



Fig. S9 Sequence alignment of proteins from four groups of predicted SUMO proteases

A_AT3948860.1	-----TDECT-R-----RGR-S-----E-----E-----RRIRKXIL-----D-SKLRKLNKSAFVGY-LE-----D-VNRFGRDEK--KNSF	122
A_POPTR_0018510280.1	-----LQTFP-C-----SKR-S-----K-----R-RRIRKKA-----IWKIIPKIKLDSGAFDCL-FE-----MHRNRFEDK--RIFI	119
A_POPTR_0018510710.1	-----LQTFP-C-----SKR-S-----K-----R-RRIRKKA-----IWKIIPKIKLDSGAFDCL-FE-----MHRNRFEDK--RIFI	119
A_GSVIVT01007539001.1	-----SMTP-R-----HER-S-----K-----R-RRIRKNI-----IIRKRNKLDYAFKFWY-FR-----NWKFSBDDK--KNSF	118
A_Soly0009007260.1.1	-----SQIKP-RPMSKKA-S-----K-----R-RTADETSEVPLRASRGGGKANNKGLGSKFLX-LE-----MIRKLPEDK--KNSF	266
A_Soly0119072220.1.1	-----LCKLSCSRHRSREGEFLK-GLSKRRN-S-----R-----R-SEGEFR-----RHSRSGKLNKSDFDCL-LE-----MIRKLPEDK--KNSF	286
A_LOC_0811910780.1	-----DQMLP-F-----HRS-S-----K-----R-IAISK-----RDKRDKKLDTEIFELY-NE-----DIWHRIDEDK--KSAV	87
A_Brad14g221605.1	-----YDMLP-Q-----HRS-S-----K-----R-MIYSE-----RERKDKKLDTEIFELY-NE-----DIWHRIDEDK--KSAV	96
A_Brad14g22300.Z	-----YDMLP-Q-----SRV-S-----E-----R-HAISR-----RDKRDKKLDTEIFELY-NE-----DIWHRIDEDK--KSAV	73
A_Brad14g22300.Z	-----YDMLP-Q-----SRV-S-----E-----R-HAISR-----RDKRDKKLDTEIFELY-NE-----DIWHRIDEDK--KSAV	73
A_GRM2MG0545326_T01	-----YDMLP-Q-----GRA-S-----R-----R-HAISR-----RDKRDKKLDTEIFELY-NE-----DIWHRIDEDK--KSAV	113
B2_AT4633620.1	-----SRKEGGVLIARDISGIDLLAFVSDVEMSRVETIR-SLDSRHK-NIWFDTIT-----ESETAFSGHDLGSL-----THLADSFEDLVY-----FG-----GDPA-----VVVRQDI-----ELNLPKRFIMDTIIDFY-IR-----ELNLPISFKE--RGRF	345
B2_AT1609730.1	-----LKD-----ENCHDEMEELIKVKNEMPKRQKIM-SLWVETP-AVWMDLE-----DDVEVS-GI-----LMDQRKFPSTDFEDVY-----FK-----GDPA-----VEISKRDV-----ELLPETVNDTIIDFY-IR-----ELNLPISFKE--RGRF	166
B2_POPTR_0008511970.1	-----KSDVADQADTQMGSGVELEVVVVEPMNRKNEETI-SLNRKYS-ALLSVIND-----MDIANN-GV-----DELDQRRTVPSDFSEKEDVYI-----FK-----GDPA-----VEISKRDV-----ELLPETVNDTIIDFY-IR-----ELNLPISFKE--RGRF	369
B2_POPTR_0002510590.1	-----SKDVAQADTQMGSGVELEVVVVEPMNRKNEETI-SLNRKYS-ALLSVIND-----MDIANN-GV-----DELDQRRTVPSDFSEKEDVYI-----FK-----GDPA-----VEISKRDV-----ELLPETVNDTIIDFY-IR-----ELNLPISFKE--RGRF	369
