFIS	YEREGISYRD	PNERVKDWKE	-VAIESVPGP	LLNTQSARCM	1701
OsNADH-GOGAT2	QAPNGISVKT	E-----KVMNE	EPSSRPSRVS	NAVKYRGFIK	YEREGTSYRD	PNERVKDWNE	-VAIELVPGP	LLKTQSARCM	1723
SbNADH-GOGAT2	KAPNGISVIT	K-----KVQNK	KSSSRPTQVF	NAERPRGFVE	YEQQGISYRD	ENERVKDWGE	-VTNELVPGP	LLNTQSARCM	1734
BdNADH-GOGAT2	KASNGSSVVT	K-----QMNDR	KPSGQPTQVS	NAIKEQGFI	FGREEVSCRD	PNERTKDWDE	LVKNELVPGP	LLRTQSARCM	1719
Consensus	KXXNGASVXT	K-----KVQXE	QSSSRPTRVX	NAVKYRGFIA	YEREGISYRD	PNERVKDWKE	-VAXESVPGP	LLNTQSARCM	
SpNADH-GOGAT	DCGTPFCHQD	NSG--CPLGN	KIPEFNELVH	QERWREALDR	LLETNNFPEF	TGRVCPAPCE	GSCVLGIIEN	PVSIKSIIECS	1821
AINADH-GOGAT	DCGTPFCHQE	NSG--CPLGN	KIPEFNELVY	QNRWQREALNR	LLETNNFPEF	TGRVCPAPCE	GSCVLGIIEN	PVSIKSIIECA	1824
NnNADH-GOGAT1	DCGTPFCHQE	NSG--CPLGN	KIPEFNELVY	QNRWREALDR	LLETNNFPEF	TGRVCPAPCE	GSCVLGIIEN	PVSIKSIIECT	1821
NnNADH-GOGAT2	DCGTPFCHQE	NSG--CPLGN	KIPEFNELVY	QNRWREALDR	LLETNNFPEF	TGRVCPAPCE	GSCVLGIIEN	PVSIKSIIECA	1818
OsNADH-GOGAT1	DCGTPFCHQE	SSGAGCPLGN	KIPEFNELVH	QNRWREALDR	LLETNNFPEF	TGRVCPAPCE	GSCVLGIIEN	PVSIKSIIECA	1785
SbNADH-GOGAT1	DCGTPFCHQE	SSGAGCPLGN	KIPEFNELVH	QNRWREALDR	LLETNNFPEF	TGRVCPAPCE	GSCVLGIIEN	PVSIKSIIECA	1781
BdNADH-GOGAT1	DCGTPFCHQE	SSGAGCPLGN	KIPEFNELVH	QNRWREALDR	LLETNNFPEF	TGRVCPAPCE	GSCVLGIIEN	PVSIKSIIECS	1781
OsNADH-GOGAT2	DCGTPFCHQE	SSGAGCPLGN	KIPEFNELVH	QNRWREALDR	LLETNNFPEF	TGRVCPAPCE	GSCVLGIIEN	PVSIKSIIECA	1803
SbNADH-GOGAT2	DCGTPFCHQE	SSGAGCPLGN	KIPEFNELVH	QNRWREALDR	LLETNNFPEF	TGRVCPAPCE	GSCVLGIIEN	PVSIKSIIECA	1814
BdNADH-GOGAT2	DCGTPFCHQE	SSGAGCPLGN	KIPEFNELVH	QNRWREALDR	LLETNNFPEF	TGRVCPAPCE	GSCVLGIIEN	PVSIKTIIECA	1799
Consensus	DCGTPFCHQE	NSGAGCPLGN	KIPEFNELVH	QNRWREALDR	LLETNNFPEF	TGRVCPAPCE	GSCVLGIIEN	PVSIKSIIECA	
SpNADH-GOGAT	IIDKAFEEGW	MVPRPPLK--	RTGKKIAIVG	SGPAGLAAAD	QLNKMGHVT	VFERADRIIG	LMMYGVPNMK	ADKVDIVQRR	1899
AINADH-GOGAT	IIDKAFEEGW	MVPRPPLK--	RTGKKIAIVG	SGPAGLAAAD	QLNKMGHVT	VYERSDRIGG	LMMYGVPNMK	TDKIDVVQRR	1902
