**Supplemental Table 1. VirE2 differentially expressed genes tested using RT-qPCR**

|  |  |  |
| --- | --- | --- |
| **Gene Name** | **Gene\_ID** | **Encoded Protein** |
| *ADH1* | At1g77120 | Alcohol dehydrogenase 1 |
| *PRKP* | At1g51840 | Protein kinase-related protein |
| *lncRNA* | At3g25795 | Trans-acting siRNA 4 |
| *PR* | At4g33720 | Putative pathogenesis-related protein |
| *LSU1* | At3g49580 | Response to low sulfur 1 |
| *LRRPK* | At1g51830 | Putative leucine-rich repeat protein kinase |
| *AGP21* | At1g55330 | Arabinogalactan protein 21 |
| *NTR2.6* | At3g45060 | High affinity nitrate transporter 2.6 |

**Supplemental Table 2. Bacterial strains used in this study**

aAmp, ampicillin;Gent, gentamicin; Kan, kanamycin; Rif, rifampicin; Spec, spectinomycin

\*ABRC: Arabidopsis Biological Resource Center (www.arabidopsis.org)

|  |  |  |  |
| --- | --- | --- | --- |
| **Strain name** | **Description** | **Antibiotic resistancea** | **Reference** |
|  | ***E. coli* strains** |  |  |
| DH10B | F- [mcrA](http://ecoliwiki.net/colipedia/index.php/mcrA) Δ(*mrr*-*hsd*RMS-*mcr*BC) Φ80d*lac*ZΔM15 Δ*lac*X74 *end*A1 *rec*A1 *deo*R Δ(*ara*,*leu*)7697 *ara*D139 *gal*U *gal*K *nup*G *rps*L λ- | None | Durfee et al., 2008 |
| TOP10 | F- *mcrA* Δ( *mrr-hsd*RMS-*mcr*BC) Φ80*lac*ZΔM15 Δ *lac*X74 *rec*A1*ara*D139 Δ( *araleu*)7697 *gal*U *gal*K *rps*L (StrR) *end*A1 *nup*G | None | Invitrogen |
| Stable | F’ *proA+B+ laclq Δ(lacZ)M15 zzf::Tn10* (TetR) Δ(*ara-leu*) *7697 araD139 fhuA* Δ*lacX74 galK16 galE15 e14- Φ80dlacZ*Δ*M15 recA1 relA1 endA1 nupG rpsL* (StrR) *rph spoT1* Δ(*mrr-hsdRMS-mcrBC)* | None | New England Biolabs |
| E886 | pBluescript (pBS) II KS (+) in DH5α | Amp | Stratagene |
| E3542 | pSAT1-Venus-C | Amp | Lee et al., 2008 |
| E3561 | pSAT1-P35S-Venus-VirD2 | Amp | Lee et al., 2008 |
| E3759 | pSAT6-VirE2-Venus | Amp | Lee et al., 2008 |
| E4145 | pPZP-RCS2-Pocs-*hpt*II-RI | Spec | Lee et al., 2012;  This study |
| E4215 | T-DNA binary vector XVE- *hptII* | Spec | Lapham et al., 2018 |
| E4223 | T-DNA binary vector XVE-Pnos-mCherry-*ABD2*-*hptII* | Spec | This study |
| **Strain name** | **Description** | **Antibiotic resistancea** | **Reference** |
|  | ***E. coli* strains** |  |  |
| E4224 | pSAT1-Inducible Promoter (minimal 35S-LexA operator; pI) | Amp | Lapham et al., 2018; This study |
| E4229 | pSAT5-P35S-VirE2 | Amp | Lee et al., 2008 |
| E4276 | pSAT1-pI-VirE2 | Amp | This study |
| E4282 | pSAT1-pI-VirE2-Venus | Amp | This study |
| E4289 | T-DNA binary vector XVE-inducible VirE2 | Spec | This study |
| E4292 | T-DNA binary vector XVE-inducible VirE2-Venus- Pnos-mCherry-*ABD2*-*hptII* | Spec | This study |
| E4297 | pSAT1A-P35S-Multi-cloning Site (MCS)-T35S | Amp | Lee et al., 2008 |
| E4372 | pSAT5-P35S-mCherry-ABD2 | Amp | This study |
| E4373 | pSAT4-Pnos-Cerulean-VirD2NLS | Amp | Lee et al., 2008 |
| E4375 | pSAT4-Pnos-Cerulean-SV40NLS | Amp | Lee et al., 2008 |
| E4376 | T-DNA binary vector XVE-inducible VirE2-Venus- Pnos-mCherry-*ABD2*-*hptII*-Pnos-Cerulean-SV40NLS | Spec | This study |
| E4377 | T-DNA binary vector XVE-inducible VirE2-Venus-*hptII*-Pnos-Cerulean-SV40NLS | Spec | This study |
