

Genomic characterization of the LEED..PEEDs, a gene family unique to the Medicago lineage

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 | ATAATGCTTA
 | ACCATT <mark>G</mark> TT <mark>G</mark> T | AGATGGAAGG
 | CATGATGT | | TTT <mark>G</mark> ATAT | TCAACCT
 | ACAT | TAGATCC | AGAAGAA | GATTGO |
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 | AATAOTAA | A.A. | TTUGALA |
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| HM056_LP2 ATGGGCT | CTAAATAI
 | ITCATTAGTAI | TACTITIACTI
 | GGAATG
 | ATAATGUTTA
 | ACCACC <mark>GT</mark> GG | TGGTGAAAGAA
 | AATAGTAAT | AAT | TTTC <mark>G</mark> ACA |
 | AIGI | TAGATCC | AGAAGAT | GATIGG |
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 | ETCATTA <mark>gt</mark> at | TACTTTTACTT
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 | AA <mark>TA<mark>gt</mark>aat</mark> | AAT | TTT <mark>CG</mark> ACA | TTCTCCT-
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| A17_LP_3 ATGAGET | C T A A A T A T
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 | <mark>АТ</mark> СТ | TA <mark>G</mark> ATCC | A GAAGAT | <mark>g a t t</mark> gg |
| HM056 LP3 ATGAGCT | CTAAATA
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| HM056_LP5 ATGAGCT |
 | TCATTAGTA | TACTITIACTI
 | GGAATG
 | ATAATGCTTA
 | ACCACTGTGA | TGG TG AAAGG
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 | ATGT | TAGATCC | AGAAGAT | TATIGG |
| A17_LP_4 ATGGCCT | CTAAATA(
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 | CA <mark>t</mark> aa <mark>t</mark> aaa | | TTT <mark>GGG</mark> TA | T <mark>gcg</mark> cca
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| HN/056_LP4 ATGGCCT | C T A A A T A C
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 | ATGGTTCTTA
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| A17_LP_7 ATGGCCT | CTAAATAG
 | CTCACTAGTAI | TACTICIACII
 | G G A A T G
 | ATGGTACTTA
 | ACCACAGTAG | GAGTGATAGG <i>A</i>
 | A <mark>gg d d ag</mark> a d | | TTT <mark>GGGT</mark> A | T <mark>GTGCCT</mark> -
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| R108_LP_7 ATOOCCT | C T A A A T A C
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 | CTGGTGCTAA
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| HM056_LP9 A TGGCCT | CTACATAC
 | CTCATTA <mark>GT</mark> AT | ТАСТТСТАСТТ
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 | ACCACTGTCG | GGG <mark>TGCTCG</mark> AA
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 | A <mark>ttac</mark> ic cat | TT <mark>GAGCT</mark> | A <mark>g</mark> aa <mark>g</mark> aa | <mark>g a t t</mark> gg |
| R108_LP_9 A <mark>tggcct</mark> | CTACATAC
 | CTCATTAGTAT | TACTTCTACTT
 | G G G A A C G
 | A TGG TGG TT A
 | ACCAC <mark>TGT</mark> C <mark>G</mark> | GGGTGCTCCA#
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 | A <mark>tt</mark> acccat | TT <mark>G</mark> AGCT | A <mark>G</mark> AA <mark>G</mark> AA | <mark>g a tt</mark> gg |
| A17_LP_10 A <mark>TGGCCT</mark> | CTACATAC
 | CTCAA <mark>T</mark> A <mark>gta</mark> t | TACTTCTACTT
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 | ACCACTTT <mark>C</mark> O | GGGTGCTGGAA
 | A <mark>GGTTT</mark> AAT | ATG | TTT <mark>GG</mark> ATA | TCCA <mark>G</mark> ATT.
 | A <mark>TT</mark> AC <mark>CCTG</mark> | TA <mark>G</mark> ATTT | A <mark>G</mark> AA <mark>G</mark> AT | <mark>g a t t</mark> gg |
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 | ATGATGGTT 4
 | ACCACTTTC. | GGGTGCTGGA
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 | ATTACCCTG | TAGATTT | AGAAGAT | GATTGG |
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 | A <mark>TAGCTT</mark> A <mark>G</mark> | AAGAAAT | AGAAGAA | GAA <mark>T</mark> GG |
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Figure S1 Aligned LP DNA sequences from A17, HM056 and R108. Columns that were omitted for the phylogenetic analysis are highlighted with red headers. Phylogenetic trees were based on the remaining 144 nucleotides.

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A17_LP_1	A TGGCCTCT	ACA <mark>TGCT</mark> CACTA	A T A T T A T T	TT <mark>CT</mark> ACTT · · · <mark>GG</mark>	TA <mark>TG</mark> A <mark>T</mark> AA <mark>TGC</mark>	TT <mark>acca</mark> tt <mark>g</mark> 1	T <mark>g tagatgg</mark> aa <mark>gg</mark>	CATGAT	. <mark>G T </mark> G T T	T <mark>g</mark> a <mark>tatt</mark> caacc	T ACA1	TA <mark>G</mark> ATCCA	<mark>G A A G</mark> A A <mark>G</mark> A <mark>T T G G</mark>
HM056_LP_1	A TGGCCTCT	A C A <mark>T G</mark> C T C A C T A	ATATTATT	TTCTACTT · · · <mark>GG</mark>	TATGATAATGC	TT <mark>accatt</mark> g T	T <mark>g tag</mark> a tgg aagg	CATGAT	. <mark>G T G T T</mark>	T <mark>g</mark> atattcaacc	T A C A 1	TA <mark>G</mark> ATCCA	<mark>g a a g</mark> a a <mark>g a t t g g</mark>
