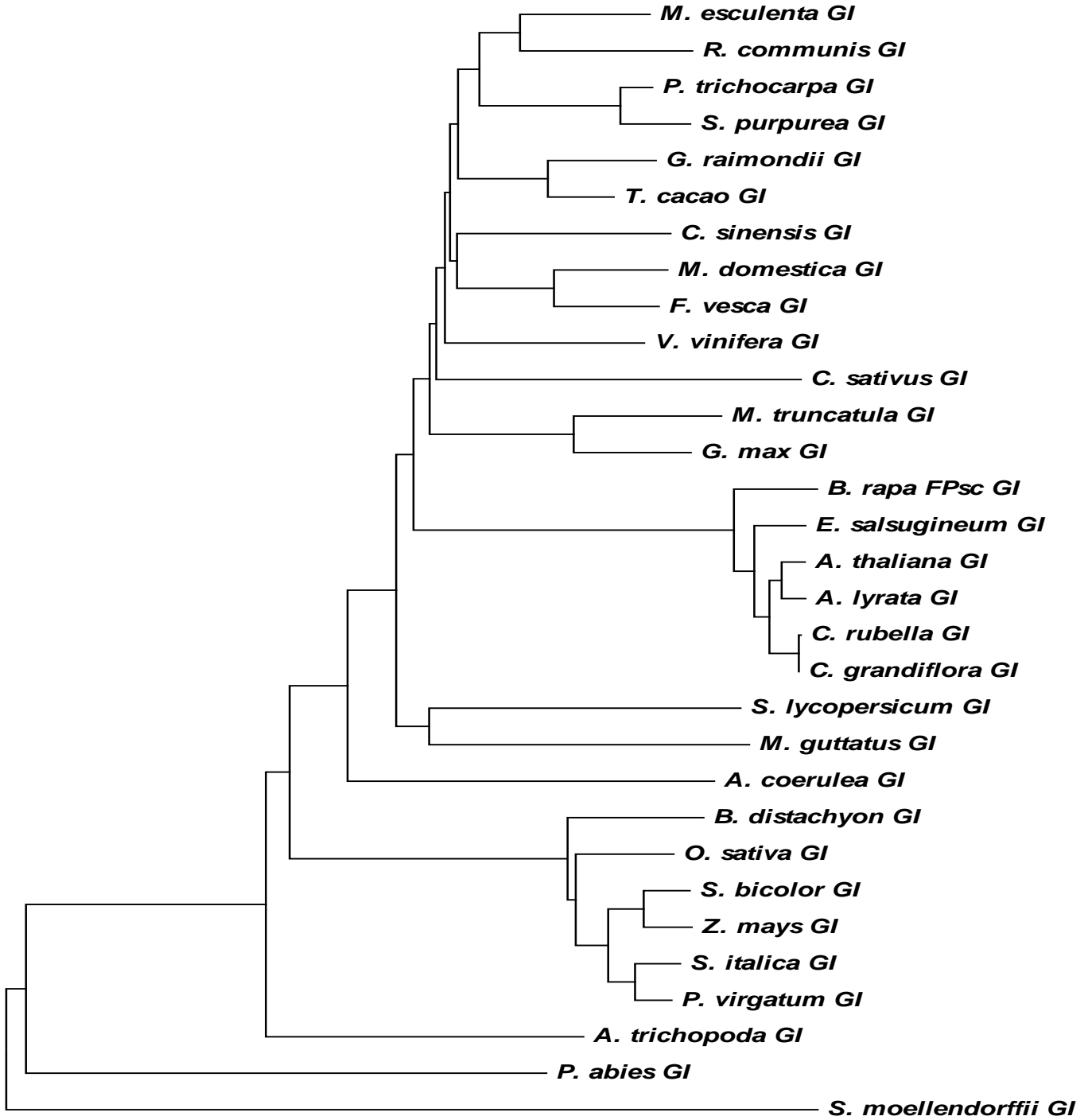


a



0.05

S. moellendorffii_GI 181 KRLLIPWETD SLLAAPLGTK SDYFRWCGGV LGKYAGGD L RPPTTGDGKCG HGKHPQLSS TPRWAVANGA AVTSVVDDE VLRVETALIT AAAPALLLP

Table with 18 rows (M. truncatula_GI to S. moellendorffii_GI) and 16 columns (310-400). Each row contains a species name and a sequence of amino acid single-letter codes.

Table with 18 rows (M. truncatula_GI to S. moellendorffii_GI) and 16 columns (410-500). Each row contains a species name and a sequence of amino acid single-letter codes.

Table with 18 rows (M. truncatula_GI to A. trichopoda_GI) and 16 columns (510-600). Each row contains a species name and a sequence of amino acid single-letter codes.

Multiple sequence alignment of a protein region across various species including P. abies_GI, S. moellendorffii_GI, M. truncatula_GI, and others. The alignment shows conserved amino acid sequences with positions 610-800 and 810-900. Species names are listed on the left, and residue numbers are indicated at the top and bottom. The sequences consist of single-letter amino acid codes.

A. trichopoda_GI 739 LMKCKWNEI HTRASSLYHL IDIHCKAVAS IVCKAEPLA NIVHASDRND APISFKGRKH IKSSS---FE EDNIPHEKTE STKESSEFLK SEKAN-FLTD
P. abies_GI 768 MRRCKMDSLEI CARASTVLAAL IDVNRKAVAS IIDKSESSVS IVQVRAENNY STDRAAYSQV GIHTEVAIDQ NHEGGNSLSL ENCHGQVEVK SHNGQEKFKM
S. moellendorffii_GI 723 IVRCKWDPGV SSKAASLAL VDGNDKAVFA VFVYADKLSG DEKRTLSSXQ AOKIISGFTK D-----

910 920 930 940 950 960 970 980 990 1000
M. truncatula_GI 868 EASGVNLLGKG VTSFSLDASD LANFLTMDRH IGLNNGTIF LISLSEKQE LCFSVSLLW HKLIASPETQ PCESTSAQO GWRQVDALC NVVASPAKA
G. max_GI 868 -ASDYTLGKG VTSFSLDASD LANFLTMDRH IGLNNGTIF LRSVLAEKQE LCFSVSLLW HKLIASPETQ PCESTSAQO GWRQVDALC NVVASPAKA
C. sativus_GI 861 VDLENLTKGR IASFLDASE LANFLTDRL IGFNGCAITL LRSVLAEKQE LCFSVSLLW HKLIASPETQ PSAEFTSAQO GWRQVDALC NVVASPAKA
M. domestica_GI 861 EGSNTLTKGK IASFLDASE LANFLTKDRH IGFNGCAITL LRSVLAEKQE LCFSVSLLW YKLIASPETQ PSAEFTSAQO GWRQVDALC NVVASPAKA
F. vesca_GI 870 GGS--TFGKG IASFLDASE LANFLTDRL IGFNGCAITL LRSVLAEKQE LCFSVSLLW HKLIASPETQ PSAEFTSAQO GWRQVDALC NVVASPAKA
A. thaliana_GI 860 SG--RPSEKGI IASFLDASE LANFLTDRL AGFYGTQKL LRSVLAEKQE LCFSVSLLW HKLIASPETQ PTAESTSAQO GWRQVDALC NVVASPAKA
A. lyrata_GI 860 SG--RPSEKGI IASFLDASE LANFLTDRL AGFYGTQKL LRSVLAEKQE LCFSVSLLW HKLIASPETQ PTAESTSAQO GWRQVDALC NVVASPAKA
C. rubella_GI 858 SG--RPSEKGI IASFLDASE LANFLTDRL AGFYGTQKL LRSVLAEKQE LCFSVSLLW HKLIASPETQ PTAESTSAQO GWRQVDALC NVVASPAKA
C. grandiflora_GI 858 SG--RPSEKGI IASFLDASE LANFLTDRL AGFYGTQKL LRSVLAEKQE LCFSVSLLW HKLIASPETQ PTAESTSAQO GWRQVDALC NVVASPAKA
B. rapa Fpsc_GI 851 SGRSSSEKGI IKDILLDASD LANFLTDRL AGFYGTQKL LRSVLAEKQE LCFSVSLLW HKLIASPETQ PTAESTSAQO GWRQVDALC NVVASPAKA
E. salsgineum_GI 855 SGT-RHSEKGI IKDILLDASD LANFLTDRL AGFYGTQKL LRSVLAEKQE LCFSVSLLW HKLIASPETQ PTAESTSAQO GWRQVDALC NVVASPAKA
G. raimondii_GI 860 EGLNLSGKG IASFLDASE LANFLTDRL IGFNGCAITL LRSVLAEKQE LCFSVSLLW HKLIASPETQ PSAEFTSAQO GWRQVDALC NVVASPAKA
T. cacao_GI 861 EGSNSLTKGK IASFLDASE LANFLTMDRH IGFNGCAITL LRSVLAEKQE LCFSVSLLW HKLIASPETQ PSAEFTSAQO GWRQVDALC NVVASPAKA
C. sinensis_GI 856 ESSGNLTKGK IASFLDASE LANFLTMDRH IGFNGCAITL LRSVLAEKQE LCFSVSLLW NKLIAAPETQ PSAEFTSAQO GWRQVDALC NVVASPAKA
M. esculenta_GI 863 EGSNTLTKGK IASFLDASE LANFLTMDRH IGFNGCAITL LRSVLAEKQE LCFSVSLLW HKLIASPETQ PSAEFTSAQO GWRQVDALC NVVASPAKA
R. communis_GI 852 EGSNTLTKGK IASFLDASE LANFLTMDRH IGFNGCAITL LRSVLAEKQE LCFSVSLLW HKLIASPETQ PSAEFTSAQO GWRQVDALC NVVASPAKA
P. trichocarpa_GI 862 EGSNTLTKGK IASFLDASE LANFLTMDRH IGFNGCAITL LRSVLAEKQE LCFSVSLLW QKLIASPETQ PSAEFTSAQO GWRQVDALC NVVASPAKA
S. purpurea_GI 861 EGSNTLTKGK IASFLDASE LANFLTMDRH IGFNGCAITL LRSVLAEKQE LCFSVSLLW QKLIASPETQ PSAEFTSAQO GWRQVDALC NVVASPAKA
V. vinifera_GI 863 EGTGNSLTKGK IASFLDASE LANFLTMDRH IGFNGCAITL LRSVLAEKQE LCFSVSLLW HKLIASPETQ PSAEFTSAQO GWRQVDALC NVVASPAKA
S. lycopersicum_GI 859 AAO--TSGKGI IASFLDASE LANFLTMDRL IGFNGCAEDL IKSVLTEBEE LCFSVSLLW HKLIASPETQ PSAEFTSAQO GWRQVDALC NVVASPAKA
M. guttatus_GI 855 VER--CSTGKI ISSPFDASD LANFLTMDRH IGFNGCAITL IKSVLTEBEE LCFSVSLLW HKLIASPETQ PSAEFTSAQO GWRQVDALC NVVASPAKA
A. coerulea_GI 862 ANARNTGKG IASLPTDASD LANFLTMDRH IGFNGCAITL IKSVLTEBEE LCFSVSLLW HKLIASPETQ PSAEFTSAQO GWRQVDALC NVVASPAKA
S. bicolor_GI 853 VAS--TSKGI IASLQVEASD LANFLTMDRN GGYRG--SOTL LRSVLAEKQE LCFSVSLLW QKLIASPETQ PSAEFTSAQO GWRQVDALC NVVASPAKA
Z. mays_GI 851 VAS--TSKGI IASLQVEASD LANFLTMDRN GGYRG--SOTL LRSVLAEKQE LCFSVSLLW QKLIASPETQ PSAEFTSAQO GWRQVDALC NVVASPAKA
S. italica_GI 852 VAS--TSKGI IASLQVEASD LANFLTMDRN GGYRG--SOTL LRSVLAEKQE LCFSVSLLW QKLIASPETQ PSAEFTSAQO GWRQVDALC NVVASPAKA
P. virgatum_GI 853 VAS--TSKGI IASLQVEASD LANFLTMDRN GGYRG--SOTL LRSVLAEKQE LCFSVSLLW QKLIASPETQ PSAEFTSAQO GWRQVDALC NVVASPAKA
O. sativa_GI 852 VAS--TSKGI IASLQVEASD LANFLTMDRN GGYRG--SOTL LRSVLAEKQE LCFSVSLLW QKLIASPETQ PSAEFTSAQO GWRQVDALC NVVASPAKA
B. distachyon_GI 858 VAS--TSKGI IASLQVEASD LANFLTMDRN GGYRG--SOTL LRSVLAEKQE LCFSVSLLW QKLIASPETQ PSAEFTSAQO GWRQVDALC NVVASPAKA
A. trichopoda_GI 835 VMLS--GKGI IASLQVEASD LANFLTMDRN IGFNGCAITL LRSVLAEKQE LCFSVSLLW HKLIASPETQ PSAEFTSAQO GWRQVDALC NVVASPAKA
P. abies_GI 868 DVVIAGSGK IANLSMDGSD VVSLTVDRH KVVNHVGNF VTAVLEKRD LGVAVPPLL QRLTAPETQ PSAEFTSAQO GWRQVDALC NVVASPAKA
S. moellendorffii_GI 783 -----GVK DASLSLNASD VTNLTCG--C NGVSTVSDL IKAFLKQRD LAVALPPLL QRLTAPETQ PSAEFTSAQO GWRQVDALC NVVASPAKA

