**Supplemental Table S1. Primers used in this study.**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Application | Gene name | Locus | Primer name | Primer sequence (5'-3') |
| Primers used for constructing pRNAi-SlDRM7 | SlDRM7 | Solyc04g005250.2 | pSlDRM7i-F | CGACGACAAGACCCTGTTTACAATGAGAAGT |
| pSlDRM7i-R | GAGGAGAAGAGCCCTTATGTTCGGGTAGTGGA |
| Primers used for constructing SlDRM7-KO induced by CRISPR-CAS9 | SlDRM7 | Solyc04g005250.2 | sgRNA oligo-F | ATATATGGTCTCGATTGAGACAATGACAGCATTGACTGTT |
| sgRNA oligo-R | AACGGAATGAACTTAGATTGACACAATCTCTTAGTCGACTCTAC |
| sgRNA oligo-F1 | TGAGACAATGACAGCATTGACTGTTTTAGAGCTAGAAATAGC |
| sgRNA oligo-R1 | ATTATTGGTCTCTAAACGGAATGAACTTAGATTGACAC |
| Primers used for RT-qPCR | SlDRM7 | Solyc04g005250.2 | SlDRM7-F | CCAAGACGTCTCCGTTCAGC |
| SlDRM7-R | GAACAATGTGGTCGCCGTAG |
| SlSAG12 | Solyc02g076970.1 | SlSAG12-F | ACATCTCGCGAGTTGAACGA |
| SlSAG12-R | AAAATGCCCAGCAACATCCG |
| SlSAG13 | Solyc03g096640.2 | SlSAG13-F | CTCAACGAACGCTTACAAGAGTG |
| SlSAG13-R | GGGCTTCCTAATGTTAGTTCCCA |
| SlSAG15 | Solyc03g117950.2 | SlSAG15-F | GGAGTTGGAAAATCTGAACTGGC |
| SlSAG15-R | CGGATAGCTTCAGTTAGAGTCCC |
| SlSRG1 | Solyc02g071430.2 | SlSRG1-F | CCTGATGCCTTTGTTGTCAACAT |
| SlSRG1-R | TAGGAGCTGGACCTAAATCTCCA |
| SlGLK1 | Solyc07g053630.2 | SlGLK1-F | TGGGAATTGATTGTCTCACTCGT |
| SlGLK1-R | ATTCATCTCTCTCTTTCCTCCGC |
| SlORE1S03 | Solyc03g115850.2 | SlORE1S03-F | ACATTTCAGGGCTTGTGAGA |
| SlORE1S03-R | AGGTGAATTGTTGAAGGAATTGAT |
| SlORE1S06 | Solyc06g069710.2 | SlORE1S06-F | GATTCTGCTACTGCTACTGCTT |
| SlORE1S06-R | GGATCTTGAACCCCAAATGAAG |
| SlNAP2 | Solyc04g005610.2 | SlNAP2-F | GTGTCTGGTTATTGGAAAGCCAC |
| SlNAP2-R | GATCCATTTGGCCTAGTTGGTTG |
| HAD | Solyc02g069410.2 | HAD-F | TGCTGATGTACCTGTGCACA |
| HAD-R | TGCACCACCAAATCCATCCA |
| PsbP-2 | Solyc03g114930.2 | PsbP-2-F | AACAATTGTCCCGTTGCTGC |
| PsbP-2-R | TGGCGAACCAAAATCCCGTA |
| GAPB | Solyc12g094640.1 | GAPB-F | ACTCTCACGAGGTTGCCAAT |
| GAPB-R | TCAAGTCACGGTGTGATGCA |
| PPR2 | Solyc12g098990.1 | PPR2-F | CAACAACGTCATCGAAGCGT |
| PPR2-R | TGGACAGCGTTGATCACCTT |
| THF1 | Solyc07g054820.2 | THF1-F | ACTCAATCGGCGGAAAGGAA |
| THF1-R | AGCTGAACTGGACGTGCAAT |
|  | Solyc12g009070.1 | 009070-F | ACAAACCCTCAGCAGCTTGT |
| 009070-R | AGCCATTGCCAATTAAGCCT |