B2_POPTR_0017601140.F	-----VDLKNFVSDVEMSRVETIR-SLWVETP-AVWMDLE-----DDVEVS-GI-----LMDQRKFPSTDFEDVY-----FK-----GDPA-----VEISKRDV-----ELLPETVNDTIIDFY-IR-----ELNLPISFKE--RGRF	378
B2_POPTR_0007503240.1	-----KVSQGNMNDTQMGSGVELEVVVVEPMNRKNEETI-SLNRKYS-ALLSVIND-----MDIANN-GV-----DELDQRRTVPSDFSEKEDVYI-----FK-----GDPA-----VEISKRDV-----ELLPETVNDTIIDFY-IR-----ELNLPISFKE--RGRF	378
B2_GSVIVT01009173001.F	-----RAM-----WIELKAFVVDENRVEGRKTI-SLNRKYS-ALLSVIND-----MDIANN-GV-----DELDQRRTVPSDFSEKEDVYI-----FK-----GDPA-----VEISKRDV-----ELLPETVNDTIIDFY-IR-----ELNLPISFKE--RGRF	362
B2_Soly0019105830.1.1	-----CNDSDVYVNDNESGAVLVLFDLFDVNSIEGALK-MLNVRKA-DKWNIDTA-----LDPTREYGFYGRKISIVLENDHPNTRFPEIIF-----FE-----GDPA-----VEISKRDV-----ELLPETVNDTIIDFY-IR-----ELNLPISFKE--RGRF	215
B2_Soly0119017040.1.1	-----KRTTAGENMAGTSSIEEVEFAVDVDSSEKCAIQ-SLDV-YK-AVWNSHSE-----NEKWRNSQGET-----SNQLPKKXTPSYTEPELVY-----FK-----GDPA-----VCISKRDF-----DLLPETVNDTIIDFY-IR-----ELNLPISFKE--RGRF	366
B2_LOC_080511170.1	-----VSGSTEZGMSKDRIDFCLIDSDVPRKQNIW-HLASKYQ-EIWNHIPS-----GDFASEMNIIEP-----SLFPFQVYFDTE-EPEDVYI-----FK-----GDPA-----VEISKRDV-----ELLPETVNDTIIDFY-IR-----ELNLPISFKE--RGRF	338
B2_Brad14g60830.1	-----VGSKARAKNSGPRVUFGLADVEMNRKQEKIW-HLASKYQ-EIWNHIPS-----GDFASEMNIIEP-----SLFPFQVYFDTE-EPEDVYI-----FK-----GDPA-----VEISKRDV-----ELLPETVNDTIIDFY-IR-----ELNLPISFKE--RGRF	293
B2_Soly02040230.F	-----PVKAGFSLDQVPRKQEKIW-HLASKYQ-EIWNHIPS-----GDFASEMNIIEP-----SLFPFQVYFDTE-EPEDVYI-----FK-----GDPA-----VEISKRDV-----ELLPETVNDTIIDFY-IR-----ELNLPISFKE--RGRF	226
B2_GSM2MG0117324.F	-----SFCVGVDEVAIVGVEDTCSGGPVRKFELEDSGPRKQEKIW-HLASKYQ-EIWNHIPS-----GDFASEMNIIEP-----SLFPFQVYFDTE-EPEDVYI-----FK-----GDPA-----VEISKRDV-----ELLPETVNDTIIDFY-IR-----ELNLPISFKE--RGRF	184
B1_AT160420.1.UPLID	-----EAGPSTVAEQAL-ELFEGG-F-----D-ICY-----FTK-----DDPHF-----VQVCLKDL-----KCLAPKAYLISPVNHFY-IR-----YVQDIPVADK-TAANC	373
B1_AT1610870.1.0T82	-----EFLSPVVEAC-ELFEGG-F-----D-ICY-----FTK-----DDPHF-----VQVCLKDL-----KCLAPKAYLISPVNHFY-IR-----YVQDIPVADK-TAANC	373
B1_POPTR_0010804980.F	-----EFG-LGTTELAK-ELCHKH-D-----AKIYS-ADPA-S-----R-----R-IRLQASFAVAKKVD-----KCLAPKAYLISPVNHFY-IR-----YVQDIPVADK-TAANC	332
B1_GSVIVT01002028001.F	-----EFLDKPMQAT-KITDRK-E-----D-ICY-----FTK-----DDPHF-----VQVCLKDL-----KCLAPKAYLISPVNHFY-IR-----YVQDIPVADK-TAANC	100
