

10.1071/CP19557_AC

© CSIRO 2020

Supplementary Material: *Crop & Pasture Science*, 2020, **71, 768–775.**

Development of SSR markers and association studies of markers with phenology and yield-related traits in grass pea (*Lathyrus sativus*)

Khela Ram Soren^{A,D}, Aravind Kumar Konda^A, Priyanka Gangwar^B, Vijay A. Tiwari^C, P. S. Shanmugavadivel^A, Ashok Kumar Parihar^{A,D}, Girish Prasad Dixit^A and Narendra Pratap Singh^A

^AICAR Indian Institute of Pulses Research, Kanpur, UP 208024, India.

^BAmity Institute of Biotechnology, Amity University, Gomti Nagar Extension, Lucknow, UP 226028, India.

^CDepartment of Biotechnology, Chatrapati Shahu Ji Maharajah University, Kanpur, UP 208024, India.

^DCorresponding authors. Email: sorenars@gmail.com; ashoka.parihar@gmail.com

Supplementary Table S1. List of 143 microsatellite loci information identified with repeat motif & putative functions

Sequence ID	Forward primer sequence (5'-3')	Reverse primer sequence (5'-3')	Product size (kb)	Repeat Motif	Putative Functions
gi 700160457 gb GBSS01000496.1	AAGGGGTAACAGGCTTAGAG	CCTTTGGTAGGAGAGTTAGGAG	144	(CAC)12	CDGSH iron-sulfur domain-containing NEET
gi 700160459 gb GBSS01000495.1	AGAGTGGGATGACAAGGAG	TCTGTAGTGCTCTCCAGCTC	123	(GAT)12	probable 26S proteasome complex subunit sem1-3
gi 700160475 gb GBSS01000482.1	CTCGAACAAACCCGAAAG	CCTTCGATCATGAACTCTCC	195	(GAA)12	CBL-interacting serine threonine- kinase 26
gi 700160477 gb GBSS01000480.1	GCCACCTCCTTATGAGTACA	GTGGAGGTGGTGATGTGTAT	182	(CAC)12	extensin-2-like isoform X4
gi 700160489 gb GBSS01000470.1	CAACCCGACCACAATACC	TACGTTTTACCCACAC	152	(AACA)12	E3 ubiquitin- ligase RING1-like
gi 700160492 gb GBSS01000468.1	CTTAATGCTCGGGCTTCT	GCATTGGTAGAGGATGAAGG	153	(GAA)12	lactoylglutathione lyase glyoxalase I family
gi 700160496 gb GBSS01000464.1	TATCCTCACCGCATCTTC	GGTACGGCAGTGATGTTAGA	138	(ATTC)12	2-methylene-furan-3-one reductase-like
gi 700160498 gb GBSS01000463.1	CTCTCGAACTCTTCCAACAC	CCGACTCTTGAAGTTCTTGC	180	(TTC)12	ATP synthase delta chloroplastic
gi 700160503 gb GBSS01000459.1	ATAGAGGCGCATTTTCGAG	GGTAGATCTTTCACCCTG	114	(CCA)12	60S ribosomal L24-3
gi 700160506 gb GBSS01000456.1	CCTGATCCTCCTCAAAC	TAGGTGGTGGTTCAGGAAG	148	(CCA)12	glycine-rich cell wall structural
gi 700160508 gb GBSS01000455.1	GATATAGCCGAGGTGATTGC	CTCCACCTTCTCTTTCT	147	(TGG)12	60S acidic ribosomal
gi 700160508 gb GBSS01000455.1	AGAGCCGTACATGCAAAG	CGGAGTAGAACATGTGGTGT	152	(AGGG)12	60S acidic ribosomal
gi 700160510 gb GBSS01000453.1	CTTGTATGTCTCCACGCTCT	GAAGAAGTCCACCATAGCAG	136	(TCT)12	---NA---
gi 700160525 gb GBSS01000441.1	GCTGGCTTGATTGTCATC	AGCAGCGGCATGTTATGT	151	(TGC)12	DUF3820 family
gi 700160525 gb GBSS01000441.1	GCTGGCTTGATTGTCATC	AGCAGCGGCATGTTATGT	151	(GCT)12	DUF3820 family
gi 700160526 gb GBSS01000440.1	CCAGGCTCAAAGGTTACA	TGTGGAGAAGGATGTTGC	187	(ATT)12	1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase 2-like
gi 700160528 gb GBSS01000438.1	CCTGATTTGGGGCCATT	CACTAGCAACATGGCAGAAC	176	(TTC)12	---NA---
gi 700160537 gb GBSS01000431.1	AGAGTGAGACCAACAGCATC	CCAACGCTCTATCTTCTACC	220	(TGGT)12	rubisco subunit binding- alpha subunit
gi 700160539 gb GBSS01000430.1	CACCACCCTAAACCTTAC	AGGAGGTGAGGGATACTTGT	185	(CCA)12	auxin response factor 2
gi 700160539 gb GBSS01000430.1	CCTCCAATAGGACCCATC	CAACCCTTCATGGTTCAC	150	(AACC)12	auxin response factor 3
gi 700160549 gb GBSS01000422.1	GTTACAGGGCTTTTCAGGAC	GCTCCATGAGAGCAGCATA	295	(CTG)12	plant F25P12-19
gi 700160557 gb GBSS01000416.1	CTTCAACCCTTCTCACACC	GGAAGAGGAAGAAGAAGGAG	175	(TTC)12	monothiol glutaredoxin-S10-like
gi 700160559 gb GBSS01000414.1	TCTCCACCATGCTTTGAC	GTGAGGAGGAAGATGATGAG	127	(CAT)12	Something about silencing 11
gi 700160560 gb GBSS01000413.1	CTCACAGTTAGCTGCAATGG	CCATCATTGTGGTGTCTT	147	(CAG)12	hypothetical protein MTR_8g099366
gi 700160562 gb GBSS01000412.1	GTAAGGGATGGGTCTGTTCT	CTGTGAGCAACTAGGGTTTC	165	(CTT)12	60S ribosomal L39-4
gi 700160569 gb GBSS01000406.1	GGGGAAACAATACTCATCC	CCCAACATCAACAACACC	143	(AAC)12	B2 -like
gi 700160571 gb GBSS01000405.1	GGCCACCATTTTCTCATC	TGTGGCTGCTGTTAAGGT	136	(CTC)12	thylakoid luminal 19 kDa chloroplastic
gi 700160571 gb GBSS01000405.1	CCATTTTCTCTCTCTCT	GCTGTAAAGGTGGTGGTTAG	103	(CCA)12	thylakoid luminal 19 kDa chloroplastic
gi 700160580 gb GBSS01000398.1	GTTCCCATGGTGAATGGT	CCCTTCTTCTTCTTGTCT	204	(GAA)12	plant F10N7-171

