

**Supplementary Table 1. Amino acid sequence identity between AtINP1, AtINP2 and their respective orthologs from a variety of angiosperm taxa.**

Species	Clade	Sub Clade	Sub clade	Order	Family	INP1	INP2	INP1: identity to AtINP1	INP2: identity to AtINP2
Arabidopsis thaliana	Eudicots	Eurosids	Malvids	Brassicales	Brassicaceae	At4g22600	At1g15320	100%	100%
Arabidopsis lyrata	Eudicots	Eurosids	Malvids	Brassicales	Brassicaceae	XM_002867712	XM_002892814	94%	90%
Capsella rubella	Eudicots	Eurosids	Malvids	Brassicales	Brassicaceae	XM_006285378	XM_006303615	92%	90%
Eutrema salsugineum	Eudicots	Eurosids	Malvids	Brassicales	Brassicaceae	XM_006413577	XP_006416922	84%	82%
Tarenaya hassleriana	Eudicots	Eurosids	Malvids	Brassicales	Cleomaceae	XP_010539222	XP_010538005	70%	70%
Carica papaya	Eudicots	Eurosids	Malvids	Brassicales	Caricaceae	XM_022046188	XM_022042844	56%	44%
Theobroma cacao	Eudicots	Eurosids	Malvids	Malvales	Malvaceae	XP_007039914	XP_007023253	54%	47%
Gossypium raimondii	Eudicots	Eurosids	Malvids	Malvales	Malvaceae	XP_012471971	XP_012442564	50%	49%
Herrania umbratica	Eudicots	Eurosids	Malvids	Malvales	Malvaceae	XM_021435636	XM_021442724	55%	48%
Manihot esculenta	Eudicots	Eurosids	Fabids	Malpighiales	Euphorbiaceae	XP_021631264	Manes.04G112100	54%	45%
Ricinus communis	Eudicots	Eurosids	Fabids	Malpighiales	Euphorbiaceae	XP_002529792	XP_002517657	53%	45%
Hevea brasiliensis	Eudicots	Eurosids	Fabids	Malpighiales	Euphorbiaceae	XM_021805081	XM_021780609	55%	44%
Populus trichocarpa	Eudicots	Eurosids	Fabids	Malpighiales	Salicaceae	XM_024587580	XP_006369313	52%	52%
Linum usitatissimum	Eudicots	Eurosids	Fabids	Malpighiales	Linaceae	Lus10028923 (Phytosome)	Lus10025746 (Phytosome)	49%	38%
Citrus cinensis	Eudicots	Eurosids	Fabids	Sapindales	Rutaceae	XM_015529742	XP_015386244	50%	48%
Pistacia vera	Eudicots	Eurosids	Fabids	Sapindales	Anacardiaceae	XM_031405325	XM_031431563	50%	48%
Fragaria vesca	Eudicots	Eurosids	Fabids	Rosales	Rosaceae	XM_004300662	XP_004305502	47%	47%
Prunus persica	Eudicots	Eurosids	Fabids	Rosales	Rosaceae	XM_007210501	XP_020416177	49%	47%
Ziziphus jujuba	Eudicots	Eurosids	Fabids	Rosales	Rhamnaceae	XM_016045621	XP_015870799	49%	47%
Cannabis sativa	Eudicots	Eurosids	Fabids	Rosales	Cannabaceae	XM_030645895	XM_030632112	51%	48%