| E4380 | T-DNA binary vector XVE-inducible VirE2-Venus- P35S-mCherry-*ABD2*-*hptII*-Pnos-Cerulean-SV40NLS | Spec | This study |
| E4386 | T-DNA binary vector XVE-inducible VirE2-Venus- P35S-mCherry-*ABD2*-*hptII* | Spec | This study |
| E4389 | T-DNA binary vector XVE-inducible VirE2-Venus- P35S-mCherry-*ABD2*-*hptII*- Pnos-Cerulean-VirD2NLS | Spec | This study |
| E4433 | pSAT1-P35S-Venus-VirD2NLS | Amp | This study |
| E4434 | pSAT6-P35S-VirE2-Venus-VirD2NLS | Amp | This study |
| E4435 | T-DNA binary vector XVE-inducible VirE2-Venus-VirD2NLS- P35S-mCherry-*ABD2*-*hptII*- Pnos-Cerulean-VirD2NLS | Spec | This study |
| E4436 | pSAT1-pI-VirE2-Venus-VirD2NLS | Amp | This study |
| E4438 | T-DNA binary vector XVE-inducible VirE2-Venus-*hptII*- Pnos-Cerulean-VirD2NLS | Spec | This study |
| E4439 | T-DNA binary vector XVE-inducible VirE2-Venus-VirD2NLS-*hptII*- Pnos-Cerulean-VirD2NLS | Spec | This study |
| E4515 | pSAT1-P35S-MCS-T35S | Kan | Lee et al., 2008; This study |
| E4590 | *PIP2A*: DKLAT3G53420 cDNA clone from ABRC\* | Spec | This study |
| E4592 | *FLA9*: DKLAT1G03870 cDNA clone from ABRC\* | Spec | This study |
| **Strain name** | **Description** | **Antibiotic resistancea** | **Reference** |
|  | ***E. coli* strains** |  |  |
| E4594 | *PERX34*:DKLAT3G49120 cDNA clone from ABRC\* | Spec | This study |
| E4596 | *PIP1A*: DKLAT3G61430 cDNA clone from ABRC\* | Spec | This study |
| E4597 | *AGP31*: DKLAT1G28290 cDNA clone from ABRC\* | Spec | This study |
| E4601 | *HDA3*: DKLAT3G44750 cDNA clone from ABRC\* | Spec | This study |
| E4602 | *HD2C*: DKLAT5G03740 cDNA clone from ABRC\* | Spec | This study |
| E4603 | *ROC2*: DKLAT3G56070 cDNA clone from ABRC\* | Spec | This study |
| E4604 | *ROC3*: DKLAT2G16600 cDNA clone from ABRC\* | Spec | This study |
| E4612 | pSAT1A-P35S-*PIP2A*-T35S | Amp | This study |
| E4613 | pPZP-P35S-*PIP2A*-T35S- Pocs-*hptII*-RI | Spec | This study |
| E4617 | pSAT1A-P35S-*FLA9*-T35S | Amp | This study |
| E4618 | pPZP-P35S-*FLA9*-T35S- Pocs-*hptII*-RI | Spec | This study |
| E4622 | pSAT1A-P35S-*PERX34*-T35S | Amp | This study |
| E4623 | pPZP-P35S-*PERX34*-T35S- Pocs-*hptII*-RI | Spec | This study |
| E4624 | pSAT1A-P35S-*PIP1A*-T35S | Amp | This study |
| E4625 | pPZP-P35S-*PIP1A*-T35S- Pocs-*hptII*-RI | Spec | This study |
| E4626 | pBS-*AGP31* | Amp | This study |
| E4627 | pSAT1A- P35S-*AGP31*-T35S | Amp | This study |
| E4628 | pPZP-P35S-*AGP31*-T35S- Pocs-*hptII*-RI | Spec | This study |
| E4629 | pBS-*HDA3* | Amp | This study |
| E4630 | pSAT1- P35S*-HDA3*-T35S | Kan | This study |
| E4631 | pPZP-P35S-*HDA3*-T35S- Pocs-*hptII*-RI | Spec | This study |
| E4633 | pBS-*HD2C* | Amp | This study |
| E4634 | pSAT1A- P35S-*HD2C*-T35S | Amp | This study |
| E4635 | pPZP-P35S-*HD2C*-T35S- Pocs-*hptII*-RI | Spec | This study |
| E4637 | pBS-*ROC2* | Amp | This study |
| E4638 | pSAT1- P35S*-ROC2*-T35S | Kan | This study |
| E4639 | pPZP-P35S-*ROC2*-T35S- Pocs-*hptII*-RI | Spec | This study |
| E4640 | pBS-*ROC3* | Amp | This study |
| E4641 | pSAT1- P35S*-ROC3*-T35S | Kan | This study |
| E4642 | pPZP-P35S-*ROC3*-T35S- Pocs-*hptII*-RI | Spec | This study |