gi 700160580 gb GBSS01000398.1	GTTCCCATGGTGAATGGT	CCCTTCTTCTTCTCCTTGTC	204	(TTC)12	plant F10N7-172
gi 700160580 gb GBSS01000398.1	GGCCAAATGCTTGGATTG	GGTGGTCGTGGAGAATTA	162	(ATGA)12	plant F10N7-173
gi 700160580 gb GBSS01000398.1	AGAGGAAGGAGACAAAGGTG	CGATCAGCAAACACCATC	140	(AGAA)12	plant F10N7-174
gi 700160581 gb GBSS01000397.1	CTCACTTACTTCCCTTGG	GATGGTGTGAGAATGTGTGG	143	(GATA)12	light harvesting
gi 700160582 gb GBSS01000396.1	TCCCTTTACCCTTTCCTG	GGCTAGAGGAGCTGAAAAAG	147	(GCA)12	peptidyl-prolyl cis-trans isomerase FKBP20-2
gi 700160583 gb GBSS01000395.1	TCCGGTGTATCAGTGG	TCGGTGTAGGTGTAACCAG	127	(TTTC)12	photosystem I P700 apo A1 (chloroplast)
gi 700160584 gb GBSS01000394.1	TATAACGAGACGCGTGT	GATGGAGGTGATAGTAGAGAGG	149	(AAT)12	V-type proton ATPase subunit c2-like
gi 700160596 gb GBSS01000385.1	CATCTCAAACCCATCCAC	CGTAGATTCCGGTGTTC	148	(ACA)12	rubredoxin
gi 700160599 gb GBSS01000383.1	GTGGGAATTGTGTGCTTG	CAGCATCTTCTCAGACCAG	148	(TGC)12	plasma membrane ATPase 5
gi 700160609 gb GBSS01000375.1	GCTGTTCAAGCTCAATACCC	CTTCTTCTCAAGTCCTTCC	170	(CAA)12	homeobox-leucine zipper ATHB-6-like
gi 700160609 gb GBSS01000375.1	TGAGAGGTGCGAATAGGA	CACCTTCAACCTCTCTCTCTC	124	(ATG)12	homeobox-leucine zipper ATHB-6-like
gi 700160609 gb GBSS01000375.1	TGAGAGGTGCGAATAGGA	CACCTTCAACCTCTCTCTCTC	124	(GAG)12	homeobox-leucine zipper ATHB-6-like
gi 700160618 gb GBSS01000368.1	GCTTAGAGCCAAAACCAGAG	CCAGCCCCTGTTTGAATA	146	(TGC)12	50S ribosomal chloroplastic
gi 700160618 gb GBSS01000368.1	GCTTAGAGCCAAAACCAGAG	CCAGCCCCTGTTTGAATA	146	(TGA)12	50S ribosomal chloroplastic
gi 700160624 gb GBSS01000363.1	GGATGAGTTCTGTTCAGCTC	GTGTTCCGGAGCTAGGGTTAT	155	(CAC)12	copper ion-binding
gi 700160624 gb GBSS01000363.1	GAGGAGGATCCATCTGTTG	CTTTTACCGCACAGGTTG	195	(GAA)12	copper ion-binding
gi 700160624 gb GBSS01000363.1	CAACCTGTGCGGTAAAAG	GTCTACTGGAGTACGGCTAGG	136	(ATG)12	copper ion-binding
gi 700160630 gb GBSS01000358.1	GTCCATGTTCCCAACTGA	GGAGTACCAAGTCCAAGAAC	244	(ATC)12	ASPARTIC PROTEASE IN GUARD CELL 2-like
gi 700160630 gb GBSS01000358.1	GTCCATGTTCCCAACTGA	GGAGTACCAAGTCCAAGAAC	244	(TTC)12	ASPARTIC PROTEASE IN GUARD CELL 2-like
gi 700160631 gb GBSS01000357.1	GGCTAAAGTCAGCACATCTAGG	CTGCTTGGATTTGTCCAG	173	(ACCA)12	CBL-interacting serine threonine- kinase 5-like
gi 700160639 gb GBSS01000351.1	CCTACAAGCCTGTGAATACG	CCTTCTTCTTCCCTCAA	150	(GTT)12	probable carboxylesterase 13
gi 700160648 gb GBSS01000344.1	GCGTCACCGTTTATGCTA	CCATCCACACTCATTACACC	225	(TTGA)12	phosphatase 2C and cyclic nucleotide-binding kinase domain-containing
gi 700160653 gb GBSS01000340.1	GAGTCACCATAGCCACCA	GGTGGAGATCGTATCTTAGG	149	(CCA)12	ribonuclease T2 family
gi 700160653 gb GBSS01000340.1	TCCTTCATCAGCATCACC	CTTTAGTGGCTCAGGAGAGA	148	(CAC)12	ribonuclease T2 family
gi 700160653 gb GBSS01000340.1	GCAGCTAAAGCTTCATGG	CACAAGGTGTGAAAGAGG	204	(TTG)12	ribonuclease T2 family
gi 700160656 gb GBSS01000338.1	GTCACCACCACACTCACC	GTCAGTGAAGAAGTTGACG	181	(TCC)12	---NA---
gi 700160668 gb GBSS01000328.1	GGAACAAGATCTCCACAACC	GAGTGATGATGGAAGAGAGG	253	(TCT)12	CURVATURE THYLAKOID chloroplastic-like
gi 700160685 gb GBSS01000314.1	CTCTACCTCCTCTGAAACCTC	CCGGGTCAACCCGTTATC	238	(GATG)12	mediator of RNA polymerase II transcription subunit 36a-like
gi 700160688 gb GBSS01000312.1	CTTTGAAGGGTTCTCCTCTC	TCCTGGCTCTGTAATCAGTC	180	(CT)12	60S ribosomal L6
gi 700160693 gb GBSS01000307.1	CCACTCAAAGGAAACTGC	AGTGGGATCTGGTGGATT	274	(TTA)12	---NA---
gi 700160709 gb GBSS01000293.1	CCACATTCACAAAGGCACTC	GCTAGAACCCCAATTT	132	(TAA)12	---NA---
gi 700160717 gb GBSS01000287.1	AGAGGAAGAAGAAGGTGGAG	CCTAGAGGACGGACAAGATAC	162	(ATG)12	---NA---