1010 1020 1030 1040 1050 1060 1070 1080 1090 1100
M. truncatula_GI 968 ATAVVLOAEK ELQPWIAKDD DLGQKMMWRIN QRIVKLIVEL MRNHDSAESL VILASASDILL LRATDGMVLD GEACTLPQLE LLEATARAIV PVLEWGESGL
G. max_GI 968 ATAVVLOAER ELQPWIAKDD DLGQKMMWRIN QRIVKLIVEL MRNHDSAESL VILASASDILL LRATDGMVLD GEACTLPQLE LLEATARAIV PVLEWGESGL
C. sativus_GI 961 AAAVVLOADR ELQPWIAKDD DLGQKMMWRIN QRIVKLIVEL MRNHDSAESL VILASASDILL LRATDGMVLD GEACTLPQLE LLEATARAIV PVLEWGESGL
M. domestica_GI 961 ATAVVLOAER ELQPWIAKDD DLGQKMMWRIN QRIVKLIVEL MRNHDSAESL VILASASDILL LRATDGMVLD GEACTLPQLE LLEATARAIV PVLEWGESGL
F. vesca_GI 969 AAAVVLOAER ELQPWIAKDD DLGQKMMWRIN QRIVKLIVEL MRNHDSAESL VILASASDILL LRATDGMVLD GEACTLPQLE LLEATARAIV PVLEWGESGL
A. thaliana_GI 958 AAAVVLOAER ELQPWIAKDD DLGQKMMWRIN QRIVKLIVEL MRNHDSAESL VILASASDILL LRATDGMVLD GEACTLPQLE LLEATARAIV PVLEWGESGL
A. lyrata_GI 959 AAAVVLOAER ELQPWIAKDD DLGQKMMWRIN QRIVKLIVEL MRNHDSAESL VILASASDILL LRATDGMVLD GEACTLPQLE LLEATARAIV PVLEWGESGL
C. rubella_GI 956 AAAVVLOAER ELQPWIAKDD DLGQKMMWRIN QRIVKLIVEL MRNHDSAESL VILASASDILL LRATDGMVLD GEACTLPQLE LLEATARAIV PVLEWGESGL
C. grandiflora_GI 956 AAAVVLOAER ELQPWIAKDD DLGQKMMWRIN QRIVKLIVEL MRNHDSAESL VILASASDILL LRATDGMVLD GEACTLPQLE LLEATARAIV PVLEWGESGL
B. rapa Fpsc_GI 951 AAAVVLOAER ELQPWIAKDD DLGQKMMWRIN QRIVKLIVEL MRNHDSAESL VILASASDILL LRATDGMVLD GEACTLPQLE LLEATARAIV PVLEWGESGL
E. salsgineum_GI 954 AAAVVLOAER ELQPWIAKDD DLGQKMMWRIN QRIVKLIVEL MRNHDSAESL VILASASDILL LRATDGMVLD GEACTLPQLE LLEATARAIV PVLEWGESGL
G. raimondii_GI 960 TIAVVLOADR ELQPWIAKDD DLGQKMMWRIN QRIVKLIVEL MRNHDSAESL VILASASDILL LRATDGMVLD GEACTLPQLE LLEATARAIV PVLEWGESGL
T. cacao_GI 961 ATAVVLOAER ELQPWIAKDD DLGQKMMWRIN QRIVKLIVEL MRNHDSAESL VILASASDILL LRATDGMVLD GEACTLPQLE LLEATARAIV PVLEWGESGL
C. sinensis_GI 956 ATAVVLOAER ELQPWIAKDD DLGQKMMWRIN QRIVKLIVEL MRNHDSAESL VILASASDILL LRATDGMVLD GEACTLPQLE LLEATARAIV PVLEWGESGL
M. esculenta_GI 963 ATAVVLOAER ELQPWIAKDD DLGQKMMWRIN QRIVKLIVEL MRNHDSAESL VILASASDILL LRATDGMVLD GEACTLPQLE LLEATARAIV PVLEWGESGL
R. communis_GI 952 AAAVVLOAER ELQPWIAKDD DLGQKMMWRIN QRIVKLIVEL MRNHDSAESL VILASASDILL LRATDGMVLD GEACTLPQLE LLEATARAIV PVLEWGESGL
P. trichocarpa_GI 962 ATAVVLOAER ELQPWIAKDD DLGQKMMWRIN QRIVKLIVEL MRNHDSAESL VILASASDILL LRATDGMVLD GEACTLPQLE LLEATARAIV PVLEWGESGL
S. purpurea_GI 961 ATAVVLOAER ELQPWIAKDD DLGQKMMWRIN QRIVKLIVEL MRNHDSAESL VILASASDILL LRATDGMVLD GEACTLPQLE LLEATARAIV PVLEWGESGL
V. vinifera_GI 963 ATAVVLOAER ELQPWIAKDD DLGQKMMWRIN QRIVKLIVEL MRNHDSAESL VILASASDILL LRATDGMVLD GEACTLPQLE LLEATARAIV PVLEWGESGL
S. lycopersicum_GI 958 ATAVVLOADR ELQPWIAKDD DLGQKMMWRIN QRIVKLIVEL MRNHDSAESL VILASASDILL LRATDGMVLD GEACTLPQLE LLEATARAIV PVLEWGESGL
M. guttatus_GI 954 ATAVVLOADR ELQPWIAKDD DLGQKMMWRIN QRIVKLIVEL MRNHDSAESL VILASASDILL LRATDGMVLD GEACTLPQLE LLEATARAIV PVLEWGESGL
A. coerulea_GI 962 SAATVLOAEK DLQPWIAKDD DLGQKMMWRIN QRIVKLIVEL MRNHDSAESL VILASASDILL LRATDGMVLD GEACTLPQLE LLEATARAIV PVLEWGESGL
S. bicolor_GI 950 STAVVLOAEK DLQPWIAKDD DLGQKMMWRIN QRIVKLIVEL MRNHDSAESL VILASASDILL LRATDGMVLD GEACTLPQLE LLEATARAIV PVLEWGESGL
Z. mays_GI 948 SAATVLOAEK DLQPWIAKDD DLGQKMMWRIN QRIVKLIVEL MRNHDSAESL VILASASDILL LRATDGMVLD GEACTLPQLE LLEATARAIV PVLEWGESGL
S. italica_GI 949 SAATVLOAEK DLQPWIAKDD DLGQKMMWRIN QRIVKLIVEL MRNHDSAESL VILASASDILL LRATDGMVLD GEACTLPQLE LLEATARAIV PVLEWGESGL
P. virgatum_GI 950 STAVVLOAEK DLQPWIAKDD DLGQKMMWRIN QRIVKLIVEL MRNHDSAESL VILASASDILL LRATDGMVLD GEACTLPQLE LLEATARAIV PVLEWGESGL
O. sativa_GI 949 SAATVLOAEK DLQPWIAKDD DLGQKMMWRIN QRIVKLIVEL MRNHDSAESL VILASASDILL LRATDGMVLD GEACTLPQLE LLEATARAIV PVLEWGESGL
B. distachyon_GI 955 STAVVLOAEK DLQPWIAKDD DLGQKMMWRIN QRIVKLIVEL MRNHDSAESL VILASASDILL LRATDGMVLD GEACTLPQLE LLEATARAIV PVLEWGESGL
A. trichopoda_GI 934 STAVVLOAEK DLQPWIAKDD DLGQKMMWRIN QRIVKLIVEL MRNHDSAESL VILASASDILL LRATDGMVLD GEACTLPQLE LLEATARAIV PVLEWGESGL
P. abies_GI 968 ATAVVLOAER DLQPWIAKDD DLGQKMMWRIN QRIVKLIVEL MRNHDSAESL VILASASDILL LRATDGMVLD GEACTLPQLE LLEATARAIV PVLEWGESGL
S. moellendorffii_GI 875 TSVVVLOAER DLQPWIAKDD DLGQKMMWRIN QRIVKLIVEL MRNHDSAESL VILASASDILL LRATDGMVLD GEACTLPQLE LLEATARAIV PVLEWGESGL

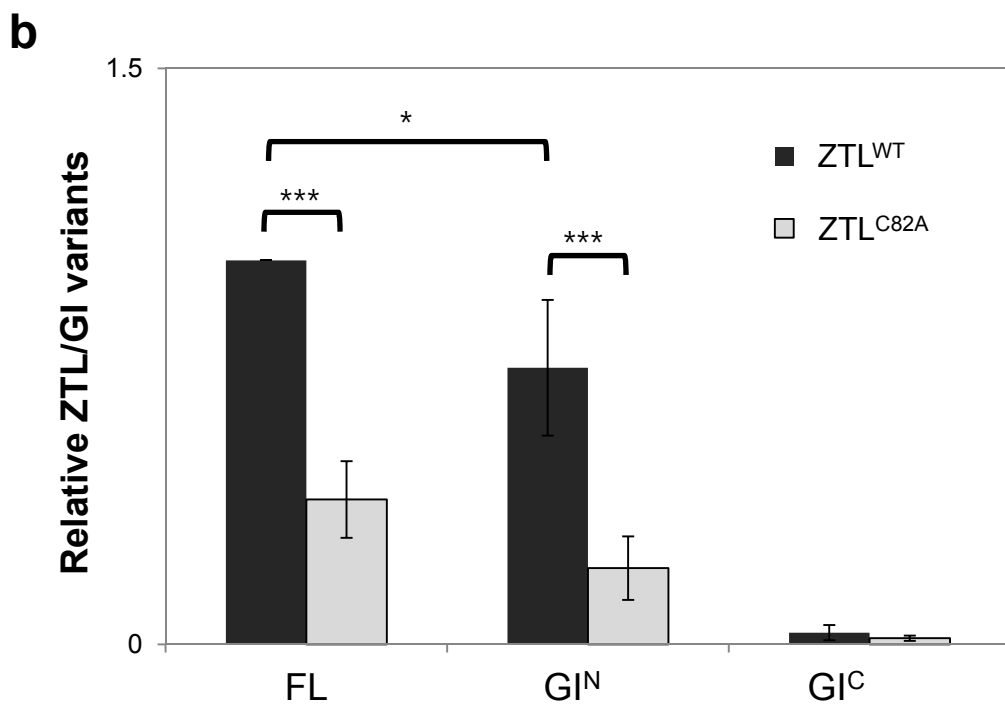
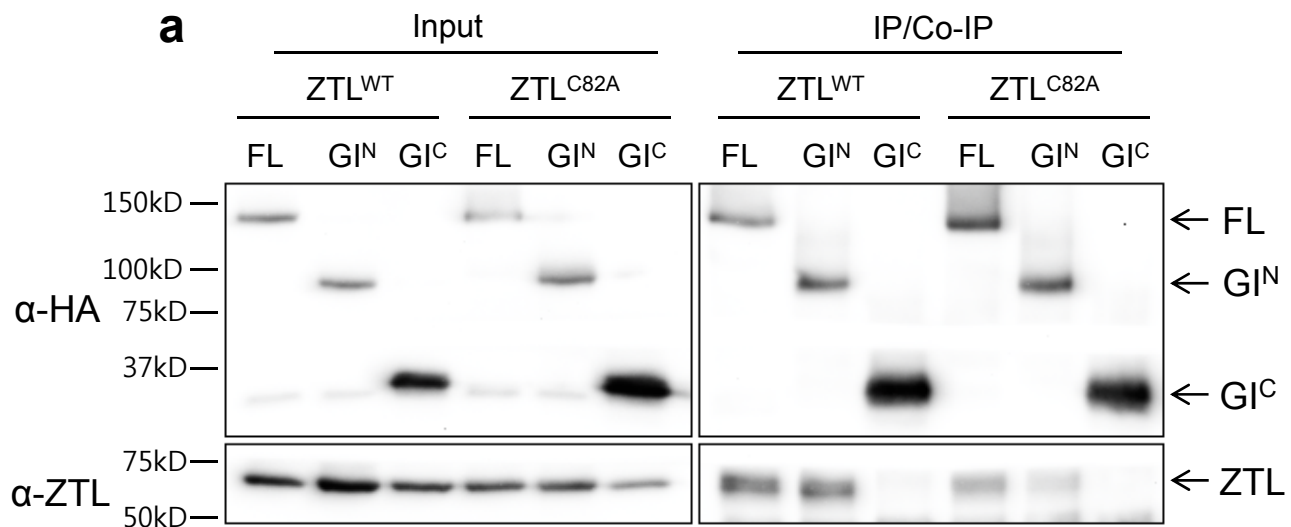
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M. truncatula_GI 1068 AVADGLSNLL KCRLATIIRC LSHPSAHVRA LSTSVDRLDI HTGSTR---C SPKP-----L RINGSHNSY QYFKLDVDW QADIEKCLTW EAHSRLSAGL
G. max_GI 1068 AVADGLSNLL KCRLATIIRC LSHPSAHVRA LSTSVDRLDI HTGSTR---C SPKP-----R RINGSHNSY QYFNLDADW QADIEKCLTW EAHSRLSAGL
C. sativus_GI 1061 STADGLSNLL KCRLPATIRC LSHPSAHVRA LSTSVDRLDI QTSYV---H RSTP-----N NINGVHSPSE QYFNREATW KVDIEKCLTW EAHSRLVTGM
M. domestica_GI 1061 AVADGLSNLL KCRLPATIRC LSHPSAHVRA LSTSVDRLDI QASTIR---P NPNP-----V EIDGHPGXY KYFNLDVDW QXIEKCLTW XAHSRLATGM
F. vesca_GI 1069 AVADGLSNLL KCRLPATIRC LSHPSAHVRA LSTSVDRLDI QTSYV---P NPNP-----V QINGHGPSY KYFNLDVDW QADIEKCLTW EAHSRLATGM
A. thaliana_GI 1058 AVVDGLSNLL KCRLPATIRC LSHPSAHVRA LSTSVDRLDI NOSSTIP-IKV TPK---LPTT EKNGMHSPSY RFFNAASIDW KADIQKCLNW EAHSRLSTTW
A. lyrata_GI 1059 AVVDGLSNLL KCRLPATIRC LSHPSAHVRA LSTSVDRLDI NOSSTIP-IKV TPK---LPTT EKNGMHSPSY RFFNAATIDW KADIQKCLNW EAHSRLSTTW
C. rubella_GI 1056 AVVDGLSNLL KCRLPATIRC LSHPSAHVRA LSTSVDRLDI NOSSTIP-IKV TPK---LPTT EKNGMHSPSY RFFNAATIDW KADIQKCLNW EAHSRLSTTW
C. grandiflora_GI 1056 AVVDGLSNLL KCRLPATIRC LSHPSAHVRA LSTSVDRLDI NOSSTIP-IKV TPK---LPTT EKNGMHSPSY RFFNAATIDW KADIQKCLNW EAHSRLSTTW
B. rapa Fpsc_GI 1051 AVVDGLSNLL KCRLPATIRC LSHPSAHVRA LSTSVDRLDI NOSGITTKA TPKPPPTITV RFFNAATIDW KADIQKCLNW EAHSRLSTTW
E. salsgineum_GI 1054 AVVDGLSNLL KCRLPATIRC LSHPSAHVRA LSTSVDRLDI NOSSVT-ITV TPKQ---RPAT EKNVMHSPSY RFFNAATIDW KADIQKCLNW EAHSRLSTTW
G. raimondii_GI 1060 AVADGLSNLL KCRLPATIRC LSHPSAHVRA LSTSVDRLDI HIGSTN---S KSK-----E EYGTGSPSY QFFNIGAITW QDIEKCLTW EYVSLATGM
T. cacao_GI 1061 AVADGLSNLL KCRLPATIRC LSHPSAHVRA LSTSVDRLDI HAGSTK---P NSKQ-----V EINGHGPSY QYFNIGVIDW QDIEKCLTW EAHSRLATGM
C. sinensis_GI 1056 AVADGLSNLL KCRLPATIRC LSHPSAHVRA LSTSVDRLDI HTSSEK---S NIEQ-----V ERNGHGSLL HYFNIDAITW QSDIEKCLTW EAHSRLATGM
M. esculenta_GI 1063 AVADGLSNLL KCRLPATIRC LSHPSAHVRA LSTSVDRLDI HTSTIK---P TANQ-----A DINDIRGPSY QLFKVDVDW QDIEKCLTW EAHSRLATGM
R. communis_GI 1052 AVADGLSNLL KCRLPATIRC LSHPSAHVRA LSTSVDRLDI YTGSTIK---R TSNR-----V DINDIRGPSY QYFNIDVDW QDIEKCLTW EAHSRLATGM
P. trichocarpa_GI 1062 AVADGLSNLL KCRLPATIRC LSHPSAHVRA LSTSVDRLDI HTGSTIK---P ASKL-----T HRNGHGPSY QYLRSDVDW QADIEKCLTW EAHSRLATGM
S. purpurea_GI 1061 AVADGLSNLL KCRLPATIRC LSHPSAHVRA LSTSVDRLDI HTGSTIK---P VSNL-----T HRNGHGPSY PYFRSDVDW QADIEKCLTW EAHSRLATGM
V. vinifera_GI 1063 AVADGLSNLL KCRLPATIRC LSHPSAHVRA LSTSVDRLDI QSGSTIK---P HIKQ-----G GRNGHGSY QYVNLGIDW QADIEKCLTW EAHSRLATGM
S. lycopersicum_GI 1058 AVVDGLSNLL KCRLPATIRC LSHPSAHVRA LSTSVDRLDI QTSYV---H RSTP-----N NINGVHSPSE QYFNREATW KVDIEKCLTW EAHSRLATGM
M. guttatus_GI 1054 AVADGLSNLL KCRLPATIRC LSHPSAHVRA LSTSVDRLDI HAGSEK---S ISA---KS QVNGFR---SQ PYISVGIRDC KAHEVEKCLTW EAHSRLATGM
A. coerulea_GI 1062 AVADGLSNLL KCRLPATIRC LSHPSAHVRA LSTSVDRLDI FLGPIK---F NVKQ-----EK RYSVQGPSH RCLSSSIDW QDIEKCLTW EAHSRLATGM
S. bicolor_GI 1050 SVADGLSNLL KCRLPATIRC LSHPSAHVRA LSTSVDRLDI NNGSNPSKI IQGE-----Q QRNGTSPSY RCLAAGITW QADVERCIEW EAHSRLATGM
Z. mays_GI 1048 SVADGLSNLL KCRLPATIRC LSHPSAHVRA LSTSVDRLDI DHGVSVPNKI SRGE-----Q QRNGTSPSY RCLVAAGITW QADVERCIEW EAHSRLATGM
S. italica_GI 1049 SVADGLSNLL KCRLPATIRC LSHPSAHVRA LSTSVDRLDI NNGHTPSKI IQGE-----Q QRNGTSPSY RCLAASINW QADVERCIEW EAHSRLATGM
P. virgatum_GI 1050 SVADGLSNLL KCRLPATIRC LSHPSAHVRA LSTSVDRLDI NNGHTPSKI IQGE-----Q QRNGTSPSY RCLAASINW QADVERCIEW EAHSRLATGM
O. sativa_GI 1049 SVADGLSNLL KCRLPATIRC LSHPSAHVRA LSTSVDRLDI NNGHTPSKI IQGE-----E HRNGTSPSY RCLAASINW QADVERCIEW EAHSRLATGM