NnNADH-GOGAT1	IIDKAFKEGW	MVPRPPLR--	RTGKRVAIVG	SGPAGLAAAD	QLNKMGHVT	VLERADRIIG	LMMYGVPNMK	ADKVDIVQRR	1899
NnNADH-GOGAT2	IIDKAFNEGW	MVPRPPPK--	RTGKRVAIVG	SGPAGLAAAD	QLNKMGHVT	VFERADRIIG	LMMYGVPNMK	ADKVDIVQRR	1896
OsNADH-GOGAT1	IIDKGFEFGW	MVPRPPLQ--	RTGKKIAIVG	SGPAGLAAAD	QLNKMGHVT	VFERADRIIG	LMMYGVPNMK	TDKIEIVQRR	1863
SbNADH-GOGAT1	IIDKGFEFGW	MVPRPPLQ--	RTGKRVAIVG	SGPAGLAAAD	QLNKMGHVT	VFERADRIIG	LMMYGVPNMK	TDKIGIVQRR	1859
BdNADH-GOGAT1	IIDKGFEFGW	MVPRPPLQ--	RTGKKIAIVG	SGPAGLAAAD	QLNKMGHVT	VYERSDRIGG	LMMYGVPNMK	TDKIGVVQRR	1859
OsNADH-GOGAT2	IIDKGFEFGW	MVPRPPLR--	RTGKRVAIVG	SGPAGLAAAD	QLNKMGHVT	VFERADRIIG	LMMYGVPNMK	ADKEGIVQRR	1881
SbNADH-GOGAT2	IIDKGFEFGW	MVPRPPLQSQ	RTGMTVAIVG	SGPAGLAAAD	QLNKMGHVYV	VFERADRIIG	LMMYGVPNMK	ADKARIVKRR	1894
BdNADH-GOGAT2	IIDKGFEFGW	MVPRPPVH--	RTGKEVAIVG	SGPAGMAAAD	QLNKMGHVT	VYERSDRIGG	LMMYGVPNMK	ADKTRIVQRR	1877
Consensus	IIDKGFEFGW	MVPRPPLQ--	RTGKKVAIVG	SGPAGLAAAD	QLNKMGHVT	VFERADRIIG	LMMYGVPNMK	ADKIDIVQRR	
SpNADH-GOGAT	VNLMAEEGVN	FVVNAHIGVD	PSYSLDILRS	ENDAILLACG	ATKPRDLPVP	GREFSGVHFA	MEFLHANTKS	LLDSNLDGDK	1979
AINADH-GOGAT	VDLMTKEGIN	FVVNANIGKD	PSYSLDGLKE	ENDAIVLAVG	STKPRDLPVP	GRDLSGVHFA	MEFLHANTKS	LLDSNHEDGN	1982
NnNADH-GOGAT1	VNLMAEEGVN	FVVNANVGTD	PLYSIDLRLA	ENDAIVLALG	ATKPRDLPVP	GRELKGVHFA	MEFLHANTKS	LLDSNLQDGN	1979
NnNADH-GOGAT2	VNLMAEEGVN	FVVNANVGTD	PLYSIDLRLA	ENDAIVLALG	ATKPRDLPVP	GRELKGVHFA	MEFLHANTKS	LLDSNLQDGN	1976
OsNADH-GOGAT1	VNLMAEEGIV	FVVNANVGSD	PLYSIERLRS	ENDAVILACG	ATKPRDLGIP	GRELSGVHFA	MEFLHANTKS	LLDSNLEDGR	1943
SbNADH-GOGAT1	VNLMAEEGIV	FVVNASVGS	PLYSIERLRS	ENDAVILACG	ATKPRDLTIP	GRELSGVHFA	MEFLHANTKS	LLDSNLEDGK	1939
BdNADH-GOGAT1	VNLMAEEGIV	FVVNAHVGS	PLYSIERLRS	ENNAVILACG	ATKPRDLSIP	GRELSGVHFA	MEFLHANTKS	LLDSNLEDGR	1939
OsNADH-GOGAT2	VELMAKEGVQ	FIVNAHVGS	PLYSVEKLRS	ENDAILLACG	ATKPKDLPVP	GRELAGIHFA	MEFLHANTKS	LLDSNLEDGN	1961