gi 700160717 gb GBSS01000287.1	ATCTTGTCCTCCTCTAGGT	ACACCAGCCTTCTTCTCAC	148	(GAG)12	---NA---
gi 700160718 gb GBSS01000286.1	CCTAGTCCTATGCCTATCCTC	ACCATCATAGAGACCGACAC	131	(ATC)12	U2 snRNP auxilliary large splicing factor
gi 700160723 gb GBSS01000282.1	TACTGAGCTCACCGAAA	GCAGCATCTTCTTCTCAC	150	(GATG)12	glycine decarboxylase multi-enzyme H subunit
gi 700160731 gb GBSS01000275.1	CCTAGAGCTGTTGAGAGGAAG	GGCATCAGGAAACCTACAAC	151	(TTTC)12	30S ribosomal chloroplastic
gi 700160732 gb GBSS01000274.1	GATCTTGCTTCCCTTGGA	CCAACCATTGTACCCACTAGG	188	(TTA)12	Universal stress A
gi 700160737 gb GBSS01000270.1	TCAATCTTACCCACACTC	CTTCTCGGGGTGAAACT	165	(CGC)12	CBL-interacting serine threonine- kinase 11-like
gi 700160755 gb GBSS01000255.1	GTGAGGACTCACTCCAGAAG	GCCGGAAGAAAACAACCT	247	(ACA)12	homeobox domain
gi 700160756 gb GBSS01000254.1	GTCAACACGTGTCATCCAC	GTAGCTGAAGCCATCTTGTG	145	(TTCA)12	ribulose-phosphate 3- chloroplastic
gi 700160757 gb GBSS01000253.1	CTTGACAGTACCTCTACTCG	ACTTACGAGCCACGGTTT	148	(CAC)12	Indole-3-acetic acid-induced ARG3
gi 700160761 gb GBSS01000250.1	AGGAGGAAGAAGTGAAGGAG	GAACGGTACACAACAGCAC	198	(TAAA)12	S-adenosylmethionine decarboxylase proenzyme
gi 700160766 gb GBSS01000246.1	CTCTCAAGGGTCTTCTAT	TGTAGAATCTCTGCACTGG	146	(TCA)12	GTP-binding nuclear Ran-3-like
gi 700160777 gb GBSS01000238.1	CACAAACACAGACACGAAGG	GCCACACCAATCCCATTA	298	(AAGA)12	zeaxanthin chloroplastic-like
gi 700160780 gb GBSS01000236.1	GTGTAGCCGAGAGAAAGAGA	AGCCTTACCATTCCAGT	153	(TCTT)12	actin-8
gi 700160785 gb GBSS01000232.1	GCTCAGCAGTTCAATGGT	GAGGACCTCTAGAACGAGAAC	175	(CCT)12	30 kDa ribonucleo chloroplastic
gi 700160789 gb GBSS01000229.1	GGGTGAGGGAGTACACAATA	GGAAGAGATTGGCTAGAGAGG	141	(CATG)12	crocetin chloroplastic-like
gi 700160798 gb GBSS01000222.1	GAGACCTTGAGAGGGTGAA	GAGGATGCTCTTAAGGAAGG	161	(CCA)12	dnaJ homolog
gi 700160798 gb GBSS01000222.1	GAGACCTTGAGAGGGTGAA	GAGGATGCTCTTAAGGAAGG	161	(CCA)12	dnaJ homolog
gi 700160818 gb GBSS01000207.1	GGGTTTGGTTCTGGAAAG	CCAACACCAACACCAACT	167	(TGT)12	30S ribosomal chloroplastic
gi 700160819 gb GBSS01000206.1	ACCAACCCTCTACCACTCTC	CTCTCAGTGACGGAGACTT	177	(CAC)12	Rieske (2Fe-2S) domain
gi 700160820 gb GBSS01000205.1	CTGGATCATGCATTCTC	GTGGTGTGCAGTTTCACCTA	141	(TCT)12	chaperone dnaJ chloroplastic
gi 700160830 gb GBSS01000198.1	GCAAAGTATGGCCTCACA	TAACCTCTGCTTGCTTGG	202	(ACAA)12	fructose-bisphosphate aldolase chloroplastic
gi 700160832 gb GBSS01000196.1	CACCACTCTCTTCTTGCTC	CCACCAACTGTTTGAAGG	150	(CAG)12	PSRP5_PEA ame: Full=50S ribosomal chloroplastic ame: Full=50S ribosomal L18 ame: Full=CL18 ame: Full=Plastid-specific 50S ribosomal 5 Short=PSRP-5 Flags: Precursor
gi 700160848 gb GBSS01000184.1	AGGTAGGCATACGACGTACA	AGGGGGTTTGTTTAGAGC	122	(AACC)12	photosystem II CP47 chlorophyll apo (chloroplast)
gi 700160851 gb GBSS01000181.1	ACCTTCTCCTTCTGCTTACC	TCGTAATCCCTCTCTCTGC	155	(CTT)12	40S ribosomal S25-3
gi 700160856 gb GBSS01000177.1	GGATCCTTCAGGAGCAAT	CACATAGGCCCATTCAGA	150	(TGT)12	aquaporin PIP2-8
gi 700160856 gb GBSS01000177.1	AACCCACACTCACTACTCTCTC	GGTGGTGGATCTTGGAATC	143	(AACC)12	aquaporin PIP2-9
gi 700160856 gb GBSS01000177.1	AACCCACACTCACTACTCTCTC	GGTGGTGGATCTTGGAATC	143	(AACA)12	aquaporin PIP2-10
gi 700160867 gb GBSS01000169.1	GTTAGCCTCTGCTAATGCTC	CGATTCACCCCTGGATT	235	(ATGA)12	hypothetical protein TSUD_206781
gi 700160869 gb GBSS01000167.1	CAGCAGAACATCACAAGC	GTTGGGGTACTGGTAATGG	151	(AAAC)12	mechanosensitive ion channel 10-like
gi 700160870 gb GBSS01000166.1	GTGATTGTAGACGGAGTTGC	CCAGCATCCAAGTAAAGC	213	(TGGT)12	cytochrome b6f complex subunit