B1_Soly0046028200.1.1	-----EFLDKPMQAT-KITDRK-E-----D-ICY-----FTK-----DDPHF-----VQVCLKDL-----KCLAPKAYLISPVNHFY-IR-----YVQDIPVADK-TAANC	240
B1_Soly0086009530.1.1	-----EFDVVEFQDQAN-HVSEKX-A-----D-ICY-----FTK-----DDPHF-----VQVCLKDL-----KCLAPKAYLISPVNHFY-IR-----YVQDIPVADK-TAANC	246
B1_LOC_080629310.1	-----TCI-----SDRAE-KSSACD-A-----MKNHY-FSW-----DTPN-----LELSYSDM-----KCLPEPELSSPVNHFY-IR-----YVQDIPVADK-TAANC	285
B1_LOC_081291380.1	-----DQVE-----GQVDC-FMMDRN-E-----MKNHY-FSW-----DTPN-----LELSYSDM-----KCLPEPELSSPVNHFY-IR-----YVQDIPVADK-TAANC	370
B1_LOC_080193830.F	-----DQVE-----GQVDC-FMMDRN-E-----MKNHY-FSW-----DTPN-----LELSYSDM-----KCLPEPELSSPVNHFY-IR-----YVQDIPVADK-TAANC	387
B1_Brad14g22280.1	-----MKNHY-FSW-----DTPN-----LELSYSDM-----KCLPEPELSSPVNHFY-IR-----YVQDIPVADK-TAANC	215
B1_Brad14g22360.1	-----DQVE-----EFVDC-VSDKI-E-----MKNHY-FSW-----DTPN-----LELSYSDM-----KCLPEPELSSPVNHFY-IR-----YVQDIPVADK-TAANC	335
B1_Sb04g001916.1.F	-----DQVE-----EFVDC-VSDKI-E-----MKNHY-FSW-----DTPN-----LELSYSDM-----KCLPEPELSSPVNHFY-IR-----YVQDIPVADK-TAANC	271
B1_Sb04g020230.1.F	-----DQVE-----EFVDC-VSDKI-E-----MKNHY-FSW-----DTPN-----LELSYSDM-----KCLPEPELSSPVNHFY-IR-----YVQDIPVADK-TAANC	280
B1_Sb08g020823.F	-----DQVE-----EFVDC-VSDKI-E-----MKNHY-FSW-----DTPN-----LELSYSDM-----KCLPEPELSSPVNHFY-IR-----YVQDIPVADK-TAANC	276
B1_Sb08g020827.F	-----DQVE-----EFVDC-VSDKI-E-----MKNHY-FSW-----DTPN-----LELSYSDM-----KCLPEPELSSPVNHFY-IR-----YVQDIPVADK-TAANC	84
B1_Sb03g03030.1	-----DQVE-----EFVDC-VSDKI-E-----MKNHY-FSW-----DTPN-----LELSYSDM-----KCLPEPELSSPVNHFY-IR-----YVQDIPVADK-TAANC	327
B1_Sb10g014910.1	-----DQVE-----EFVDC-VSDKI-E-----MKNHY-FSW-----DTPN-----LELSYSDM-----KCLPEPELSSPVNHFY-IR-----YVQDIPVADK-TAANC	26
B1_GRM2MG0432931.F	-----DQVE-----EFVDC-VSDKI-E-----MKNHY-FSW-----DTPN-----LELSYSDM-----KCLPEPELSSPVNHFY-IR-----YVQDIPVADK-TAANC	26
B1_GRM2MG072939_T01	-----DQVE-----EFVDC-VSDKI-E-----MKNHY-FSW-----DTPN-----LELSYSDM-----KCLPEPELSSPVNHFY-IR-----YVQDIPVADK-TAANC	317
B1_GRM2MG0138175.F	-----DQVE-----EFVDC-VSDKI-E-----MKNHY-FSW-----DTPN-----LELSYSDM-----KCLPEPELSSPVNHFY-IR-----YVQDIPVADK-TAANC	317