Quercus suber	Eudicots	Eurosids	Fabids	Fagales	Fagaceae	XM_024052895	XM_024036728	50%	45%
Juglans regia	Eudicots	Eurosids	Fabids	Fagales	Juglandaceae	XM_018992647	XP_018851749	50%	47%
Vitis vinifera	Eudicots	Rosids	Vitales	Vitales	Vitaceae	XM_010648242	XP_010654806	46%	45%
Solanum lycopersicum	Eudicots	Euasterids	Lamiids	Solanales	Solanaceae	XM_004245692	XP_004236461	46%	43%
Ipomoea nil	Eudicots	Euasterids	Lamiids	Solanales	Convolvulaceae	XM_019340312	XP_019159957	48%	42%
Mimulus guttatus	Eudicots	Euasterids	Lamiids	Lamiales	Phrymaceae	XM_012990426	XP_012856236	45%	41%
Olea europea	Eudicots	Euasterids	Lamiids	Lamiales	Oleaceae	XM_023026469	XM_022994362	45%	43%
Sesamum indicum	Eudicots	Euasterids	Lamiids	Lamiales	Pedaliaceae	XM_011083080	XM_020692503	47%	45%
Coffea arabica	Eudicots	Euasterids	Lamiids	Gentianales	Rubiaceae	XM_027226234	XM_027270435	46%	42%
Lactuca sativa	Eudicots	Euasterids	Campanulid	Asterales	Asteraceae	XP_023753693	XM_023894801	45%	37%
Helianthus annuus	Eudicots	Euasterids	Campanulid	Asterales	Asteraceae	XM_022149160	XM_022162388	44%	37%
Daucus carota	Eudicots	Euasterids	Campanulid	Apiales	Apiaceae	XM_017377544	XM_017362523	44%	41%
Camellia sinensis	Eudicots	Asterids	Ericales	Ericales	Theaceaceae	XM_028205791	XM_028195317	49%	48%
Spinacia oleracea	Eudicots	Core eudicots/Superast	Caryophyllales	Caryophyllales	Amaranthaceae	XM_022000275	XM_022007145	41%	42%
Nelumbo nucifera	Basal eudicots			Proteales	Nelumbonaceae	XP_010259014	XP_010241626	46%	46%
Papaver somniferum	Basal eudicots			Ranunculales	Papaveraceae	XM_026602809	XM_026587879	40%	36%
Aquilegia coerulea	Basal eudicots			Ranunculales	Ranunculaceae	Aqcoe7G079000 (Phytosome)	Aqcoe7G382900 (Phytosome)	46%	42%
Elaeis guineensis	Monocots	Commelinids		Arecales	Arecaceae	XM_010921594	XP_010928340	44%	34%
Phoenix dactylifera	Monocots	Commelinids		Arecales	Arecaceae	XM_008788847	XM_026804442	44%	34%
Ananas comosus	Monocots	Commelinids		Poales	Bromeliaceae	Aco011729, Phytosome	XM_020246879	39%	25%
Oryza sativa	Monocots	Commelinids		Poales	Poaceae	XP_025878546	XM_015755361	35%	21%
Brachypodium distachyon	Monocots	Commelinids		Poales	Poaceae	XM_024460675	XP_003576910	35%	20%