SbNADH-GOGAT2	VDLMDKEGVK	FIVNAHVGS	PRYSIERLRS	ENDAVILACG	ATPRDLPIP	GRELSDIHFA	MDFLHSNTKS	LLDTNLEDGN	1974
BdNADH-GOGAT2	VDLMTKEGIV	FVVNAHVGRD	PSYSIDLRLS	KNNAVILACG	ATKPRDLPIP	GRQLSGIHFA	MEFLHANTKS	LLDSKLEDGN	1957
Consensus	VNLMAEEGVX	FVVNAHVGS	PLYSIXRLRS	ENDAXILACG	ATKPRDLPIP	GRELSGVHFA	MEFLHANTKS	LLDSNLEDGN	
SpNADH-GOGAT	YISAKGKKVV	VIGGGDTGTD	CIGTSIRHGC	TSVNVLELLP	EPPAKRAPGN	PWPQWPRIFR	VDYGHQEAAT	KFGKDPRSIE	2059
AINADH-GOGAT	YISAKGKKVV	VIGGGDTGTD	CIGTSIRHGC	TNIVNLELLP	QPPSTRAPGN	PWPQWPRVFR	IDYGHQEAAT	KFGKDPRTYE	2062
NnNADH-GOGAT1	YISAKGKKVV	VIGGGDTGTD	CIGTSIRHGC	TNIVNLELLP	QPPQTRAPGN	PWPQWPRIFR	VDYGHQEAAT	KFGKDPRSIE	2059
NnNADH-GOGAT2	YISAKGKKVV	VIGGGDTGTD	CIGTSIRHGC	TNIVNLELLP	QPPKTRAPGN	PWPQWPRIFR	VDYGHQEAAT	KFGKDPRSIE	2056
OsNADH-GOGAT1	YISAKGKKVV	VIGGGDTGTD	CIGTSIRHGC	TSVNVLELLT	KPPSKRAADN	PWPQWPRIFR	VDYGHQEAAS	KFGNDPRTYE	2023
SbNADH-GOGAT1	YISARGKKVV	VIGGGDTGTD	CIGTSIRHGC	TNLVNLELLS	KPPSNRAADN	PWPQWPRIFR	VDYGHQEAAT	KFGKDPRTYE	2019
BdNADH-GOGAT1	YISAGKKVV	VIGGGDTGTD	CIGTSIRHGC	SSVNVLELLT	KPPSKRAADN	PWPQWPRVFR	VDYGHQEAAS	KFGKDPRTYE	2019
OsNADH-GOGAT2	YISAQGRKVV	VIGGGDTGTD	CIGTSIRHGC	TNLVNLELLP	EPPRKRAPDN	PWPQWPRIFR	VDYGHQEATS	KFGKDPRSIE	2041
SbNADH-GOGAT2	YISARGKKVV	VIGGGDTGTD	CIGTAIRHGC	SNLVNLELLP	EPPRERAPDN	PWPQWPRIFR	RDYGHQEAAS	KFGKDPRTYQ	2054
BdNADH-GOGAT2	YISAGKKVV	VIGGGDTGTD	CIGTSIRHGC	SNLVNLELLP	EPPTRAPDN	NWPKFPRIFR	LDYGHQEAAS	KFGKDPRTYQ	2037
Consensus	YISAKGKKVV	VIGGGDTGTD	CIGTSIRHGC	TNIVNLELLP	EPPSKRAPDN	PWPQWPRIFR	VDYGHQEAAT	KFGKDPRTYE	
SpNADH-GOGAT	VLTKRFIGDD	NGVVKGLEVV	RVRWAKDASG	RFQFKEIAGS	EEIEADLV	LAMGFLGPEQ	KIAEELGVER	DNRSNFKADF	2139
AINADH-GOGAT	VLTKRFIGDD	NGVVKGLEVV	RVSWEKDETS	RFQFKEIAGS	EEIEADLV	LAMGFLGPEP	TLAEKLGLEK	DNRSNFKAEY	2142
NnNADH-GOGAT1	VLTKRFLGDE	NGAVKGLEVV	RVRWEKDESG	RFQFKEIAGS	EEIEADLV	LAMGFLGPES	TIAEKLGLEK	DNRSNFKADY	2139
NnNADH-GOGAT2	VLTKRFLGDE	NGTVKGLEVV	RVQWEKDGAN	KFQFKEIAGS	EEMIEADLV	LAMGFLGPES	TIAEKLGLEK	DNRSNFKAEY	2136