<i>B. distachyon_GI</i>	1055	AVADGLSNLL	KCRLLSTIRG	LSHPSAHVRA	LSWSVLRDIL	NSGPIINSTKI	IQG-----E	QRNGVOSPTV	QCAAASMVNM	QADMERCIEW	EARSRRATGM
<i>A. trichopoda_GI</i>	1034	SVADGLSNLL	KCRLPATITG	LSHPSAHVRA	LSTSLLRDIL	NIGSPK--S	NFAE-----E	DIRGHPVPPY	RNISIGTIDM	RSDLEKCLAW	EARNRRATGM
<i>P. abies_GI</i>	1068	AMAEGLNLL	KYRLPATVQG	LSHSSAHVRA	LSTSVLRDIL	HAESLN--FR	YCKN----FS	EKNHHSEHLV	YGKDIVVQDW	NKAVEQCLAW	EAHNRQARGM
<i>S. moellendorffii_GI</i>	969	--SRGLTLL	KERLPATVRC	LSHSPRTIRA	SSASLLREIV	STDVLR----	-----A	-----A	SYPGDKAGAW	LEIVEOSTAW	ETHYVRAEGL

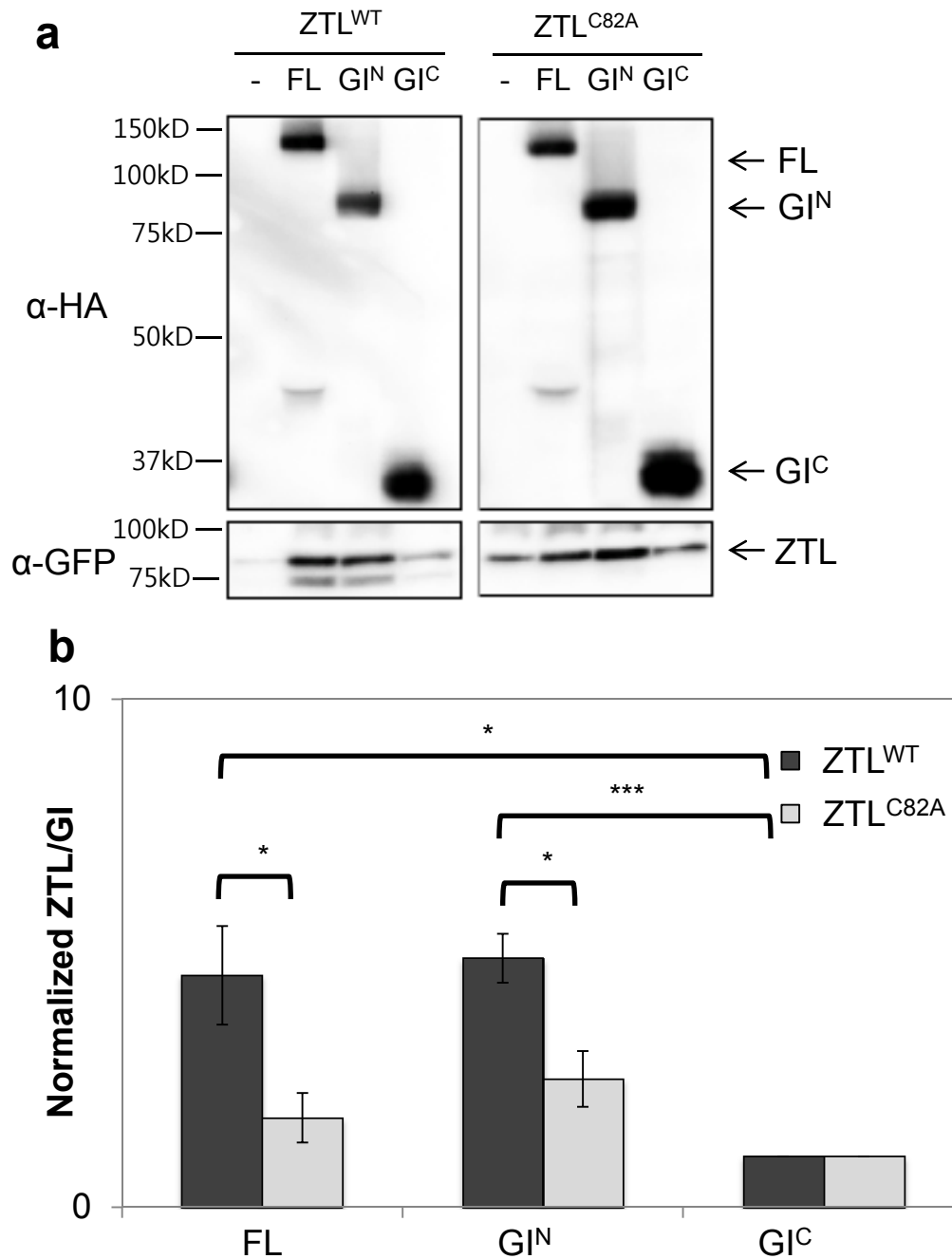
		1210	1220
	
<i>M. truncatula_GI</i>	1160	PIKFLDTAAK	ELGGATISV--
<i>G. max_GI</i>	1160	SINFLDTAAK	ELGCTISM--
<i>C. sativus_GI</i>	1153	PTEVLHVAAK	ELGGSTISL--
<i>M. domestica_GI</i>	1153	QIKFLDTAAK	ELGGSTISL--
<i>F. vesca_GI</i>	1161	PIKFLDTAAK	ELGCTISV--
<i>A. thaliana_GI</i>	1154	PTQFLDTAAR	ELGCTISLSQ-
<i>A. lyrata_GI</i>	1155	PTQFLDTAAR	ELGCTISLSQ-
<i>C. rubella_GI</i>	1152	PTQFLDTAAQ	ELGCTISLSQ-
<i>C. grandiflora_GI</i>	1152	PTQFLDTAAQ	ELGCTISLSQ-
<i>B. rapa FPsc_GI</i>	1151	PTQFLDTAAR	ELGCTISMSSQ
<i>E. salsugineum_GI</i>	1151	PTQFLDTAAR	ELGCTISLSSQ
<i>G. raimondii_GI</i>	1151	TIQFLDTAAK	ELGGNISI--
<i>T. cacao_GI</i>	1153	PIRFLDTAAK	ELGGSTISL--
<i>C. sinensis_GI</i>	1148	PIQFLDTAAK	ELGCTISL--
<i>M. esculenta_GI</i>	1155	AIQFLDTAAK	ELGCTVSI--
<i>R. communis_GI</i>	1144	PIQFLDTAAK	ELGCTISL--
<i>P. trichocarpa_GI</i>	1154	PVHFLDTAAK	ELGCTISL--
<i>S. purpurea_GI</i>	1152	SVHFLDTAAK	ELGCTISL--
<i>V. vinifera_GI</i>	1153	TNQFLDVAAK	ELGCTISL--
<i>S. lycopersicum_GI</i>	1150	CTQFLDMAAK	ELGCTISL--
<i>M. guttatus_GI</i>	1143	PIQFLDTAAK	ELGCTISL--
<i>A. coerulea_GI</i>	1155	STTFLDTAAK	ELGCTISL--
<i>S. bicolor_GI</i>	1145	TLAFLSAAAK	ELGGPLPC--
<i>Z. mays_GI</i>	1143	TLAFLSAAAK	ELGGPLPC--
<i>S. italica_GI</i>	1143	TLAFLSAAAK	ELGGPLPC--
<i>P. virgatum_GI</i>	1144	TLAFLSAAAK	ELGGPLPC--
<i>O. sativa_GI</i>	1143	TLAFLSAAAK	ELGGPLPC--
<i>B. distachyon_GI</i>	1149	TLAFLSAAAN	ELGGPLPC--
<i>A. trichopoda_GI</i>	1126	TLTFLSAAAK	ELGGATISV--
<i>P. abies_GI</i>	1162	SIALHALLAAN	ALGFSANV--
<i>S. moellendorffii_GI</i>	1045	SESEFLASAAI	ALGCKLPPS--

Supplementary Fig. 1. A phylogenetic tree and alignments of GI orthologs.

(a) Evolutionary relationships of taxa used in the GI alignment. The evolutionary history was inferred using the Neighbor-Joining method ¹. The optimal tree with the sum of branch lengths = 2.88320250 is shown. The tree is drawn to scale, with branch lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree. The evolutionary distances were computed using the Poisson correction method and are in the units of the number of amino acid substitutions per site. The analysis involved 31 amino acid sequences. All ambiguous positions were removed for each sequence pair. There were a total of 1220 positions in the final dataset. Evolutionary analyses were conducted in MEGA6 ². The scale bar corresponds to an evolutionary distance of 0.05 substitution per amino acid position. (b) Multiple alignment of GI orthologs obtained from ClustalW implemented in MEGA. Identical and similar amino acid residues are indicated by black and gray shading, respectively.

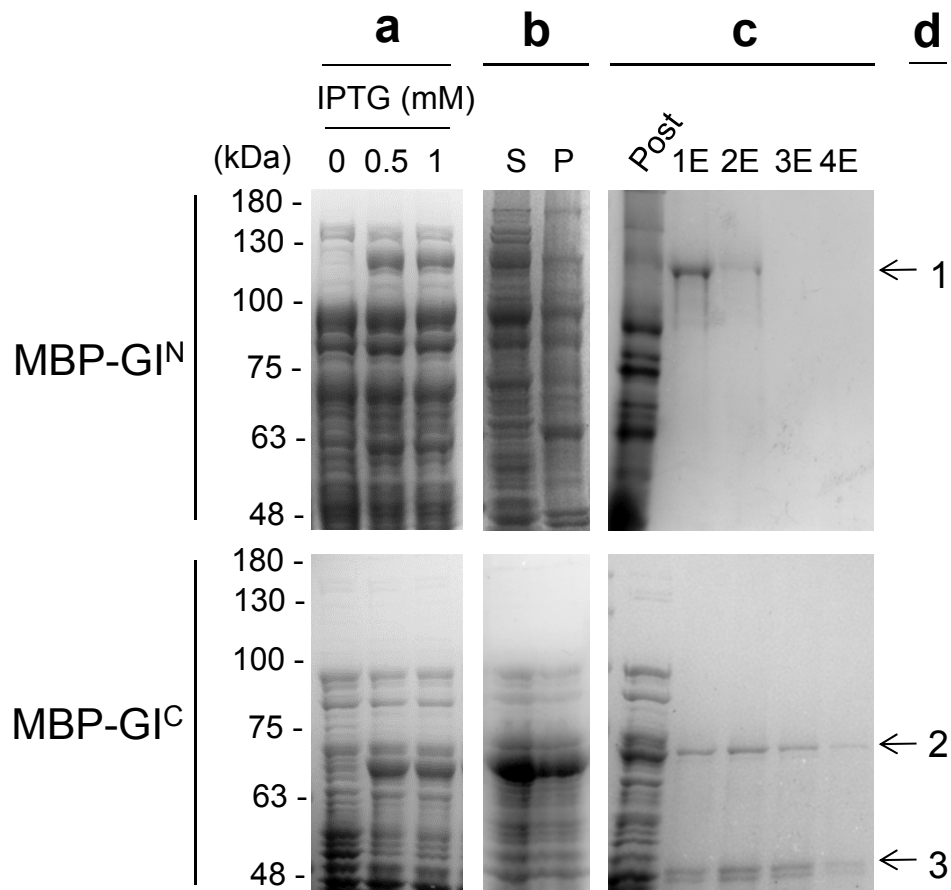


Supplementary Fig. 2. GI^N recapitulates full-length GI specificity of ZTL interaction *in planta*. (a) HA-tagged GI full length (FL), GI^N and GI^C were separately co-infiltrated with wild type (WT) ZTL or photochemically dead ZTL^{C82A} in *N. benthamiana*. Immunoprecipitation was performed with anti-HA antibody, followed by immunoblotting and probing for GI (anti-HA) and ZTL (anti-ZTL). (b) Quantification of densitometric ratio of co-immunoprecipitated ZTL to immunoprecipitated GI. Relative to WT ZTL, GI^N shows significantly poorer interaction with ZTL^{C82A}, similar to that of FL GI. Error bars indicate s.e. (n=9). For t-test: 0.01 < * < 0.05, *** < 0.001.

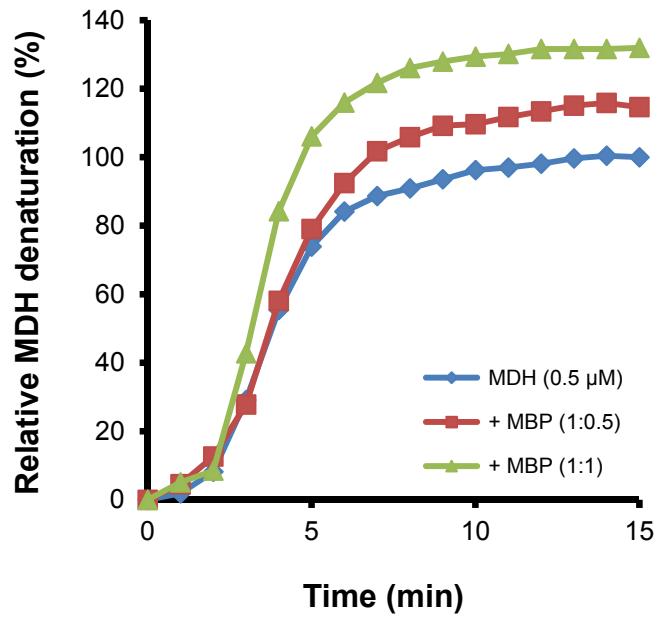


Supplementary Fig. 3. GI^N recapitulates full-length GI stabilization of ZTL *in planta*.

(a) HA-tagged GI full length (FL), GI^N, and GI^C were separately co-transformed with GFP-tagged wildtype (WT) ZTL or ZTL^{C82A} into *A. thaliana gi-201* protoplasts. Stabilization of ZTL is seen as increased band intensity when co-transformed with GI-FL or GI^N, but not with GI^C. Immunoblots were performed with anti-HA antibody and anti-GFP antibody. **(b)** Quantification of densitometric ratio of ZTL to GI variants. Values normalized to GI^C. Error bars indicate s.e. (n=6 for WT ZTL, and n=4 for C82A ZTL). For t-test: 0.01 < * < 0.05, *** < 0.001.

