

Tagged genes and sequences of DNA primers used for their amplification.

Gene Name	Accession Number	Position on Chromosome		Primer Sequence (5' => 3')			
		Start	End	P1	P2	P3	P4
MFP2	AT3G06860	2161875	2166315	GCTCGATCCACCT AGGCTCATTGTTA TGAACGGTTGGT CTTTGG	CACAGCTCCACCTCCACCT CCAGGCCGGCCGCTCTGTA ATACAAATGGAAG	TGCTGGTGCTGCTGCGG CCGCTGGGGCCGCTCC CGTGAAACAAGCC	CGTAGCGAGACCA CAGGAGTTGGTCGT CGACTATCC
PEX5	AT5G56290	22803755	22809345	GCTCGATCCACCT AGGCTTTCGGAT CCTAGATCGGGT CTT	CACAGCTCCACCTCCACCT CCAGGCCGGCCGAGATTC CTTGACTCACAAGCTTCTA T	TGCTGGTGCTGCTGCGG CCGCTGGGGCCGATCT CTTGAGAAAGAATTC CCGCTGTG	CGTAGCGAGACCA CAGGATCCGTGAG ACCCCTTTTT
AtFIM1	AT4G26700	13463674	13467605	GCTCGATCCACCT AGGCTCGCCAAA TTAAACAGCAAC AA	CACAGCTCCACCTCCACCT CCAGGCCGGCCGATTTC GAAACCGCATCACCAAC	TGCTGGTGCTGCTGCGG CCGCTGGGGCCACCAC GGTCTCAGAGGAAGC	CGTAGCGAGACCA CAGGAAAGTCATTT TTGCGCCAGATTA
PME	AT1G69940	26408907	26410581	GCTCGATCCACCT AGGCTCATGTAA ACAAATAGCAG	CACAGCTCCACCTCCACCT CCAGGCCGGCCTCCTTGA TGAGCCGAG	TGCTGGTGCTGCTGCGG CCGCTGGGGCCTCCAA GTGGCTTCTCCCACC	CGTAGCGAGACCA CAGGAAGCAGAGA GAGTAACACC
VIP2	AT5G59710	24075560	24079144	GCTCGATCCACCT AGGCTGCAATCG TCGGTTCGTCACT	CACAGCTCCACCTCCACCT CCAGGCCGGCCGTAATTG ATAACAAAATGTTCTGCG ATA	TGCTGGTGCTGCTGCGG CCGCTGGGGCCGAGCT TATGGAAGAGACCA AGC	CGTAGCGAGACCA CAGGAGGATGAAG AGAGAATGTTCTTC GAG
SYP21	AT5G16830	553574 (-) strand	5532877	GCTCGATCCACCT AGGCTGTTGGAC TTCTCCTTGTTTT TGGC	TCCACCTCCACCTCCAGGC CGGCCATCGTCTCTTCTC TCGA ATCTCTCGA	TGGTGCTGCTGCGGCC GCTGGGGCCATGAGTT TCCAAGATCTCGAAGC T	CGTAGCGAGACCA CAGGAGATCATGA AGATCCTTATGATG AG
SYP41	AT5G26980	9491041 (-) strand	9488299	GCTCGATCCACC TAGGCTCAGCCC GCACGAATGCAT GCCGTT	TCCACCTCCACCTCCAGGC CGGCCATGATCGTCAAA ATTTGAAATCCCTAG	TGGTGCTGCTGCGGCC GCTGGGGCCATGGCGA CGAGGAATCGTACGTT G	CGTAGCGAGACCAC AGGATCCACCATGT AGTGCTCGCAGCTA G
SYP42	AT4G02195	972487 (-) strand	969776	GCTCGATCCACCT AGGCTAGCCGCC ACGAATCTACGG GCATT	TCCACCTCCACCTCCAGGC CGGCCATCAATACCAAA TCAATTGATTCTCTT	TGGTGCTGCTGCGGCCG CTGGGGCCATGGCGAC GAGGAATCGAACGACG	CGTAGCGAGACCA CAGGAGTCTGTGAA GCCAACGCATTCTG
SYP51	AT1G16240	5556728 (-) strand	5555072	GCTCGATCCACCT AGGCTGCTACCC GGTGCGTGACAG GTTGAA	TCCACCTCCACCTCCAGGC CGGCCATTATTCCTATAT AATTAAAAGCTAATC	TGGTGCTGCTGCGGCC GCTGGGGCCATGGCGT CTTCATCGGATTCAATG G	CGTAGCGAGACCA CAGGAGCTCAGCC ACAAATGTGGAAT GAGA

PIP2A	AT3G53420	19819151 (-) strand	19814307	5'- TTGGTCGGATC TACGATGTTCT C-3'	5'- CGTTCTGAGAGCTTCAG GTTCTAAGTCT-3'	5'- CTTGGATCATTGAGAA GTGCTG-3'	5'- CTCGAACTTGGCT GAGGATT-3'
PRP2	AT2G21140	9072115 (-) strand	9067216	5'- CACCGTCTCCG AGTCTCTTC-3'	5'- TTGTCTGCCCTCCTCTCA CT-3'	5'- TGATCTAAAAACATCC CCTTGAT-3'	5'- AATGCACATAGAT TCTACAGTTCCAT AG-3'
ELP	AT1G05850	1769995 (-) strand	1764130	5'- CGGAAGCATGC AGAGATTGT-3'	5'- GTTGTAAAGGAAGGAAC TTGGAATC-3'	5'- ATGAAGCTTGGGCTTT TCAC-3'	5'- CCATAAGAAGAAA AACAATAAACTTT G-3'
SEC12	AT2G01470	216526	211116	5'- ATATGTTGCGG TTGAACACG-3'	5'- TCGAGAGACAGACACGG AGG-3'	5'- ATGGCGAATCAGAGT ACAGAG-3'	5'- TGCTTCTTTGTTAG CGCCTT-3'
SYP61	AT1G28490	10014143	10018466	5'- TAAGGATGTGC GTCACAGGA-3'	5'- GCAAAATTTTGTGATTT CGGG-3'	5'- ATGTCTTCAGCTCAAG ATCCATT-3'	5'- GCTGATAAGGCCC AACGTAA-3'