Zea mays	Monocots	Commelinids		Poales	Poaceae	NP_001130869	XP_008649809	36%	21%
Setaria italica	Monocots	Commelinids		Poales	Poaceae	XM_004953314	XP_004956307	35%	21%
Sorghum bicolor	Monocots	Commelinids		Poales	Poaceae	XM_002452752	XP_002441305	36%	21%
Laurelia sempervirens	Magnoliids			Laurales	Atherospermataceae	gnl onekp WAIL_scaffold_2020264	gnl onekp WAIL_scaffold_2068545	46%	48%
Austrobaileya scandens	Basal angiosperm	ANA		Austrobaileyales	Austrobaileyaceae	gnl onekp FZIL_scaffold_2015050	?	46%	N/A
Nymphaea colorata	Basal angiosperm	ANA		Nymphaeales	Nymphaeaceae	XM_031628012	XM_031628356	40%	31%
Amborella trichopoda	Basal angiosperm	ANA		Amborellales	Amborellaceae	No	No	N/A	N/A

Color coding according to order/clade is the same as in Fig. 5

**Supplementary Table 2. Primers used in this study.**

Construct/Purpose	Primer name (restriction enzyme)	Sequence (5' to 3'; restriction enzyme recognition sites are underlined)
<i>INP2pr:INP2 ORF</i> ( <i>INP2</i> promoter and <i>INP2</i> ORF fragments)	INP2pr-IF-F ( <i>SacI</i> )	ACAAAAGCTGGAGCTCGCTGTGATCTTCTTTGCTCTTC
	INP2pr-IF-R ( <i>Bam</i> HI)	<u>GGATCCTGC</u> CACTCAAATCCTAAAATGC
	INP2-ORF-IF-F ( <i>Bam</i> HI)	GAGTGTGCAGGATCCATGAGATTACAAGAGTTGGTTC
	INP2-stop-SpeI-R ( <i>SpeI</i> )	GGAA <u>ACTAGIT</u> TCAACTAGATGATCCTGATCC
<i>INP2pr:gINP2</i> (Fragment composed of <i>INP2</i> genic + ~0.5kb downstream regions)	INP2-ORF-IF-F ( <i>Bam</i> HI)	GAGTGTGCAGGATCCATGAGATTACAAGAGTTGGTTC
	gINP2-SpeI-R ( <i>SpeI</i> )	GGAA <u>ACTAGIT</u> TGCTGTATGGCGCGGGTTATC
<i>INP2pr:H2B-RFP</i> ( <i>H2B-RFP</i> fragment)	H2BRFPinfAF ( <i>AgeI</i> )	ATCCCCGGGTACCGGTGAATTCATGGCGAAGGCAGATAAGAAACC
	H2BRFPinfAR ( <i>SpeI</i> )	AGCGTACCGGACTAGTTTAGGCGCCGGTGGAGTGGCGGC
<i>INP2pr:gSIINP2</i> ( <i>SIINP2</i> genomic fragment)	BamHI-SIINP2-BF ( <i>Bam</i> HI)	GGAAGGATCCATGAAGCGGCCTTCTTCTCTG
	SpeI-SIINP2-AR ( <i>SpeI</i> )	GGAA <u>ACTAGIT</u> CTTTTCTAAAGCCGAACGGTAAAC
Genotyping for <i>SIINP1</i> transgene	2-SI-F	GGCGACTCAGAATCCGAAATTGAC
	Sly INP1-R- <i>NcoI</i> ( <i>NcoI</i> )	GGAACCATGGCTAATTCCAAGAACAACCTTGTCAAATTGAC
Genotyping for <i>SIINP2</i> transgene	AD23	TTTGTCTTCCTGCAACGTAACAAAGGAAAATCTATACTCGAAGATGAAGAC
	AD8	CTCTTCGATGCGTATCTCGTTGATCAATTGGGGCAATGCCAC
CAPS marker for <i>inp1-1</i> (mutant allele cut with <i>SacI</i> )	22600-DF	ccatttagacaagggcttg