gi 700160872 gb GBSS01000165.1	GGAAAAGAGAGGACGTGAAG	CACCATCCACGAAATCCT	191	(TG)12	serine mitochondrial
gi 700160875 gb GBSS01000162.1	CTCCACGTCTCTTCTCTCT	GCTGAGTTCCCAACTAATGG	154	(CCTC)12	2-Cys peroxiredoxin chloroplastic-like
gi 700160878 gb GBSS01000160.1	CCGCTTCTAGGTGGAAT	GCACTCCAGAAGAAGTAGCA	184	(TAG)12	1-deoxy-D-xylulose 5-phosphate chloroplastic-like
gi 700160882 gb GBSS01000157.1	GCTGCAGCTGTTAGTCTAGA	ACCAAAGTCACCTGGTAGC	141	(TGC)12	chlorophyll a-b binding CP24 chloroplastic
gi 700160887 gb GBSS01000153.1	GTGGGTGATCGATTTACG	CCCTAAGGAAAACCAGGA	142	(TCT)12	leguminosin group485 secreted peptide
gi 700160888 gb GBSS01000152.1	ATCACCCAACGCACTCAC	TCCAACGGTTTGTGGTAG	191	(TAA)12	probable aquaporin PIP-type 7a
gi 700160888 gb GBSS01000152.1	GCCTCCATTTCTCAGTCTCT	CACTTTCGCTGTTCCAG	169	(GTG)12	probable aquaporin PIP-type 7a
gi 700160899 gb GBSS01000143.1	ACCACGGCTATAACCTCCT	CTAGATGGCCGTAACATCAC	150	(CCA)12	chlorophyll a-b binding chloroplastic
gi 700160899 gb GBSS01000143.1	ACCACGGCTATAACCTCCT	CTAGATGGCCGTAACATCAC	150	(CCG)12	chlorophyll a-b binding chloroplastic
gi 700160907 gb GBSS01000135.1	GCACAGAAGTGCCTCTTTC	AACACACCAGTCTCTTGGAG	132	(CTT)12	dehydrin b
gi 700160926 gb GBSS01000118.1	CTCTATGTCTGTTCCGGTGT	AGGGTTTTGAGGAAGCAG	126	(CCT)12	calreticulin-3-like isoform X2
gi 700160933 gb GBSS01000113.1	ACACAAGCTGGGAACCTAC	GGGTGAGTTGAAGAAGACG	177	(TTC)12	ATP synthase gamma chloroplastic
gi 700160937 gb GBSS01000110.1	AAAACCTGCAGTCATCC	CTATTGACACCACCATGGAC	243	(CTTC)12	metallothionein type 4
gi 700160938 gb GBSS01000109.1	CATGGAGATTGGAGACCT	TTCCATGCACATGGTGTC	239	(AAT)12	peroxidase 43
gi 700160938 gb GBSS01000109.1	GTTTCATGGAGATTGGAGACC	TGGACCACATGCAATACC	147	(TTTA)12	peroxidase 44
gi 700160939 gb GBSS01000108.1	GCCTAGTTTGGTCACTGGTA	GCACTCTCTACTCTCTCTCA	193	(TTC)12	40S ribosomal S2-5
gi 700160944 gb GBSS01000104.1	GTTACAAAGGGGGTGGTG	TACCATTGTCGGAAGCAC	153	(GGT)12	---NA---
gi 700160944 gb GBSS01000104.1	GTTACAAAGGGGGTGGTG	TACCATTGTCGGAAGCAC	153	(TGG)12	---NA---
gi 700160948 gb GBSS01000101.1	GTCCACCACCAATTCCTC	GGAGGTGGTGGTACAGGT	163	(CAC)12	---NA---
gi 700160952 gb GBSS01000098.1	CCGGATATCCTTCTTCTCAC	AGAAGGTAAGGCCTGACTC	151	(ACTG)12	exocyst subunit exo70 family
gi 700160953 gb GBSS01000097.1	CTAGGTGGTGGTGGTGGGA	AGAAGATCTCCACCAAGGAG	128	(GGT)12	hypothetical protein
gi 700160953 gb GBSS01000097.1	CTAGGTGGTGGTGGTGGGA	AGAAGATCTCCACCAAGGAG	128	(TGG)12	hypothetical protein
gi 700160956 gb GBSS01000095.1	GACAAATGTTGCCACGTC	TGCAGAGGTGTCCTAAGTGT	234	(ACA)12	glutaredoxin (GRX) family
gi 700160957 gb GBSS01000094.1	ACTCGAACCGTAGACCTTCT	AATCAGAGCACAGGGAGTC	197	(TAT)12	ATP synthase CF1 beta subunit (chloroplast)
gi 700160962 gb GBSS01000090.1	GTCTAAACACAGCCATACCC	GGTAAGAGCCTTTGGTAGGT	107	(AAC)12	photosystem II core complex s chloroplastic-like
gi 700160964 gb GBSS01000088.1	GTCCTTCCTCAGGACACAG	CTCTTGAGTCCATCTGGTG	163	(CCA)12	MLO 5
gi 700160964 gb GBSS01000088.1	TAGCACCTTGTTCCAACC	GCTGACAGCAGTTCATAC	160	(TTCA)12	MLO 6
gi 700160976 gb GBSS01000079.1	GAGTTGATGGCACCTACAAG	CATCCACTTCTCTGATACC	148	(ACC)12	CURVATURE THYLAKOID chloroplastic
gi 700160976 gb GBSS01000079.1	CGCGACTCTGAAAACGTG	CAGTGTTAGTCCCTCCTCTTC	136	(GTG)12	CURVATURE THYLAKOID chloroplastic
gi 700160982 gb GBSS01000075.1	CGACTTCCTCAATCTTAGGG	CAGAGGCAGATGAGTTGAG	168	(CAT)12	heat shock cognate 70 kDa 2-like
gi 700160992 gb GBSS01000067.1	GTACCTAGCTGGACTCTGGTT	ATACCTCGAGGGCTCGAA	282	(TA)12	photosystem II K (chloroplast)
gi 700160994 gb GBSS01000066.1	GGTGACTCTTGTTGTAATGC	GAGTGACGATGAGGAGAAAC	161	(TCA)12	pro-resilin, putative