B1_GRM2MG0174667.F	-----DQVE-----EFVDC-VSDKI-E-----MKNHY-FSW-----DTPN-----LELSYSDM-----KCLPEPELSSPVNHFY-IR-----YVQDIPVADK-TAANC	182
B1_GRM2MG0142553_mod	-----DQVE-----EFVDC-VSDKI-E-----MKNHY-FSW-----DTPN-----LELSYSDM-----KCLPEPELSSPVNHFY-IR-----YVQDIPVADK-TAANC	347
C_AT4615880.1.E8D4	-----FRVEDISVGLDSELDVVDN-DASSLEAZKMLQMSAE-KRNKSLK-ZALGFEVLNENKLLSRSRPTVE-----KRVEVFRPFIETLDEEAEVYKAFSGRN-RKRVLAHNSHNS-IDTIGEDL-----KCLIPSAWLNDEVINLY-LE-----LIEREREPKFLK	230
C_AT4606690.1.UPLID	-----RTEFPRKRLACKRFLNFKLLVRASVLEKKAARCSQGVVNDKRIEHSNSRGRFGKGNFVSSDET-----KRLVAQGEFQFLMDEEVALVNSALSKRN-RKRVLAHNSHNS-IDTIGEDL-----KCLIPSAWLNDEVINLY-LE-----LIEREREPKFLK	181
C_AT3606910.1.UPLID	-----RVEGCSKANSBSLVNRPVPT-----DVTGFVAKRNVLEGAV-NRKSRLK-DRGFVDFKRRGALLRSLSSVWQDEEPEVQREAFVLSPEEETAVRRAFSN-----DENLIVYRNSHNS-IDTIGEDL-----KCLIPSAWLNDEVINLY-LE-----LIEREREPKFLK	342
C_POPTR_00106001730.1	-----LAVENRGMGLSGLALNHPT-----GVLVTEVTKLLEDEE-RNRKRLG-SLAFEILYVNRKMSFKALRFPVKE-----FVEKISNPFIEETPEEIVKQAFVFN-RKRVLAHNSHNS-IDTIGEDL-----KCLIPSAWLNDEVINLY-LE-----LIEREREPKFLK	358
C_POPTR_0008522250.1	-----LAVENRGMGLSGLALNHPT-----GVLVTEVTKLLEDEE-RNRKRLG-SLAFEILYVNRKMSFKALRFPVKE-----FVEKISNPFIEETPEEIVKQAFVFN-RKRVLAHNSHNS-IDTIGEDL-----KCLIPSAWLNDEVINLY-LE-----LIEREREPKFLK	358
C_GSVIVT0101729001	-----LAVENRGMGLSGLALNHPT-----GVLVTEVTKLLEDEE-RNRKRLG-SLAFEILYVNRKMSFKALRFPVKE-----FVEKISNPFIEETPEEIVKQAFVFN-RKRVLAHNSHNS-IDTIGEDL-----KCLIPSAWLNDEVINLY-LE-----LIEREREPKFLK	358
C_Soly0129099520.1.1	-----LAVENRGMGLSGLALNHPT-----GVLVTEVTKLLEDEE-RNRKRLG-SLAFEILYVNRKMSFKALRFPVKE-----FVEKISNPFIEETPEEIVKQAFVFN-RKRVLAHNSHNS-IDTIGEDL-----KCLIPSAWLNDEVINLY-LE-----LIEREREPKFLK	362
C_Soly0019068830.1.1	-----LAVENRGMGLSGLALNHPT-----GVLVTEVTKLLEDEE-RNRKRLG-SLAFEILYVNRKMSFKALRFPVKE-----FVEKISNPFIEETPEEIVKQAFVFN-RKRVLAHNSHNS-IDTIGEDL-----KCLIPSAWLNDEVINLY-LE-----LIEREREPKFLK	358
C_Brad11g18100.1	-----LAVENRGMGLSGLALNHPT-----GVLVTEVTKLLEDEE-RNRKRLG-SLAFEILYVNRKMSFKALRFPVKE-----FVEKISNPFIEETPEEIVKQAFVFN-RKRVLAHNSHNS-IDTIGEDL-----KCLIPSAWLNDEVINLY-LE-----LIEREREPKFLK	234
C_LOC_080329630.1	-----LAVENRGMGLSGLALNHPT-----GVLVTEVTKLLEDEE-RNRKRLG-SLAFEILYVNRKMSFKALRFPVKE-----FVEKISNPFIEETPEEIVKQAFVFN-RKRVLAHNSHNS-IDTIGEDL-----KCLIPSAWLNDEVINLY-LE-----LIEREREPKFLK	237
