**Supplemental Table 1. HMR peptides identified by LC-MS/MS analysis.**

| Sequence | Prob | Start | Stop |
|---|---|---|---|
| (C)KKEDGDGDVSEGSKKSEEGFE(Y) | 95% | 58 | 78 |
| (E)YVTVER(H) | 50% | 79 | 84 |
| (E)RHPYHSYmD(S) | 96% | 84 | 92 |
| (E)RHPYHSYMD(S) | 92% | 84 | 92 |
| (E)RHPYHSYmD(S) | 17% | 84 | 92 |
| (E)RHPYHSYmDSTSGKLEPASG(A) | 82% | 84 | 103 |
| (E)RHPYHSYMDSTSGKLEPASG(A) | 60% | 84 | 103 |
| (E)RHPYHSYmDSTSGKLEPASGAR(A) | 100% | 84 | 105 |
| (E)RHPYHSYmDSTSGKLEPASGAR(A) | 100% | 84 | 105 |
| (E)RHPYHSYmDSTSGKLEPASGAR(A) | 100% | 84 | 105 |
| (E)RHPYHSYMDSTSGKLEPASGAR(A) | 100% | 84 | 105 |
| (E)RHPYHSYmDSTSGKLEPASGAR(A) | 100% | 84 | 105 |
| (E)RHPYHSYmDSTSGKLEPASGAR(A) | 98% | 84 | 105 |
| (E)RHPYHSYMDSTSGKLEPASGAR(A) | 95% | 84 | 105 |
| (E)RHPYHSYMDSTSGKLEPASGAR(A) | 56% | 84 | 105 |
| (E)RHPYHSYMDSTSGKLEPASGARASIPGE(D) | 11% | 84 | 111 |
| (E)RHPYHSYMDSTSGKLEPASGARASIPGEDYWPE(G) | 93% | 84 | 116 |
| (E)RHPYHSYMDSTSGKLEPASGARASIPGEDYWPE(G) | 87% | 84 | 116 |
| (E)RHPYHSYmDSTSGKLEPASGARASIPGEDYWPE(G) | 74% | 84 | 116 |
| (E)RHPYHSYMDSTSGKLEPASGARASIPGEDYWPE(G) | 53% | 84 | 116 |
| (E)RHPYHSYmDSTSGKLEPASGARASIPGEDYWPE(G) | 49% | 84 | 116 |
| (E)RHPYHSYMDSTSGKLEPASGARASIPGEDYWPE(G) | 45% | 84 | 116 |
| (E)RHPYHSYMDSTSGKLEPASGARASIPGEDYWPE(G) | 28% | 84 | 116 |
| (E)RHPYHSYmDSTSGKLEPASGARASIPGEDYWPE(G) | 28% | 84 | 116 |
| (E)RHPYHSYMDSTSGKLEPASGARASIPGEDYWPE(G) | 9% | 84 | 116 |
| (H)SYmDSTSGKLEPASGARASIPGEDYWPE(G) | 35% | 89 | 116 |
| (D)STSGKLEPASGAR(A) | 99% | 93 | 105 |
| (D)STSGKLEPASGAR(A) | 95% | 93 | 105 |
| (D)STSGKLEPASGARASIPGEDYWPE(G) | 77% | 93 | 116 |
| (D)STSGKLEPASGARASIPGEDYWPE(G) | 40% | 93 | 116 |
| (S)GKLEPASGARASIPGEDYWPE(G) | 35% | 96 | 116 |
| (A)SGARASIPGEDYWPE(G) | 91% | 102 | 116 |
| (S)GARASIPGEDYWPE(G) | 87% | 103 | 116 |
| (G)ARASIPGEDYWPE(G) | 78% | 104 | 116 |
| (G)ARASIPGEDYWPE(G) | 38% | 104 | 116 |
| (R)ASIPGEDYWPE(G) | 47% | 106 | 116 |
| (R)ASIPGEDYWPE(G) | 29% | 106 | 116 |
| (E)GTSSRVRAARAPQPAGE(S) | 10% | 117 | 133 |
| (R)VRAARAPQPAGE(S) | 100% | 122 | 133 |
| (R)VRAARAPQPAGE(S) | 53% | 122 | 133 |
| (R)AARAPQPAGE(S) | 27% | 124 | 133 |
| (E)SSSFPSYGK(N) | 16% | 134 | 142 |
| (E)SSSFPSYGKNPGSR(R) | 99% | 134 | 147 |
| (E)SSSFPSYGKNPGSR(R) | 99% | 134 | 147 |