gi 700160996 gb GBSS01000064.1	CCTTCCTCATCACTCCACT	GTGTAGACGCAATTCTCACC	169	(AGA)12	transmembrane protein, putative
gi 700160999 gb GBSS01000062.1	GTTGCTTCCTAGGAGTTGGT	TACACACACATCCACTCCAC	159	(TTG)12	phospholipase A1-IIdelta
gi 700161013 gb GBSS01000051.1	GAGAAACTCATGGAGGGAGT	CACACAATCCACAGAGGAAG	170	(CAT)12	photosystem I reaction center subunit chloroplastic
gi 700161015 gb GBSS01000050.1	GAGTGAGAGGTGTAGTGTCCA	AGCAGCACGGATCCTAGT	152	(ATA)12	phosphoglycerate chloroplastic
gi 700161019 gb GBSS01000047.1	TCTGCAACTAGCAACAGC	AAGGTTGGAGAAGAGAGAGC	193	(CAT)12	---NA---
gi 700161027 gb GBSS01000041.1	GTCACTGCTGCTGCTACTATC	TCCATGGTGGAAAGTGATG	119	(CTT)12	unknown
gi 700161028 gb GBSS01000040.1	CGGAGATGAATCGGAGAT	TATCTCCTCCGAACCTTGAC	118	(AAG)12	transcription activator GLK1
gi 700161029 gb GBSS01000039.1	GTGAGGTGGTTTTTAGCC	CGTATTTTCGAGACTCCTCCA	130	(TTCT)12	peroxisomal (S)-2-hydroxy-acid oxidase GLO1 isoform X1
gi 700161031 gb GBSS01000038.1	GGAAGCCTGATTGATCTCC	GGTCGAACGTCTTCAATG	144	(TAG)12	S-adenosylmethionine decarboxylase proenzyme
gi 700161035 gb GBSS01000035.1	GCTTCTGGCAACAGACATAG	GAGAGTGGTGGTGGTAAAGA	190	(TCAC)12	fructose-bisphosphate aldolase chloroplastic
gi 700161036 gb GBSS01000034.1	CGGTATCTCACCTTCTTCT	CGGTGGTGTGTTGTAGAGA	146	(CTT)12	ATP synthase delta chloroplastic-like
gi 700161039 gb GBSS01000032.1	CATTTGTGGCAACCTCAC	GTTACCATGGTGGTGGATAC	132	(CCA)12	hypothetical protein TSUD_106180
gi 700161039 gb GBSS01000032.1	TGTAACCACCTCCACCAC	GGTTACCATGGAGGCTATG	154	(CCA)12	hypothetical protein TSUD_106180
gi 700161039 gb GBSS01000032.1	GCCGCAAATTACCGCTTT	GTGGTTACATTGGTGGTGAG	127	(CATG)12	hypothetical protein TSUD_106180
gi 700161053 gb GBSS01000021.1	TCGAACTGTGTTTCAGTCTCC	GTACGAGCGTTCTTCTCCTA	157	(ACAA)12	retrotransposon 1
gi 700161055 gb GBSS01000020.1	ACCGTAGCCTCCTCCATA	CACAATGGTTACGGTGGT	159	(ACC)12	leguminosin group485 secreted peptide
gi 700161062 gb GBSS01000014.1	CCAAAACCTCACACCACAC	AGAGAGAGGCTTGTGTTGC	151	(ATTC)12	photosystem I reaction center subunit chloroplastic-like
gi 700161062 gb GBSS01000014.1	CCAAAACCTCACACCACAC	AGAGAGAGGCTTGTGTTGC	151	(CTCA)12	photosystem I reaction center subunit chloroplastic-like
gi 700161062 gb GBSS01000014.1	CCAAAACCTCACACCACAC	AGAGAGAGGCTTGTGTTGC	151	(CATT)12	photosystem I reaction center subunit chloroplastic-like
gi 700161077 gb GBSS01000002.1	CTGTAGTCACAGCTGAAGAGG	GTGGCACTCTCATAGTGATG	235	(TTG)12	ribulose bisphosphate carboxylase small chain

Table S2. Genetic characterization of 60 polymorphic microsatellite loci in *L. sativus*

Primer name	Major. Allele Frequency	Gene Diversity (GD)	PIC	Na	Ne	Ho	He	F
IPL-8	0.7700	0.3542	0.2915	2.000	1.600	0.500	0.375	-0.2895
IPL-22	0.4900	0.5538	0.4534	1.000	1.000	0.000	0.000	0.9646
IPL-30	0.4800	0.6294	0.5563	0.000	0.000	0.000	0.000	0.5307
IPL-31	0.4200	0.6536	0.5798	1.000	1.000	0.000	0.000	0.9400
IPL-32	0.5400	0.4968	0.3734	1.000	1.000	0.000	0.000	1.0000
IPL-41	0.5100	0.4998	0.3749	1.000	1.000	0.000	0.000	0.9608
IPL-42	0.4900	0.6298	0.5589	0.000	0.000	0.000	0.000	0.5938
IPL-43	0.5200	0.6072	0.5352	1.000	1.000	0.000	0.000	0.9354
IPL-44	0.4800	0.6342	0.5627	0.000	0.000	0.000	0.000	0.6589

IPL-45	0.5500	0.4950	0.3725	2.000	1.180	0.167	0.153	0.8016
IPL-50	0.5200	0.5176	0.4028	2.000	2.000	0.333	0.500	0.9242
IPL-51	0.6100	0.4758	0.3626	1.000	1.000	0.000	0.000	0.9588
IPL-52	0.5500	0.5950	0.5280	1.000	1.000	0.000	0.000	0.5699
IPL-56	0.5700	0.4902	0.3701	2.000	1.180	0.167	0.153	0.8799
IPL-57	0.7300	0.4042	0.3371	1.000	1.000	0.000	0.000	-0.0290
IPL-59	0.4400	0.6368	0.5608	2.000	1.471	0.400	0.320	0.8767
IPL-60	0.4900	0.6118	0.5344	1.000	1.000	0.000	0.000	0.9680
IPL-62	0.4400	0.6424	0.5677	1.000	1.000	0.000	0.000	0.3241
IPL-63	0.3500	0.6662	0.5921	0.000	0.000	0.000	0.000	0.9117
IPL-65	0.5100	0.4998	0.3749	2.000	1.800	0.000	0.444	0.8822
IPL-66	0.5700	0.4902	0.3701	1.000	1.000	0.000	0.000	0.8799
IPL-68	0.5000	0.5000	0.3750	2.000	1.180	0.167	0.153	0.9215
IPL-76	0.5400	0.4968	0.3734	2.000	2.000	0.333	0.500	0.9210
IPL-78	0.7700	0.3542	0.2915	2.000	1.600	0.500	0.375	-0.2895