R108_LP_1	ATGGCCTCT	ACATGCTCACTA	ATATTATT	ITCTACTT - GG	TATGATAATGC	TTACCATTGT	TG TAGATGGAAGG	CATGAT	- GTGTT	TGATATTCAACC		TAGATCCA	G A A G A A G A T T G G
Ms_LP_1	ATGGCCTCT	ACATOCICACIA	GTATTACT	GG CTACTT GG	TATGATGATGC	CACCATIG		CATGAT	AIGII	TGATATTCAACC	ACA	TAGATCCA	GAAGAAGATIGG
HM056 / P 2	ATGGGCTCT		GTATTACT				GGTTGGTGAAAGA			TCGACATTCTCC			G A A G A T G A T T G G
R108 LP 2	ATGGACTCT	AAATATTCATTA	GTATTACT	TTTACTT GG	AATGATAATGC	TACCACC	GGTTGGTGAAAGA		AATTT	TCGACATTCTCC	T	TAGATCCA	GAAGATGATTGG
Ms_LP_2	ATGGGCTCT	AAATATTCATTA	GTATTACT	ГТТТ <mark>АСТТ</mark> <mark>66</mark>	AA <mark>tg</mark> ataatac	TTACCACT <mark>S</mark>	GGTTGGTGAAAGG	AATAGTAAT	AATTT	T <mark>gg</mark> acattctcc	т <mark></mark>	TA <mark>G</mark> ATCCA	<mark>g a a g a t g</mark> a t t <mark>g g</mark>
A17_LP_3	A TG A G C T C T	ΑΑΑ <mark>Τ</mark> ΑΤΤ <mark></mark> ΟΑΤΤ	<mark>g tattac</mark> t	TTTTACTT <mark>GG</mark>	AA <mark>tg</mark> ataat <mark>g</mark> c	T <mark>CACCACT</mark> G T	<mark>G a t t g g t g</mark> a a a <mark>g g</mark>	ΑΑ <mark>Τ</mark> ΘΑΤΑΑΤ	AAATT	T <mark>g</mark> aatat <mark>g</mark> atcc	T A T <mark>G</mark> 1	TA <mark>G</mark> ATCCA	<mark>g a a g a t g a t t g g</mark>
HM056_LP_3	А <mark>ТС</mark> А <mark>СТСТ</mark>	ААА <mark>Т</mark> АТТ <mark>С</mark> АТТ	<mark>g tattac</mark> t	ГТТТ <mark>АСТТ</mark> · · · <mark>GG</mark>	ΑΑ <mark>Τ</mark> ΘΑΤΑΑΤ <mark>Θ</mark> Ο΄	T C A C C A C T <mark>G</mark> T	<mark>GATTGGTG</mark> AAA <mark>GG</mark>	ΑΑ <mark>Τ</mark> ΘΑΤΑΑΤ · ·	• AAA <mark>TT</mark>	Т <mark>б</mark> аатат <mark>б</mark> атса	т <mark>А т </mark>	TA <mark>G</mark> ATCCA	<mark>g a a g a t g a t t g g</mark>
R108_LP_3	A TG A G C T C T	AAA <mark>T</mark> ATTCA <mark>TT</mark> A	<mark>g ta tta c t</mark>	ГТТТ <mark>АСТТ</mark> <mark>GG</mark>	AA <mark>TG</mark> ATAAT <mark>G</mark> C	TT <mark>accac<mark>tg</mark>i</mark>	G <mark>attggtg</mark> aaa <mark>gg</mark>	AA <mark>TGAT</mark> AAT	- AAA <mark>TT</mark>	T <mark>g</mark> aatat <mark>g</mark> atcc	T A T <mark>G</mark> 1	TA <mark>G</mark> ATCCA	<mark>G A A G A T G G T T G G</mark>
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A17_LP_5	ATGAGCTCT	AAATATTCATTA	GTATTACT	ITTTACTT GG	AATGATAATGC	TTACCACTGT	G A T T G G T G A A A G G	AATAATAAT	AAATT	TGAATATGATCC	T · · · · · · A T G I	TAGATCCA	G A A G A T T A T T G G
HM056_LP_5	ATGAGCICI	AAATATTCATTA	GTATTACT	GG TROTACTT	AATGATAATGC	TACCACTO	GATTGGTGAAAGG		AAATT	TGAATATGATCC	AIG	TAGATCCA	GAAGATTATTGG
HM056 LP 4	ATGGCCTCT		GTATTATT	ACTICIACTIC			AGTGAGTTATGGG	CATAAT		TGGGTATGCGCC			
A17 LP 6	ATGGCCTCT	AAATACTCACAA	GTATTACT	TCTACTT GG	AATGATGGTTC	TACTACTO	AGTGAGTGATGGG	CATAAT	AGTTT	TGGGTATGCGCC	A A T G 1	TAGATCCA	GAGGAGGATTGG
HM056 LP 6	ATGGCCTCT	AAATACTCACAA	GTATTACT	TCTACTT · · · GG	ΑΑ <mark>Τ</mark> ΘΑΤΘΘΤΤΟ	Т Т А С Т А С Т <mark>З</mark> Т	AGTGAGTGATGGG	CATAAT	- AGTTT	TGGGTATGCGCC	аат <mark>ат</mark> ат	TAGATCCA	G A G G A G G A T T G G
R108_LP_6	A TGG C C T C T	ААА <mark>Т</mark> А <mark>стс</mark> асаа	<mark>g tattac</mark> t	TTCTACTT <mark>GG</mark>	ΑΑ <mark>Τ</mark> ΘΑ <mark>ΤΘΘ</mark> ΤΤΟ	ТТ <mark>аст</mark> аст <mark>с</mark> т	A G T G A G T G A T G G G	CATAAT	- A <mark>GTTT</mark>	T <mark>gggt</mark> a <mark>tgcg</mark> cc	4 A T <mark>G T</mark>	TA <mark>G</mark> ATCCA	<mark>g agg agg a t t</mark> g g
Ms_LP_6					A TOG TTC	TT <mark>actact</mark> o 1	A G T G A G T G A T G G G	CATAAT	A G T T T	T <mark>gggt</mark> a <mark>tgct</mark> cc	с <mark>А Т <mark>С</mark> 1</mark>	TA <mark>G</mark> ATCCA	<mark>g agg agg a t t</mark> g g
A17_LP_7	A TGGCCTCT	ААА <mark>Т</mark> АСТСАСТА	<mark>G TATTACT</mark>	ГТСТАСТТ <mark>GG</mark>	AA <mark>TG</mark> A <mark>TGGT</mark> AC	TT <mark>accac</mark> a <mark>g</mark> 1	A G T G A G T G A T A G G	A <mark>G G C C A G</mark> A C C T	ттт <mark>с</mark> тт	T <mark>gggtatgtgcc</mark>	т <mark>G Т А</mark> 1	TA <mark>G</mark> ATCTA	<mark>g a a g a g g a t t g g</mark>
HM056_LP_7	ATGGCCTCT	AAATACTCACTA	GTATTACT	TTCTACTT · · · GG	AA <mark>TGATGGTAC</mark>	TTACCACA <mark>G</mark>	AG TG AG TG A TAG G	A G G C C A G A C C T	TTTCTT	T G G G T A T G T G C C	T · · · · · · G T A I	TAGATCCA	G A A G A G G A T T G G
R108_LP_7	ATGGCCTCT	AAATACTCACTA	GTATTACT	ITCTACTT - GG	AATGATGGTAC	TTACCACAG	AG TG AG TG A TAG G	AGGCCAGACCT	тттстт	TGGGTATGTGCC	T · · · · · · G T A 1	TAGATCCA	GAAGAGGATTGG
MS_LP_7	ATGGCCTCT	AAATAUTUAUTA	OT ATTACT		AATOCTOCTOC		AGTGAGTGATAGA	COTAGACCI		TOGOTATOTOCC			GAAGAGGATIGG
HM056 LP 8	ATGGCCTCT		GTATTAGT		AATGCTGGTGC			COTAAT	BCAAT	TGGGTATGTGCC			
R108 LP 8	ATGGCCTCT	ааататтсаста	GTATTACT	TCTACTT GG	AATTATGGTGC	Т Т А С <mark>С</mark> А С Т С Т	AGTGAGTGACAAG	CGTAAT	GCAAT	TGGGTATGTGCC	T	TAGAACCA	G A A G A G G A T T G G