| (E)SSSFPSYGKNPGSR(R) | 97% | 134 | 147 |
| (E)SSSFPSYGKNPGSRR(K) | 92% | 134 | 148 |
| (E)SSSFPSYGKNPGSRR(K) | 70% | 134 | 148 |
| (E)SSSFPSYGKNPGSRRKK(N) | 56% | 134 | 150 |
| (E)SSSFPSYGKNPGSRRKK(N) | 11% | 134 | 150 |
| (E)SSSFPSYGKNPGSRRKKNR(K) | 10% | 134 | 152 |
| (R)KATEENVTVE(T) | 59% | 153 | 162 |
| (S)SEEEENDSSDGFVTYKNE(F) | 13% | 174 | 191 |
| (E)EEENDSSDGFVTYKNE(F) | 56% | 176 | 191 |
| (E)ENDSSDGFVTYKNE(F) | 68% | 178 | 191 |
| (E)NDSSDGFVTYKNE(F) | 100% | 179 | 191 |
| (E)NDSSDGFVTYKNE(F) | 100% | 179 | 191 |
| (E)NDSSDGFVTYKNE(F) | 99% | 179 | 191 |
| (E)NDSSDGFVTYKNEFE(R) | 71% | 179 | 193 |
| (N)DSSDGFVTYKNE(F) | 92% | 180 | 191 |
| (D)SSDGFVTYKNE(F) | 99% | 181 | 191 |
| (E)FEREEEE(T) | 90% | 192 | 198 |
| (E)FEREEEETGFE(L) | 100% | 192 | 202 |
| (E)FEREEEETGFE(L) | 100% | 192 | 202 |
| (E)FEREEEETGFE(L) | 99% | 192 | 202 |
| (E)TGFELDK(K) | 90% | 199 | 205 |
| (E)TGFELDKK(L) | 78% | 199 | 206 |
| (E)LDKKLGRPHPFIDPTK(K) | 30% | 203 | 218 |
| (E)LDKKLGRPHPFIDPTKK(K) | 97% | 203 | 219 |
| (E)LDKKLGRPHPFIDPTKK(K) | 37% | 203 | 219 |
| (E)LDKKLGRPHPFIDPTKKK(Q) | 99% | 203 | 220 |
| (E)LDKKLGRPHPFIDPTKKK(Q) | 75% | 203 | 220 |
| (E)LDKKLGRPHPFIDPTKKK(Q) | 72% | 203 | 220 |
| (E)LDKKLGRPHPFIDPTKKK(Q) | 57% | 203 | 220 |
| (E)LDKKLGRPHPFIDPTKKK(Q) | 31% | 203 | 220 |
| (E)LDKKLGRPHPFIDPTKKKQIE(K) | 99% | 203 | 223 |
| (E)LDKKLGRPHPFIDPTKKKQIE(K) | 98% | 203 | 223 |

| | | | |
|---|---|---|---|
| (E)LDKKLGRPHPFIDPTKKKQIE(K) | 98% | 203 | 223 |
| (E)LDKKLGRPHPFIDPTKKKQIE(K) | 97% | 203 | 223 |
| (E)LDKKLGRPHPFIDPTKKKQIE(K) | 97% | 203 | 223 |
| (E)LDKKLGRPHPFIDPTKKKQIE(K) | 97% | 203 | 223 |
| (E)LDKKLGRPHPFIDPTKKKQIE(K) | 96% | 203 | 223 |
| (E)LDKKLGRPHPFIDPTKKKQIE(K) | 96% | 203 | 223 |
| (E)LDKKLGRPHPFIDPTKKKQIE(K) | 92% | 203 | 223 |
| (E)LDKKLGRPHPFIDPTKKKQIE(K) | 82% | 203 | 223 |
| (E)LDKKLGRPHPFIDPTKKKQIE(K) | 80% | 203 | 223 |
| (E)LDKKLGRPHPFIDPTKKKQIE(K) | 72% | 203 | 223 |
| (E)LDKKLGRPHPFIDPTKKKQIE(K) | 65% | 203 | 223 |
| (E)LDKKLGRPHPFIDPTKKKQIE(K) | 47% | 203 | 223 |
| (E)LDKKLGRPHPFIDPTKKKQIE(K) | 32% | 203 | 223 |
| (E)LDKKLGRPHPFIDPTKKKQIE(K) | 23% | 203 | 223 |
| (E)LDKKLGRPHPFIDPTKKKQIEK(T) | 43% | 203 | 224 |
| (E)LDKKLGRPHPFIDPTKKKQIEK(T) | 29% | 203 | 224 |