IPL-82	0.4900	0.5538	0.4534	1.000	1.000	0.000	0.000	0.9646
IPL-85	0.5100	0.4998	0.3749	2.000	1.800	0.000	0.444	0.8822
IPL-88	0.5700	0.4902	0.3701	1.000	1.000	0.000	0.000	0.8799
IPL-92	0.4900	0.6118	0.5344	1.000	1.000	0.000	0.000	0.9680
IPL-95	0.5700	0.4902	0.3701	2.000	1.180	0.167	0.153	0.8799
IPL-102	0.5400	0.4968	0.3734	1.000	1.000	0.000	0.000	1.0000
IPL-103	0.4800	0.6246	0.5499	0.000	0.000	0.000	0.000	0.4001
IPL-105	0.4400	0.6368	0.5608	2.000	1.471	0.400	0.320	0.8767
IPL-110	0.3600	0.6648	0.5907	2.000	1.923	0.000	0.480	0.7636
IPL-111	0.4900	0.6118	0.5344	1.000	1.000	0.000	0.000	0.9680
IPL-113	0.5100	0.4998	0.3749	1.000	1.000	0.000	0.000	0.9608
IPL-119	0.4900	0.6298	0.5589	0.000	0.000	0.000	0.000	0.5938
IPL-120	0.4900	0.5538	0.4534	1.000	1.000	0.000	0.000	0.9646
IPL-123	0.5500	0.4950	0.3725	2.000	1.180	0.167	0.153	0.8016
IPL-126	0.5200	0.6072	0.5352	1.000	1.000	0.000	0.000	0.9354

IPL-129	0.5000	0.5000	0.3750	2.000	1.180	0.167	0.153	0.9215
IPL-130	0.4800	0.6294	0.5563	0.000	0.000	0.000	0.000	0.5307
IPL-131	0.5700	0.4902	0.3701	1.000	1.000	0.000	0.000	0.8799
IPL-136	0.5500	0.4950	0.3725	2.000	1.180	0.167	0.153	0.8016
IPL-139	0.7300	0.4042	0.3371	1.000	1.000	0.000	0.000	-0.0290
IPL-143	0.5400	0.4968	0.3734	2.000	2.000	0.333	0.500	0.9210
IPL-144	0.3600	0.6648	0.5907	2.000	1.923	0.000	0.480	0.7636
IPL-147	0.5100	0.4998	0.3749	2.000	1.800	0.000	0.444	0.8822
IPL-148	0.5500	0.5950	0.5280	1.000	1.000	0.000	0.000	0.5699
IPL-152	0.6100	0.4758	0.3626	1.000	1.000	0.000	0.000	0.9588
IPL-154	0.4800	0.6294	0.5563	0.000	0.000	0.000	0.000	0.5307
IPL-158	0.5500	0.5950	0.5280	1.000	1.000	0.000	0.000	0.5699
IPL-160	0.4200	0.6536	0.5798	1.000	1.000	0.000	0.000	0.9400
IPL-166	0.7300	0.4042	0.3371	1.000	1.000	0.000	0.000	-0.0290
IPL-169	0.4400	0.6368	0.5608	2.000	1.471	0.400	0.320	0.8767

IPL-178	0.5400	0.4968	0.3734	1.000	1.000	0.000	0.000	1.0000
IPL-179	0.6400	0.4608	0.3546	1.000	1.000	0.000	0.000	1.0000
IPL-181	0.6100	0.4758	0.3626	1.000	1.000	0.000	0.000	0.9588
IPL-183	0.3500	0.6662	0.5921	0.000	0.000	0.000	0.000	0.9117
IPL-192	0.4900	0.6298	0.5589	0.000	0.000	0.000	0.000	0.5938
IPL-193	0.5200	0.6072	0.5352	1.000	1.000	0.000	0.000	0.9354
Mean	0.52	0.54	0.45	1.16	1.01	0.073	0.10	0.077

Table S3. Basic characterization of the 60 polymorphic microsatellite loci in grasspea, including the product size, repeat motif, and putative functions of each locus.

Sequence ID	Primers Name	Forward Primer sequence (5'-3')	Product size (bp)	Repeat Motif	Putative function
gi 700077338 gb GBSN01000363.1	IPL-8	F-5'GGATGAGTTCTGTTTCAGCTC3' R-5'GTGTTCCGGAGCTAGGGTTAT3'	155	(ATA)21	Copper ion-binding
gi 700077248 gb GBSN01000429.1	IPL-22	F-5'CATACACCCCAAGTTGAGC3' R-5'GGCTCTCTCTCAAGATTCTC3'	217	(TCCAT)15	Small EDRK-rich factor 2
gi 700077809 gb GBSN01000017.1	IPL-30	F-5'CATCACCACATCCACACA3' R-5'CTCTGCCCTGTCATTTTG3'	174	(ACACA)20	Photosystem ii 22 KDachloroplastic-like
gi 700077442 gb GBSN01000288.1	IPL-31	F-5'GAGTCTGCTTCATTCTGGTC3' R-5'ACCTCCCTCTCTTCAAACCTC3'	191	(TGC)15	Probable sugar phosphate phosphatetranslocator at3g11320-like

gi 700077444 gb GBSN01000287.1 	IPL-32	F-5'GGCGTGGAATTTGCCTA3' R-5'CTCCACCTTCTTCTCCTCT3'	145	(GACTTA)24	---NA---
gi 700077703 gb GBSN01000095.1 	IPL-41	F-5'GAGAATAGGAGGAGGGAGAG3' R-5'GAAGTCGCCGTATAACCAG3'	156	(TGGTGT)18	Glutaredoxin domain-containing cysteine-rich protein 1
gi 700077671 gb GBSN01000119.1 	IPL-42	F-5'ACACCACTCACCACAGAAAG3' R-5'GAAAGTATCCGGCGAAGT3'	158	(AGAAAA)18	Probable protein s-acyltransferase 7- like
gi 700077657 gb GBSN01000129.1 	IPL-43	F-5'AGTGGCACATTGTCACGA3' R-5'GGAGGGAAGAAGAAGTAGGT3'	225	(CAATTA)18	50s ribosomal protein 131
gi 700077641 gb GBSN01000141.1 	IPL-44	F-5'CCCTTTCCTTGTTCTTC3' R-5'CCCTATAGCTTGGTTCACAC3'	151	(CTTATT)18	Eukaryotic translation initiation factor 1a
gi 700077551 gb GBSN01000208.1 	IPL-45	F-5'CCTCCTTGGTATTGACCTG3' R-5'GGAGGAGACAAGAAAGAAGG3'	164	(CCATGT)18	---NA---
gi 700077384 gb GBSN01000331.1 	IPL-50	F-5'GAGTAACGCGAGATATGGAC3' R-5'AATCCATGGAGGGTGCTT3'	137	(TTTATT)18	ADP-ribosylation factor 2