OsNADH-GOGAT1	VLTKRFIGDE	NGNVKALEVV	RVKWEK-VDG	RFQFKEIAGS	NETIEADLV	LAMGFLGPEA	TIAEKLGLEK	DNRSNFKAEY	2102
SbNADH-GOGAT1	VLTKRFIGDE	NGVKVKALEVV	RVKWEK-VDG	RFQFKEIAGS	EEIEADLV	LAMGFLGPEA	TIAEKLGLEK	DNRSNFKAEY	2098
BdNADH-GOGAT1	VLTKRFIGDE	NGKVKALEVV	RVKWEK-VDG	RFQFKEIAGS	QEIEADLV	LAMGFLGPEA	TIAEKLGLEK	DNRSNFKAEY	2098
OsNADH-GOGAT2	VLTKRFIGDE	NGNVKALEVI	RVEWKG-VDG	RFQFKEIAGS	EEIEADLV	LAMGFLGPEA	TVANKLGLEQ	DNRSNFKAEY	2120
SbNADH-GOGAT2	VLTKRFIGDE	NGKVKALEVV	RVEWSK-VDG	RFQFKEIAGS	QEIEADLV	LAMGFLGPEA	AIKKLGLEQ	DNRSNFKAEY	2133
BdNADH-GOGAT2	YMAKRFIGDE	DGKVKALEVV	HVEWEK-VDG	RLQFKEVEGS	EETIEADLV	LAMGFLGPEV	TLADKLGLEQ	DNRSNFKAEY	2116
Consensus	VLTKRFIGDE	NGKVKALEVV	RXWWEK-VDG	RFQFKEIAGS	EEIEADLV	LAMGFLGPEA	TIAEKLGLEK	DNRSNFKAEY	
SpNADH-GOGAT	GRFSTNVEGI	FAAGDCRRGQ	SLVWVAIAEG	RQAAQVDRY	LKDDGSFGGD	DMASKISCHG	DLEDLVKNPG	SKRRVAA-	2216
AINADH-GOGAT	GRFSTTVEGV	FAAGDCRRGQ	SLVWVAISEG	RQAAQVDRY	LTKTDD---	---EDAKLQ	DLNQMKHNTI	TN-----	2208
NnNADH-GOGAT1	GKFSTNVEGV	FAAGDCRRGQ	SLVWVAISEG	RQAAQVDRY	LMR-DSDPGT	-SDSQ-----	---DVQKQD	SSRLTLMT	2207
NnNADH-GOGAT2	GKFSTNMEGV	FATGDCRRGQ	SLVWVAISEG	RQAAQVDRY	LTR-EGKHS	TSQSQC----	---DSAKQD	KNQFTART	2207
OsNADH-GOGAT1	GNFATSVGDI	FAAGDCRRGQ	SLVWVAITEG	RQAAAADVY	LSR-NEQ---	DAEDITPSG	---AGFVQVA	A-----	2167
SbNADH-GOGAT1	GDFATSVGDI	FAAGDCRRGQ	SLVWVAITEG	RQAAAADVY	LSR-YDQ---	NAAGDITPSG	---AGLVQVA	A-----	2163
BdNADH-GOGAT1	GDFATSVGDI	FAAGDCRRGQ	SLVWVAITEG	REAAAADVY	LSRDEQ---	NSTQGITPSG	---AGLVQIT	A-----	2163
OsNADH-GOGAT2	GNFATNVEGV	FAAGDCRRGQ	SLVWVAITEG	RQAAAADVY	LSK-DDEGET	NGTEDIAVSS	---EGLVQPV	A-----	2188
SbNADH-GOGAT2	ENFATNVEGV	FAAGDCRRGQ	SLVWVAIAEG	REAAAADVY	LSR-E---KT	NVDENVVAPG	PCECLVQVA	A-----	2200
BdNADH-GOGAT2	GNFATNVEGV	FAAGDCRRGQ	SLVWVAITEG	REAAAADVY	LS---DETCT	NDADDAIASS	---IGLLQVA	AWRHQON-	2188
Consensus	GNFATNVEGV	FAAGDCRRGQ	SLVWVAITEG	RQAAAADVY	LSR-XDX--T	NSAEDITPSG	---XGLVQVA	A-----	