	22600-DR	AACTTGATACGACGAGACC
<i>dCAPS</i> marker for <i>inp2-1</i>	At1g15320-BF	GAGAGATCTCACCAACACGAATC

(mutant allele cut with AccI)		
	AD402	CGCAATGCTGTTCTGTTCTTGCCTC
<i>SIINP2</i> ORF-pGEM-T- Easy (subcloning <i>SIINP2</i> ORF into pGEM-T-Easy with IVA)	AD19 ( <i>Bam</i> HI)	CAACGCGTTGGGGGATCCATGAAGCGGCCTTCTT CTCTG
	AD16 ( <i>Spe</i> I)	CCGGCCGCCATGACTAGTCTACTTAAGTGGGCTA CCACCAGAC
	AD17 ( <i>Bam</i> HI)	<u>GGATCCCCCAACGCGTTGGATGC</u>
	AD14 ( <i>Spe</i> I)	<u>ACTAGTCATGGCGGCCGGGA</u>
<i>SIINP2</i> ORF-pGEM-T- Easy (subcloning <i>SIINP2</i> ORF into pGEM-T-Easy with IVA)	pGEM-INP2- IF-F ( <i>Bam</i> HI)	ATCCAACGCGTTGGGGGATCCATGAGATTACAAG AGTTGGTTCT
	INP2-pGEM- IF-R ( <i>Spe</i> I)	CTCCCGGCCGCCATGACTAGTTCAACTAGATGAT CCTGATCCCT
1- <i>At</i> INP2 <sup>SIN</sup>	AD19 ( <i>Bam</i> HI)	CAACGCGTTGGGGGATCCATGAAGCGGCCTTCTT CTCTG
	AD20	AAATCCATTCTCTTCACTAGAATTGACATCAACGT GATGAGTTCC
	AD17 ( <i>Bam</i> HI)	<u>GGATCCCCCAACGCGTTGGATGC</u>
	AD18	AGTGAAGAGAATGGATTGAAGAACCAAAC
2- <i>At</i> INP2 <sup>Slacid</sup>	AD23	TTTGTCTTCCTGCAACGTAACAAAGGAAAATCTAT ACTCGAAGATGAAGAC
	AD24	TGATATATTACTAGCAGCTGTGCTGATTCTCTCGA AATCGATGATC
	AD21	ACGTTGCAGGAAGACAAACC
	AD22	GCTGCTAGTAATATATCATCTAAAAGATCTCATGC
3- <i>At</i> INP2 <sup>Slmid</sup>	AD27	GATGATCTGGAGAGAGAACCCTGTAATTTGCAAAA CAGTACAAAATTGG
	AD28	TTCAATCAGTTCATCGAGTGCCCATCTTGCTTTTA GCTGTTTCTC
	AD25	TTCTCTCTCCAGATCATCCAGGAAAG
	AD26	CTCGATGAACTGATTGAAGAACAGCTGAG
4- <i>At</i> INP2 <sup>SIDOG1</sup>	AD3	CTAAAATCCAGGTGGGAAGTGGATGGACTTATCG AAGAAGAACTC
	AD4	GAAGGAGGGGTTTTGAGCGGCTAAGTATTGAAGA AGATCCAGGATTG
	AD1	TTCCACCTGGATTTTAGCTCTTTGTC
	AD2	GCTCAAACCCCTCCTTCTCTC
5- <i>At</i> INP2 <sup>SILCR</sup>	AD7	CTTGTCCGCATTCTGGCACATTCATCTGGGCTTT CAAATCTCTAC
	AD8	CTCTTCGATGCGTATCTCGTTGATCAATTGGGGC AATGCCAC
	AD5	TGCCAGAATGCGGACAAGGTC

	AD6	GAGATACGCATCGAAGAGGCCGTTA
6-AtINP2 <sup>SICTR</sup>	AD11	CTCTCTCAGCTTTTACGTGAGTTACGAATCGAGG AGGCGGTGA
	AD12	CTGGTGTATGGCGTCTTGAATTCCAGCAAAAGCA ACCAAAACTC
	AD9	ACGTAAAAGCTGAGAGAGCACG
	AD10	CAAGACGCCATACACCAGTTTGG
	AD15	GTCGCATTTGCAGGGATTCAAGATTTGGTTCATC AATGGGCTATG
7-AtINP2 <sup>SIC-tail</sup>	AD16 ( <i>SpeI</i> )	CCGGCCGCCATGACTAGTCTACTTAAGTGGGCTA CCACCAGAC
	AD13	AATCCCTGCAAATGCGACCAC
	AD14 ( <i>SpeI</i> )	ACTAGTCATGGCGGCCGGGA