gi 700077365 gb GBSN01000344.1 	IPL-51	F-5'AGTACCCTAGCACCACAAAG3' R-5'GCGGTTATAGCAGAGAAGAG3'	134	(CACCAT)18	Protein phosphatase 2c and cyclic nucleotide-binding kinase domain-containing protein
gi 700077453 gb GBSN01000279.1 	IPL-52	F-5'ATCATCCCCATCATAGCC3' R-5'GTTGCTGGGGTTCTAGGT3'	138	(CAT)15	---NA---
gi 700077171 gb GBSN01000487.1 	IPL-56	F-5'GGAACCAAGTACAAGGACTG3' R-5'CGGAATCCCCTAATCCT3'	161	(TTAGGG)18	Serine-threonine protein plant-
gi 700077528 gb GBSN01000225.1 	IPL-57	F-5'GCTGGCAATAGACAAGTCAC3' R-5'CTCGAGTAAGATCGAGGCTA3'	227	(ATAAT)15	Auxin-induced protein aux28
gi 700077532 gb GBSN01000222.1 	IPL-59	F-5'GAGACCTTGAGAGGGTGAA3' R-5'GAGGATGCTCTTAAGGAAGG3'	161	(GCC)15	Protein like
gi 700077562 gb GBSN01000200.1 	IPL-60	F-5'GAGTCTACGAGCACGTTCC3' R-5'CAACCTTCACTCACACACAC3'	168	(AACAG)15	Glycine dehydrogenase
gi 700077588 gb GBSN01000180.1 	IPL-62	F-5'CCTTCTACACAACGGCTTC3' R-5'CTACTGGAGGAGGCTTTCAT3'	153	(TTC)15	Sucrose transport

gi 700077588 gb GBSN01000180.1 	IPL-63	F-5'GGAGAGGCTCCATAGTGATA3' R-5'CTCACATCACTCCCAGATTC3'	157	(GTT)15	Sucrose transport
gi 700077684 gb GBSN01000109.1 	IPL-65	F-5'TAAGCACCAGCAAGCACT3' R-5'AGGAGGCCGTTATCTTCTAC3'	146	(CACTC)15	Cationic peroxidase
gi 700077700 gb GBSN01000097.1 	IPL-66	F-5'GGAGATCTTCTTGGTGGTG3' R-5'CCTCCCACCATTTCACAT3'	162	(GGT)15	Hypothetical protein
gi 700077719 gb GBSN01000083.1 	IPL-68	F-5'ATAGCCTCTACACCTCACACC3' R-5'AGGAGTGCTTGAGAGAGATG3'	143	(CTTCA)15	Plastid transketolase
gi 700077487 gb GBSN01000255.1 	IPL-76	F-5'GAGGGTTCTTGCGATTC3' R-5'ACTCTCTCCCTCCGAACTAC3'	116	(AG)20	Homeoboxdomain protein
gi 700077351 gb GBSN01000354.1 	IPL-78	F-5'CTCTCTCTCTCTCTCTCTCG3' R-5'GGCTCTCTCTCAAGATTCTC3'	152	(CT)22	GDP-mannose -epimerase 1
gi 700077187 gb GBSN01000474.1 	IPL-82	F-5'CAACACAACACCAACACG3' R-5'GCTGAGGTTAAGAGGGTTTC3'	143	(CACAC)15	TPR1-like protein

gi 700077818 gb GBSN0100010.1 	IPL-85	F-5'TGCGGGTTACCCATATCT3' R-5'GGAAGAGGAGGAAGAAGAAG3'	166	(TTC)24	Pentatricopeptiderepeat-containing protein mitochondrial-like isoform x1
gi 700077188 gb GBSN01000473.1 	IPL-88	F-5'ATAGCCTTGCTGGAGACAC3' R-5'GAAGATCTCGAAGGAAGGA3'G	132	(CTT)15	Core histone h2a h2b h3 h4
gi 700077192 gb GBSN01000470.1 	IPL-92	F-5'GTGTGGGGGTAAAACGTA3' R-5'GGAGAAGAAGCAGAAGCTGG3'	150	(TAATT)15	E3 ubiquitin-protein ligase ring1-like
gi 700077778 gb GBSN0100040.1 	IPL-95	F-5'GGTGTAGTAGGAGGGAAGAGA3' R-5'ACTTGTAAGTGGTGGAGGA3'	142	(TCC)24	Transcription activator glk1
gi 700077321 gb GBSN01000375.1 	IPL-102	F-5'GCTGTTCAAGCTCAATACCC3' R-5'CTTCTTCCTCAAGTCCTTCC3'	170	(ACA)27	Homeobox-leucine zipper protein athb-6-like
gi 700077308 gb GBSN01000385.1 	IPL-103	F-5'GTGGTTACTCCCATCACATC3' R-5'CTGGAAACCCTCCTGTTAG3'	161	(CAT)15	Rubredoxin family protein
gi 700077192 gb GBSN01000470.1 	IPL-105	F-5'GACGGAGGGTACAAAGTCTC3' R-5'CCAACATACTGACTCACACG3'	194	(TTTGG)15	E3 ubiquitin-protein ligase ring1-like