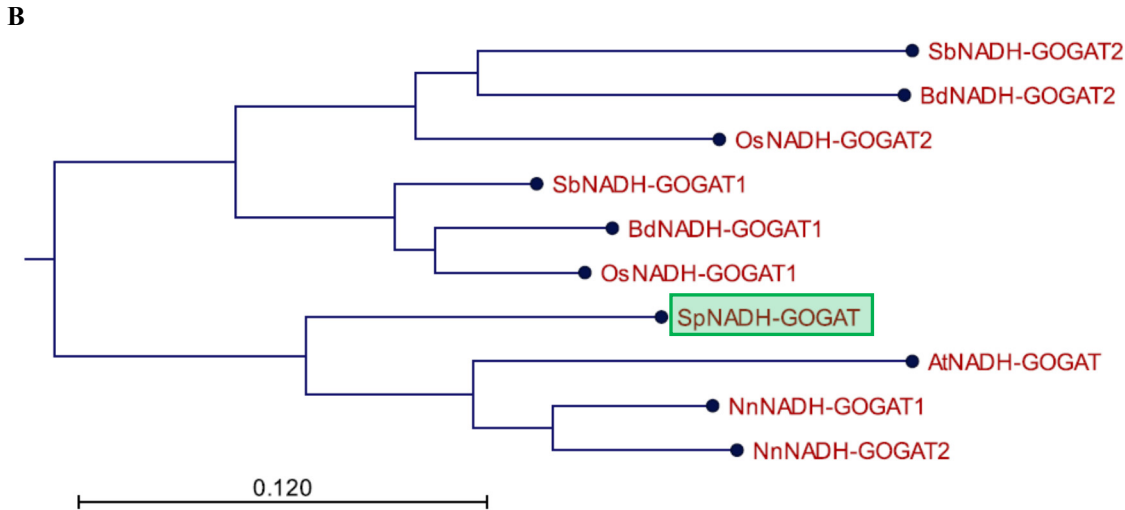


Figure S13. Sequence alignment NADH-GOGAT protein from *S.polyrhiza* with other representative species **(A)** and the resulted phylogenetic tree **(B)**. AtNADH-GOGAT - *A. thaliana*, NP_200158.2, BdNADH-GOGAT1 - *B. distachyon*, XP_003566997.1, BdNADH-GOGAT2 - *B. distachyon*, XP_024315185.1, NnNADH-GOGAT1 - *N. nucifera*, XP_010261570.1, NnNADH-GOGAT - *N. nucifera*, XP_010266511.1, OsNADH-GOGAT1 - *O. sativa*, XP_015649242.1, OsNADH-GOGAT2 - *O. sativa*, XP_015640407.1, SbNADH-GOGAT1 - *S. bicolor*, XP_002458326.1, SbNADH-GOGAT2 - *S. bicolor*, XP_021302649.1, SpNADH-GOGAT - *S. polyrhiza* (sequence translated from. Acc. OL421563)

SpNR

[illegible]

SpNiR

CAGTTTAAAGCTCTATTATGTTCAAGCCCTATGAACCCTAGAATTAATGATCAGCCCTTGCCTTTTCACTTTTTTAGATAGGC
ATCATAACCATGACTTCATTCCCTCATTGCAATTGACAAGAATATTATTTTTTAACATTATATTTACTTTTGGATAGTGGTGCTGAT
TTCCCTTGAGAAACAATACCATAGATAGAGAGAGACACAAAAATCTTGATTTAGCCATGATTAAAAAATTTTATTGTTCAAGGGAG
AGTAATGGAGGAAAACAGACAGACAAATTCCAAATTTGGCATGTTTTGCAAGGACTTCCAGCAACAGGTGAAAAGGTGAGGGACT
CTTCTCTAAATCTAGTAGTTTACGAGTACCCCGATTTCTTTTTATAGTATAATAATACGATCTCCTTGAAAATAGAACCCCTTTG
ACTGGTCGTCCACGTGACGAGCTCTTGAGCTGCCGTGGAGCCAGCGGAGCGTTGACCAGCAAGAAGAATGTTGCGACAGGAAACA
TTTCGACGTGCAGCTGAAACTAATGGCGAGGATTTTTCTAACATTGTATTGCGACACAGTTTTTCTGTGGCGCCGATCGTCTTAT
CAAGAAACGAAAGCGGTGCCCGGGAGGCCTCGGTCCGACGGGCTGGCCCTGCTGTGCGGCTCACC GCCTGCGGTACGCGCCCCC
CTCACGGCCGAGGGAGCCGCTGACCTGTGGCCCCACCCACCATCCCCCCCCCTCGCTGCCGCCGTCTTCTTCCGTCCCTAAGACC
CTTCTCTCGTCCGTGAGTCCCGCGTCGTCTTTAGAGAGAGCGAAGAGCCC AAGGCCAGATGCCCTCTCGTGCGACCGACTCTC
CGCCGCCGCTCGCTTGGGGGGGCAACTCCGTCTCCCTCGTCGTCTACCTCTCGAGGTGTTAAGAACCCTGCGGCCCTTCCCACTGCC
CCGATGGAGTCGCCACCGCCGCAGAGCAGCCCGCTGCCACCATCACC CGCGACCTCGTACCGCCatg