A17_LP_9	ATGGCCTCT	ACATACTCATTA	GTATTACT	TTCTACTT <mark>GG</mark>	AACGATGG TGG	TT <mark>ACCACTG</mark>	C <mark>g t g g g t g c t c g</mark> a	AGATCTAAT	- A T G T T	T G G A T A T C C A G A	TATTACCCAT	TTT <mark>G</mark> AGCTA	G A A G A A G A T T G G
HM056_LP_9	A T <mark>G G C C T</mark> C T	ACATACTCATTA	GTATTACT	TT <mark>CT</mark> ACTT <mark>GG</mark>	AA <mark>cg</mark> a <mark>tggtgg</mark>	TT <mark>accact</mark> g	C <mark>gtgggtgctcg</mark> a	A <mark>gatet</mark> aa <mark>t</mark>	- A <mark>T </mark> G T T	T <mark>gg</mark> a <mark>tatcc</mark> a <mark>g</mark> a	TATTACCCA1	TT <mark>G</mark> A <mark>GCT</mark> A	<mark>g aag aag attgg</mark>
R108_LP_9	A <mark>T G G C C T</mark> C T	ACATACTCATTA	G T A T T A C T	TT <mark>CTACTT</mark> · · · <mark>GG</mark>	AA <mark>cg</mark> a <mark>tgg</mark> tgg	TTACCACT <mark>G</mark> T	C <mark>G T G G G T G C T C C</mark> A	A GATCTAAT · ·	- A T <mark>G</mark> T T	T <mark>gg</mark> a <mark>t</mark> atccaga	TATTACCCA1	TTGAGCTA	GAAGAA <mark>G</mark> A <mark>TT</mark> GG
Ms_LP_9	ATAGCCTCT	ACATACTCATTA	GTATTACT	GG TACTT GG	AACGATGATGG	ACCACTO	COTOGOTOCTCOA		ATGTT	TOGATATCCAGA	TATTICCCA	TGAGCTA	GAAGAAGAATGG
A1/_LP_10	ATGGCCTCT	ACATACTCAATA	A TATTACT	G ACTT GG	AATGATGATGG	TACCACTT	COTOGOTOCTOGA			TOGATATCCAGA	AT ACCCT	AGATTTA	GAAGATGATTGG
P109 / P 10	ATGCCCTCT	ACATACTCAATA	CTATTACT		AATGATGATGG				ATCTT	TGGATATCCAGA			GAAGATGATTGG
Ms LP 10	ATGGCCTCT	ACATACTCAATA	GTATTACT	TCTACTT	AATGATGATCA	TACCACTT	CGTCGGTGCTAGA	AGGTTTAAT	ATGTT	TGGATATCCAGA	TATTACCCT	TAGATTTA	GAAGACGATTGA
A17_LP 11	ATGGCCTCT	ACATATTCAATA	GTATTACT	TTCTACTT GA	AATGATGATGG	TACCACTT	CGTGGGTGCTGGA	AAGTCTAAT	ATGTT	TGGATATCCAGA	CAATACCCA	TAGATCCA	GAAGACGATTGG
HM056_LP_1	A T G G C C T C T	Α <mark>ς Α</mark> ΤΑΤΤ <mark>ς</mark> ΑΑΤΑ	<mark>g tattac</mark> t	<mark>ГТСТ</mark> АСТТ <mark>G</mark> A	AA <mark>TG</mark> A <mark>TG</mark> AT <mark>GG</mark>	ТТ <mark>ассаст</mark> тт	C <mark>g tggg tg c tgg</mark> A	аа <mark>стст</mark> аат	- ATGTT	T <mark>gg</mark> atatcca <mark>g</mark> a	T C A A T A C C C A	TA <mark>G</mark> ATCCA	<mark>g aag a c g</mark> a t t g g
R108_LP_11	A T G G C C T C T	ACATACTCAATA	<mark>g tattac</mark> t	ΓΤ <mark>ΟΤ</mark> ΑΟΤΤ · · · <mark>66</mark>	AA <mark>tg</mark> ctgatgg	TT <mark>accact</mark> t1	<mark>CGTGGGTGCTGG</mark> A	A <mark>gatet</mark> aat	- A <mark>TG</mark> AT	T <mark>gg</mark> acatccaga	TCAATACCCA	TA <mark>G</mark> ATCCA	G A A G A C G A T T G G
Ms_LP_11					A TG A TG G	TT <mark>ACCAC</mark> TT	C <mark>g tggg tg c tgg</mark> A	AA <mark>GTCT</mark> AAT	- A T G T T	T <mark>gg</mark> a <mark>tatccag</mark> a	TCAATTCCCA	TA <mark>GATCC</mark> A	G A A G A C G A T T G G
A17_LP_12	ATGGCCTCT	ACATACTCAATA	GTATTACT	ITCTATTT GG	AATGATGATGG	TTACCACTG T	C G T G G G T G C G G G A	AGATCTAAT	ATGAT	T G G A C A T C C A G A	TATAGCTTAG	AAGAAATA	G A A G A A G A A T G G
HM056_LP_1	A TGGCCTCT	ACATACTCAATA	G TATTACT	TOTATTT · · · GG	AATGATGATGG	TACCACTO	CGTGGGGTGCGGGA		ATGAT	TGGACATCCAGA	TTATAGCTTAC		GAAGAAGAA TGG
Me / P 12	AIGOCCICI	ACATATICAATA	GIALIACI		AATOATOATO					TGGACATCCAGA			
A17 LP 13	ATGGCCTCT	ACATACTCAATA	GTATTACT	TTCTACTT GG	AATGATGATGG	TACCACTO	CGTGGGTGCTGGA	GAGTCTAAT	ATGTT	TGGATATTCAGA	TATAAAACAA	ACAGATCTC	GAAGACGATTGG
HM056_LP_1:	а <mark>тее</mark> сстст	ACATACTCAATA	GTATTACT	TTTACTT · · · GG	AA <mark>TG</mark> ATG <mark>ATGG</mark>	ТТ <mark>ассаст</mark> от	COTOGOTOCTOG A	GAGTCTAAT	ATGTT	T <mark>ggatattcag</mark> a	TATAAAAACAA	АСА <mark>с</mark> атстс	G A A G A C G A T T G G
R108_LP_13	Α <mark>ΤGGCCΤCΤ</mark>	Α <mark>ς Α</mark> ΤΑς Τς Ας ΤΑ	<mark>G T A T T A C T</mark>	<mark>ГТСТ</mark> АСТТ <mark>бб</mark>	AA <mark>tg</mark> a <mark>tg</mark> atgg	TT <mark>accact</mark> g1	C <mark>g t g g g t g c t g g</mark> A	GAGTCTAAT	. А <mark>Т</mark> БТТ	T <mark>gg</mark> atattcaga	TTATAAAACAA	A C A <mark>G</mark> A T C T A	<mark>g aag acg a t t g g</mark>
Ms_LP_13	A T G G C C T C T	ACATACTCACTA	GTATTACT	TTCTACTT · · · <mark>gg</mark>	AA <mark>TG</mark> A <mark>TG</mark> A <mark>TGG</mark>	TACCACT <mark>G</mark>	CGTGGGTGCTGGA	GAGTCTAAT	ATGTT	T <mark>ggatattcag</mark> a	TATAAAACAA	ACA <mark>G</mark> A <mark>TCT</mark> A	G A A <mark>G</mark> A C <mark>G</mark> A <mark>T T G G</mark>
	4.40	150	100	170	100	100	0000						000
	140	150	160	170	180	190	200 2	10 220		230	240 2	50	260 27
A17_LP_1	140 CCAGAAGTT	150 TTTTATGAAGCA	160	170 CTGATGTAGTAGG	180 Tggaaagca <mark>t</mark> a.	190 A <mark>T</mark> A A <mark>G T T T G G</mark>	200 2	10 220		230 6 6 6 <mark>1 1</mark> 6 6 <mark>6 6 6 6 6</mark> A	240 2 CAAC <mark>T</mark> AA	50	260 27
A17_LP_1 HM056_LP_1	140 CCAGAAGTT CCAGAAGTT	150 TTTTATGAAGCA TTTTATGAAGCA	180 	170 CTOATOTAGTAGO CTGATGTAGTAGG	180 TGGAAAGCATA. TGGAAAGCATA.	190 A TAAG TTTGG A TAAG TTTGG	200 2 ATTTAAACCTATA ATTTAAACCTATA	10 220 TTA GATCO TTA GATCO	AGAAGA AGAAGA	230 G G G T T G G C C A G A G G G T T G G C C A G A	CAACTAA	50	260 27