	pGEM-INP2- IF-F ( <i>Bam</i> HI)	ATCCAACGCGTTGGGGGATCCATGAGATTACAAG AGTTGGTTCT
1-SIINP2 <sup>AtN</sup>	AD21	ACGTTGCAGGAAGACAAACC
	AD17 ( <i>Bam</i> HI)	GGATCCCCAACGCGTTGGATGC
	AD23	TTTGTCTTCCTGCAACGTAACAAAGGAAAATCTAT ACTCGAAGATGAAGAC
	AD20	AAATCCATTCTCTTCACTAGAATTGACATCAACGT GATGAGTTCC
2-SIINP2 <sup>Atacid</sup>	AD27	GATGATCTGGAGAGAGAACCTGTAATTTGCAAAA CAGTACAAAATTGG
	AD18	AGTGAAGAGAATGGATTTGAAGAACCAAAC
	AD25	TTCTCTCTCCAGATCATCCAGGAAAG
	AD24	TGATATATACTAGCAGCTGTGCTGATTCTCTCGA AATCGATGATC
3-SIINP2 <sup>Atmid</sup>	AD3	CTAAAATCCAGGTGGGAAGTGGATGGACTTATCG AAGAAGAACTC
	AD22	GCTGCTAGTAATATATCATCTAAAAGATCTCATGC
	AD1	TTCCACCTGGATTTTAGCTCTTTGTC
	AD28	TTCAATCAGTTCATCGAGTGCCCATCTTGCTTTTA GCTGTTTCTC
4-SIINP2 <sup>AtDOG1</sup>	AD27	GATGATCTGGAGAGAGAACCTGTAATTTGCAAAA CAGTACAAAATTGG
	AD26	CTCGATGAACTGATTGAAGAACAGCTGAG
	AD5	TGCCAGAATGCGGACAAGGTC
	AD2	GCTCAAACCCCTCCTTCTCTC
5-SIINP2 <sup>AtLCR</sup>	AD9	ACGTAAAAGCTGAGAGAGCACG
	AD4	GAAGGAGGGGTTTTGAGCGGCTAAGTATTGAAGA AGATCCAGGATTG
	AD11	CTCTCTCAGCTTTTACGTGAGTTACGAATCGAGG AGGCGGTGA
	AD8	CTCTTCGATGCGTATCTCGTTGATCAATTGGGGC AATGCCAC

	AD15	GTCGCATTTGCAGGGATTCAAGATTTGGTTCATC AATGGGCTATG
	AD6	GAGATACGCATCGAAGAGGCCGTTA
	AD13	AATCCCTGCAAATGCGACCAC
7-SIINP2 <sup>AtC-tail</sup>	AD12	CTGGTGTATGGCGTCTTGAATTCCAGCAAAAGCA ACCAAAAACCTC
	AD14 ( <i>SpeI</i> )	<u>ACTAGTCATGGCGGCCGGA</u>
	AD10	CAAGACGCCATACACCAGTTTGG
	INP2-pGEM- IF-R ( <i>SpeI</i> )	CTCCCGGCCGCCATG <u>ACTAGTTCAACTAGATGAT</u> CCTGATCCCT
gRNA sequence for <i>INP2</i> CRISPR construct in pHEE401E vector	Oligo-01-F- INP2-T1	ATTGAGACTTGTACGAACTGTGG
	Oligo-R-INP2- T1	AAACCCACAGTTCGTACAAGTCT
35Spr:nYFP- <i>AtINP1</i>	AD17-BHL ( <i>PacI</i> )	CCCTTAATTAACATGCCTTTCTCTTTCTTCTCC
	AD18-BHL ( <i>XbaI</i> )	GCGTCTAGAAATTGGGCAAAGAAAGAATCTC
35Spr:cYFP- <i>AtINP2</i>	AD469 ( <i>PacI</i> )	CCCTTAATTA <del>AA</del> AATGAGATTACAAGAGTTGGTT
	AD470 ( <i>XbaI</i> )	5'-GCGTCTAGAACTAGATGATCCTGATCCCTT
<i>AtINP1</i> -pDONR207	AD326	AAAAAGCAGGCTAGAAAATGCCTTTCTCTTTC
	AD488	AGAAAGCTGGGTAGAGATTATTGGGCAAAGAA
	AD122	GGGACAAGTTTGTACAAA AAA GCA GGC T
	AD123	GGGACCACTTTGTACAAGAAAGCTGGGT
<i>AtINP2</i> -pDONR207	AD370	AAAAAGCAGGCTGATCCATGAGATTACAAGAG
	AD489	AGAAAGCTGGGTAAAGCTCACTAGATGATCCT
	AD122	GGGACAAGTTTGTACAAAAAAGCAGGCT
	AD123	GGGACCACTTTGTACAAGAAAGCTGGGT