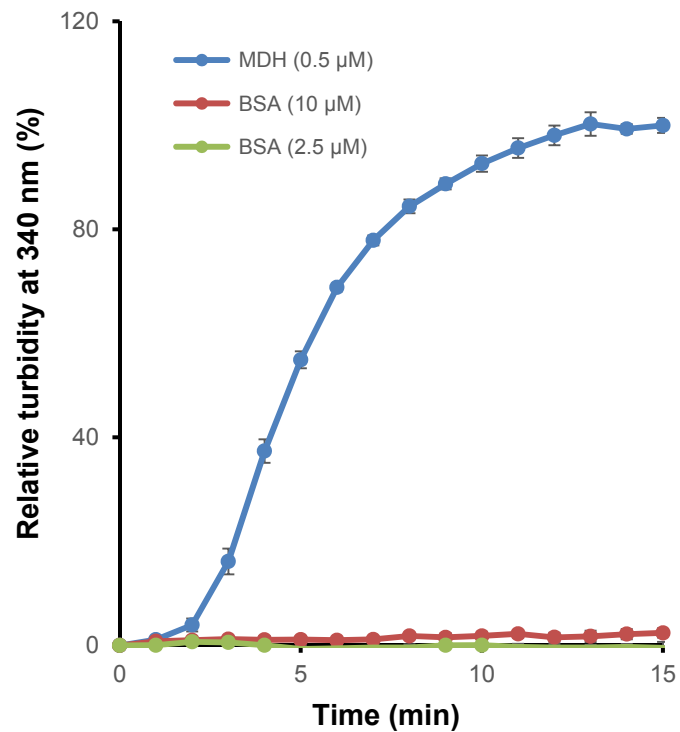


Supplementary Fig 4. Expression, purification and identification of MBP-GI^N and MBP-GI^C.
(a) IPTG-induced expression of MBP-GI in *E. coli*. **(b)**. Soluble fractionation by centrifugation. S, supernatant; P, pellet fraction. **(c)** Affinity chromatography using amylose resin. Post, post binding supernatant. 1E-4E, each eluates using 10 mM maltose elution buffer. **(d)** First eluate (1E) of each bands analyzed by MALDI-TOF/TOF MS.

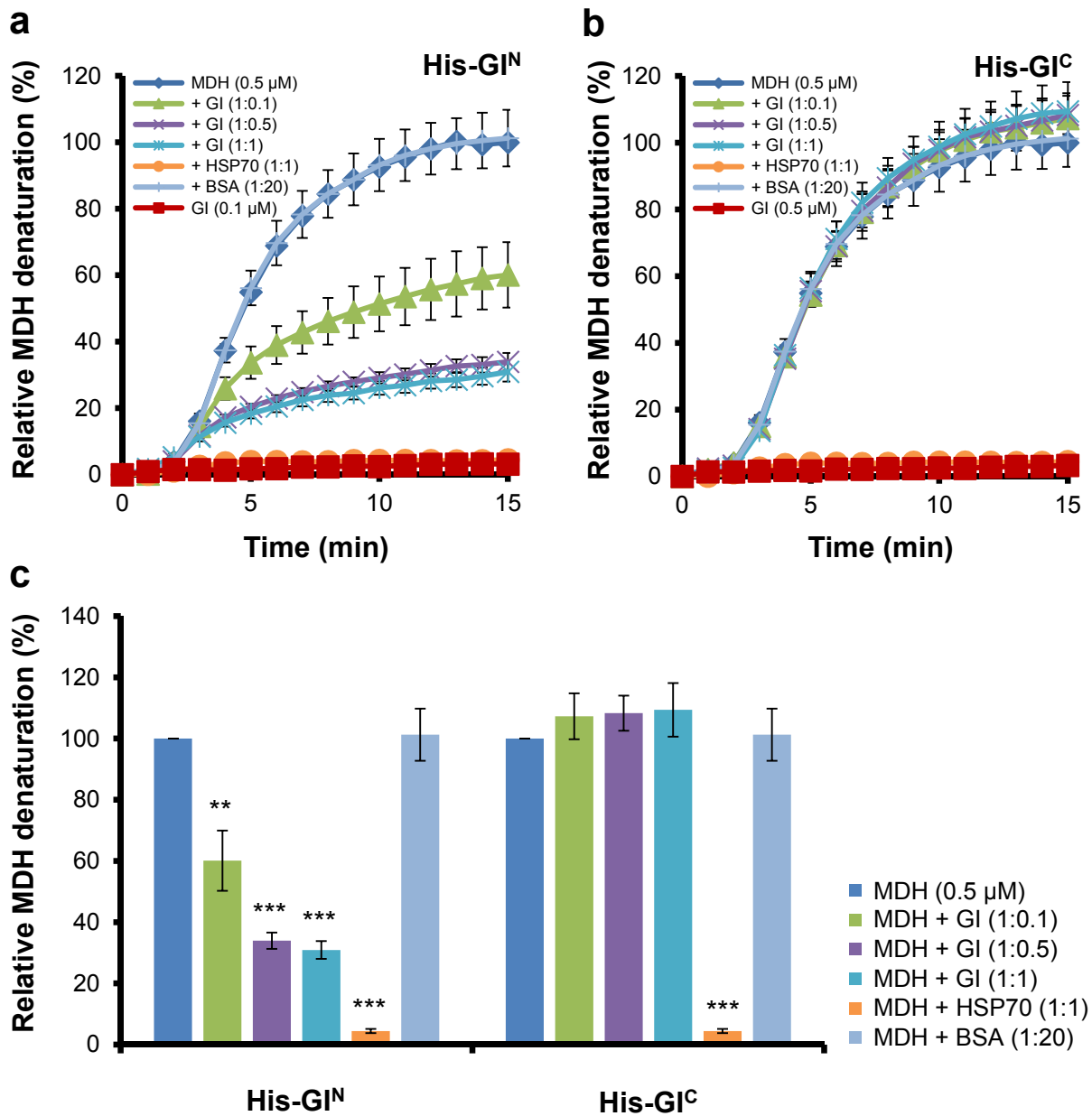


Supplementary Fig. 5. MBP does not protect MDH under heat denaturation.

The aggregation of MDH (0.5 μ M) was monitored (turbidity at 340 nm) under thermal denaturing conditions for 15 min at 45 $^{\circ}$ C in the absence or presence of MBP at different molar ratios.

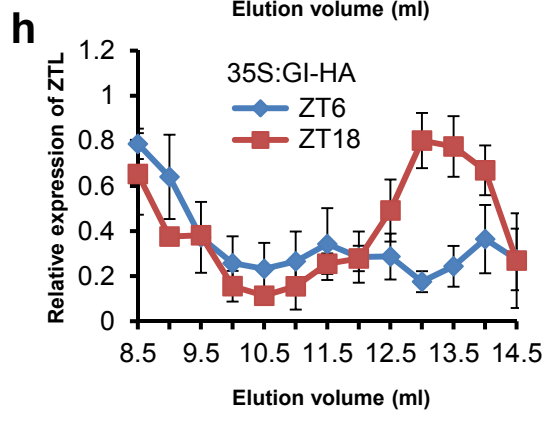
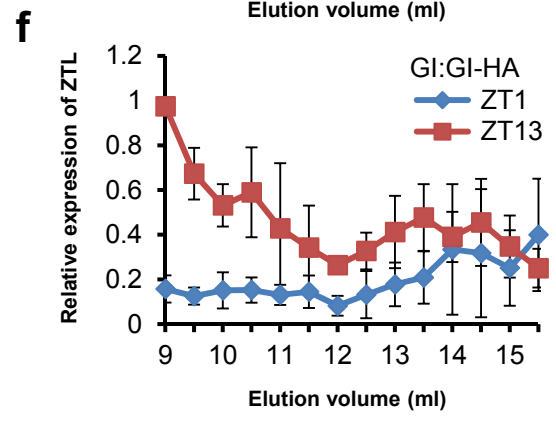
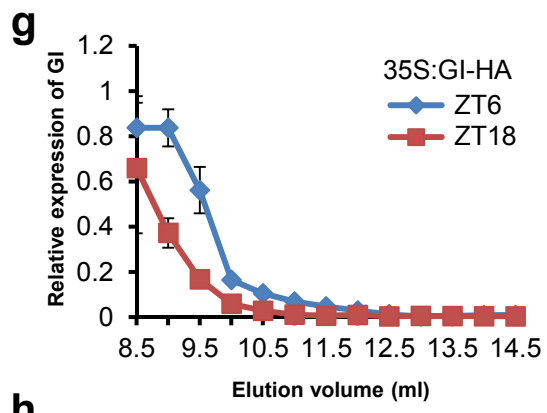
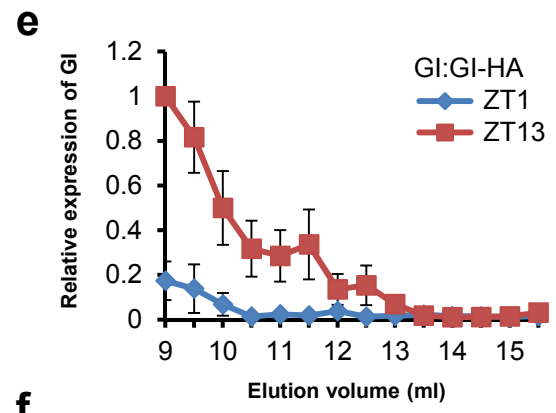
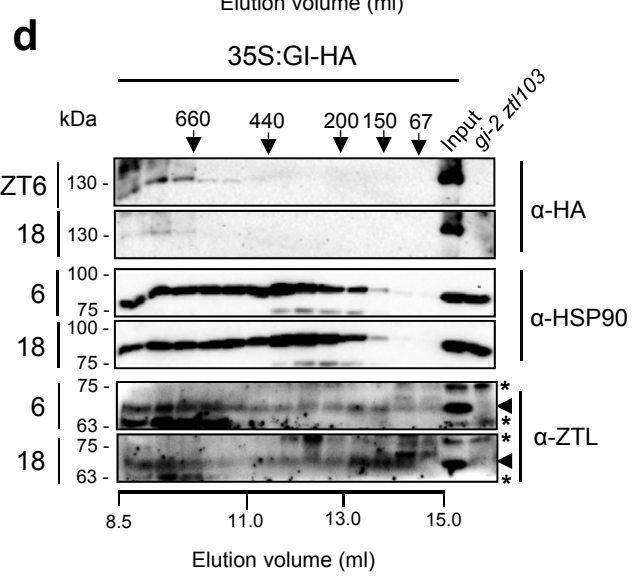
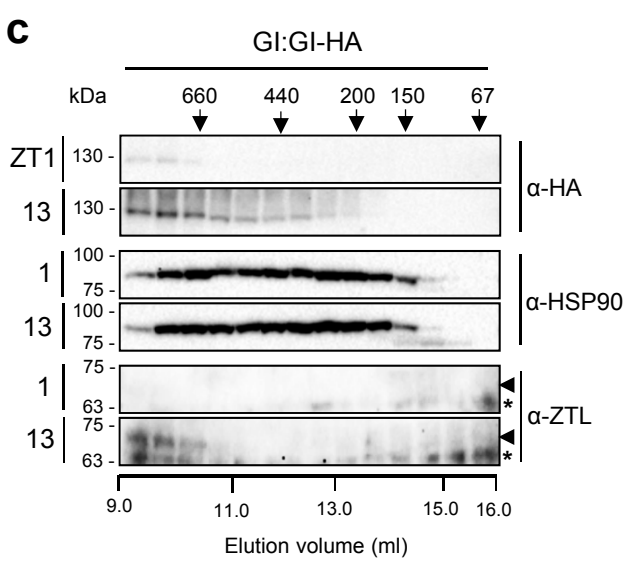
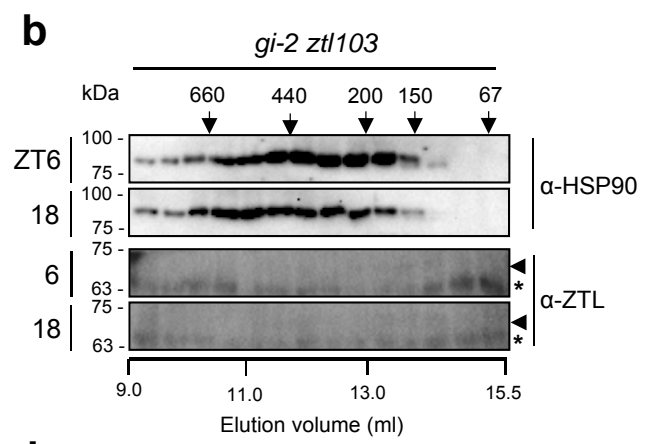
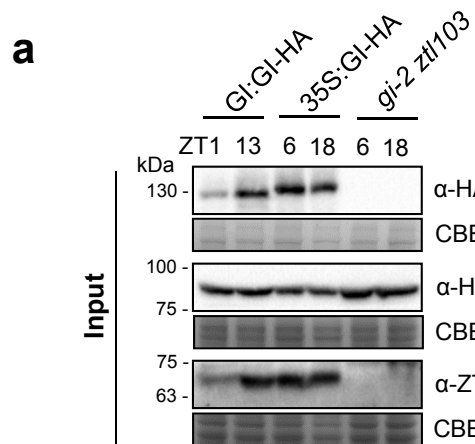


Supplementary Fig. 6. BSA alone is heat-stable compared to MDH under heat denaturation. Ten or 2.5 μM BSA, corresponding to Fig. 1a-c and Fig. 2a-c, was tested relative to the aggregation of MDH (0.5 μM) under thermal denaturing conditions for 15 min at 45 °C (turbidity at 340 nm). Data are means ± s.e ($n=3$).