A17_LP_1 HM056_LP_1 R108_LP_1 Ms LP 1	140 CCAGAAGTT CCAGAAGTT CCAGAAGTT CCAGAAGTT	150 TTTTATGAAGCA TTTTATGAAGCA TTTTATGAAGCA	160 CCTAC CCTAC CCTAC CCTAC	170 CTGATOTAGTAGG CTGATOTAGTAGG CTGATOTAGTAGG CTGATOTAGTAGG	180 TGGAAAGCATA TGGAAAGCATA TGGAAAGCATA TGGAAAGCATA	190 A TAAG TTTGG A TAAG TTTGG A TAAG TTTGG A TAAG TTTGG	200 2 ATTTAAACCTATA ATTTAAACCTATA ATTTAAACCTATA ATTTAAACCTATA	10 220 TTA GATCO TTA GATCO TTA GATCO TTA GATCO	AGAAGA AGAAGA AGAAGA AGAAGA	230 GGGTTGGCCAGA GGGTTGGCCAGA GGGTTGGCCAGA	240 2 CAACTAA CAACTAA CAACTAA	50	260 27
A17_LP_1 HM056_LP_1 R108_LP_1 Ms_LP_1 A17_LP_2	140 CCAGAAGTT CCAGAAGTT CCAGAAGTT CCAGAAGTT CCAGAAGTT	150 TTTTATGAAGCA TTTTATGAAGCA TTTTATGAAGCA TTTTATGAAGCA TTTCATGAACAA	180 ••••••••••••••••••••••••••••••••••••	170 CTGATGTAGTAGG CTGATGTAGTAGG CTGATGTAGTAGG CTGATGTAGTAGG CCAACTATAAAAT	180 T GGAAAGCATA T GGAAAGCATA T GGAAAGCATA T GGAAAGCATA A T C T AA GAGG	190 A T A A G T T T G G A T A A G T T T G G A T A A G T T T G G A T A A G T T T G G A G T C A T C A G A	200 2 ATTTAAACCTATA ATTTAAACCTATA ATTTAAACCTATA ATTTAAACCTATA	10 220 TTA - GATCO TTA - GATCO TTA - GATCO TTA - GATCO TTA - GATCO TTA - GATCO	AGAAGA AGAAGA AGAAGA AGAAGA AGAAGA	230 GGGTTGGCCAGA GGGTTGGCCAGA GGGTTGGCCAGA GGGTTGGCCAGA CATCAACCACAT	40 2 CAACTAA CAACTAA CAACTAA CAACTAA CAACTAA CGTTTGA	50	280 27
A17_LP_1 HM056_LP_1 R108_LP_1 Ms_LP_1 A17_LP_2 HM056_LP_2	140 CCAGAAGTT CCAGAAGTT CCAGAAGTT CCAGAAGTT CCAGAAATT CCAGAAATT	150 TTTTATGAAGCA TTTTATGAAGCA TTTTATGAAGCA TTTTATGAAGCA TTTCATGAACAA TTTCATGAACAA	180 	170 C TG A TO TAG TAGG C C A A C TATAAAA T C C A A C TATAAAA T	180 T G G AAAG C AT A T C T AA G AG G A T C T AA G AG G	190 A T A A G T T T G G A T A A G T T T G G A T A A G T T T G G A T A A G T T T G G A G T C A T C A G A G T C A T C A G A G T C A T C A G	200 2 ATTTAAACCTATA ATTTAAACCTATA ATTTAAACCTATA ATTTAAACCTATA ATTACGAGACAAAC	10 220 TTA GATCO TTA GATCO TTA GATCO TTA GATCO TTG TCAGA TTG TCAGA	AGAAGA AGAAGA AGAAGA AGAAGA TGAAGC	230 GGGTTGGCCAGA GGGTTGGCCAGA GGGTTGGCCAGA GGGTGGCCAGA CATCAACCACAT	240 2 CAACTAA CAACTAA CAACTAA CAACTAA CAACTAA COTTTOA	50	260 27
A17_LP_1 HM056_LP_1 R108_LP_1 M∞_LP_1 A17_LP_2 HM056_LP_2 R108_LP_2	140 C C A G A A G T T C C A G A A G T T C C A G A A G T T C C A G A A A T T C C A G A A A T T C C A G A A A T T	150 TTTTATGAAGCA TTTTATGAAGCA TTTTATGAAGCA TTTTATGAAGCA TTTTGAAGAA TTTCATGAACAA TTTCATGAACAA	160 	170 CTGATOTAGTAGG CTGATOTAGTAGG CTGATOTAGTAGG CCAACTATAAAAT CCAACTATAAAAT CCAACTATAAAAT	180 T G G A A A G C A T A T G G A A A G C A T A T G G A A A G C A T A T G G A A A G C A T A A T C T A A - G A G G A <mark>T C T</mark> A A A G A G G	190 A TAAG TTTG A TAAG TTTG A TAAG TTTG A TAAG TTTG A G TCATCAG A G TCATCAG A G TCATCAG A G TCATCAG A G TCATCAG	200 2 ATTTAAACCTATA ATTTAAACCTATA ATTTAAACCTATA ATTTAAACCTATA ATTTACACCTATA TTACGAGACAAA ATTACGAGACAAAA ATTACGAGACAAAA	10 220 TTA GATCO TTA GATCO TTA GATCO TTA GATCO TTA GATCO TTG TCAGA TTG - TCAGA	AGAAGA AGAAGA AGAAGA AGAAGA AGAAGC TGAAGC TGAAGC	230 COORTIGOCCAGA COORTIGOCCAGA COORTIGOCCAGA CATCAACCACAT CATCAACCACAT	240 2 CAACTAA CAACTAA CAACTAA CAACTAA CGTTTGA CGTTTGA	50	280 27
A17_LP_1 HM056_LP_1 Me_LP_1 A17_LP_2 HM056_LP_2 R108_LP_2 Me_LP_2	140 CCAGAAGTT CCAGAAGTT CCAGAAGTT CCAGAAGTT CCAGAAATT CCAGAAATT CCAGAAATT	150 TTTTATGAAGCA TTTTATGAAGCA TTTTATGAAGCA TTTCATGAAGCA TTTCATGAACAA TTTCATGAACAA TTTCATGAACCA TTTCATGAACCA	160 	170 CTGATOTAOTAGO CTGATOTAGTAGO CTGATOTAGTAGO CCGACTATAAAAT CCAACTATAAAAT CCAACTATAAAAT CCAACTATAAAAT	180 T G G AAAG C ATA T G T AA G AGG AT C T AA G AGG AT C T AAAG AGG AC T AAAG AGG	190 A T A A G T T T G G A T A A G T T T G G A T A A G T T T G G A T A A G T T T G G A G T C A T C A G A G T C A T C A G A G T C A T C A G A G T C A T C C G A	200 2 ATTTAAACCTATA ATTTAAACCTATA ATTTAAACCTATA ATTTAAACCTATA ATTAAACCTATA ATTACGAGACAAAA TTACGAGACAAAA TTACGAGACAAAA	10 220 11A GATCO 11G TCAGA 11G TCAGA 11G TCAGA 11G TCAGA	AGAAGA AGAAGA AGAAGA AGAAGA TGAAGC TGAAGC TGAAGC	230 6 6 6 T T 6 6 C C A 6 A 6 6 6 T T 6 6 C C A 6 A 6 6 6 T T 6 6 C C A 6 A 6 6 6 T T 6 6 C C A 6 A C A T C A A C C A C A T C A T C A A C C A C A T C A T C A A C C A C A T C A T C A A C C A C A T	240 2 CAACTAA CAACTAA CAACTAA CAACTAA CAACTAA CGTTGA CGTTGA CGTTGA CGTTGA	50	200 23
