

AiDSC1	...MESSSSPSSAEFVFLSFRGSDTRNNFTGHLQKALLGLDSEFDRLRGGDNL...AFDRITKSKLITIVSTNYANSAICLRELVVLEPCRN..	92
NgN	...MASSSSSRWSYVFLSFRGSDTRKTFTHLYEVLVNDGIRFODDKPIYGATIPGEGCKLIESOFIVVTSENVASVCIENLIMCKPT..	95
GhDSC1	MASSSAPPFPQVKHQVFLSFRGSDTRNNFTSHLLKALLLTGLVVFDEEELFGEKLDLISQ...AASNLSLLVLSKDYAS...SCLGELSDMDRRKP	100
<b>TIR</b>		
AiDSC1	<u>SNQOLVPIFYKDKSDPEKRNSTFVPEKLPDLTTEGVTPEISSWKAASASNILEVMVK..EISTSEPKIMDITAVDTFKLIDAPSGNPELVLGI</u>	190
NgN	<u>DFNCTIPIPIYDVSISVWVNOKSFKABEHEKDKD.DVEGQWRALNEAALGSCDN...RMTDQDCTIIDQISSKLCCKLSLVLQIVGI</u>	191
GhDSC1	<u>EDRHALLPIFYHVSISVWVIGTERTSSEHEKRE...LDVWKWKAFTEVGTGWHEGGKFDNTEYIDVVEYLKRLSNCRSVSEDLVGI</u>	197
<b>TIR</b>		
AiDSC1	<u>EQRNLEKLLSWEDDITVHIIGIVGMVGIGKTTLADCLYGRMC.....OFDGSIFINIRENSGFSGLISLQKLESITVINDRDIIEGAGG/AHERI</u>	284
NgN	<u>DFHEKIEISLLEFG...INGNMIGMVGKTTIARAFDITLDRMSSYDFCAFLDIKEN...RRGHSIQALIKELLREKANYNEE.DCKHQM</u>	287
GhDSC1	<u>EDQK...IILGIEQADSIVILGMGIGKTTLAIIVYKEVSP.....EEESRFFLNWSKKIKDQDLSLNDLTKLKEKECVTTSIYV</u>	287
<b>P-loop</b> <span style="margin-left: 150px;"><b>RNBS-A</b></span>		
AiDSC1	<u>ERRLKSKLLLVLDLVNPEK...IRVIMHCKYQGSRIITTRDSKLEET.IKGRKIVLPINLDRALKLFLSNANSNFPLKFFGLNMLIYAGH</u>	382
NgN	<u>ASRLRSKVLIVLDDIINKHYEYLA...DFNGSRIIITTRDHLIEK...NIIIVYVITALPHESTALEKQHARGKEVENEFFKLSLEVMVYAGL</u>	385
GhDSC1	<u>NERLNKSVLLVLDLISDDQ...DFMG...VTHEFGSKIIVTSRDIQINNGGAKTHVVKLLANDSLLESTFAKQLNBAVFRDLRKEVRYAQSS</u>	384
<b>Kinase-2</b> <span style="margin-left: 100px;"><b>RNBS-B</b></span> <span style="margin-left: 100px;"><b>RNBS-C</b></span>		
AiDSC1	<u>PLALKVLSGSLDCEPDDLYWAKDLRKRSHGDYEVLLTSYEEITTEOKVFLDIAQFRRSENVVYVTSLLNSHG...DSSVVKDLVDRCLITLSDN.RI</u>	481
NgN	<u>PLALKVWGSIDHNRLRTWRKSAHEHMKNNSYSGIDDKLKIISYDLEPKQEMFLDIACFIRREEDVILILESCHICAEYGLRLLIDKSLVFISEVNI</u>	485
GhDSC1	<u>PLALKVGSLLYKSRKWESEVDRLECAQPKLQQLSSFNLDDEIKNIFLDLAIETKRESENVVEILNICYKVDGIRSLDKLDLTKSISEI</u>	484
<b>RNBS-D</b>		
AiDSC1	<u>EMHDMLOVAREISLKVETIGIRDCRWLSRHGNQCWHIRLWSELICDLLIEGLTIRKRGILDSSKLRAIRLSAKAFGMYLKM...KLYDSHCRCG</u>	581
NgN	<u>EMHDIQDMKYLIN.....FQDDEGRRLWLAKVEVVMENITGMAEATVSS.YESTREFSNQAKMKRRLVFNMGRS.....</u>	583
GhDSC1	<u>SMHDMLEMERDITVR.....QESRPEQQRWLWPKIVDQVLYKIKGTLTRGIRKVCMSPIDVRRINPTALQNMHLRRTYFSITRWVGG..</u>	568
<b>MHD</b>		
AiDSC1	<u>EAEIKLHLRRGLSFLPNLITYHHCYPLSHELIFPRKLVLDLLEPHSQLLEIHWDEKDYGLMKWVDSLHINIRQCLGLAIAHNLRLNLEGCNSL</u>	681