| (E)LDKKLGRPHPFIDPTKKKQIEKTLTSDE(S) | 36% | 203 | 230 |
| (D)KKLGRPHPFIDPTKKKQIE(K) | 100% | 205 | 223 |
| (D)KKLGRPHPFIDPTKKKQIE(K) | 99% | 205 | 223 |
| (D)KKLGRPHPFIDPTKKKQIE(K) | 98% | 205 | 223 |
| (D)KKLGRPHPFIDPTKKKQIE(K) | 92% | 205 | 223 |
| (K)KLGRPHPFIDPTKKKQIE(K) | 88% | 206 | 223 |
| (K)KLGRPHPFIDPTKKKQIE(K) | 75% | 206 | 223 |
| (K)LGRPHPFIDPTKKKQIE(K) | 98% | 207 | 223 |
| (K)LGRPHPFIDPTKKKQIE(K) | 97% | 207 | 223 |
| (G)RPHPFIDPTKKKQIE(K) | 60% | 209 | 223 |
| (K)QIEKTLTSDE(S) | 21% | 221 | 230 |
| (E)SWWNWRKPE(K) | 97% | 231 | 239 |
| (E)SWWNWRKPE(K) | 91% | 231 | 239 |
| (E)SWWNWRKPEKE(Q) | 95% | 231 | 241 |
| (E)SWWNWRKPEKE(Q) | 36% | 231 | 241 |
| (E)SWWNWRKPEKE(Q) | 28% | 231 | 241 |
| (E)TVFLKAmAE(T) | 99% | 255 | 263 |
| (E)TVFLKAmAE(T) | 99% | 255 | 263 |
| (E)TVFLKAmAE(T) | 98% | 255 | 263 |
| (E)TVFLKAmAE(T) | 94% | 255 | 263 |
| (E)TVFLKAMAE(T) | 75% | 255 | 263 |
| (E)TVFLKAmAE(T) | 64% | 255 | 263 |
| (E)TVFLKAMAE(T) | 61% | 255 | 263 |
| (E)TVFLKAmAE(T) | 61% | 255 | 263 |
| (E)TVFLKAmAE(T) | 40% | 255 | 263 |
| (E)TVFLKAmAE(T) | 37% | 255 | 263 |
| (E)TVFLKAmAE(T) | 31% | 255 | 263 |
| (E)TVFLKAMAE(T) | 29% | 255 | 263 |
| (E)TVFLKAMAE(T) | 20% | 255 | 263 |
| (E)TVFLKAMAE(T) | 14% | 255 | 263 |
| (E)TVFLKAmAE(T) | 13% | 255 | 263 |
| (E)TGQVKLYGEEPTLTE(T) | 100% | 264 | 278 |
| (E)TGQVKLYGEEPTLTE(T) | 100% | 264 | 278 |
| (E)TGQVKLYGEEPTLTE(T) | 99% | 264 | 278 |
| (E)TGQVKLYGEEPTLTE(T) | 84% | 264 | 278 |
| (Q)VKLYGEEPTLTE(T) | 74% | 267 | 278 |
| (E)TSLYRAR(R) | 90% | 279 | 285 |
| (E)TSLYRAR(R) | 70% | 279 | 285 |
| (E)TSLYRARRHLFKEE(R) | 30% | 279 | 292 |
| (R)RHLFKEE(R) | 90% | 286 | 292 |
| (R)RHLFKEE(R) | 84% | 286 | 292 |
| (E)RLQAERE(R) | 85% | 293 | 299 |
| (E)RERLAKEGPmAFYSE(W) | 91% | 298 | 312 |
| (E)RERLAKEGPMAFYSE(W) | 17% | 298 | 312 |
| (E)RERLAKEGPmAFYSE(W) | 9% | 298 | 312 |
| (E)RLAKEGPmAFYSE(W) | 100% | 300 | 312 |
| (E)RLAKEGPMAFYSE(W) | 99% | 300 | 312 |
| (E)RLAKEGPmAFYSE(W) | 77% | 300 | 312 |
| (E)RLAKEGPMAFYSE(W) | 24% | 300 | 312 |
| (E)RLAKEGPmAFYSE(W) | 14% | 300 | 312 |
| (E)RLAKEGPmAFYSE(W) | 11% | 300 | 312 |
| (R)LAKEGPmAFYSE(W) | 22% | 301 | 312 |
| (E)GPmAFYSE(W) | 77% | 305 | 312 |
| (E)GPmAFYSE(W) | 16% | 305 | 312 |