A17_LP_1 HM056_LP_1 R108_LP_1 A17_LP_2 HM056_LP_2 R108_LP_2 A18_LP_3 A17_LP_3 A17_LP_3 HM056_LP_2	140 CCAGAAGTT CCAGAAGTT CCAGAAGTT CCAGAAGTT CCAGAAATT CCAGAAATT CCAGAAATT CCAGAAATT CCAGAAATT	150 TTTTATGAAGCC TTTTATGAAGCC TTTTATGAAGCC TTTTATGAAGCA TTTCATGAACAA TTTCATGAACAA TTTCATGAACCA TTTCATGAACCA TTTAATGAACCC		170 C T G A T O T A O T A O G C T G A T O T A O T A O G C T G A T O T A O T A O G C T G A T O T A O T A O G C T G A T O T A O T A O A A T C C A A C T A T A A A A T C C A A C T A T A A A A T C C T A C T A T A A A A T	180 T G G A A A G C A T A T G G A A A G C A T A T G G A A A G C A T A T G G A A A G C A T A T C T A A G A G G A T C T A A G A G G A T C T A A G A G G A C C T A A G C A T A A C C T A A C C A C A A C C T A A C C A C A A C C T A A C C A C A A C C T A A C C A C A A C C T A A C C A C A A C C T A A C C A C A A C C T A A C C A C A A C C T A A C C A C A A C C T A A C C A C A A C C T A A C C A C A A C C T A A C C A C A A C C T A A C C A C A A C C T A A C C A C A A C C T A A C A C A C A A C C T A A C A C A C A A C C T A A C A C A C A A C C T A A C A C A C A A C C T A A C A C A C A A C C T A A C A C A C A C A C A C A C A	190 A T A A G T T T G G A T A A G T T T G G A T A A G T T T G G A T A A G T T T G G A G T C A T C A G A G T C A T C A G A G T C A T C A G A G T C A C C T G A A G T C A C C T G A	ATTTAAACCTATA ATTTAAACCTATA ATTTAAACCTATA ATTTAAACCTATA ATTTAAACCTATA ATTTACACCTATA ATTACAGACAAAA ATTACGAGACAAAA ATTACGAGACAAAA ATTACGAGACAAAA ATTACGAGACAAAA	10 220 TTA - GATCO TTA - GATCO TTA - GATCO TTA - GATCO TTA - GATCO TTA - TCAGA TTO - TCAGA TTO - TCAGA TTO - TCAGA TTO - TCAGA	AGAAGA AGAAGA AGAAGA AGAAGA AGAAGA TGAAGC TGAAGC TGAAGC TGAAGC TGAAGC TGAAGC	230 3 0 0 T T 6 0 C C A 6 A 3 6 0 T 7 6 0 C C A 6 A 3 6 0 T 7 6 0 C C A 6 A 3 6 0 T 7 6 0 C C A 6 A C A T C A A C C A C A 7 C A T C A A C C A C C A C A 7 C A T C A A C C A C A 7 C A T C A A C C A C A 7 C A T C A A C C A C A 7 C A T C A A C C A C A 7 C A T C A A C C A C A 7 C A T C A A C C A C A 7 C A T C A A C C A C A 7 C A T C A A C C A C A 7 C A T C A A C C A C A 7 C A T C A A C C A C A 7 C A T C A A C C A C A 7 C A T C A A C C A C A 7 C A T C A A C C A C A 7 C A T C A A C C A C A 7 C A T C A A C C A C A 7 C A T C A A C C A 7 C A T C A A C C A C A 7 C A T C A A C C A C A 7 C A T C A A C C A C A 7 C A T C A A C C A C A 7 C A T C A A C C A C A 7 C A T C A 7 C A	240 C A A C T A A C A A C T A A C A A C T A A C A C T A A C A C T A A C G T T T G A	50	
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$\begin{array}{l} {\rm A17}_LP_1\\ {\rm HMO56}_LP_1\\ {\rm HMO56}_LP_1\\ {\rm HMO56}_LP_1\\ {\rm HMO56}_LP_2\\ {\rm HMO56}_LP_2\\ {\rm HMO56}_LP_2\\ {\rm HMO56}_LP_2\\ {\rm HMO56}_LP_2\\ {\rm HMO56}_LP_3\\ {\rm HMO56}_LP_3\\ {\rm HHO56}_LP_3\\ {\rm HHO56}_LP_3\\ {\rm HHO56}_LP_4\\ {\rm HHO56}_LP_4\\ {\rm HHO56}_LP_6\\ {\rm HHO56}_LP_6$\\ {\rm HH056}_LP_6$\\ {\rm HH056}_LP_$	IAC C A Q A A Q T C A Q A A Q T C A Q A A Q T C A Q A A Q T C A Q A A Q T C A Q A A Q T C A Q A A Q T C A Q A A Q T C A Q A A A T C A Q A A A T C A Q A A A T C A Q A A A T C A Q A A A T C A Q A A A T C A Q A A A T C A Q A A A T C A Q A A A T C A Q A A A T C A Q A A A T C A Q A A A A T C A Q A A A T C A Q A A A T C A Q A A A A C A A A T C A Q A A A A A C A A A T C A Q A A A A A C A A A A A C A A A A A	150 111 A <td>100 100 C C C C C C C C C C C C C C C C C C C<td></td><td></td><td></td><td></td><td></td><td></td><td>100 100<td></td><td></td><td></td></td></td>	100 100 C C C C C C C C C C C C C C C C C C C <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td>100 100<td></td><td></td><td></td></td>							100 100 <td></td> <td></td> <td></td>			
A17_LP_1 HN056_LP_1 HN056_LP_1 A17_LP_2 A17_LP_2 R106_LP_2 R106_LP_2 R106_LP_2 R106_LP_2 R106_LP_3 R106_LP_3 R106_LP_3 R106_LP_3 A17_LP_5 R106_LP_5 R1				III III III IIII IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII									
A17_LP_1 HM058_LP_1 HM058_LP_1 HM058_LP_2 A17_LP_2 R108_LP_2 R108_LP_2 R108_LP_2 R108_LP_3 R108_LP_3 R108_LP_3 R108_LP_3 A17_LP_5 A17_LP_5 A17_LP_5 A17_LP_5 A17_LP_5 A17_LP_5 A17_LP_5 A17_LP_5 A17_LP_5 A17_LP_5 R108_		150 111 A 0 A A Q C 111 T 0 A A Q C				100 100 <td></td> <td>0 0</td> <td></td> <td>100 100<td>Image: Control of the second second</td><td></td><td></td></td>		0 0		100 100 <td>Image: Control of the second second</td> <td></td> <td></td>	Image: Control of the second		
A17_LP_1 HA1056_LP_1 HA1056_LP_1 A17_LP_2 A17_LP_2 R106_LP_2 R106_LP_2 R106_LP_2 R106_LP_2 A17_LP_3 R106_LP_3 A17_LP_3 A17_LP_5 A17_LP_4 HA1056_LP_6 R106_LP_6 R106_LP_6 R106_LP_6 R106_LP_1 A17_LP_1 HA1056_LP_1 A17_LP_1 HA1056_LP_1 A17_LP_1 HA1056_LP_1 A17_LP_1 HA1056_LP_1 A17_LP_1 HA1056_LP_1 A17_LP_1 HA1056_LP_1 A17_LP_1 HA1056_LP_1 A17_LP_1 HA1056_LP_1 A17_LP_1 HA1056_LP_1 HA1056_LP_1 A17_LP_1 HA1056_LP_1HA1056_LP_1 HA1056_LP_1HA1056_LP_1 HA1056_LP_1HA1056_LP_1 HA1056_LP_1HA1056_LP_1HA1056_LP_1HA1056_LP_1HA1056_LP_1HA1													

Figure S2 Aligned LP DNA sequences from A17, HM056, R108 and *M. sativa*. Columns that were omitted for the phylogenetic analysis are highlighted with red headers. Phylogenetic trees were based on the remaining 87 nucleotides.