SpGS1;1

ATTTAAATTATTTTATAATGTATACATTATTTATGGGCTGAAAAATATAGAGTTATTGCAGAAATTCAGACCCT
GAAATTTCTCTAAATTAAGTAAATATAGGAAAAATGTCAATAATTCTTGCCAGATAGATCTCCGGCCGCAA
GTATTATTGCCAACTTTTTTTCACATCAGTCCCTCCAGGAATTCCATCCAGGCGGAAATTTCCCGAAATTATTTA
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AGCATTCTGGGGGGGCATATTACAATAATGTGGACGAATGACAGCTCTC**GATTC**GTCTGATCAGATCGCATCCGAT
GACGACGTTTGTTCCTCAATCGGAATATG**C**CACGTCATCAAGCGCGCTCTAGATACCGCCGG**GAATC**TGTTCCC
ACTGGCAGAGTATCGTGAGATGGCCTAACTAAGTGGGGCCACATGCAACACCAAATTACCTTAAAGCCCTCAC
CGGCAAGTCTAATCGCAGTCGACCCCGTTGACCGGGCCCCACCCGAAAACCTTTTTCCCTTTCATTAATACATC
TAATACTAAGTTAATTAATTGAAACATAGTACTAACGTATTTCGTATTTTAC**ATATATTTAA**AATTAATTAAAT
TTAAAAGTCAGCAGACTTGGAAGTCAAGCGTCTATAAGGGC**AATATA**GGCATTTCACCATAACCACAACCTCCTC
CGAAAGGGACGC**GAATC**ACCGTAACAAATCGGTGACGTTACCGGCCATCCCGGAGTTCCGCGCTCCGCTAATAG
AAATTAATTTATTAAACTCTCTCCGTG**ACGGCTAT**TAAAGATAGCA**GCGAGCCG**CTCCCCCTGCGCCCAATCGCGT
CATCGCCTGGTGCATCTCCCCTGCTCTCGGATCTCGCCTCCTCTCTCCCCCTCCCCCTCCCTGGGGTTCTTCCC
GCT**GAATC**TTCCCTTCCCCTCTCTCCCGTCTCTTCCGCC**atg**

SpGS1;2

CATCATATCGCCATAATTTTCCTTATAATAATCCCGCATTATTGTTTTTTAATGAGGGCCGTCGATGTGCCACG
CCAGGCCAAGTGGGCTAACAAAATAAGCCCGCGAAATTATAACAGCGAGATTCTTTTCCGCGGTTCCGATTCGA
TCAGGCGCGGAGGAAAGTAGCGGCCATTTATTGGCGACTGGGGGCTTCGAAATCTGAAGATTCCGGGTGGCGT
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CCCAGGTGGCGGGCTTCGGTTATTACGACCCCTCCCCAGGTGAGTTACTCAGTGTGGTTGAATCTAGACACAGA
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GGAGCTCGAACTTGATTATTCTGATTAAATGAGCGGATCTAGACCCGCAACCCTCTGCCAGTACGCAGCGG**AAG**
AGCCCGCCACATGCACTCGTGAGAGGAGAGGAATTTTGACCGGCATTGATGCATGCGTCACTTGTCACTGAC
 CCTCGAATGTAGTAAAGTTTTTGATCCGCGAGGGCAGTAGCGCCATTTAAGA**GAATC**GTCTCTCTCTCTAGTTG
 CGGGAAAATCGGTCAGCGGGGGAGCAAGTGGGGCCTACAGCTCCTCCGTGGCGGCGCAAAGTTACCGTACCAAC
 CAGTTTTTCGGCGCCGATGTCAGGCTTCTGACTTTTGGGTGCCTC**CTCCCTCTT**CCTGTCGCAGC**AGGAGGAA**GG
 GAGGGGAGGGTGGGGGCGGGCCACTGGAGATTTCTTCCTTGTTTTTTAAGGCTT**GAATC**CGCT**TATATAAA**GCG
 CCCCCGCCGCTTCCCCACCAATCCATTACCGCAGCGCTCTCCCTGCCCGGCGGATTGATCGCAGTTCCCTCTC
 CCGCCCCGCCTCCTGCGTCTCCAGCTTCG**G**CCGCTGCC**atg**