| (E)WVKAWKRD(T) | 13% | 313 | 320 |
| (R)EAVQKHFEETGEDE(N) | 36% | 324 | 337 |
| (E)AVQKHFEE(T) | 90% | 325 | 332 |
| (E)AVQKHFEETGEDE(N) | 100% | 325 | 337 |
| (E)AVQKHFEETGEDE(N) | 90% | 325 | 337 |
| (E)AVQKHFEETGEDE(N) | 82% | 325 | 337 |
| (E)AVQKHFEETGEDE(N) | 78% | 325 | 337 |
| (E)AVQKHFEETGEDE(N) | 9% | 325 | 337 |
| (E)AVQKHFEETGEDENTQLIE(M) | 26% | 325 | 343 |

| | | | |
|---|---|---|---|
| (K)HFEETGEDE(N) | 86% | 329 | 337 |
| (E)NTQLIEmFSHQTDRE(Y) | 100% | 338 | 352 |
| (E)NTQLIEmFSHQTDRE(Y) | 100% | 338 | 352 |
| (E)NTQLIEmFSHQTDRE(Y) | 98% | 338 | 352 |
| (E)NTQLIEMFSHQTDRE(Y) | 67% | 338 | 352 |
| (E)MFSHQTDRE(Y) | 100% | 344 | 352 |
| (E)MFSHQTDRE(Y) | 100% | 344 | 352 |
| (E)mFSHQTDRE(Y) | 100% | 344 | 352 |
| (E)mFSHQTDRE(Y) | 100% | 344 | 352 |
| (E)MFSHQTDRE(Y) | 100% | 344 | 352 |
| (E)MFSHQTDRE(Y) | 99% | 344 | 352 |
| (E)MFSHQTDRE(Y) | 99% | 344 | 352 |
| (E)mFSHQTDRE(Y) | 98% | 344 | 352 |
| (E)mFSHQTDRE(Y) | 98% | 344 | 352 |
| (E)mFSHQTDRE(Y) | 96% | 344 | 352 |
| (E)mFSHQTDRE(Y) | 96% | 344 | 352 |
| (E)mFSHQTDRE(Y) | 76% | 344 | 352 |
| (E)MFSHQTDRE(Y) | 74% | 344 | 352 |
| (E)YRImMGTD(I) | 77% | 353 | 360 |
| (E)DQIKQIWGGD(P) | 98% | 375 | 384 |
| (E)DQIKQIWGGDPVYPTINYIQD(P) | 71% | 375 | 395 |
| (D)PVYPTINYIQDPNAVmD(F) | 95% | 385 | 401 |
| (N)YIQDPNAVMDFRGPDFHEPTPNMLSYLKE(N) | 16% | 392 | 420 |
| (D)PNAVmDFRGPDFHEPTPNMLSYLKE(N) | 53% | 396 | 420 |
| (D)PNAVmDFRGPDFHEPTPNmLSYLKE(N) | 43% | 396 | 420 |
| (D)PNAVMDFRGPDFHEPTPNMLSYLKE(N) | 28% | 396 | 420 |
| (D)PNAVmDFRGPDFHEPTPNMLSYLKE(N) | 7% | 396 | 420 |
| (D)FRGPDFHEPTPNmLSYLKE(N) | 100% | 402 | 420 |
| (D)FRGPDFHEPTPNMLSYLKE(N) | 100% | 402 | 420 |
| (D)FRGPDFHEPTPNmLSYLKE(N) | 100% | 402 | 420 |
| (D)FRGPDFHEPTPNmLSYLKE(N) | 81% | 402 | 420 |
| (D)FRGPDFHEPTPNMLSYLKE(N) | 43% | 402 | 420 |
| (D)FRGPDFHEPTPNmLSYLKE(N) | 35% | 402 | 420 |
| (N)MLSYLKE(N) | 56% | 414 | 420 |
| (E)NGKVISREmHE(A) | 41% | 421 | 431 |
| (E)mHEALLTKE(K) | 17% | 429 | 437 |
| (E)ALLTKEKTE(Q) | 100% | 432 | 440 |
| (E)ALLTKEKTE(Q) | 100% | 432 | 440 |
| (E)ALLTKEKTE(Q) | 95% | 432 | 440 |
| (A)LLTKEKTE(Q) | 97% | 433 | 440 |
| (L)LTKEKTE(Q) | 90% | 434 | 440 |
| (E)KTEQLEVPDmD(D) | 85% | 438 | 448 |
| (E)KVPRNWSVLK(E) | 25% | 475 | 484 |