**Supplemental Table 2. Bacterial strains used in this study**

aAmp, ampicillin;Gent, gentamicin; Kan, kanamycin; Rif, rifampicin; Spec, spectinomycin

\*ABRC: Arabidopsis Biological Resource Center (www.arabidopsis.org)

|  |  |  |  |
| --- | --- | --- | --- |
| **Strain name** | **Description** | **Antibiotic resistancea** | **Reference** |
|  | ***Agrobacterium* strains** |  |  |
| A208 | Tumorigenic; pTiT37 in A136 | Rif | Sciaky et al., 1978 |
| EHA105 | Non-tumorigenic, disarmed pTiBO542 without Kan gene in A136 | Rif | Hood et al., 1993 |
| GV3101 | Non-tumorigenic, disarmed pTiC58 in C58 background | Rif, Gent | Koncz and Schell, 1986 |
| At2 | Non-tumorigenic; A136 | Rif | Sciaky et al., 1978 |
| At849 | pBISN1 in GV3101 | Rif, Gent, Kan | Narasimhulu et al., 1996 |
| At1529 | pBISN1 in EHA105 | Rif, Kan | This study |
| At1879 | pBISN2 in EHA105 with in-frame deletion of *virE2* | Rif, Kan, Spec | This study |
| At2091 | pE4289 in GV3101 | Rif, Gent, Spec | This study |
| At2155 | pE4438 in GV3101 | Rif, Gent, Spec | This study |
| At2156 | pE4439 in GV3101 | Rif, Gent, Spec | This study |
| At2256 | pE4613 in GV3101 | Rif, Gent, Spec | This study |
| At2257 | pE4618 in GV3101 | Rif, Gent, Spec | This study |
| At2259 | pE4623 in GV3101 | Rif, Gent, Spec | This study |
| At2260 | pE4625 in GV3101 | Rif, Gent, Spec | This study |
| At2264 | pE4628 in GV3101 | Rif, Gent, Spec | This study |
| At2265 | pE4631 in GV3101 | Rif, Gent, Spec | This study |
| At2266 | pE4642 in GV3101 | Rif, Gent, Spec | This study |
| At2267 | pE4635 in GV3101 | Rif, Gent, Spec | This study |
| At2268 | pE4639 in GV3101 | Rif, Gent, Spec | This study |