| PsaK | Solyc08g006930.2 | PsaK-F | GCTTGGTGGCAATTCAACCA |
| PsaK-R | TTTAGCCCTGCAGTTGCCTT |
| LHCB4 | Solyc09g014520.2 | LHCB4-F | ACATCCAATTCGCCGATCGA |
| LHCB4-R | CCTTTTTCGGTGCGGCTTTT |
| BE1 | Solyc07g064830.2 | BE1-F | TTCGCATGAAACAGCCTCCT |
| BE1-R | AATTGGCCCATGCAGGAACT |
| GLY1 | Solyc06g048920.2 | GLY1-F | AAACCCTTGTACTGCCGCTT |
| GLY1-R | GCTGCAATTGCTGTTCCGAA |
| PsbS | Solyc06g060340.2 | PsbS-F | TTGCTGCCTCTTTGTTGGGA |
| PsbS-R | AAGGATTTGCCAGGAGGGAT |
| PNSB5 | Solyc09g083190.2 | PNSB5-F | TCCTGTTGATCGATGGAGAACT |
| PNSB5-R | AAATCCTGTTGGGGGTGCAA |
| LFNR1 | Solyc02g083810.2 | LFNR1-F | TTGATGCCAATGGGAAGCCT |
| LFNR1-R | GGCATGAGCATTTCTTTGCCT |
| PsbP-3 | Solyc08g043180.2 | PsbP-3-F | CACCCACCAAAACCTTTGCA |
| PsbP-3-R | AGAAAAGCCGTCGCCATAGA |
| PPD2 | Solyc04g009420.2 | PPD2-F | GCTTCGCTATTGCCATTGGT |
| PPD2-R | ACCACGACGCCTACATTGTT |
| MET1 | Solyc03g096850.2 | MET1-F | TGTGGCCAGCTGATAAGCTT |
| MET1-R | ACCACAGTCGAGGCAAATGT |
|  | Solyc10g047410.1 | 047410-F | ATGCTTGGTCCCGTTCGAAA |
| 047410-R | TCAGCAATACGGCGGTGAAT |
| HEMA2 | Solyc01g106390.2 | HEMA2-F | TTCACATGCACTGCTTCGAAAG |
| HEMA2-R | AGCTTCCATTTTCTTCCGCAAC |
| GSA1 | Solyc04g009200.2 | GSA1-F | AACGAGTTTCGGTGCTCCAT |
| GSA1-R | TAGGACGGCAAGTGAAAGCA |
| HEMC | Solyc07g066470.2 | HEMC-F | TTTGACGACCTTGGATGGGT |
| HEMC--R | AAAGTAGTTCCTGGCCAGCA |
| HEME2 | Solyc06g048730.2 | HEME2-F | AGGTCCTTCATTCGCTGCTT |
| HEME2-R | TCTCAAGCAAGCCACCTGAT |
| PPOX1 | Solyc01g079090.2 | PPOX1-F | TCGTGATCCGCGTTTACCAA |
| PPOX1-R | TGCTTCGACTTCGCAGAGAA |
| CHLH | Solyc04g015750.2 | CHLH-F | AGCGATGCATGTTTCCCAGA |
| CHLH-R | AAGCTGCTTGAGTCCCTTGT |
| CHLI | Solyc10g008740.2 | CHlI-F | ATCGCCACTGTCATTCCCAA |
| CHlI-R | AGCTTGGTGCAGGGAAATGT |
| CHLD | Solyc04g015490.2 | CHlD-F | TGCCAAAGGAGCAGCACTTA |
| CHlD-R | AACTGCCGTTGTAAGCCCAT |
| CHLM | Solyc03g118240.2 | CHLM-F | AAACAGGCGCAAGAGGAGTT |
| CHLM-R | TTCGGTGCAAAGCTCAGGAT |
| PORA | Solyc12g013710.1 | PORA-F | TCAAGCTGCTGCATTGCTTC |
| PORA-R | ATGCAACCATTGTCTCGGCT |
| DVR | Solyc01g067290.2 | DVR-F | AGGAAGTTTGGGGCTTCACA |
| DVR-R | TGCAAGCACACAACTTTCCA |
| CHLG | Solyc09g014760.2 | CHLG-F | CCAATTCCTTCAGGTGCGGT |
| CHLG-R | CCCACCAAGGCAAGCTGATA |
|  | Solyc03g115980.1 | Solyc03g115980.1-F | TGGCCAACATACAAGGTGCT |
| Solyc03g115980.1-R | AATGGGGTTTCCTGGTGCAA |