C_Sb02g042620.1	-----LAVENRGMGLSGLALNHPT-----GVLVTEVTKLLEDEE-RNRKRLG-SLAFEILYVNRKMSFKALRFPVKE-----FVEKISNPFIEETPEEIVKQAFVFN-RKRVLAHNSHNS-IDTIGEDL-----KCLIPSAWLNDEVINLY-LE-----LIEREREPKFLK	247
C_GSM2MG010505_T01	-----LAVENRGMGLSGLALNHPT-----GVLVTEVTKLLEDEE-RNRKRLG-SLAFEILYVNRKMSFKALRFPVKE-----FVEKISNPFIEETPEEIVKQAFVFN-RKRVLAHNSHNS-IDTIGEDL-----KCLIPSAWLNDEVINLY-LE-----LIEREREPKFLK	377
C_LOC_080322240.1	-----LAVENRGMGLSGLALNHPT-----GVLVTEVTKLLEDEE-RNRKRLG-SLAFEILYVNRKMSFKALRFPVKE-----FVEKISNPFIEETPEEIVKQAFVFN-RKRVLAHNSHNS-IDTIGEDL-----KCLIPSAWLNDEVINLY-LE-----LIEREREPKFLK	258
C_Brad11g2760.1	-----LAVENRGMGLSGLALNHPT-----GVLVTEVTKLLEDEE-RNRKRLG-SLAFEILYVNRKMSFKALRFPVKE-----FVEKISNPFIEETPEEIVKQAFVFN-RKRVLAHNSHNS-IDTIGEDL-----KCLIPSAWLNDEVINLY-LE-----LIEREREPKFLK	243
C_GRM2MG049989_T01	-----LAVENRGMGLSGLALNHPT-----GVLVTEVTKLLEDEE-RNRKRLG-SLAFEILYVNRKMSFKALRFPVKE-----FVEKISNPFIEETPEEIVKQAFVFN-RKRVLAHNSHNS-IDTIGEDL-----KCLIPSAWLNDEVINLY-LE-----LIEREREPKFLK	264
C_GSM2MG035640.1	-----LAVENRGMGLSGLALNHPT-----GVLVTEVTKLLEDEE-RNRKRLG-SLAFEILYVNRKMSFKALRFPVKE-----FVEKISNPFIEETPEEIVKQAFVFN-RKRVLAHNSHNS-IDTIGEDL-----KCLIPSAWLNDEVINLY-LE-----LIEREREPKFLK	219
C_GSM2MG088063_T01	-----LAVENRGMGLSGLALNHPT-----GVLVTEVTKLLEDEE-RNRKRLG-SLAFEILYVNRKMSFKALRFPVKE-----FVEKISNPFIEETPEEIVKQAFVFN-RKRVLAHNSHNS-IDTIGEDL-----KCLIPSAWLNDEVINLY-LE-----LIEREREPKFLK	335
C_Sb03g013930.1	-----LAVENRGMGLSGLALNHPT-----GVLVTEVTKLLEDEE-RNRKRLG-SLAFEILYVNRKMSFKALRFPVKE-----FVEKISNPFIEETPEEIVKQAFVFN-RKRVLAHNSHNS-IDTIGEDL-----KCLIPSAWLNDEVINLY-LE-----LIEREREPKFLK	340
C_GSM2MG012601_T01	-----LAVENRGMGLSGLALNHPT-----GVLVTEVTKLLEDEE-RNRKRLG-SLAFEILYVNRKMSFKALRFPVKE-----FVEKISNPFIEETPEEIVKQAFVFN-RKRVLAHNSHNS-IDTIGEDL-----KCLIPSAWLNDEVINLY-LE-----LIEREREPKFLK	342
C_Brad1212720.1	-----LAVENRGMGLSGLALNHPT-----GVLVTEVTKLLEDEE-RNRKRLG-SLAFEILYVNRKMSFKALRFPVKE-----FVEKISNPFIEETPEEIVKQAFVFN-RKRVLAHNSHNS-IDTIGEDL-----KCLIPSAWLNDEVINLY-LE-----LIEREREPKFLK	323
C_LOC_0801925370.1	-----LAVENRGMGLSGLALNHPT-----GVLVTEVTKLLEDEE-RNRKRLG-SLAFEILYVNRKMSFKALRFPVKE-----FVEKISNPFIEETPEEIVKQAFVFN-RKRVLAHNSHNS-IDTIGEDL-----KCLIPSAWLNDEVINLY-LE-----LIEREREPKFLK	339