SpGS1;3

CCAACCTGGGTTGACCAGCGCTTTCTAATGAGATCCTCCATTTTAGTAAGGCGTAAACTTGCATTATTTCAAACAAAGAGGGGCTCAGTACATCCACGGTCGAGAACAGGGCAGTGGGCGGCGGCGGAGCGTTGGTAGATTTCTTCACTGTGCGGCGGCGGCGGTGGCGTCGGCGACCTACGAGGGCGGAGATGGGAATGGCTCAAACAGCGGCGGCGAGCAGTTCCAGAGGCCGCAGCAGCTGAAGAACCA CAGGCTGCAGAGAATTGAGGTCGAGGAGATGAGGGCAAAGAGAGAATTGACACTTGGAGGGAGGGGGAGTGAGAGACGAAGGGG **GATGCTTACC**ATGAAGCT**AAGAGCCC**GTCGGCTCCCGTGGCCTCTCAGCAGCGGCGGCGGCGGCAACGATGGCGGCGGCGGCAGGGCAGTGGGGGGGCAGCAGCAGGGGCGGCCTCTTGTGGCATGGGGGGGTCCATCGTTTCAGAGGAAGGAACAAGGGGGATGAAGGAGAGATCTGTTCTTCTTCTAGGGTGGACTCTTCTCCAGGGAGATCACCATCTGCCCTTCCAGCGCCGCCACCCAGCGGTCAGAGTCTAGAGAGCAGAGACGGAGAGAGAGAGAGAGAGTGGACTATTGGACCGAGCTGATGGGTGGAGTCTACTTTGGTGTTCAAGGCCAAATCCATATAACAGATGGGCGCTCTCCAGTGGGTTTGGGCTATCCCCCCCCCATTTGGGCCATTAGGCC**AA****TAAATATATAT**GCATGGAAGAGGCCCATCTCTGTGATCATCATCAGTGAGGGCGTCGGCCCTCGAATGCCACCTATTTTCGGCTGCCACCTCCCACCCGCCAAGAGCGCGGTGTTAGGCCGCCACGTAGGAACCTCCGAGCTCTTTTTCCGATGCTGATTTTGTGCTTCTGGTTGGTTACAGTCTCTCTCTCCCCAGGGGAGTAGCGCCTGCGTGCGAGTTCCCCAGTCGGCC**atg**

SpGS2

AGATGAATAAAAAATACCCCTTTTTGTGCAGAGCGGCAGCAGACGGATGTGTGTATGAGAGAGAGATGGCGCCCTTATCT**GAATC**CCCT
TGGTCTTTGAGGGCTCCCAAGGGACCCGT**TTTCCTCC**ACTCAAAGCG**AAGAACC**TATCTGCTGGCGAAGAGCCGCCGAGGCCGA
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TATAAACGGTCCACCCG**CTCTCTCTCCCTCTCTCTCTCTCTCTCTCT**CGCTGTGTTTGAAATCTTCTCTCCTCCTCCCAACGACG
CCGCCGCCGCCGGAGGAGCTGGTGGGCGCCCGCATTACCTCCCTGCCTCGCCGTCGCCCGGCGTCTCTCGGTTAG**CTCTCCCTCC**
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TGA**CC**CTGCAAGATGCGGTTCTCGCCCTCGCTACGTGGCGTG**GATT**CATTCTGCCCCCGGAGCGTTTCATTCTTCAGAGGGGG
ATCCCCTCCATTTTTGTCTGTCGGATCCTCTGTGTTCCCTTTTCGAGTATCTCCCATGTCTGATCCGAATGTCTCCGTTTCGCCTTGC
CG**GATTGCGGTTGATTCTCCGAGAGATT**GTTGC**TGCCTTTT**GTTTTTATGATCC**ACGAGGCG**AATTGCGAATTCTGTTTCCATCT
TCGGATCTTGATCAAAC**TA**GTTCAGAGCGGAGGAGAAGAGAGGGGACAGAAGGCGGAAGGAAAG**atg**

SpFd-GOGAT

GTCTCTTTTCCGAGGTAAGTCCAGTTATTTCAAATATTTTATTTTATCTTTCATATTCTCCAATGGGGGAGTACATCTAGGA
TCATTTTCGAAGAGAGAGAGAGCGCCGAAAAAGCCAAGAAGCGAGAGGCAGGGAGAGGAGAGAGCGGAGAGGGACAGAGAGACAGA
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AGGAGCGAGAAGAGAGAGAGAGAGAGAGAGAGAGAGTGAGAGGAGAGAGAAGAGAGATGAAGAGAGGGGGGAGAGAGAGAGAGAGA
GAGAGAGAGAGAGAGAGGGTCCGAGGATAGTGGTTGGCAGGGTGCGGTAGAGGACAAGGCAGCGGCTCCCACCAGTGCCTGTGTC
CTCCTCCCGGAGCTCTACTCCATTCCCTCTCCGCACGACGACGACGACTACGAGCGCTGGAGGCGAGTGGCTCACATCTCTCCC
CTCCCCGCTCTCTCATTCTCGCTCTAACC**TCTCTCTATC**CTCTCTCTC**TGCAGCCT**CTCTCTCTCTCTCTCTCTATCTGTTGG
CCAATCCTCCCGGCTTGGCAGCGCGGGCGCATCAGGATTATCCTGCTCTT**TGGCGTTT**CCTCTCCAC**GCGAGCCT**CTCCATTTTCG
GATTTATATATTTGCGCATCTTCAAACCTTCCTGC**ATATTTTATT**GGCGTCGCG**TATAAATTTT**CGCTTCCCTGGTTTTGTTTTCC
TGCTCTGCCGACCAGAAAAAGTCTCCTCCTCTCCACCTCGTCTCCTCCTCCTCCTTCCACTTCGGTTCCCTGGGGGATCCTG
CTCTGCCGAGCGGTGGT**GAATCA**AGCGCGGCAGAGAGGAACGGGAGGGAGGGGAGGAAGGTGGG**atg**