| (E)KVPRNWSVLKE(T) | 98% | 475 | 485 |
| (E)KVPRNWSVLKE(T) | 53% | 475 | 485 |
| (E)KVPRNWSVLKETPE(L) | 99% | 475 | 488 |
| (E)KVPRNWSVLKETPE(L) | 96% | 475 | 488 |
| (E)KVPRNWSVLKETPE(L) | 35% | 475 | 488 |
| (E)KVPRNWSVLKETPE(L) | 21% | 475 | 488 |
| (E)KVPRNWSVLKETPE(L) | 13% | 475 | 488 |
| (E)KVPRNWSVLKETPE(L) | 13% | 475 | 488 |
| (E)KVPRNWSVLKETPE(L) | 11% | 475 | 488 |
| (E)KVPRNWSVLKETPE(L) | 10% | 475 | 488 |
| (E)KVPRNWSVLKETPE(L) | 8% | 475 | 488 |
| (R)NWSVLKE(T) | 78% | 479 | 485 |
| (R)NWSVLKETPE(L) | 84% | 479 | 488 |
| (R)NWSVLKETPE(L) | 47% | 479 | 488 |
| (W)SVLKETPE(L) | 9% | 481 | 488 |
| (E)TPELRTAKPKPKKE(G) | 24% | 486 | 499 |
| (E)LRTAKPKPKKE(G) | 99% | 489 | 499 |
| (E)LRTAKPKPKKE(G) | 52% | 489 | 499 |
| (E)LRTAKPKPKKEGR(M) | 91% | 489 | 501 |
| (E)GRMSLDEAVDD(A) | 59% | 500 | 510 |
| (E)GRmSLDEAVDDAE(N) | 67% | 500 | 512 |
| (E)GRMSLDEAVDDAE(N) | 57% | 500 | 512 |
| (E)GRmSLDEAVDDAENLTDFLmDFE(E) | 62% | 500 | 522 |
| (E)AVDDAENLTDFLmDFEEE(T) | 31% | 507 | 524 |
| (E)AVDDAENLTDFLmDFEEE(T) | 22% | 507 | 524 |

**Supplemental Table 2.** Oligonucleotides used for generating constructs used in this study.

| Construct | Vector | Forward Primer | Reverse Primer | Template | Cloning Method |
|---|---|---|---|---|---|
| N20-YFP | pCHF3-YFP | GGCggatccATGGCGTCAATATCAACCAC | GGCgtcgacTCCACTGTCTGTGCATACTTG | AT2G34640 (HMR) | PCR and Ligation |
| N31-YFP | pCHF3-YFP | GGCggatccATGGCGTCAATATCAACCAC | GGCgtcgacAACCCGTCTCTGCACAATAC | AT2G34640 (HMR) | PCR and Ligation |
| N50-YFP | pCHF3-YFP | GGCggatccATGGCGTCAATATCAACCAC | GGCgtcgacAGACCGATCCCTAGAAGTAATC | AT2G34640 (HMR) | PCR and Ligation |
| N60-YFP | pCHF3-YFP | GGCggatccATGGCGTCAATATCAACCAC | GGCgtcgacCTCTTTCTTGCATTTGATAC | AT2G34640 (HMR) | PCR and Ligation |
| YFP-GUS | pCHF3-NtermYFP | CGGagatctATGTTACGTCCTGTAGAAAC | CGGggatccTTGTTTGCCTCCCTGCTGCG | GUS | PCR and Ligation |
| YG-NLS1 | pCHF3-YFP-GUS | CGGagatctAAAAAGCTTGGAAGGCCACAT | CGGgtcgacTTAGTTCCACCACGATTCATCGCT | AT2G34640 (HMR) | PCR and Ligation |
| YG-NLS2 | pCHF3-YFP-GUS | CGGagatctAAGACACTCACGAGCGATGAATCG | CGGgtcgacTTAAACATCAGGACGTCTTCTTTG | AT2G34640 (HMR) | PCR and Ligation |
| YG-2NLS | pCHF3-YFP-GUS | CGGagatctAAAAAGCTTGGAAGGCCACAT | CGGgtcgacTTAAACATCAGGACGTCTTCTTTG | AT2G34640 (HMR) | PCR and Ligation |