Fig. S9 continued

A_AT3G48480.1	-----	288
A_POPTR_0018s10280.1	-----	292
A_POPTR_0010s18760.1	-----	298
A_GSVIVT01007539001	-----	296
A_Solyc00g007260.1.1	-----	360
A_Solyc11g072220.1.1	-----	379
A_LOC_0s11g0780.1	-----	165
A_Brad1g22406.1	-----	266
A_Brad1g22360.E	-----	265
A_Sb05g009053.1	-----	238
A_GRMGM2G949329_T01	-----	300
B1_AT1G33620.1	-----	753
B2_AT1G09730.1	K-----	963
B2_POPTR_0008s17970.1	-----	956
B2_POPTR_0002s10990.1	TKSLKDLAL	1041
B2_POPTR_0017s07140.F	-----	651
B2_POPTR_0007s03240.1	-----	871
B2_GSVIVT01009173001.F	HKSLKDLAL	898
B2_Solyc01g105830.1.1	DLS-----	770
B2_Solyc11g017040.1.1	RSSVTMDLIL	855
B2_LOC_0s05g11770.1	---ATP----	991
B2_Brad1g60830.1	-----F-----	928
B2_Sb03g040230.F	ETSTD-----	1069
B2_GRMGM2G177324.F	-----	394
B1_AT1G060220.1 ULP1D	-----	584
B1_AT1G10570.1 0352	-----	571
B1_POPTR_0010s04480.F	-----	845
B1_GSVIVT01020235001.F	-----	382
B1_Solyc01g026200.1.1	-----	437
B1_Solyc05g006630.1.1	-----	544
B1_LOC_0s06g29310.1	-----	522
B1_LOC_0s12g1360.1	-----	725
B1_LOC_0s01g3630.F	-----	504
B1_Brad1g42280.1	-----	875
B1_Brad1g02360.I	-----	669
B1_Sb01g001916.1.F	-----	693
B1_Sb06g020821.F	-----	878
B1_Sb06g020823.F	-----	875
B1_Sb06g020827.F	-----	356
B1_Sb03g034020.1	-----	537
B1_Sb10g016910.1.	-----	220
B1_GRMGM2G432931.F	-----	335
B1_GRMGM2G072529_T01	-----	629
B1_GRMGM2G381786.F	-----	547
B1_GRMGM2G174667.F	-----	472
B1_GRMGM2G142853_mod	-----	553
C_AT4G18880.1 ESD4	-----	489
C_AT1G000590.1 ULP1B	-----	315
C_AT3G06910.1 ULP1A	-----	802
C_POPTR_0010s01730.1	-----	511
C_POPTR_0082s00230.1	-----	516
C_POPTR_0008s22280.1	-----	516
C_GSVIVT01017729001	-----	556
C_Solyc12g099830.1.1	-----	522
C_Solyc01g066830.1.1	-----	515
C_Brad1g18100.1	-----	403
C_LOC_0s03g29630.1	-----	397
C_Sb02g042620.1	-----	306
C_GRMGM2G010608_T01	-----	524
C_LOC_0s03g22400.1	-----	418
C_Brad1g62760.1	-----	403
C_GRMGM2G849959_T01	-----	413
C_Sb01g038640.1	-----	409
C_GRMGM2G088683_T01	-----	493
C_Sb03g013930.1	-----	498
C_GRMGM2G012601_T01	-----	500
C_Brad1g12720.1	-----	381
C_LOC_0s01g25370.1	-----	197
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Fig. S9 continued