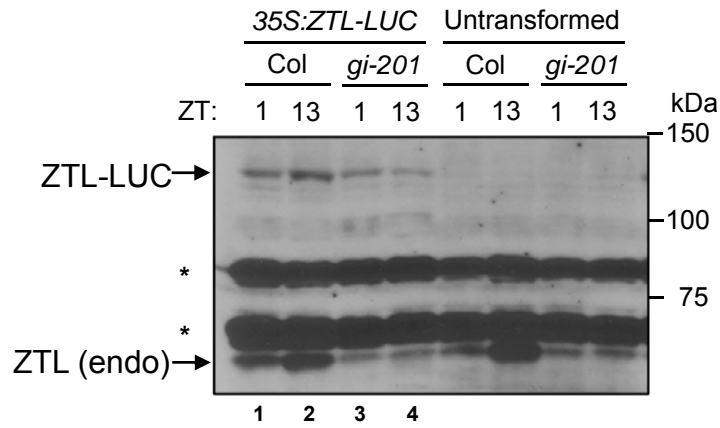
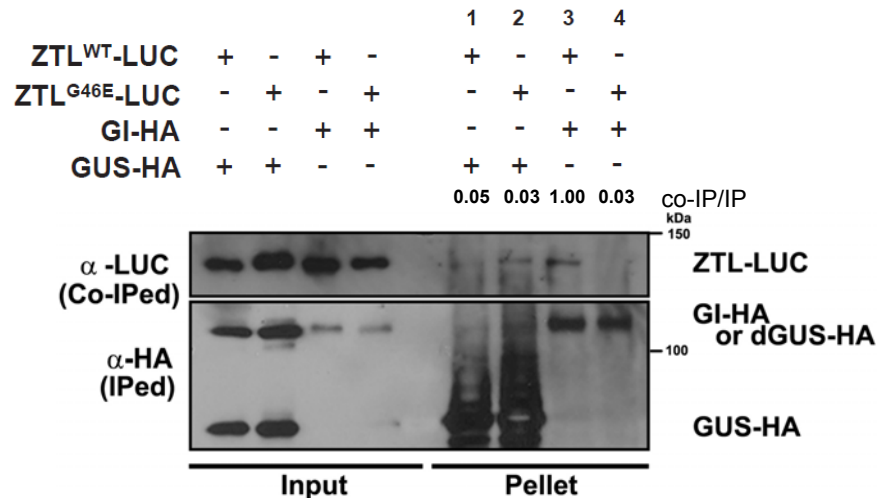
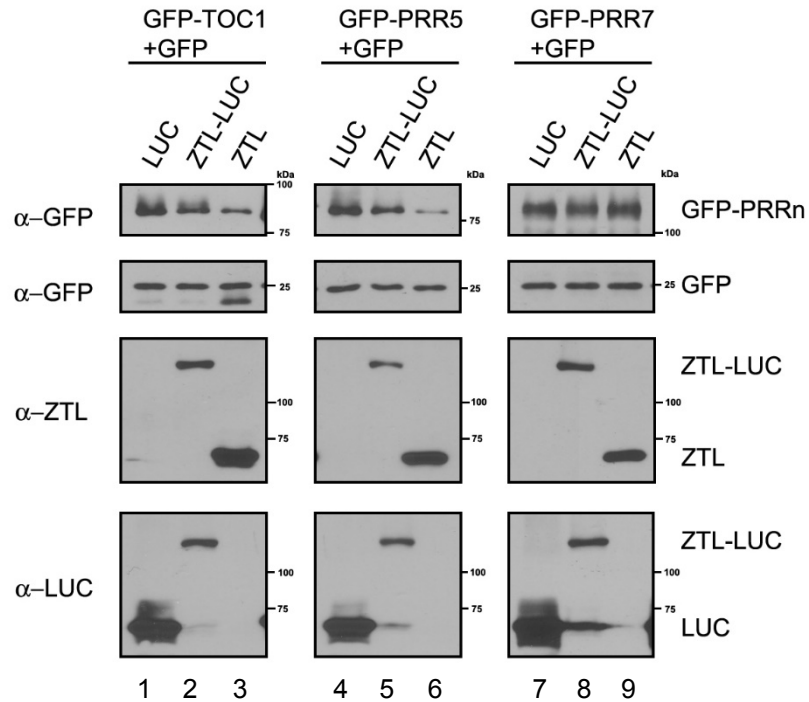


Supplementary Fig. 7. His-GI^N exhibits general holdase chaperone activity *in vitro*.

Recombinant His-GI^N or His-GI^C was expressed and purified from *E. coli* BL21 (DE3). The aggregation of MDH (0.5 μ M) was monitored by measuring the turbidity at 340 nm under thermal denaturing conditions for 15 min at 45 °C. The turbidity of MDH alone at 15 min was set to 100%, and that from each treatment expressed relative to it. HSP70 and BSA used as positive and negative controls, respectively. **(a)** His-GI^N effectively protects heat-induced MDH aggregation as similar as MBP-GI^N. **(b)** His-GI^C does not display chaperone activity *in vitro*. **(c)** The mean denaturation rate at the treatment endpoint (15 min) of (a) and (b) relative to thermal-denaturation of MDH alone. * $P < 0.05$; ** $P < 0.01$; *** $P < 0.001$; two-tailed Student's t-test. Data are means \pm s.e. ($n=3$).

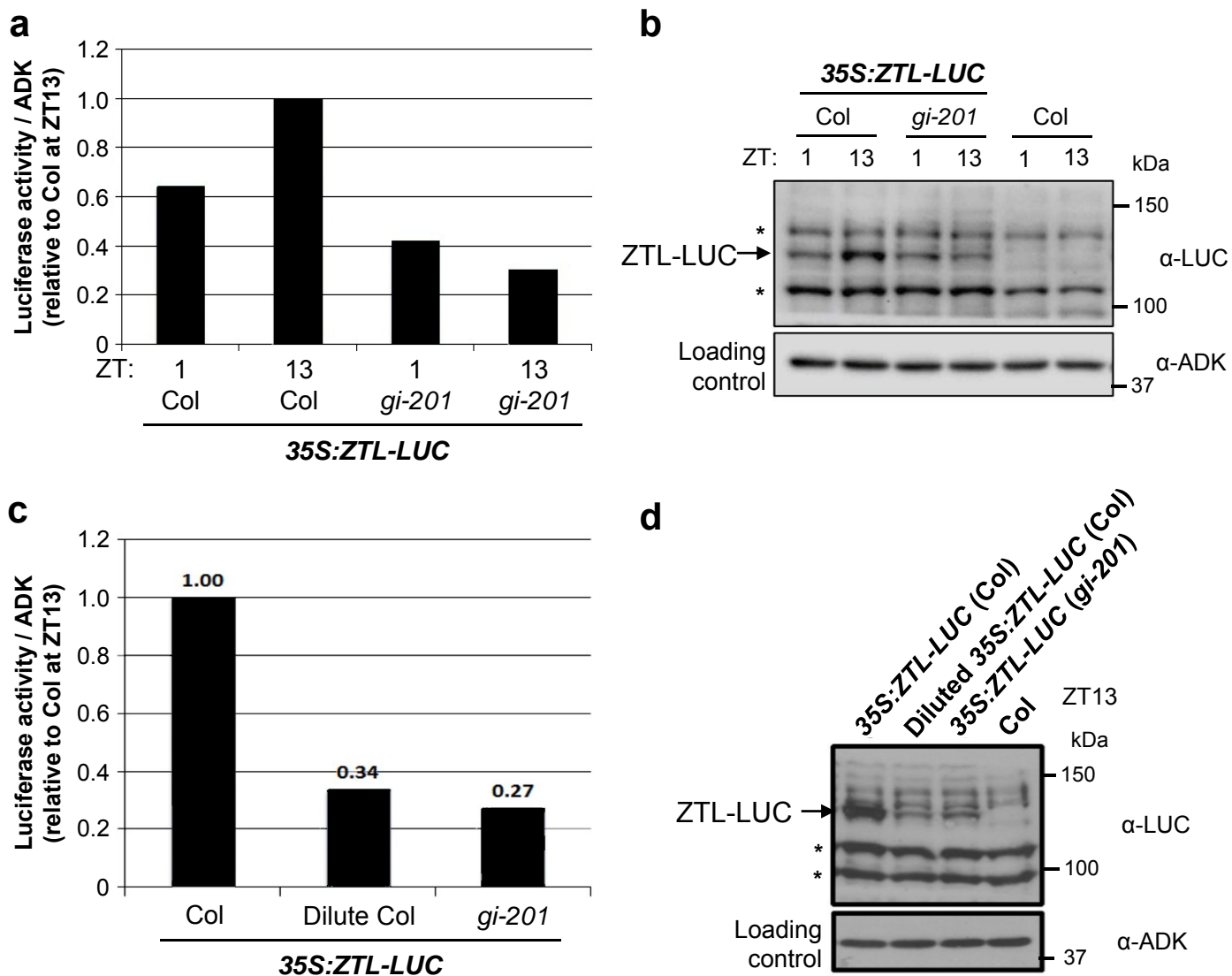


Supplementary Fig. 8. GI , ZTL and HSP90 co-elution in large complexes is light-dependent. (a) Input and (b-d) protein migration profiles of GI-HA, ZTL and HSP90 proteins in (b) *gi-2 ztl-103* (ZT6 and ZT18), (c) *GI:GI-HA* (ZT1 and ZT13) and (d) *35S:GI-HA* (ZT6 and ZT18) seedlings grown under 12 h L/12 h D. (a) shows the expressions of GI-HA, HSP90 and ZTL in independent lines before gel-filtration. CBB: Coomassie blue-stained gel. (b) shows the migration patterns of HSP90 in the absence of GI and ZTL. (c) shows co-elution of HSP90, GI-HA and ZTL in the same high molecular weight elution fraction at times of maximum GI-HA expression, consistent with presence of all three in the same complex. (d) shows co-elution of HSP90, GI-HA and ZTL in the same high molecular weight elution fraction is enhanced during the photoperiod under constitutive expression of GI-HA, consistent with light-enhanced presence of GI and ZTL in the same complex. Band intensity of GI-HA and ZTL in (e,f) *GI:GI-HA* and (g,h) *35S:GI-HA* was quantitated using Image Lab software (ver. 4.1, Bio-Rad) and all bands were normalized to the band of each protein showing highest intensity (set to 1). Total protein was extracted from 10-day old seedlings and eluted using a Superdex200 10/300 column. Eluted samples were TCA-precipitated, immunoblotted and probed with anti-HA (for GI-HA), anti-HSP90 and anti-ZTL antibodies. Molecular mass markers (blue dextran, 2000 kDa; thyroglobulin, 660 kDa; ferritin, 440 kDa; β -amylase, 200 kDa; alcohol dehydrogenase, 150 kDa; BSA, 67 kDa) were independently eluted using same equilibrated column. Arrowhead in (c) and (d) shows ZTL position. Data represent means \pm s.e ($n=3$).

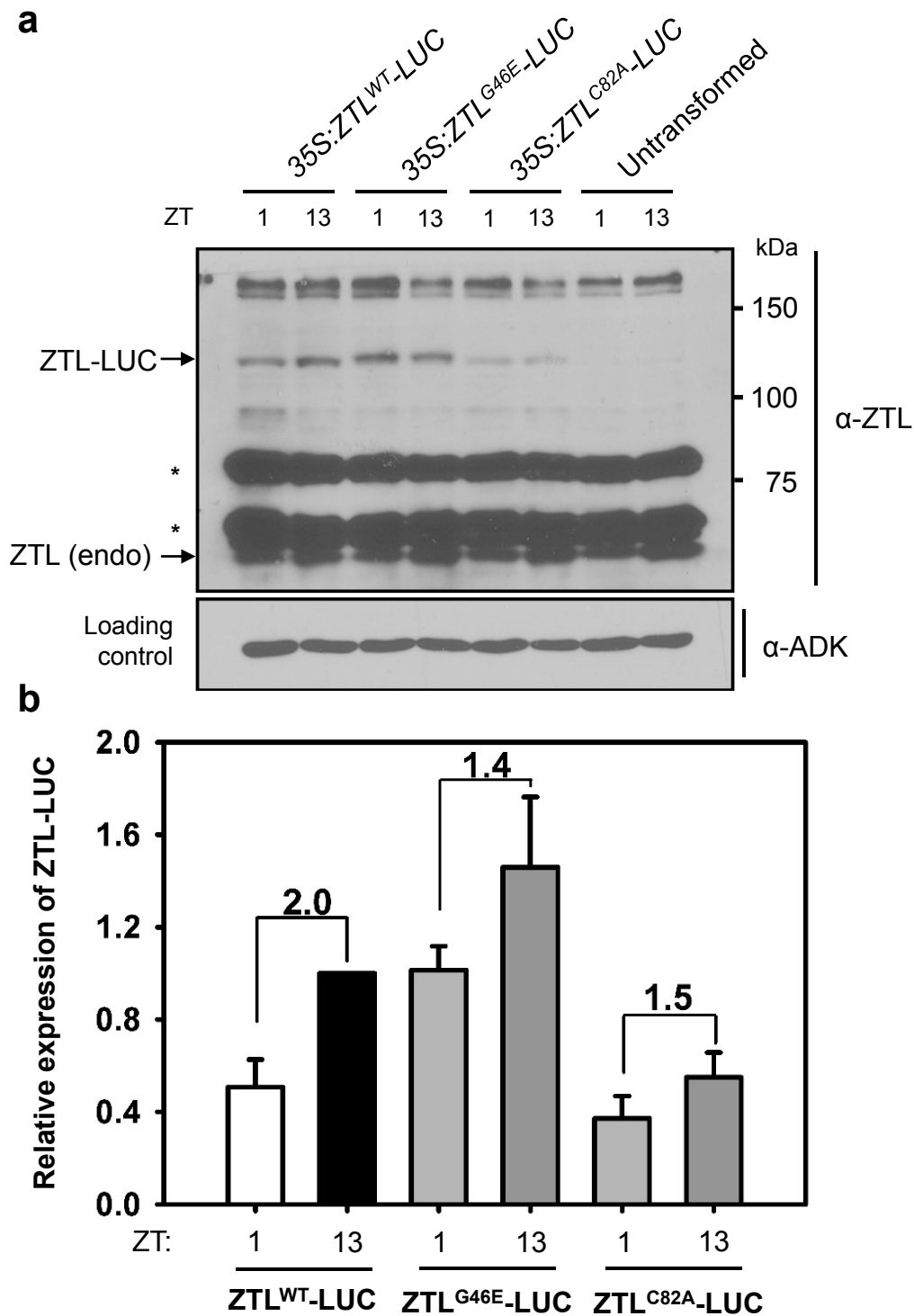
a**b****c**

Supplementary Fig. 9. ZTL-LUC properties are similar to those of endogenous ZTL.

(a) Protein abundance of ZTL-LUC reflects endogenous ZTL levels. *35S:ZTL-LUC* in Col and *gi-201*, and untransformed Col and *gi-201* seedlings were grown under 12L/12D and harvested at ZT1 and ZT13. SDS-PAGE separated protein extracts were immunoblotted with anti-ZTL antibody. Arrows indicate ZTL-LUC and endogenous ZTL. ZTL-LUC proteins migrated between 100 and 150 kDa and endogenous ZTL below 75kDa. * indicates non-specific proteins. The *35S:ZTL-LUC* line used in all subsequent experiments was chosen as the one that best approximated the level of endogenous ZTL. **(b)** ZTL-LUC and GI protein interaction is allele specific. *35S:ZTL^{WT}-LUC* and *35S:ZTL^{G46E}-LUC* were co-transformed with *CsVMV:GI-HA* or *CsVMV:GUS-HA* into Arabidopsis mesophyll protoplasts. Protein expression from protoplasts was determined by immunoblotting. Soluble fraction (input) and eluates (pellet) after IP with anti-HA antibody are shown. The co-IP/IP ratios of ZTL-LUC to GI-HA or GUS-HA, normalized to the ratio of the GI-HA/ZTL WT value, are shown above the blots for each of the four combinations. **(c)** Abundance of GFP-TOC1 and GFP-PRR5 proteins are reduced in response to *35S:ZTL-LUC* co-expression. GFP-PRRn (TOC1, PRR5, or PRR7) and GFP were co-expressed with *35S:LUC*, *35S:ZTL-LUC*, or *35S:ZTL* in *N. benthamiana* and protein levels were determined by immunoblotting with anti-GFP, anti-ZTL and anti-LUC antibody. In **(c)** GFP was used as a reference protein for expression. In **(b)** the dGUS-HA band is a presumed dimer of GUS-HA that migrates at a similar position as GI-HA. Data are representative of two trials.