SpNADF-GOGAT

[illegible]

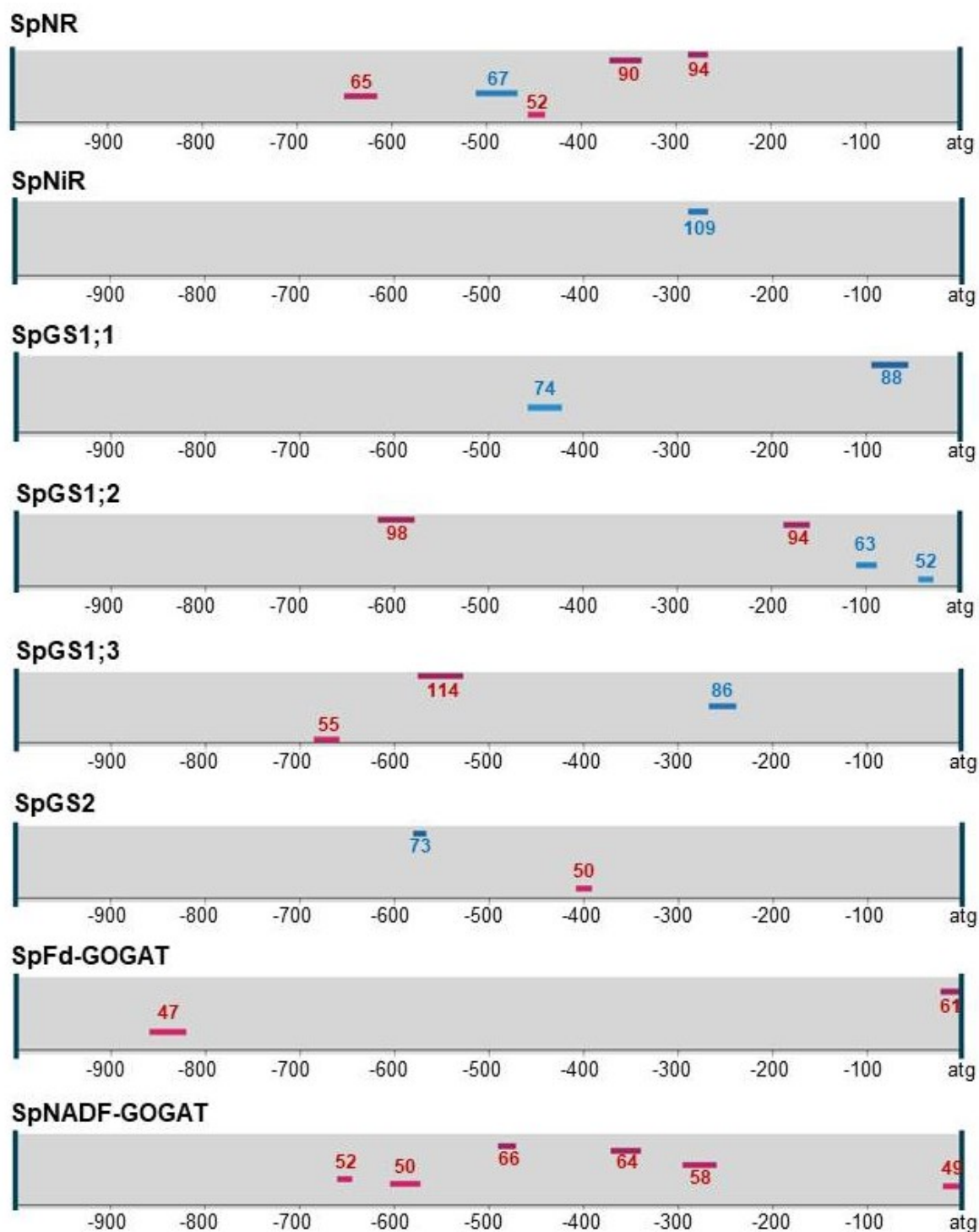


Figure S15. Patterns of G-quadruplex structures predicted for promoters of key *S. polyrhiza* genes involved in nitrogen assimilation, using the *pqsfinder* tool (<https://pqsfinder.fi.muni.cz>). Positions of G-quadruplex structures are indicated by horizontal lines (**red** for forward DNA strand, **blue** for reverse strand); Numbers next to bars indicate the relative strength of each G-quadruplex structure, and the negative (–) numbers indicate positions relative to the genes' translation start.