		10	. 2	20	30	. 40	. c	50	60	70	80	90
A17 LP 1	MASTCS	LIL <mark>F</mark> LL -	GMIMLT	IVVDGRH		TLD	PEEDWP	EVFYEA P	T D V V G G K H N K F	GFKPIL - DP	E G W P D N	
HM056 LP 1	MASTCS	LIL <mark>F</mark> LL -	GMIML T	IVVDGRH		T LD	PEEDWP	EVFYEA-P	TDVV <mark>ggkhn</mark> kr	GFKPIL-DPI	EEGWPDN	
R108 LP 1	MASTCS	LIL <mark>F</mark> LL -	GMIML T	IVVDGRH		<mark>T</mark> LD	PEEDWP	EVFYEA-P	TDVV <mark>ggkhn</mark> kr	GFKPIL-DPI	EEGWPDN	
Ms LP 1	MASTCS	LVLLLL-		IVVVGRE		T LD	PEEDWP	EVFYEA-P	TDVV <mark>ggkhn</mark> kr	GFKPIL-DPI	EEGWPDN	
A17 LP 2	M <mark>GSKY</mark> S	LVLLLL-	GMIMLT		SN-NFRHS	ML D	PEDDWP		SNYKISKRSHO		STTSFEPVH	TAKISYHYK
HM056 LP 2	MRSKYS	LVLLLL-	GMIML T		ISN - NERHS	ML D	PEDDWP		SN <mark>y</mark> kiskrsho		PSTTSFEPVH	TAKTSYHYK
R108 LP 2	MDSKYS	LVLLL.	<mark>g</mark> miml <mark>t</mark>	TVVGERN	ISN - NFRHS	ML D			SN <mark>y</mark> kisk <mark>ee</mark> ss	DYETNL - SDI	AINHIV	
Ms LP 2	M <mark>gskys</mark>	LVLLLL-	<mark>g</mark> miil <mark>t</mark>	TVVGERN	ISN - NFGHSI	ML D			SNYKIPKEESS	S D Y E T N L - S D I	AINHIV	
A17 LP 3	MSSK <mark>y</mark> s	LVLLLL-	GMIMLT	TVIGERN	DN-KFEYD	ML D	PEDDWP	EIFNEPLPS	SYYKIPKEESF	DYETNL - SN	AINHTV	
HM056 LP 3	MSSK <mark>y</mark> s	LVLLLL-	<mark>g</mark> miml <mark>t</mark>	TVIGERN	DN-KFEYD	ML D	PEDDWP	E I F N E P L P S	SYYKI PKEES F	DYETNL - SN	AINHTV	
R108 LP 3	MSSK <mark>y</mark> s	LVLLLL.	<mark>g</mark> miml <mark>t</mark>	TVIGERN	DN-KFEYDI	ML D	PEDDWP	E I F N E P L P S	SYYKI PKEESF	DYETNL - SN	AINHTV···	
Ms_LP_3	MSSK <mark>y</mark> s	LVLLLL-	<mark>g</mark> miml <mark>t</mark>	TAIGERN	IGN - KFEYDI	ML D	PEDDWP	E I F N E P L P S	SYYKI <mark>pkees</mark> r	DYETNL - SDI	AINHTV	
A17_LP_5	MSSK <mark>y</mark> s	LVLLLL-	<mark>g</mark> miml <mark>t</mark>	TVIGERN	INN - KFEYDI	ML D	PEDYWP	E I F H E P L P S	SH <mark>y</mark> kipk <mark>ee</mark> lf	PDYETN		
HM056_LP_5	MSSK <mark>y</mark> s	LVLLLL-	<mark>g</mark> miml <mark>t</mark>	TVIGERN	INN - KFEYDI	ML D	P E D YWP	E I F H E P L P S	SH <mark>y</mark> kipkeelf	<mark>P D Y E T N</mark>		
A17_LP_4	MA <mark>sky</mark> s	QVLLLLL	. <mark>G</mark> MM∨L <mark>T</mark>	TVV <mark>SYG</mark> H	IN K <mark>fgy</mark> ai	ML D	LEEDWP	D <mark>QFFPP</mark> -L <mark>1</mark>	TII <mark>EG</mark> RKSHS <mark>B</mark>	GYPPIL - DPI	<u> </u>	
HM056_LP_4	MA <mark>sky</mark> s	QVLLLLL	. <mark>G</mark> MM∨L <mark>T</mark>	T V V <mark>S Y G</mark> ⊢	IN K <mark>fgy</mark> ai	ML D	PEEDWP	D <mark>QFFPP</mark> -L <mark>1</mark>	TII <mark>EG</mark> RKSHS <mark>b</mark>	GYPPIL - DPI	<u> </u>	
A17_LP_6	MA <mark>sky</mark> s	QVLLLL -	<mark>G</mark> MM∨L <mark>T</mark>	TVV <mark>S</mark> DGH	IN <mark>SFGY</mark> AI	M L D	PEEDWP	D <mark>QFFPP</mark> -L <mark>1</mark>	TII <mark>Eg</mark> rkshs <mark>r</mark>	GYPPIL - DPI	<u> </u>	
HM056_LP_6	MA <mark>sky</mark> s	QVLLLL-	<mark>G</mark> MM∨L <mark>T</mark>	T V V <mark>S D G ⊢</mark>	IN <mark>SFGY</mark> AI	ML D	PEEDWP	D <mark>QFFPP</mark> -L <mark>1</mark>	TII <mark>EG</mark> RK <mark>S</mark> HS <mark>B</mark>	GYPPIL - DPI	<u> </u>	
R108_LP_6	MA <mark>sky</mark> s	QVLLLL -	<mark>G</mark> MM∨L <mark>T</mark>	T V V <mark>S D G ⊢</mark>	IN <mark>SFGY</mark> AI	ML D	PEEDWP	D <mark>QFFPP</mark> -L <mark>1</mark>	TII <mark>E</mark> GRKSHS <mark>b</mark>	GYPPIL-DPI	<u>= E D</u>	
Ms_LP_6	??????	777777	??MVLT	TVV <mark>SDG</mark> H	IN SFGYAI	ML D	PEEDWP	D L F F P P - L <mark>1</mark>	TMIV <mark>grkp</mark> nsp	AYPLIL-DPI	<u> </u>	
A17_LP_7	MA <mark>sky</mark> s	LVLLLL-	<mark>G</mark> MM∨L <mark>T</mark>	TVV <mark>SD</mark> RF	PDLFFGYVI	• • V L D	LEEDWP	D L F F P P - <mark>S 1</mark>	TIIV <mark>ggkp</mark> ns <mark>r</mark>	RYPPIL - DPI	<u>ED</u>	
HM056_LP_7	M A <mark>S K </mark> Y S	LVLLLL-	<mark>G</mark> MM∨L <mark>T</mark>	TVV <mark>SD</mark> RF	PDLFFGYVI	• • • V L <mark>D</mark>	PEEDWP	D L F F P P - <mark>S 1</mark>	TIIV <mark>ggkp</mark> nsf	RYPPIL - DPI	<u>E D</u>	