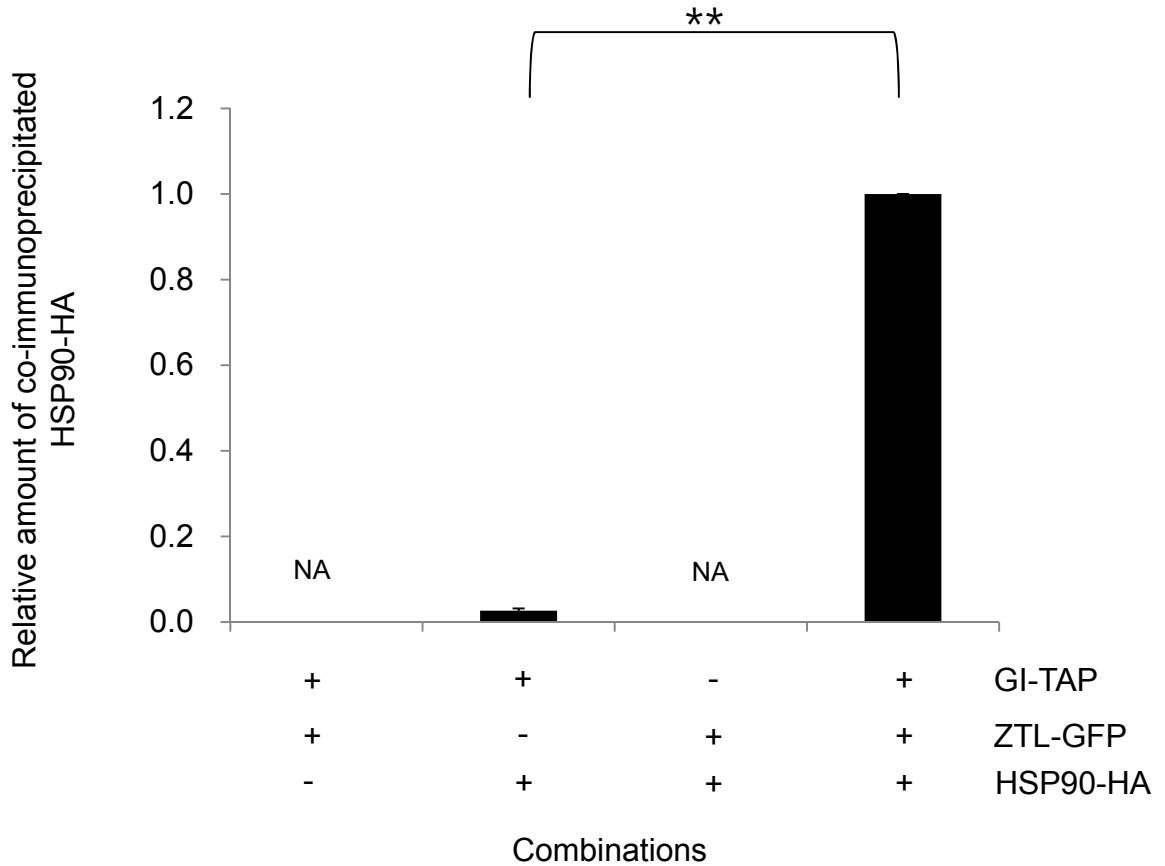


Supplementary Fig. 10. Luciferase activity and protein levels of ZTL-LUC in Col and *gi-201*. (a) Col and *gi-201* plants harboring 35S:ZTL-LUC were grown in 12L/12D and harvested at ZT1 and ZT13. Total protein was extracted and assayed for luciferase activity. (b) The same extracts were separated by SDS-PAGE and immunoblotted with anti-LUC and anti-adenosine kinase (ADK) antibody. Luciferase activity in (a) is adjusted relative to ADK protein level and normalized to luciferase activity in Col (35S:ZTL-LUC) harvested at ZT13. Arrow indicates ZTL-LUC. * indicates non-specific cross-reactivity. WT Col used to identify ZTL-LUC band. ADK protein used as loading control. Data are representative of four trials. Luciferase activity (c) and protein amount (d) of ZTL-LUC in Col and *gi-201* at ZT13. Luciferase activity and protein amount were measured as in (a) and (b) but with dilution of total protein extracts from 35S:ZTL-LUC in Col at ZT 13 with protein extracts from untransformed Col by a ratio of 1 to 3. This was done to bring ZTL-LUC protein in the WT background to levels similar to ZTL-LUC in *gi-201* to allow for more accurate quantitation at this time point. This approach was used for the final data presented in Fig. 3. Data are representative of eight trials.

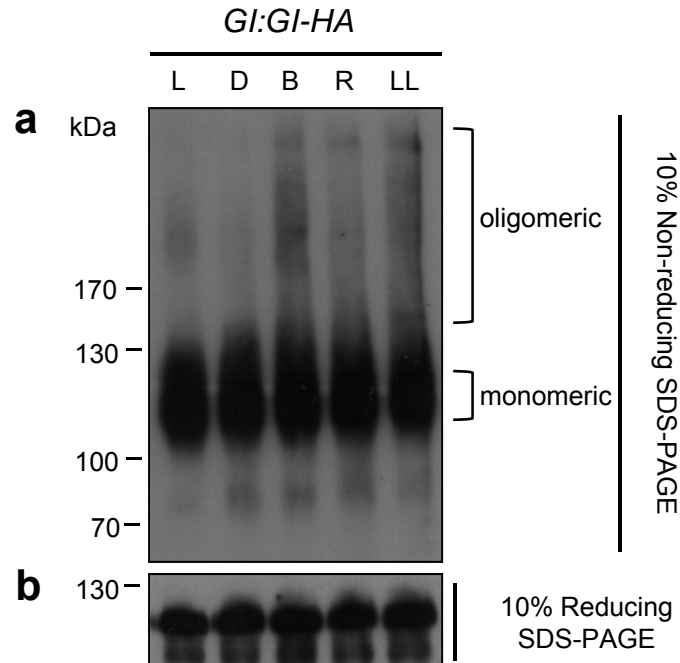


Supplementary Fig. 11. Expression levels of ZTL^{WT}-LUC, ZTL^{G46E}-LUC and ZTL^{C82A}-LUC.

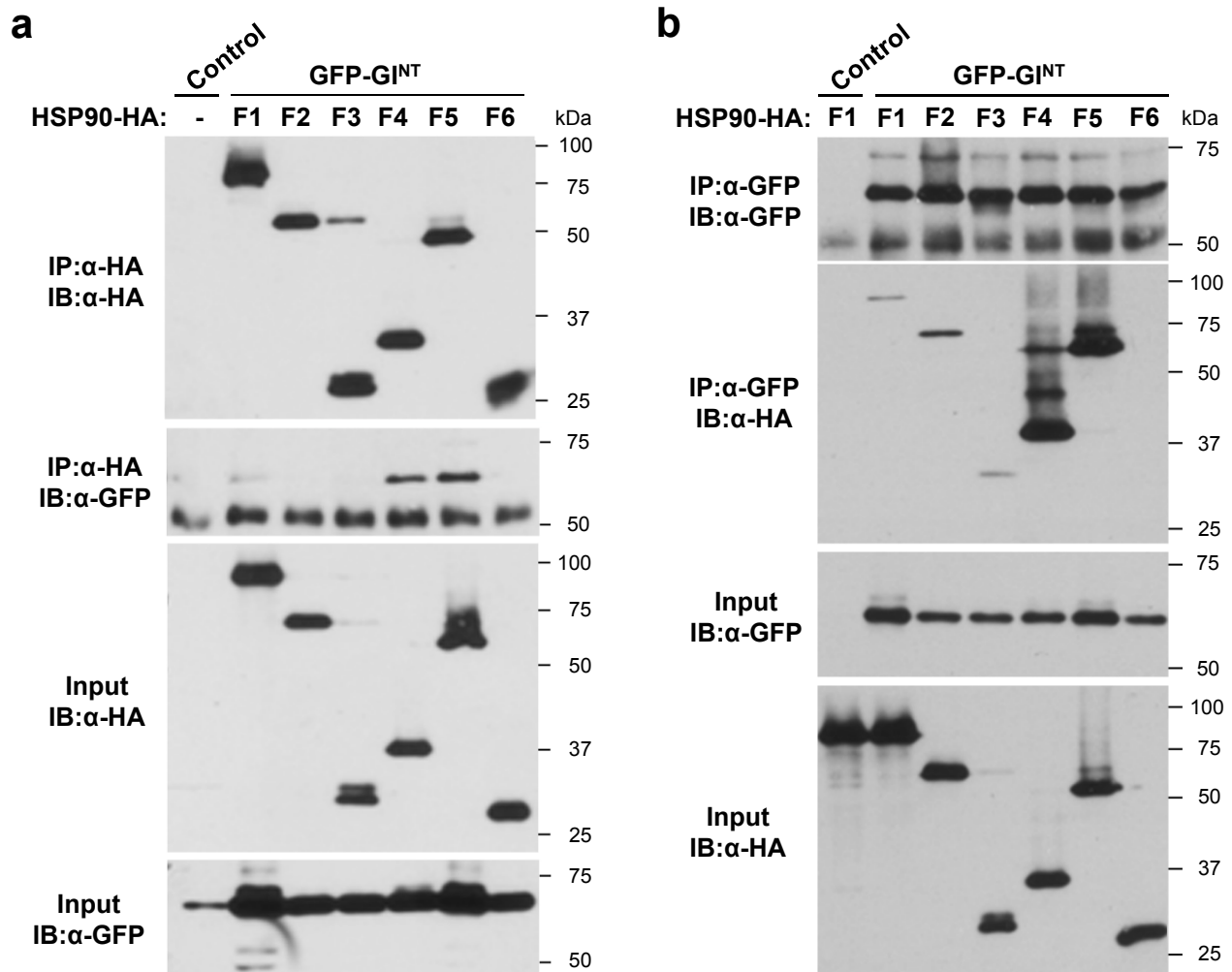
(a) 35S:ZTL(^{WT}, ^{G46E}, or ^{C82A})-LUC and untransformed plants seedlings were grown under 12L/12D, harvested at ZT1 and ZT13 and immunoblotted protein extracts were probed with anti-ZTL antibody. Arrows indicate ZTL-LUC and endogenous ZTL. * indicates non-specific proteins. Data are representative of three trials. ZTL^{G46E}-LUC migrates more slowly than ZTL^{WT}-LUC. **(b)** Quantitation of relative expression ZTL-LUC proteins from **(a)**. ZTL-LUC levels in each sample were normalized to ADK and further normalized to ZTL^{WT}-LUC at ZT13 within each trial. Data are means ± s.e. of three independent trials. Numbers indicate the ratio of ZTL-LUC proteins expressed at ZT 13 to at ZT1 for each ZTL variant.



Supplementary Fig. 12. Graphical summary of the serial detections of co-immunoprecipitated HSP90-HA from the 2nd supernatants (2nd Sup.) of Figure 4c. ** P<0.001 calculated from one-way ANOVA. Quantitations based on long exposures of 3 independent experiments. NA = “not acquired” since the initial HSP90-HA in the 2nd Sup. is not detectable in these instances.



Supplementary Fig. 13. Light-dependent oligomeric complex of Gl. Ten-day-old *Gl:Gl-HA* plants grown in 12L/12D were harvested at ZT6 (L) and ZT18 (D). The plants were also harvested at ZT18 under blue (B), red (R) and constant light (LL). Total protein was extracted and separated by **(a)** 10 % non-reducing SDS-PAGE and **(b)** 10 % reducing SDS-PAGE. Immunoblot analysis was performed using anti-HA antibody.



Supplementary Fig. 14. N-terminus of GI interacts with HSP90 and its deletion *in vivo*. HSP90 deletion interactions with GI^{NT} (aa 1-391). The co-IP assays were performed either with HA antibody (**a**) or GFP antibody (**b**) as the primary antibody. In both cases, the strongest interactions between GI^{NT} and HSP90 are found in HSP90 F4 (HSP90 264-524aa; MD) and HSP90 F5 (HSP90 264-706aa; MD+DD), indicating the middle domain of HSP90 is sufficient to interact with GI^{NT}, but the presence of the NBD weakens this interaction (as in F1-F3). *Agrobacteria* harboring GFP-GI^{NT} and HSP90 or respective deletions (3xHA-tagged) were co-infiltrated into *N. benthamiana* leaves. Anti-GFP immunoprecipitations (IP) were followed by detection of co-immunoprecipitated HSP90-HA (co-IP). Representative of three trials with similar results. HSP90 domain structure and respective deletion scheme as in Fig. 4. IP: immunoprecipitation antibody; IB: immunoblot antibody.

Supplementary Fig. 15

Note: The following pages (Supplementary Figure 15) show original images of immunoblots and gels used in various main and supplementary figures when those images were cropped. They are shown in the context of the annotation of the original figure.