| GST-HMRm | pET42b | GGCgaattcTAAGAAAGAGGATGGAGATGGTG | GGCctgcagTTAAGGATCAGTCTCCTCTTCAAAG | AT2G34640 (HMR) | PCR and Ligation |
| | | | | | |
| HMRm-HA | pCHF3 | cccggggatcctctagagATGAAGAAAGAGGATGGAGATGGTGATG | cgaaagctctgcaggTTAGGCGGCCGGAGCGTA | HMR-HA | Gibson Assembly |
| TPrbcS-HMRm-HA | pCHF3 | cccggggatcctctagagATGGCTTCCTCTATGCTC | ctttcttcatAGTCTCAAACTTCTTCTTTCC | AT1G67090 (RBCS1A) | Gibson Assembly |
| | | tttgagactATGAAGAAAGAGGATGGAGATGGTGATG | cgaaagctctgcaggTTAGGCGGCCGGAGCGTA | HMR-HA | Gibson Assembly |
| | | | | | |
| YG | pCHF3-YFP-GUS | gatccTAATACCCATACGATGTTCCAGATg | tcgacATCTGGAACATCGTATGGGTATTAg | - | Adapter Ligation |
| YG-NLS SV40 | pCHF3-YFP-GUS | gatccCCTAAGAAGAAGCGCAAGGTCTAAg | tcgacTTAGACCTTGCGCTTCTTCTTAGGg | - | Adapter Ligation |

**Supplemental Table 3.** Primers used for cDNA synthesis and qRT-PCR analysis of PEP-dependent plastidial genes.

| Accession | Gene Name | cDNA Synthesis Primer | Primer Pair for qRT-PCR |
|---|---|---|---|
| ATCG00630 | PSAJ | GGGAAATGTTAATGCATCTGG | AAACATATCTTTCCGTAGCAC<br>CTCTATTAATAAACCTGCTAACG |
| ATCG00020 | PSBA | TAGATGGAGCCTCAACAGCAGCTA | ACATTTCTTCTTAGCGGCTT<br>CGTCCTTGACTATCAACTACTGA |
| ATCG00680 | PSBB | CATCCAAATCTGGATCAATACCAG | GAATTAGATCGTGCGACTTTGA<br>CTAGCACCATGCCAAATGTGTC |
| ATCG00490 | RBCL | CTTCACAAGCAGCAGCTAGTTCAGG | GGAGATGATTCTGTACTACAAT<br>GTCCCTCATTACGAGCTTGTAC |

**Supplemental Table 4.** Primers used for qRT-PCR analysis of nuclear-encoded genes.

| Accession | Gene Name | Forward Primer | Reverse Primer |
|---|---|---|---|
| AT1G69960 | PP2A | TATCGGATGACGATTCTTCGTGCAG | GCTTGGTCGACTATCGGAATGAGAG |
| AT2G38530 | LTP2 | GCATGCAAAGTCAATATTCC | AATATTCGAAACATCCGCTA |
| AT5G14180 | MPL1 | TCAGCTACGGTGGTTTAGAT | TTCACAAACTGCACATTCAT |
| AT2G45210 | SAUR36 | GTTCAGGATACAACCGGATA | TTGAGTTTGGCTAATGGTCT |
| AT1G19530 | - | CAAGTTGGTAACTCAGGAAGGTG | TTCTCCACCATCCACTACTCTTG |
| AT2G46970 | PIL1 | AAATTGCTCTCAGCCATTCGTGG | TTCTAAGTTTGAGGCGGACGCAG |
| AT4G16780 | ATHB-2 | TCACAGTACTCTCAATCCGAAGC | CCGTAAGAACTCGCAGTCTAC |
| AT4G32280 | IAA29 | CACCATCATTGCCCGTATCA | CCACAGTAGCCGTTGTTGGA |
| AT4G14130 | XTR7 | CACCGTCACTGCTTACTACTTG | CATTGGTGTGAAGAACATAAG |