R108_LP_7	M A <mark>S K Y</mark> S	LVLLLL-	<mark>G</mark> MM∨L <mark>T</mark>	TVV <mark>SD</mark> RF	PDLFFGYV	• • V L <mark>D</mark>	PEEDWP	D L F F P P - <mark>S</mark> 1	TIIV <mark>ggkp</mark> nsb	RYPPIL - DPI	<u>E D</u>	
Ms_LP_7	MA <mark>sky</mark> s	LVLLLL.	<mark>G</mark> MM∨L <mark>T</mark>	TVV <mark>SD</mark> RF	PDLFFGYV	• • • V L <mark>D</mark>	P E E D W P	D L F F P P - P	TIIV <mark>ggkp</mark> nsf	GYPPIL - DPI	<u> </u>	
A17_LP_8	MA <mark>sky</mark> s	LVLLIL.	<mark>g</mark> mlvl <mark>t</mark>	TVV <mark>SD</mark> KF	IN AI <mark>gy</mark> vi	• • I L <mark>E</mark>	LEEDWP	D H F F P P - P 1	TVMV <mark>grkp</mark> is <mark>)</mark>	<mark>(g y p s h n</mark> - r -)		
HM056_LP_8	MA <mark>sky</mark> s	LVLVIL-	<mark>g</mark> mlvl <mark>t</mark>	TVVSDKF	IN AI <mark>GY</mark> VI	• • I L <mark>E</mark>	LEEDWP	DHFFPP-P	TVMV <mark>GRKP</mark> IS <mark>)</mark>	<mark>(g y p s h n</mark> - <mark>r</mark> -)		
R108_LP_8	MA <mark>sk</mark> ys	LVLLLL.	<mark>g</mark> im∨l <mark>t</mark>	T V V <mark>S D</mark> K F	N AI <mark>gy</mark> vi	• • I L <mark>E</mark>	P E E D WP	HH <mark>FFPP-P</mark>	TITV <mark>grkp</mark> is <mark>)</mark>	(GY <mark>PSHN</mark> - <mark>P</mark> -)		
A17_LP_9	M A <mark>S T Y</mark> S	LVLLLL.	<mark>G T</mark> M∀∀ <mark>T</mark>	T V V <mark>g</mark> a r f	I <mark>SN</mark> - M <mark>FGYP</mark> I	YY <mark>P</mark> FE	LEEDWF	DV <mark>HSN</mark> PSDI	I <mark>rvggrp</mark> iil <i>A</i>	A <mark>RPPP</mark> LV - DLI	E E <mark>K</mark> F Y <mark>D L D </mark> S D	L H
HM056_LP_9	M A <mark>S T Y</mark> S	LVLLLL.	<mark>G T</mark> M∨∨ <mark>T</mark>	T V V <mark>g</mark> a r f	I <mark>SN</mark> - MFGYPI	YY <mark>P</mark> FE	LEEDWF	DV <mark>HSN</mark> PSDI	I <mark>rvggrp</mark> iil <i>A</i>	A <mark>RPPP</mark> LV - <mark>D</mark> LI	EE <mark>NFY</mark> DLD <mark>S</mark> -	L H
R108_LP_9	M A <mark>S T Y</mark> S	LVLLLL-	<mark>G T</mark> M∨∨ <mark>T</mark>	T V V <mark>g</mark> a <mark>p f</mark>	I <mark>SN</mark> - MFGYPI	YY <mark>P</mark> FE	LEEDWF	D <mark>VHSN</mark> PSDI	I I V <mark>ggrp</mark> iil <i>a</i>	A <mark>RPPP</mark> LV - DL	E E <mark>N</mark> F Y D L D <mark>S</mark> D	L <u>H</u>
Ms_LP_9	I A <mark>S T </mark> Y S	LVLLLL-	<mark>G</mark> TMM∨T	T V V <mark>g</mark> a r f	I <mark>SN</mark> - MFGYPI	YFPFE	LEEEWF	NVHSDPSDI	I <mark>R V G G</mark> ? ? ? ? ? ?	, <u>,,,,,,,,,,,</u> ,,,,,,,,,,,,,,,,,,,,,,,,	,,,,,,,,,,,,	
A17_LP_10	M A <mark>S T Y</mark> S	IVLLLL-	<mark>G</mark> MMM∨ <mark>T</mark>	TFV <mark>G</mark> AGF	FN-MFGYPI	YY <mark>P</mark> VD	LEDDWF	EVL <mark>SDPS</mark> DI	I I V <mark>GGKPKS</mark> LA	A <mark>RPPPIF - DPI</mark>	EDDL <mark>S</mark> DMD <mark>S</mark> -	L H
HM056_LP_10	M A <mark>S T Y</mark> S	IVLLLL-	<mark>G</mark> MMM∨ <mark>T</mark>	TFV <mark>G</mark> AGF	FN-MFGYPI	Y Y <mark>P</mark> V D	L E D D WF	EVL <mark>SDPS</mark> DI	I I V <mark>GGKPKS</mark> LA	A <mark>rpppif - Dpi</mark>	EDDL <mark>S</mark> DMD <mark>S</mark> -	L H
R108_LP_10	M A <mark>S T Y</mark> S	ILLLL.	<mark>G</mark> MMM∨ <mark>T</mark>	TFV <mark>G</mark> A <mark>G</mark> F	FN-MFGYPI	YY <mark>P</mark> VD	LEDDWF	EVL <mark>SDTSD</mark> I	ILV <mark>GGKPKS</mark> LA	ARPPPLF - DPI	EDDL <mark>S</mark> DMD <mark>S</mark> -	L H
Ms_LP_10	MA <mark>ST</mark> YS	IVLLLL.	<mark>G</mark> MMM∨ <mark>T</mark>	TFV <mark>G</mark> ARF	FN-MFGYP	Y Y <mark>P</mark> V D	LEDDWF	EVL <mark>SDPS</mark> DI	IIV <mark>ggkpks</mark> la	A <mark>rpppif - D</mark> l	EEDL <mark>S</mark> DLD <mark>S</mark> -	L H
A17_LP_11	M A <mark>S T Y</mark> S	IVLLLL-	ЕМММ∨Т	TFV <mark>G</mark> AGK	(<mark>SN</mark> - MFGYPI	D <mark>QY</mark> PVD	P E D D W I	D L L <mark>Y D P</mark> A E N	и <mark>к</mark> ∕	A <mark>r</mark> ll <mark>piy</mark> - <mark>Dpi</mark>	E E D L <mark>S</mark> D F D <mark>S</mark> -	L H
HM056_LP_11	M A <mark>S T Y</mark> S	IVLLLL-	ЕМММ∨Т	TFV <mark>G</mark> AGK	(<mark>SN</mark> - M <mark>FGYP</mark> I	D <mark>QYP</mark> VD	PEDDWI	DLL <mark>YDP</mark> AEN	и <mark>к</mark> /	A <mark>rllpiy</mark> - <mark>dpi</mark>	E E D L <mark>S</mark> D F D <mark>S</mark> -	L H