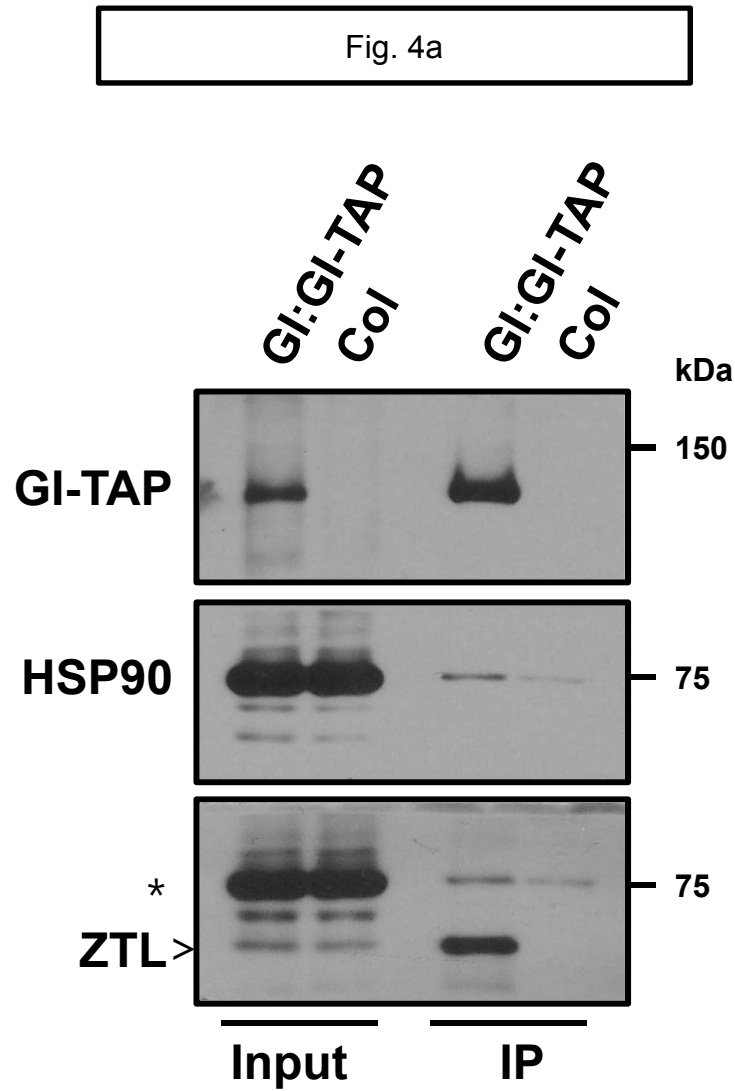


Fig. 4b

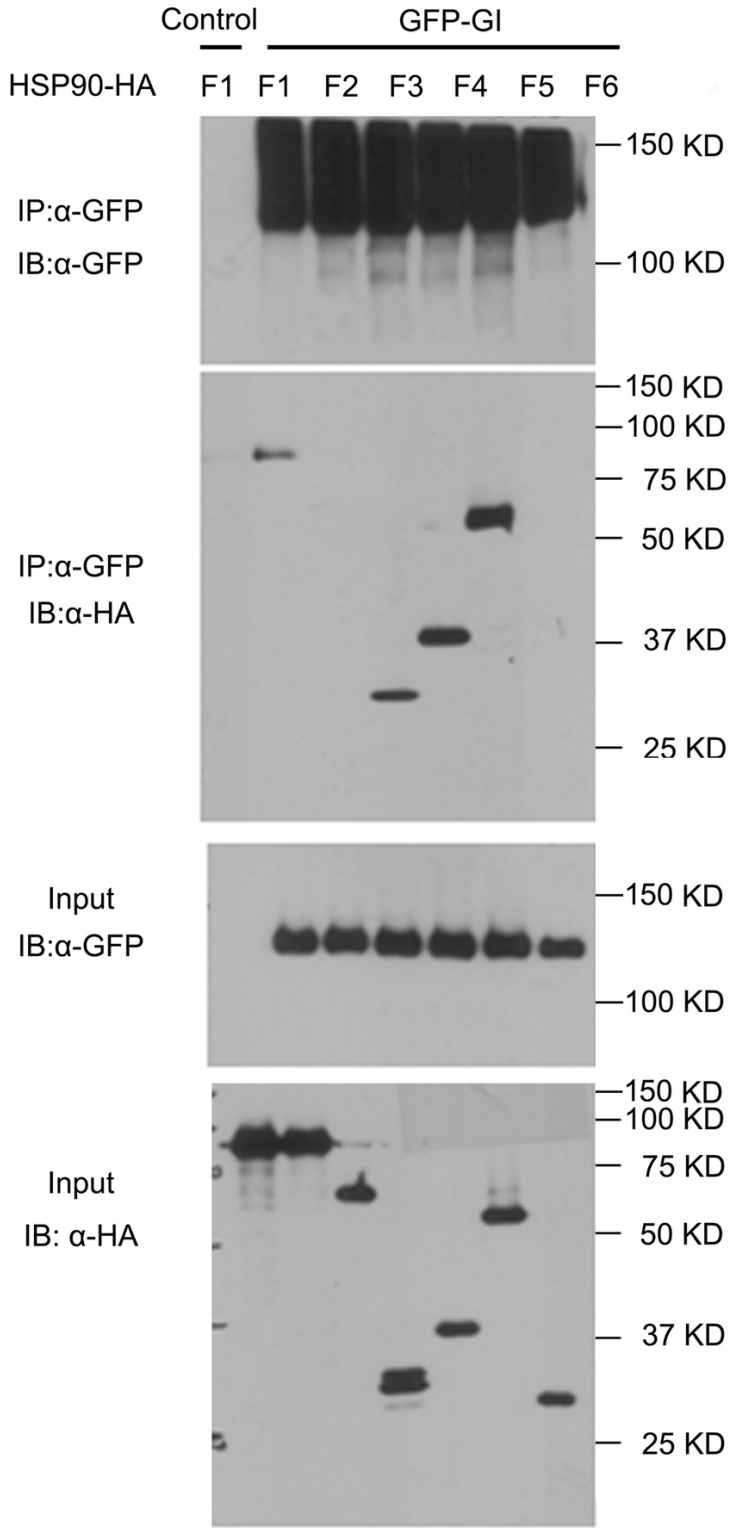
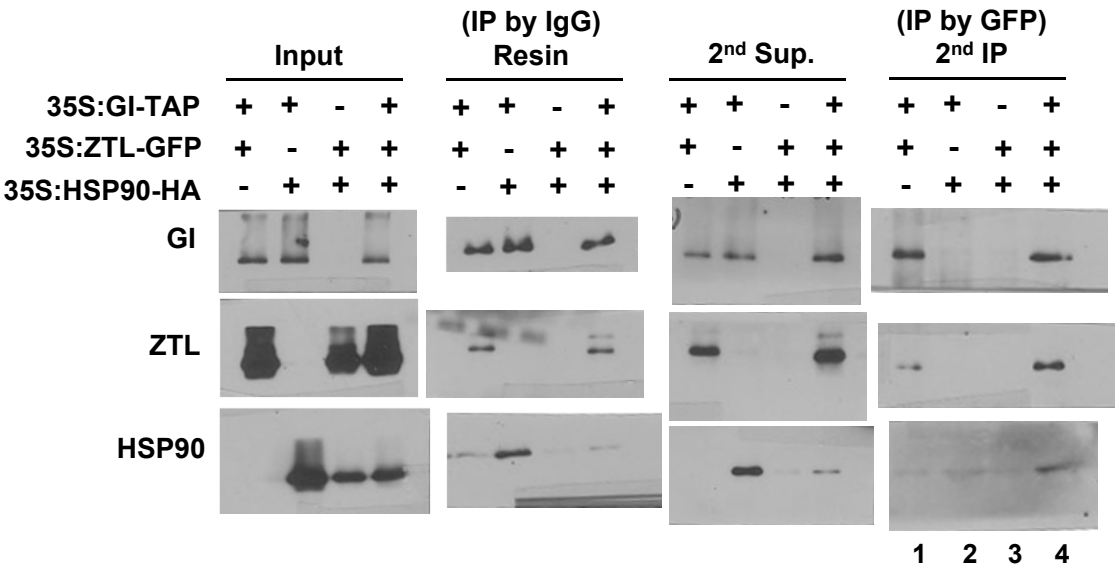
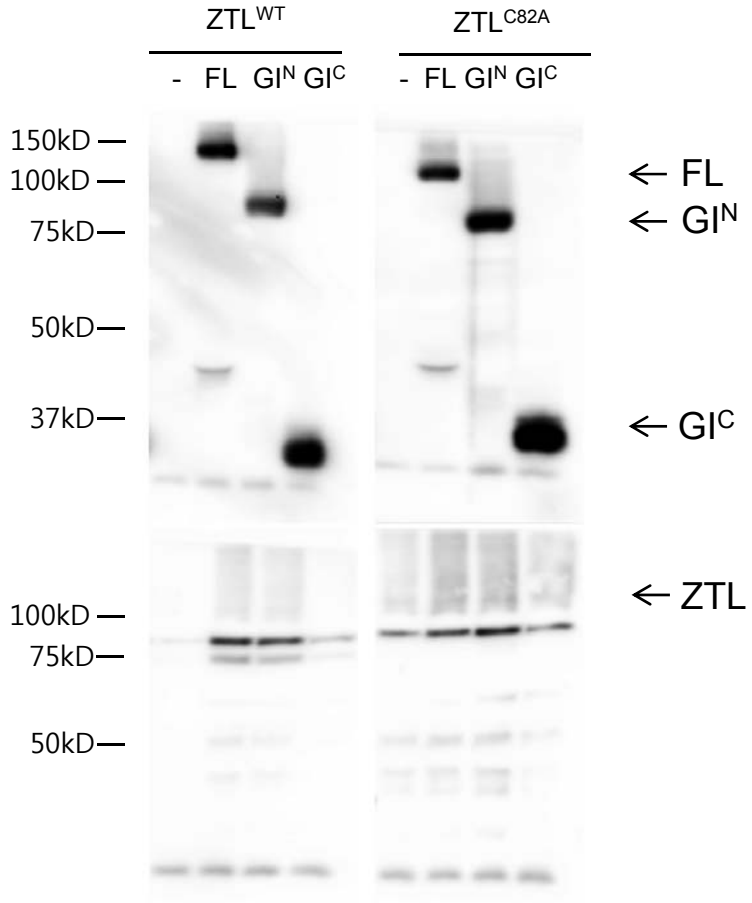