| PGI1 | Solyc04g076090.2 | PGI1-F | AGATTCCATGTTCACGCGGT |
| PGI1-R | TCTGCAAACGAGGCTCCATT |
| PGM1 | Solyc03g006870.2 | PGM1-F | TGCCACTGGAAGATTTCGGA |
| PGM1-R | TAGCATCTTGGGCATTGGCA |
| APS1 | Solyc07g056140.2 | APS1-F | TTGATGGGGGCAGATTACTACG |
| APS1-R | GCCGCTTCTTGAACATTGTCTT |
| APL1 | Solyc01g079790.2 | APL1-F | TGCTAAGCCTGCTGTTCCAA |
| APL2-R | TGTGACCCCATTGCCAAAGT |
| APL2 | Solyc07g019440.2 | APL2-F | AGGAACAACCAACGGCAGAT |
| APL2-R | ATTATACGTGCGGGCAAGGT |
| APL3 | Solyc01g109790.2 | APL3-F | AAGGATGTGGCTGCAGTCAT |
| APL3-R | ACGATTCAGGGCAGCAGAAT |
| GBSS | Solyc08g083320.2 | GBSS-F | TGCGATGTTGTTGACCCAGA |
| GBSS-R | TGGCAAGTGGAGCGATTTCT |
| SS1 | Solyc03g083090.2 | SS1-F | TCCTGGGAAAATGCAGCCAT |
| SS1-R | ATTCCGCGTCCAATGACAGT |
| SS2 | Solyc02g088000.2 | SS2-F | AAGGTGGTTGGGGATTGCAT |
| SS2-R | ACATTGAGGCTTGCCAGTCT |
| SS3 | Solyc02g080570.2 | SS3-F | AGAAAGGCTTGCCGAGGAAA |
| SS3-R | TGGGAACATGGATCGTGCAA |
| SS4 | Solyc02g071040.2 | SS4-F | TTCCCACGCAAAAATGGTGC |
| SS4-R | ATCAACATCTGGTGGGCGTT |
| BE1 | Solyc07g064830.2 | BE1-F | TTCGCATGAAACAGCCTCCT |
| BE1-R | AATTGGCCCATGCAGGAACT |
| BE2 | Solyc04g082400.2 | BE2-F | TCGGTGACAAGACCATTGCA |
| BE2-R | TCAGGATGGCCAAACTCGTT |
| BE3 | Solyc09g009190.2 | BE3-F | CCACGGCCAAAGAAACCAAA |
| BE3-R | TGTTCCAAAACGGCTGCTTG |
| ISA1 | Solyc07g014590.2 | ISA1-F | TGCCCTGTCACGAGTTCAAT |
| ISA1-R | TATTGCACCGAGGCCACAAT |
| ISA2 | Solyc09g064800.1 | ISA2-F | ACTTTGAAGGCCGATGCTGA |
| ISA2-R | AAAAGGGAGGGCTGTGTCAA |
| GWD | Solyc05g005020.2 | GWD1-F | GCAATTTTGTGGGGATGCCA |
| GWD1-R | TCCATCAAGTCAGCCGCAAT |
| PWD | Solyc09g098040.2 | PWD-F | ACATGCTGTAGCCCGTGTTT |
| PWD-R | TGAAGCGAGTGTTTCACCGA |
| SEX4 | Solyc03g111160.2 | SEX4-F | TCCTGCAGTTGCGTTGACAT |
| SEX4-R | TCAACGTGACAGGCGTCTTT |
| SEX4-2 | Solyc11g007830.1 | SEX4-2-F | TGCGTGCCGAAATAAGGGAT |
| SEX4-2-R | GTTTCGGAAAACAGGAGCGT |
| LSF2 | Solyc06g050230.2 | LSF2-F | ATCACTGGAGTGGGCGATTT |
| LSF2-R | TGACCTTTTGTTGGGACCACA |
| LSF1 | Solyc12g062250.1 | LSF1-F | AATGGGCGCATGGGAATTTC |
| LSF1-R | TTTTCAGCCTCGATGCCACT |
| BAM | Solyc08g077530.2 | BAM-F | TTTGCACAAGCCAAGCCATC |
| BAM-R | CAACGCCATCAAACTCGCAT |
| BAM1 | Solyc09g091030.2 | BAM1-F | ATCCTTCAAGCGTCCTCGTT |
| BAM1-R | TGTTCGCGGCATTTGTTAGC |
| BAM2 | Solyc08g005780.2 | BAM2-F | TCCAGAAACTGATGACGCGT |