R108_LP_11	M A <mark>S T Y</mark> S	IVLLLL-	<mark>G</mark> MLM∨ <mark>T</mark>	TFV <mark>G</mark> AGF	I <mark>SN</mark> - MIGHPI	D <mark>QY</mark> PVD	PEDDWL	DLL <mark>YDPA</mark> DN	и <mark>к</mark> /	A <mark>rrpp</mark> i <mark>yy</mark> dpi	E E D L <mark>S</mark> D F D <mark>S</mark> -	L H
Ms_LP_11	??????	???????????????????????????????????????	?? <mark>MMV</mark> T	TFV <mark>G</mark> A <mark>G</mark> K	(<mark>SN</mark> -MFGYPI	D <mark>QFP</mark> VD	PEDDWF	D L L <mark>Y D P S</mark> D I	<mark>K</mark> /	A <mark>rpppiy</mark> - <mark>Dpi</mark>	EEDL <mark>S</mark> DFD <mark>S</mark> -	L <mark>H</mark>
A17_LP_12	M A <mark>S T Y</mark> S	IVLLL <mark>F</mark> -	<mark>G</mark> MMM∨ <mark>T</mark>	TVV <mark>G</mark> AGF	I <mark>SN</mark> - MI <mark>GH</mark> PI	Y <mark>s</mark> lee	I EEEWY	H L <mark>F S D P R</mark> A I	IIM <mark>ggkr</mark> m <mark>rf</mark>	A <mark>rppptf</mark> - VL	EEDVW <mark>EN</mark> LWE	
HM056_LP_12	M A <mark>S T Y</mark> S	IVLLL <mark>F</mark> -	<mark>G</mark> MMM∨ <mark>T</mark>	TVV <mark>G</mark> A <mark>G</mark> F	ISN - MI <mark>GHP</mark>	Y <mark>s</mark> lee	I E E E WY	H L F <mark>S D P R</mark> A I	IIM <mark>ggkr</mark> m <mark>rf</mark>	A <mark>rppptf</mark> - v <mark>p</mark>	EEDVWE <mark>N</mark> LWE	
R108_LP_12	MA <mark>ST</mark> YS	IVLLLL.	<mark>G</mark> MMM∨ <mark>T</mark>	T V V <mark>G</mark> A <mark>G F</mark>	I <mark>SN</mark> - MI <mark>GHP</mark>	Y <mark>s</mark> lee	IEEEWY	H L F <mark>S D P R</mark> A I	IIM <mark>ggkr</mark> m <mark>rf</mark>	A <mark>RPPPTF</mark> - V <mark>P</mark>	EEDVW <mark>EN</mark> LWE	
Ms_LP_12	??????	???????	222222	? V V <mark>G</mark> A <mark>G</mark> F	ISN - MI <mark>GHP</mark>	YSLEE	I EEEWY	HL <mark>FSDPR</mark> AI	IIM <mark>ggkrm</mark> rf	A <mark>rppptf</mark> - v <mark>p</mark>	EEDVWENLWE	
A17_LP_13	MA <mark>ST</mark> YS	IVLLLL-	<mark>G</mark> MMM∨ <mark>T</mark>	TVV <mark>G</mark> A <mark>G</mark> E	SN - MFGYS	Y K T T D	LEDDW-	FEQPRAI	I I M <mark>gg</mark> krrr <mark>f</mark>	RPPPTL - DPI	E E N S S E L <mark>G F S</mark>	PLKFL
HM056_LP_13	M A <mark>S T </mark> Y S	IVLLLL.	<mark>G</mark> MMM∨ <mark>T</mark>	TVV <mark>G</mark> A <mark>G</mark> E	SN - MFGYS	Y K T T D	LEDDW-	FEQPRAI	I I M <mark>gg</mark> krrr <mark>f</mark>	RPPPTL - DPI	E N S S E L <mark>G</mark> F S	PLKFF
R108_LP_13	M A <mark>S T </mark> Y S	LVLLL.	<mark>G</mark> MMM∨ <mark>T</mark>	T V V <mark>G</mark> A <mark>G</mark> E	SN - MFGYS	Y K T T D	LEDDW-	FEQPRAI	I I M <mark>gg krrr</mark> f (RPPPTL - DPI	E N S S E L G F S	P L K F L
Ms_LP_13	MA <mark>STY</mark> S	LVLLLL -	<mark>G</mark> MMM∨ <mark>T</mark>	TVVGAGE	SN - MFGYS	YKTTD	LEDDW-	FEQPRAI	I I M <mark>ggk</mark> ?????	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	******	????

Figure S3 Multiple sequence alignment of LPs from *M. truncatula* accessions A17 and HM056, R108 and *M. sativa*. Unknown *M. sativa* residues are indicated with "?".









Figure S4 Dotplot comparisons between *M. truncatula* and *G. max* in regions surrounding *M. truncatula* LPs. Panels show syntenic regions of *G. max* chromosomes 8 a) and 15 b) compared against a 2 Mb region in A17 chromosome 4, corresponding to 0.5% of the total *M. truncatula* genome. Syntenic regions of *G. max* chromosomes 8 c) and 18 d) are compared against a 3-4 Mb region of A17 chromosome 7. Red dots indicate regions of sequence similarity with a forward orientation, while blue dots indicate reverse matches. The LP region in *M. truncatula* is shown with green rectangles.



Figure S5 Phylogenetic tree of A17, HM056, R108 and *M. sativa* LP nucleotide sequences. The tree was generated through Bayesian Inference and visualized with FigTree software. Posterior probability values of the clades are indicated at the nodes.