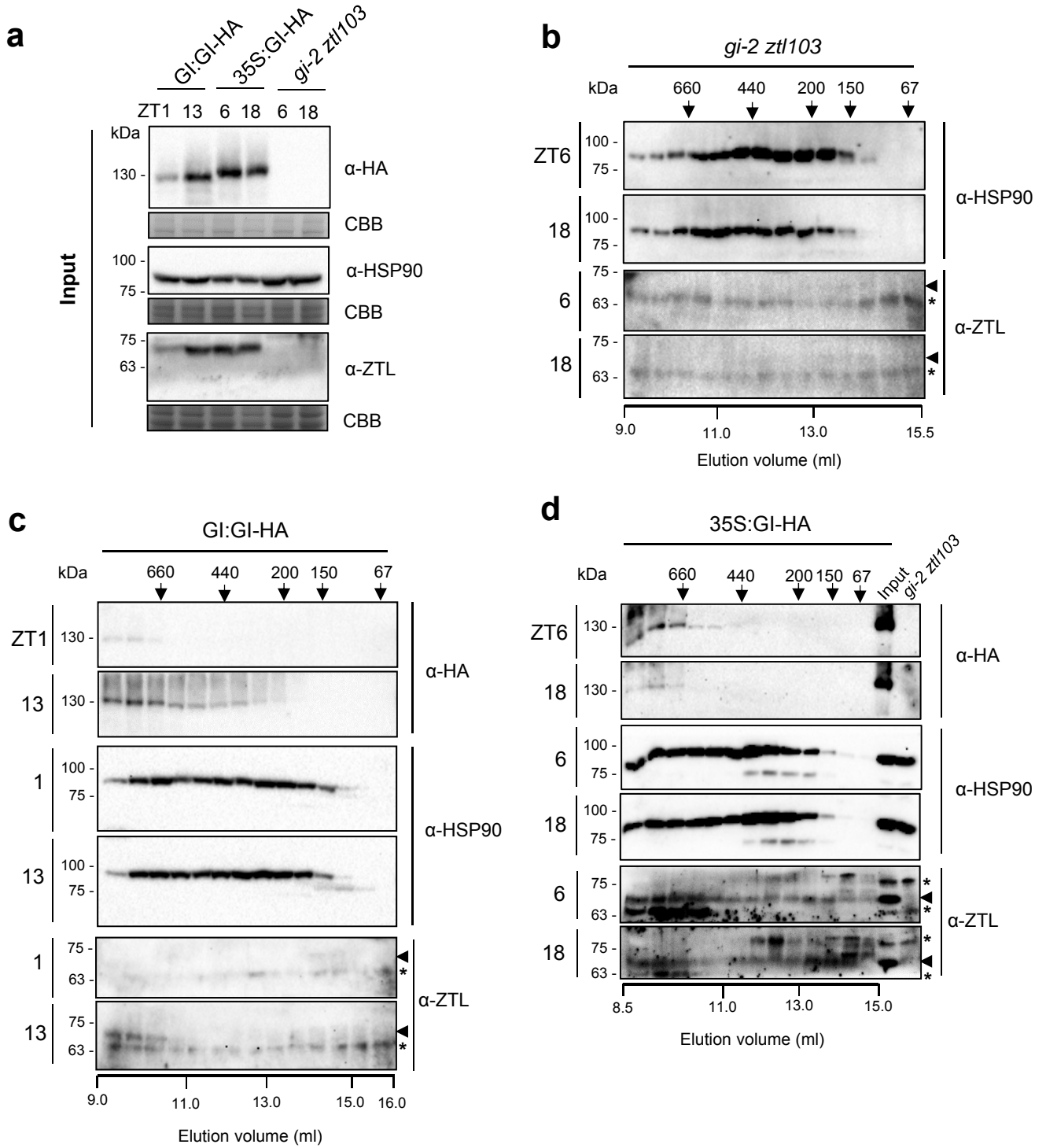
Fig. 4c



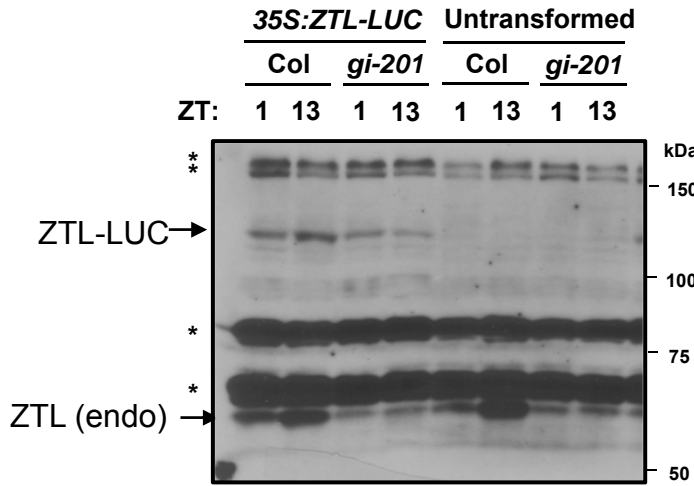
Supplementary. Fig. 3a



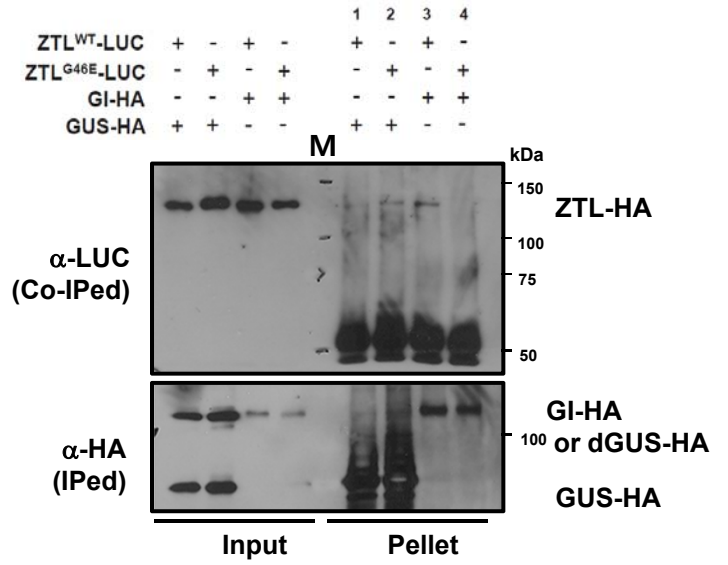
Supplementary. Fig. 8



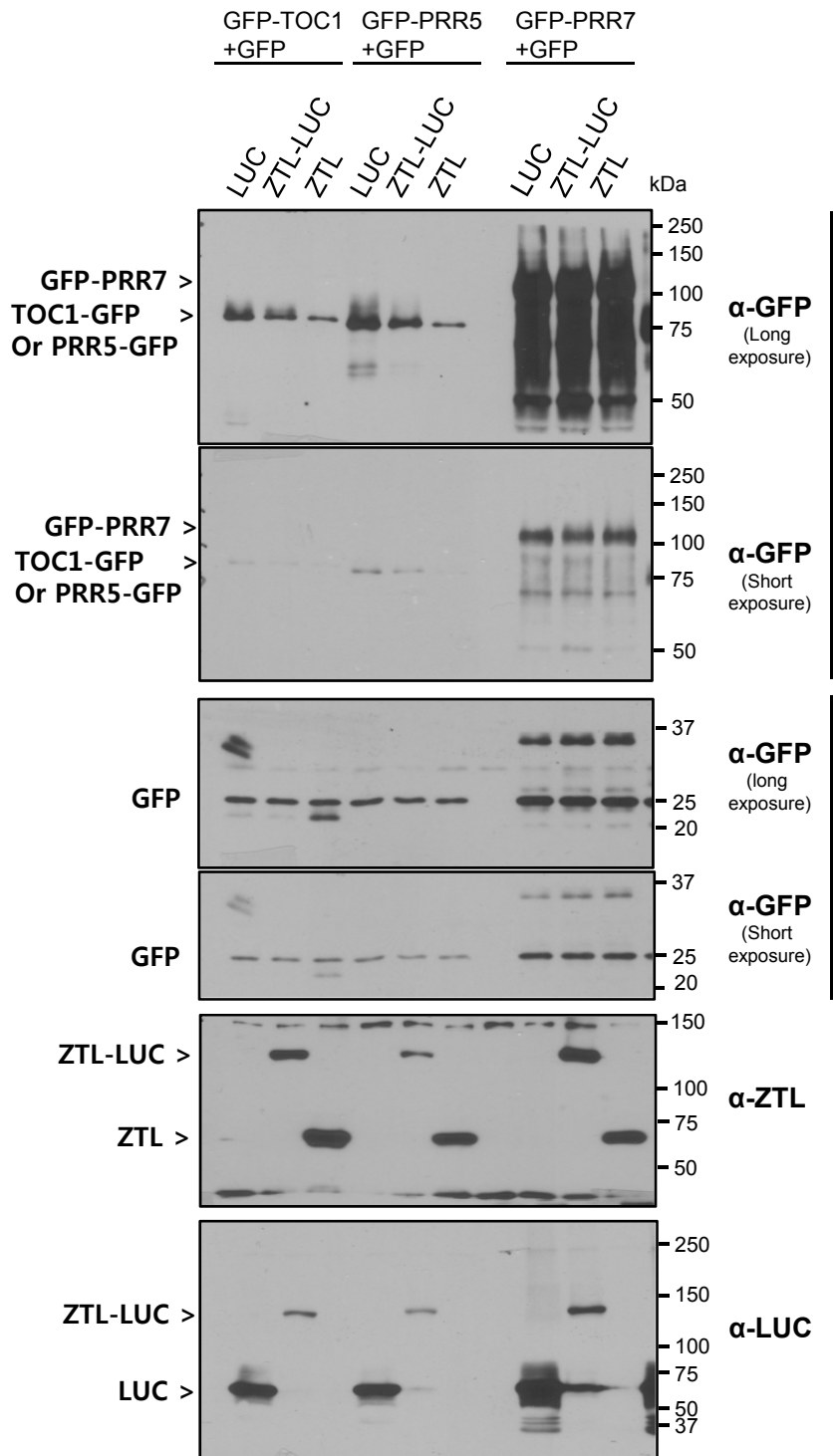
Suppl. Fig. 9a



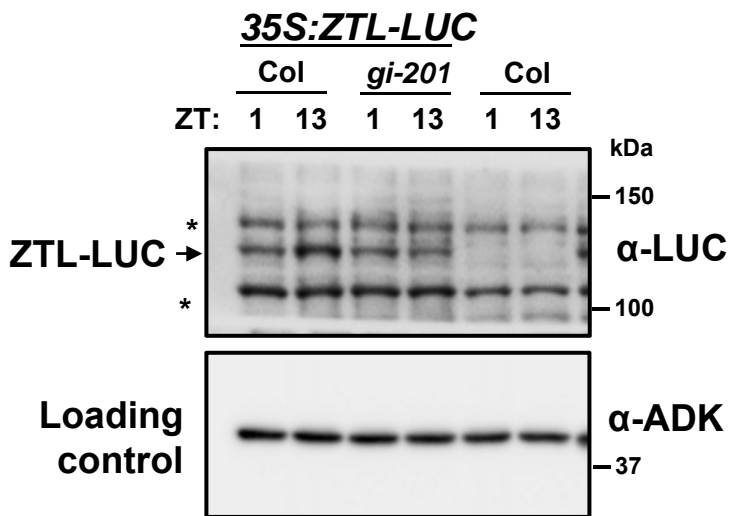
Suppl. Fig. 9b



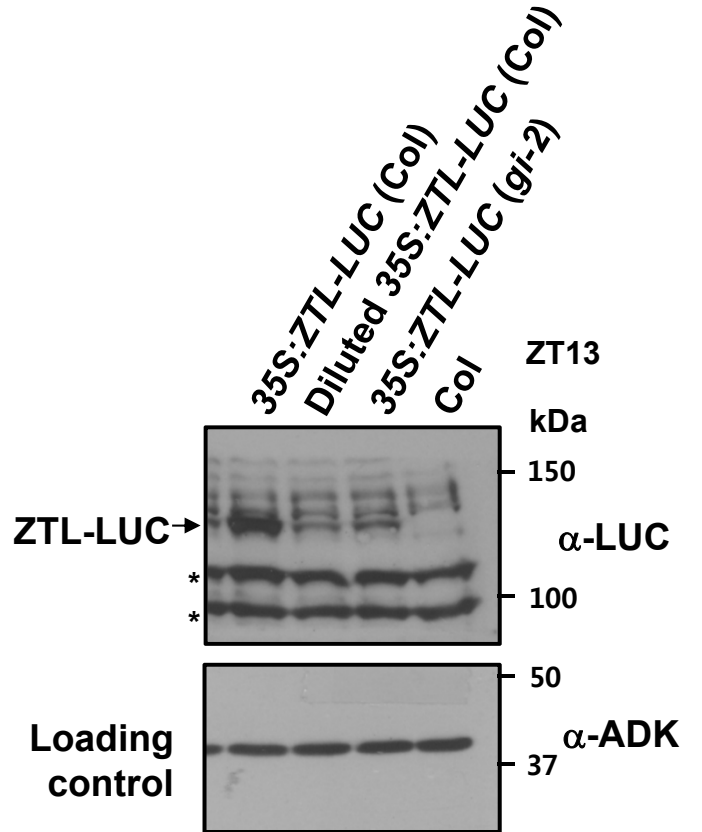
Supplementary. Fig. 9c



Supplementary. Fig 10b

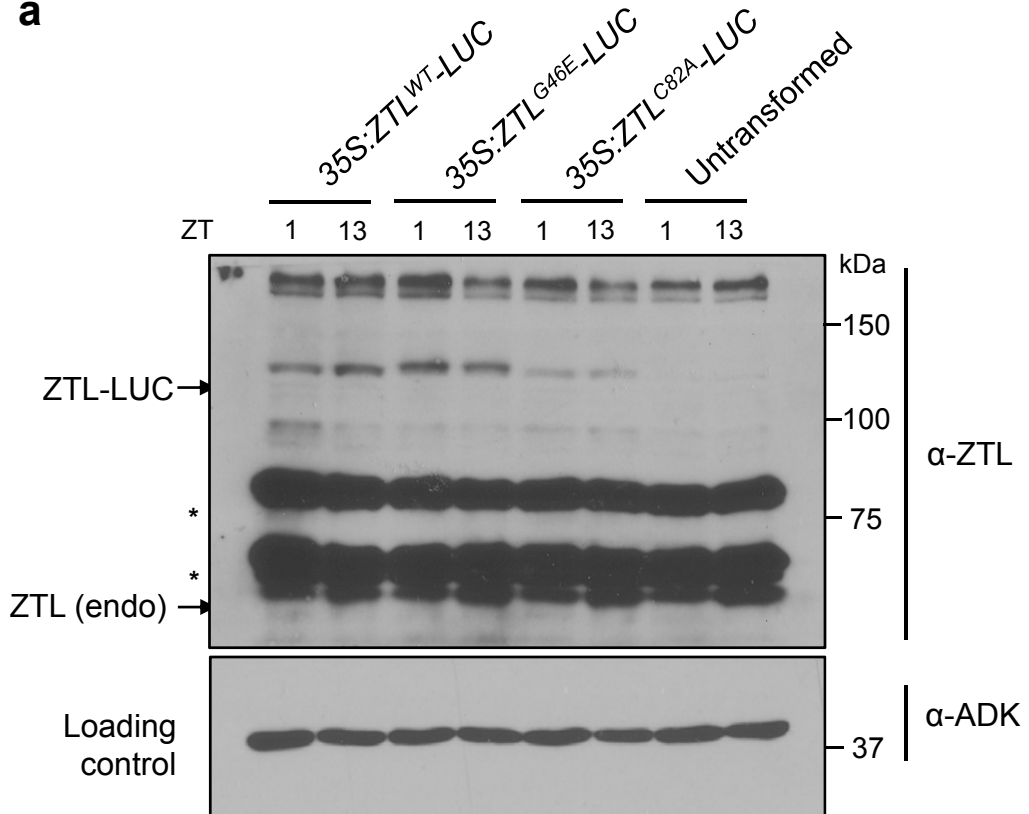


Supplementary. Fig 10d

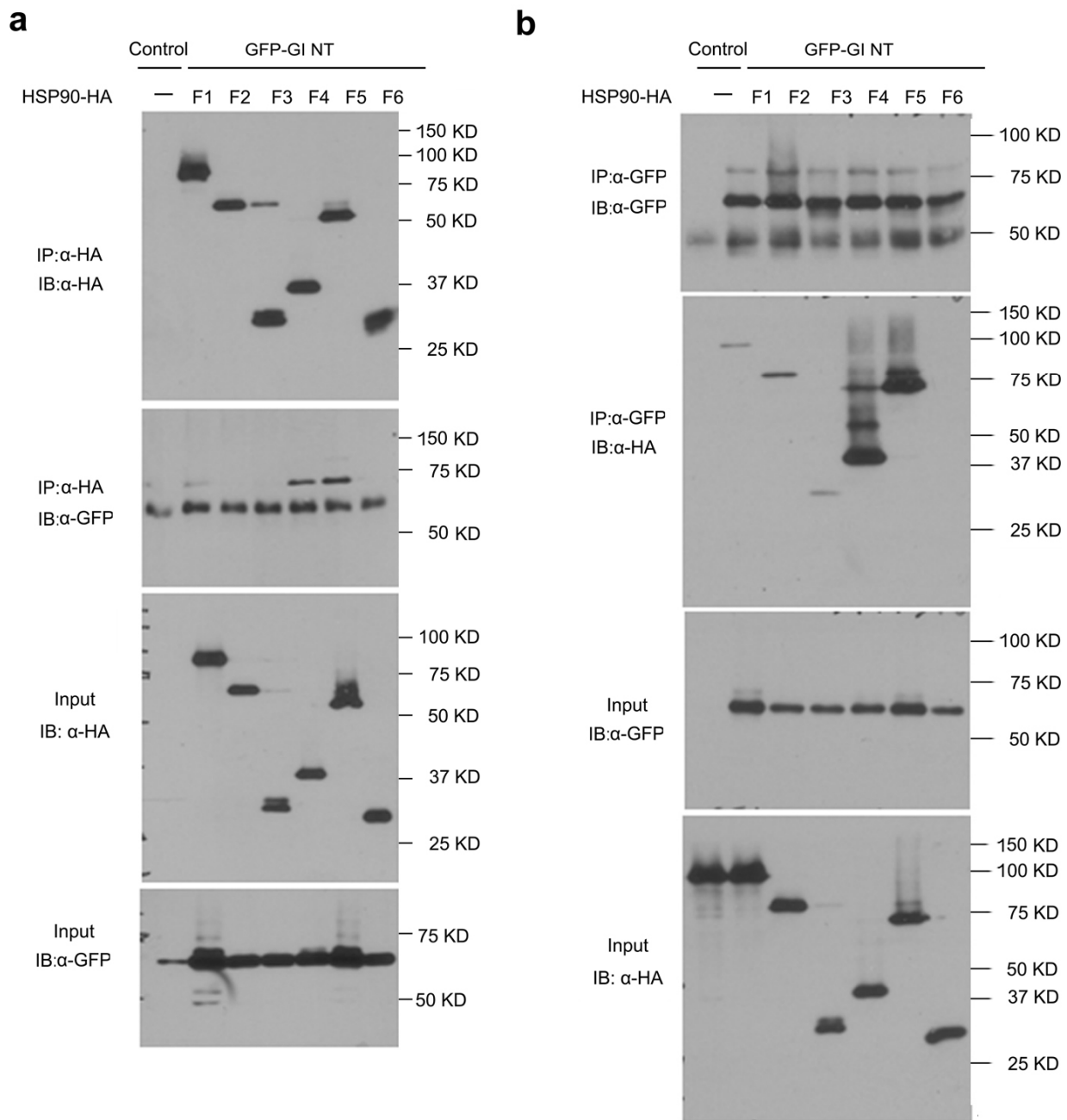


Supplementary. Fig 11

a



Supplementary. Fig. 14



Supplementary Fig. 15. Uncropped images of immunoblots and gels.

Gels and blots used in various main and supplementary figures when those images were cropped are shown. They are presented in the context of the annotation of the original figure.

Supplementary Table1. Identification of the expressed proteins by MALDI-TOF/TOF-MS.

No ^{a)}	Accession	Description (Mr/pI ^{b)})	Covered protein %	Matched peptide #	Matched peptide sequence
1	At1G22770	Protein GIGANTEA (<i>Arabidopsis thaliana</i>) (129163/6.6)	10% (82/858AA's)	6	RWIDGLQFSSLLWPPPRD RYYAIATPSATQRL RNWMHLHFLRA RAGVAADAAAALLFRI KVLEYLPRG KIFVATVETILSRT
2	At1G22770	Protein GIGANTEA (<i>Arabidopsis thaliana</i>) (129163/6.6)	25% (62/253AA's)	3	KAAAAVVLQAERE RNHDRPESLVILASADLLRA RATDGMLVDGEACTLPQLELLEATARA
3	P0AEY0 (P02928)	Maltose-binding periplasmic protein (<i>Escherichia coli</i> O157:H7) (43360/5.53)	30% (118/396AA's)	7	KFPQVAATGDGPDIIFFWAHDRF RFGGYAQSGLLAEITPDKA KLYPFTWDAVRY KLIAYPIAVEALSIIYNKD KAGLTFLVDLIKN KEFLENYLLTDEGLEAVNKD KSYEEELAKDPRI

a) Numbers correspond to the bands marked on Supplementary Fig 4.

b) Theoretical MW (Da) and pI values.

Supplementary Table 2. Primer sequences used in this study.

Name	Primer sequence (5' to 3')	Purpose
GI ^N	Forward: 5'-GGGGACAAGTTTGTACAAAAAAGCAGGCTCCATGGCTAGTTCATCTTCA-3' Reverse: 5'-GGGGACCACTTTGTACAAGAAAGCTGGGTCTTATTCATCTGAATGTCTAGCATA-3'	Gateway cloning
GI ^C	Forward: 5'-GGGGACAAGTTTGTACAAAAAAGCAGGCTCCATGATTGCTGCTCCTGAAATC-3' Reverse: 5'-GGGGACCACTTTGTACAAGAAAGCTGGGTCTTATGGGACAAGGATATAG-3'	Gateway cloning
GI ^{NT}	Forward: 5'-ACTGGATCCGATGGCTAGTTCATCTTCATC-3' Reverse: 5'-CTAGATATCTTAAGCGGCTGCAGCATCAGCAG-3'	Gateway cloning
ZTL ^{C82A}	Forward: 5'-GTTCTCGGAGGAAATGCCCGCTTCTTGCAATGT-3' Reverse: 5'-ACATTGCAAGAAGCGGGCATTTCCTCCGAGAAC-3'	Mutagenesis
HSP90.1 F1	Forward: 5'-TTTGGATCCGGATGGCGGATGTTTCAGATGGCTG-3' Reverse: 5'-TTTGCGGCCGCTTAGTCGACTTCCTCCATCTTGCT-3'	Gateway cloning
HSP90.1 F2	Forward: 5'-TTTGGATCCGGATGGCGGATGTTTCAGATGGCTG-3' Reverse: 5'-TTTGCGGCCGCTTATTCTTTAGTCGCAGAAACAAG-3'	Gateway cloning
HSP90.1 F3	Forward: 5'-TTTGGATCCGGATGGCGGATGTTTCAGATGGCTG-3' Reverse: 5'-TTTGCGGCCGCTTAAGGGTAACTGATGAACTCAGA-3'	Gateway cloning
HSP90.1 F4	Forward: 5'-TTTGGATCCGGTGGGAACTCATCAACAAGCAG-3' Reverse: 5'-TTTGCGGCCGCTTATTCTTTAGTCGCAGAAACAAG-3'	Gateway cloning
HSP90.1 F5	Forward: 5'-TTTGGATCCGGTGGGAACTCATCAACAAGCAG-3' Reverse: 5'-TTTGCGGCCGCTTAGTCGACTTCCTCCATCTTGCT-3'	Gateway cloning
HSP90.1 F6	Forward: 5'-TTTGGATCCGGTTCGAGAATCTGTGCAAGACG-3' Reverse: 5'-TTTGCGGCCGCTTAGTCGACTTCCTCCATCTTGCT-3'	Gateway cloning

References

1. Saitou, N., Nei, M. The neighbor-joining method: a new method for reconstructing phylogenetic trees. *Molecular Biology and Evolution* **4**, 406 (1987).
2. Tamura, K.*et al.* MEGA6: Molecular Evolutionary Genetics Analysis version 6.0. *Molecular Biology and Evolution* **30**, 2725 (2013).