NgN	<u>.....STHYADYLEPNLRGFCVCTNYPPSESTBELMLVHQLRNSLRHLEWTRKHLPSLRRIDLWKRTRTPDFTGPNLLYVNLVQCINLEE</u>	657
GhDSC1	<u>..GAYLDQVDDIAYLENLRLGICNDGYFRKLSNSYNENLVLELNGNVNRLWEDD.....HDDVNLRHLDLISYKKR</u>	645
AiDSC1	<u>LESINCLELILYINRIRCTLSLEKGIKTOSLITLILSICSSLKKEPLLS...ENVELLIDETVTLSTFESTQTRRALALIKKCKKIKHLSL</u>	777
NgN	<u>VHHSFGCSVWGHYNCKELRFFWN...TESLIYIGLRSQDLELPELYGRMKPEIQRMQSSIRELSSIQWTHYTKLMLMANNVALPSSH</u>	756
GhDSC1	<u>ENLNRALNLRKTKVCSQDNLVEPELDHIESLDELEFECCNLMEKWP...NIFSLDELSTLEVEVDSIGYLD.MLECDLIS.HSYVQSVSH</u>	739
<b>LRRs</b>		
AiDSC1	<u>YKLLKIQBLILSFCSCQLVPEPIKEQMBSELELLMDISSTEMKMHLSNKTFSICGTSSHVS...SMFEMPTLCSRRTDLYSRQSY...LADITE</u>	875
NgN	<u>CRIKSFVSTSYSCSRLSLEPPEIGDLNIRVFDASDILLRPSSIRLAKLILMFRGFKDG...HFEPEVAEGHSWEYLNLSYCNIDGGLEETE</u>	855
GhDSC1	<u>LKLNLDLDSLSYSPKFPETPKNLISN.....LSCGKNEVSLSSNP.....LSNRRELNGSSIQ...LQCLIA</u>	806
<b>LRRs</b>		
AiDSC1	<u>GLSSIQSICISGNNIENPEFNOINNKWFLEFKMKRSLEVLPONQOYLDHESELLETIAN.....PITPTVGERIHSMFIFSNCYKIQDAQA</u>	969
NgN	<u>SLSSIKKDLSSRNPEHPPSAAGALQSLDLDQQRPTOLPELPEENLHVYCHALKETHLVTKRKKLHRKIDIAHNDIYVNLFAVMEQNISS</u>	955
GhDSC1	<u>.....LFCSEETTGGAPEFLRFRKSLGCTVHEHNSKLLSELPEYVMDLANYLCLSEVVS...SAQHQDLYELHSEFNFCMLFSNCEFLVQSDID</u>	899
AiDSC1	<u>SIVGHRIRKQLANASAKRYRGFPEPVGICYATIPSP...FCHQRLGRSLETFLPPHGDIN...FVGLRSLVVSFKDYEDAKRSVRCGNGFENK</u>	1067
NgN	<u>MRHDISASDLSLSTVFGQPP.....EKIPS...FHHQWGDSSVGNLENKYIPDFLFLFAVQYSR...SLIDITAHLPVGDDEKMSRM</u>	1036
GhDSC1	<u>NIAANMLKIRFLKCKWVSYH...LRRPFYSYEGNIPSNKREHQSNESSLKRTANCSGSRFLVSEICLVADLTELDCSEFCECQLTAASG</u>	996
AiDSC1	<u>DSSFT...DFTLAEMPEGCSISHESRKLTS...DHVFMGYNCSFLVNVHESNSCCPTKASFEFYVDDTRKKIETCEVIKCSMLMVPEPDDDCMLLKT</u>	1167
NgN	<u>TONLALSCEDTSSNYSEWDL.....HFFVPEPAFLDTSKANG...KTPNDYGIIRLSFSGEK.....MYGIRLLKKEGPE.....VN</u>	1108
GhDSC1	<u>.AHEK...KSVQCKQMHSAVSGMG...DHLLIFGDMVKDEG.....VQASFEFYKYLGE.....</u>	1052
AiDSC1	<u>NIVQSLKGPSY...DDIMDDVREFRGLCFVGEPEPGKRRKEEKITVR.....</u>	1219
NgN	<u>ALLQRENSEPTHESTGIIRTYNNRSTFYELN.....</u>	1144
GhDSC1	<u>.....ENMKVKGCVVSYVDEPREQSTT.....</u>	1077

**Figure S2 | Structure-based multiple sequence alignment of the subdomains in *GhDSC1* to known TIR-NBS-LRR proteins.** The secondary structure assignments of the known TIR-NBS-LRR proteins are underlined. Conserved residues are marked by asterisks. *N. glutinosa* *NgN* (Genebank ID: AAA50763.1), and *A. thaliana* *AtRPP5* (Genebank ID: AAF08790.1).