

AtNudC1	1	-----MAEKLAPEK-----RHDFVHN-----GQKVFWDQTLLEEVNMY
AtBOB1	81	VKPVEK-KAEKEIVKLVEKKVEKESVKPTIAASSAEPTEVEKPKDEEEKESGPIVENKNGNDLENLSWQNLQEVTVN
AtBOB2	77	VKSMEVEKPKKDSLKPTELEKPKKE--ESIMAT--DPMEIEKPKDE--KESGPIVENKNGNGLDFEKSWGQNLQEVTVN
Zm	1	-----MAENLAPEK-----RHDFVHN-----GQKVFWDQTLLEEVNMY
Sb	1	-----MAEKLGPKEK-----RHDFVHN-----GQKVFWDQTLLEEVNMY
Os	1	-----MAEKLGPKEK-----RHDFVHN-----GQKVFWDQTLLEEVNMY
Bd	1	-----MAEKLAPEK-----RHDFVHN-----GQKVFWDQTLLEEVNMY
Gm	1	-----MAEKLAPEK-----RHDFVHN-----GQKVFWDQTLLEEVNMY
Rc	1	-----MAEKLAPEK-----RHDFVHN-----GQKVFWDQTLLEEVNMY
Vv	1	-----MAEKLAPEK-----RHDFVHN-----GQKVFWDQTLLEEVNMY
Hs	1	-----MSAPFEE-----RSGVPC-----GTPWGQWQTLLEEVNMY

AtNudC1	34	ITLPPNVKPKSEKQKISKHEVGIKGNPPYLNHDLSPVKTDCSFWTLEDIMH--ITLQREKGTWASPILGQGGI
AtBOB1	160	IPVPTGTARTVVEIKKNRKVGKGGDLVDGELYRSVKPDDCWNIEDQKVIS--ITLQKSTQMEWKKCCVKEPEP
AtBOB2	149	IPMPEGTASRSVVEIKKNRKVGKGGDLVDGFFNSVKPDDCWNIEDQKVIS--ITLQKSTQMEWKKCCVKEPEP
Zm	34	IELPKGVPTKLEHONICASHVEVGIRGNPPYLNHDLTHPVKTDSSFWTIEDGEMH--ITLQREKGTWSSPIQGQGI
Sb	34	IELPKGVPTKLEHONICASHVEVGIRGNPPYLNHDLTHPVKTDSSFWTIEDGEMH--ITLQREKGTWSSPIQGQGI
Os	34	IELPKGVPTKLEHONICASHVEVGIRGNPPYLNHDLTHPVKTDSSFWTIEDGEMH--ITLQREKGTWSSPIQGQGI
Bd	34	IELPKGVPTKLEHONICASHVEVGIRGNPPYLNHDLTHPVKTDSSFWTIEDGEMH--ITLQREKGTWSSPIQGQGI
Gm	34	ITLPPNVKPKSEKQKISKHEVGIKGNPPYLNHDLSPVKTDCSFWTLEDIMH--ITLQREKGTWASPILGQGGI
Rc	34	ITLPPNVKPKSEKQKISKHEVGIKGNPPYLNHDLSPVKTDCSFWTLEDIMH--ITLQREKGTWASPILGQGGI
Vv	34	ITLPPNVKPKSEKQKISKHEVGIKGNPPYLNHDLSPVKTDCSFWTLEDIMH--ITLQREKGTWASPILGQGGI
Hs	32	IQVPPGTADIDCGICSRHVAISVGGRE-ILKGIKFDSTIADEGTWTLLEDRKVRIVITKTKRDAKNCWTSLESEYAA

AtNudC1	111	DPYATDLEQKRI--MLQRFQENPGFDFSQAQFSGNCPD-----PRTFMGGIRSD
AtBOB1	238	DTQKVEPETSILGDLDPETRSVVKMMFDQKQKMGFLPTSDELQKQEIILKKFMSEHPEMDFSNAKFN
AtBOB2	227	DTQKVEPETSILGDLDPETRSVVKMMFDQKQKMGFLPTSDELQKQEIILKKFMSEHPEMDFSNAKFN
Zm	111	DPYATDLEQKRI--MLQRFQENPGFDFSQAQFSGNCPD-----PRTFMGGIRSD
Sb	111	DPYATDLEQKRI--MLQRFQENPGFDFSQAQFSGNCPD-----PRTFMGGIRSD
Os	111	DPYATDLEQKRI--MLQRFQENPGFDFSQAQFSGNCPD-----PRTFMGGIRSD
Bd	111	DPYATDLEQKRI--MLQRFQENPGFDFSQAQFSGNCPD-----PRTFMGGIRSD
Gm	111	DPYATDLEQKRI--MLQRFQENPGFDFSQAQFSGNCPD-----PRTFMGGIRSD
Rc	111	DPYSTDLEQKRI--MLQRFQENPGFDFSQAQFSGNCPD-----PRTFMGGIRSD
Vv	111	DPYSTDLEQKRI--MLQRFQENPGFDFSQAQFSGNCPD-----PRTFMGGIRSD
Hs	111	DPYVDDQKRI--MLQRFQENPGFDFSQAQFSGNCPD-----GGPDFSNLEK-

At, *Arabidopsis thaliana*; **Zm**, *Zea mays*; **Sb**, *Sorghum bicolor*; **Os**, *Oryza sativa*; **Bd**, *Brachypodium distachyon*; **Gm**, *Glycine max*; **Rc**, *Ricinus communis*; **Vv**, *Vitis vinifera*; **Hs**, *Homo sapiens*

FIGURE S1. Multiple alignment of amino acid sequences of the NudC domain proteins from *Arabidopsis thaliana* and their homologs generated by Clustal Omega. The presented species are *A. thaliana* (At), *Zea mays* (Zm), *Sorghum bicolor* (Sb), *Oryza sativa* (Os), *Brachypodium distachyon* (Bd), *Glycine max* (Gm), *Ricinus communis* (Rc), *Vitis vinifera* (Vv), and *Homo sapiens* (Hs). The two conserved domains are underlined with black (NudC domain) and red (CS domain) lines. Black background represents 90–100% sequence identity and grey background represents 80–90% identity.