gi 700077199 gb GBSN01000465.1 	IPL-110	F-5'GTCAAAGGAGTGACAAGTCG3' R-5'GAGAGGTCCTAAGAGAGCATC3'	162	(GCTTT)15	40s ribosomal protein s6
gi 700077201 gb GBSN01000463.1 	IPL-111	F-5'GTTGTGGAGGACGATTAGG3' R-5'CCTCTGGTTAGGTTCTTCG3'	168	(TTG)15	ATP synthase delta chain
gi 700077208 gb GBSN01000458.1 	IPL-113	F-5'GTTACTACTGCCACCCTTCC3' R-5'GGTGGTGAAGAAGTAGTGGA3'	128	(TTC)15	60s ribosomal protein 110-2
gi 700077211 gb GBSN01000456.1 	IPL-119	F-5'ACCTAGCCCTCCTCCACT3' R-5'GGTGCTCTTGTCTGTAGTAGC3'	162	(ACC)15	Hypothetical protein MTR_3g052810
gi 700077219 gb GBSN01000450.1 	IPL-120	F-5'GAGGAAGATGACAGAAGCAC3' R-5'CCATGTCTCCA ACTCTCTTG3'	173	(TTTTG)15	Limonoindudp-glucosyltransferase-like protein
gi 700077247 gb GBSN01000430.1 	IPL-123	F-5'AATACACTCACCACCTCCAC3' R-5'AGGAGGTGAGGGATACTTGT3'	142	(CAC)15	Auxinresponse factor 1
gi 700160569 gb GBSS01000406.1 	IPL-126	F-5'GGGGAAACA ACTACTCATCC3' R-5'CCCAACATCAACAACACC3'	143	(CAA)18	B2 protein

gi 700077735 gb GBSN0100071.1 	IPL-129	F-5'ACTCGTTCATACTCCACCAC3' R-5'CAAGTGTCTCTCCGACTTC3'	157	(GTG)18	Phloem specific protein
gi 700077525 gb GBSN01000227.1 	IPL-130	F-5'TGATCTGAAGGACTGACCAC3' R-5'CAGTTGCTCACAACCACA3'	202	(TTG)18	Hypothetical protein MTR_4g127690
gi 700077465 gb GBSN01000271.1 	IPL-131	F-5'CAACAGCACGACTCTCAA3' R-5'CTTCACAGGTCCAATACCAC3'	156	(CAA)18	Transcriptional corepressorseuss
gi 700077280 gb GBSN01000406.1 	IPL-136	F-5'GCGGTTTCAACAAAGGAG3' R-5'GCACCACCGAACTTAACTC3'	121	(AAC)15	B2 protein
gi 700077282 gb GBSN01000404.1 	IPL-139	F-5'GAGGTTGAGGAACAAGAGG3' R-5'GCACCACCGAACTTAACTC3'	267	(ATA)15	Hypothetical protein MTR_2g022610
gi 700077308 gb GBSN01000385.1 	IPL-143	F-5'GTGGTTACTCCCATCACATC3' R-5'CTGGAAACCCTCCTGTTAG3'	161	(CCA)27	Rubredoxinfamily protein
gi 700077330 gb GBSN01000369.1 	IPL-144	F-5'GAAGTGAGGTGAAGTCCAAG3' R-5'ACCAAACGCGTCACTCTT3'	188	(GAAT)20	DS12 from 2d-page of leaf

gi 700077162 gb GBSN01000494.1 	IPL-147	F-5'TATGGATCCCCATAAGC3' R-5'GACACCACAAAGTGATCCTC3'	295	(ATTT)20	Temperature-induced lipocalin
gi 700077336 gb GBSN01000365.1 	IPL-148	F-5'GGAGTAGTGGTGGATGAGTT3' R5'ATAGGGAAGAGGAGGTAGAGC3'	188	(TCAC)16	NAD H-quinoneoxidoreductase subunit I
gi 700077338 gb GBSN01000363.1 	IPL-152	F-5'TCTTCATGGGCTGATGTG3' R-5'CTTCCTCACTCTCAGTATCCTC3'	136	(GAT)15	Copper ion-binding
gi 700160523 gb GBSS01000442.1 	IPL-154	F-5'GTGTTCGTGCCTTCATACTC3' R-5'GAACTACCGGTGGTGCTAC3'	145	(TGACCA)30	Dehydrin3
gi 700160483 gb GBSS01000475.1 	IPL-158	F-5'CAGTACATTCCCTCTTCAGC3' R-5'CCTCCCGAGTATAGCAGTTT3'	173	(CTCTTC)30	30s ribosomal protein s6
gi 700077263 gb GBSN01000418.1 	IPL-160	F-5'ATATCCATCCACCACCAGAC3' R-5'GAGGTACCTGCAACCATAGA3'	143	(AAAATA)18	Rubredoxin family protein
gi 700077450 gb GBSN01000282.1 	IPL-166	F-5'GAAAGGATGAGGCATTGG3' R-5'GCTTGTGTTTGTGAGGAGTG3'	151	(TCATT)15	Glycine decarboxylase multi-enzyme h subunit

gi 700077743 gb GBSN01000065.1 	IPL-169	F-5'CCTTACCACTAACCCAAGC3' R-5'AGCTGTTAGACCCTTCACTG3'	173	(ACCCTT)18	Thermosperminesynthase acaulis5-like
gi 700077738 gb GBSN01000069.1 	IPL-178	F5'GAGGTGAGTGATTAGTGGTAGC3' R-5'CTCATGGCCTTGACTCTAAC3'	159	(GCCATT)18	hypothetical protein MTR_3g086650
gi 700077712 gb GBSN01000088.1 	IPL-179	F-5'GCACCAGCTTTGTATGGA3' R-5'GATCTCCACGTTTGAGACTG3'	142	(GCCAAT)18	Seven transmembraneMLO family protein isoform 2
gi 700077528 gb GBSN01000225.1 	IPL-181	F-5'CACCTTCTTTGGGAGAGAG3' R-5'GGAAGTGGGTTGGGATT3'	152	(TCACTC)18	Auxin-induced protein aux28
gi 700077476 gb GBSN01000263.1 	IPL-183	F-5'CTTCTTCCACCTCCTAGAGTC3' R-5'CTTCAGACGCTGGTTTTTC3'	207	(CCTCTG)18	THO complex subunit
gi 700077409 gb GBSN01000314.1 	IPL-192	F-5'CTCTACCTCCTCTGAAACCTC3' R-5'CTTCTGATTCGCTCCAG3'	206	(GGTTTT)18	Mediator of RNAPolymerase ii transcription subunit 36a
gi 700077211 gb GBSN01000456.1 	IPL-193	F-5'ACCTAACCTCCTCCACTAC3' R-5'GGAGGAGGTGGTGGTTTT3'	147	(CCACCT)18	Hypothetical protein MTR_3g052810