| BAM2-R | TTTGCAGTCTCAACCAGCCT |
| BAM3  | Solyc08g007130.2 | BAM3-F | CACACAGCGCGAATTGTTCA |
| BAM3-R | AGTCTGCTCTGCTTGTGCTT |
| BAM5  | Solyc07g052690.2.1  | BAM5-F | TGGTACAAAGATGCCAGCCA |
| BAM5-R | AAGCGCATTCTCACCTGCTA |
| BAM7  | Solyc01g094580.2 | BAM7-F | TCTGCTGAAAAACCTGCGGA |
| BAM7-R | TTTGCAGCAATGCATGTCCC |
| BAM9  | Solyc01g067660.2 | BAM9-F | AGAAGAACGTGTTGCCAGCA |
| BAM9-R | TGACTGCAACTTTCAGCTGC |
| AMY1  | Solyc03g095710.2 | AMY1-F | TGCTAACCTTTTGCTCCCAAAA |
| AMY1-R | AACAGAGTGAGATGATGGTGGT |
| AMY2  | Solyc04g082090.2 | AMY2-F | TCAATTGGATTGATGGCGCG |
| AMY2-R | TGATGTGAAGGGAAAGGCCA |
| AMY3  | Solyc05g007070.2 | AMY3-F | TGCGAAAAACTGGCGTCTTG |
| AMY3-R | TGTTTCCGCTGGATATGGCA |
| ISA3 | Solyc06g009220.2 | ISA3-F | ATAAAGGGCGATGCTGGCAT |
| ISA3-R | TTCATTTGCCGTGAACGCAG |
| LDA | Solyc11g008050.1 | LDA-F | TTTCGGAAAATGGTGCAGGC |
| LDA-R | ATGAAATGCTCACTGGCGGT |
| PHS1  | Solyc03g065340.2 | PHS1-F | TCGGACACCCAAACGTTCTT |
| PHS1-R  | TCACGAACACTTTGAGCGGT |
| PHS2  | Solyc09g031970.2 | PHS2-F | GGCGAGCTTTGACAAATGCA |
| PHS2-R | TTGGCCAGCCTTCGTGATAA |
| DPE1  | Solyc04g053120.2 | DPE1-F | TCTTGCTGGTTGCTCCCTTT |
| DPE1-R | AGAAGCCTCTTTGCTGCCTT |
| DPE2  | Solyc02g020980.2 | DPE2-F | ATGGGGCCGGTTTTCTGAAT |
| DPE2-R | ATCCCCAATTCTGGCCGTTT |
| MEX1 | Solyc04g064720.2 | MEX1-F | TCTAGCAGGAAATCAAGCTGCA |
| MEX1-R | TTACGGGATTGAGCAAGTGGAA |
| GLT1  | Solyc02g086160.2 | GLT1-F | TACGGTGTACATGGGATTTGCA |
| GLT1-R | TGATTCATGAAGCCGGTGTGTA |
| GPT1  | Solyc07g064270.2 | GPT1-F | GTTGTGGTCTTTCTGCGCTT |
| GPT1-R | TCCCTCAACAGCAATGGCAA |
| GTP2 | Solyc05g045670.2 | GPT2-F | CATGGTGGGCTTTGAATGTTGT |
| GPT2-R | TTTGACATGCTCACTGTTGCAG |
| PPT2 | Solyc02g086650.2 | PPT2-F | TACGGCCTCACAATTTGGCT |
| PPT2-R | CAAGAAACAGCGCGGAAAGA |
| TPT | Solyc10g008980.2 | TPT-F | AATGGAGTCTCGCGTGTTGA |
| TPT-R | TCCGACTGGTTTTGCCGTAA |
| SlDML1 | Solyc09g009080.2 | SlDML1-F | CACAGCAGAAACGAAGGAAGAAG |
| SlDML1-R | GGAGGGTCCTCAATCTTGTTTCT |
| SlDML2 | Solyc10g083630.1 | SlDML2-F | GGACTCTGTGGTTGGGGTATATC |
| SlDML2-R | GTTGCACACTCTTCAGGTTCTTC |
| SlDML3 | Solyc11g007580.1 | SlDML3-F | GAGAGACACAGCATACACAGACA |
| SlDML3-R | CTTGACGGGAACTTTGTTGAGTC |
| SlDML4 | Solyc03g123440.2 | SlDML4-F | TGACTTTGTCTCCACTAGTCACG |
| SlDML4-R | GGGGCACTCTTCAATATCATTGC |