**Supplemental Table 3. Primer sequences used in this study**

|  |  |  |  |
| --- | --- | --- | --- |
| **Primer Name** | **Sequence (5’ to 3’)** | **Melting Temperature (oC)** | **Purpose** |
| VirE2 qPCR Fwd | CTTGGTGAAGCAGCTGACAAATACTC | 58 | RT-qPCR |
| Universal qPCR Rev | AGACTGGTGATTTTTGCGGACTCTAG | 58.6 | RT-qPCR |
| ADH1 (AT1G77120) qPCR Fwd | CGGGGTTGTGGAAAAGTACATGAAC | 58.2 | RT-qPCR |
| ADH1 (AT1G77120) qPCR Rev | GCTTCAAGCACCCATGGTGATG | 59 | RT-qPCR |
| PRKP (AT1G51840) qPCR Fwd | TGACCCGAACTTCGACCTTTACC | 58.8 | RT-qPCR |
| PRKP (AT1G51840) qPCR Rev | TCAATGAACCGCTTTGAGTAGCGTATAC | 58.6 | RT-qPCR |
| TAS4 (AT3G25795) qPCR Fwd | AAGTCACTCAAACACTGACGTGAACC | 59.1 | RT-qPCR |
| TAS4 (AT3G25795) qPCR Rev | CGTCCTTCACCACGGCAATTTCATG | 60.6 | RT-qPCR |
| PR  (AT4G33720) qPCR Fwd | CACTATACTCAGGTTGTGTGGAGAAACTC | 58.3 | RT-qPCR |
| PR  (AT4G33720) qPCR Rev | CCACTCGCCAACCCAGTTAC | 58.3 | RT-qPCR |
| LSU1  (AT3G49580) qPCR Fwd | GAGCTGGAGGTCGAGTCTTTAGAAC | 58.5 | RT-qPCR |
| LSU1  (AT3G49580) qPCR Rev | CTTATTCTACGAGGAAGAGACGACAGAAG | 57.7 | RT-qPCR |
| LRRPK (AT1G51830) qPCR Fwd | TCCTTCATCAGCTAGAAGACCGAACATG | 59.7 | RT-qPCR |
| LRRPK (AT1G51830) qPCR Rev | CCGAGCCAATGGGGTCACTTC | 60.6 | RT-qPCR |
|  |  |  |  |
| **Primer Name** | **Sequence (5’ to 3’)** | **Melting Temperature (oC)** | **Purpose** |
| AGP21 (AT1G55330)  Geno Fwd | AAAGATCTATGGAGGCAATGAAGATG | 55 | RT-qPCR |
| AGP21 (AT1G55330)  Geno Rev | TTCTTAAGTCAAAAGATGAAACCAGATGC | 56 | RT-qPCR |
| ATNTR2.6 (AT3G45060) qPCR Fwd | GAAGAGCATTACTATGGAGCGGAATGG | 59 | RT-qPCR |
| ATNTR2.6 (AT3G45060) qPCR Rev | CTTCACTAGACATGAGCCGGAGATC | 58.4 | RT-qPCR |
| Left Border Primer (SALK) | TGGTTCACGTAGTGGGCCATCG | 61.5 | T-DNA insertion line genotyping |
| 12965 lncRNA Geno Fwd (SALK\_086573) | AAGAGCTCCTAGCTATATATTCTGGAGACTC | 58 | T-DNA insertion line genotyping |
| 12965 lncRNA Geno Rev (SALK\_086573) | TTCCGCGGGATTAACTGTTAAAAGATTCAAAAAC | 59.6 | T-DNA insertion line genotyping |
| AtPSK3 LP (SALK\_044781) | ATGTGTTACGCAGTTTCGTCC | 55.6 | T-DNA insertion line genotyping |
| AtPSK3 RP (SALK\_044781) | AGCTTTGCTTCATGTTCTTGG | 53.9 | T-DNA insertion line genotyping |
| ACS6 Geno Fwd (SALK\_054467) | AAAGATCTATGGTGGCTTTTGCAACAG | 58 | T-DNA insertion line genotyping |
| ACS6 Geno Rev (SALK\_054467) | TTCTTAAGTTAAGTCTGTGCACGGACTAG | 57.9 | T-DNA insertion line genotyping |
| TST18 Geno Fwd (CS867285) | AAAGATCTATGTCTCAATCAATCTCCTCC | 56.1 | T-DNA insertion line genotyping |
| TST18 Geno Rev (CS867285) | TTCTTAAGTTAATTAGCAGATGGCTCCTC | 56.5 | T-DNA insertion line genotyping |
| PR5 LP (SALK\_055063C) | CATTTCATTAATGGCTCGCTC | 52.1 | T-DNA insertion line genotyping |
| PR5 RP (SALK\_055063C) | ATTGCTGTTATGGCCACAGAC | 55.7 | T-DNA insertion line genotyping |
| AGP14 LP (SALK\_096806) | TTTAGGAGTTGTGCCCATGTC | 55.1 | T-DNA insertion line genotyping |
| AGP14 RP (SALK\_096806) | CCTTAACGTGTCATAAATCAATTCC | 52.4 | T-DNA insertion line genotyping |
| *tasi4* LP (SALK\_066997) | CGAGGTTAAAATTCCGAAAGG | 51.7 | T-DNA insertion line genotyping |
| *tasi4* RP (SALK\_066997) | GTCCGCAATACGTAAAACTCG | 54 | T-DNA insertion line genotyping |
| **Primer Name** | **Sequence (5’ to 3’)** | **Melting Temperature (oC)** | **Purpose** |
| miR163 LP Geno (CS879797) | ACCCGGTGGATAAAATCGAGTTC | 57 | T-DNA insertion line genotyping |
| miR163 RP (CS879797) | TCAAGCGTCCAGACTTCAGATTG | 57 | T-DNA insertion line genotyping |
| SAMP LP (SALK\_209995C) | TGTTGCATTTGTGGACAAGAC | 54 | T-DNA insertion line genotyping |
| SAMP RP (SALK\_209995C) | TGGAGTGATCTCGTAACGGAC | 56.1 | T-DNA insertion line genotyping |
| TAS3 RP2 (N432182 GABI-Kat) | TGAGAAGAGAGCAAAGAAACTTC | 52.9 | T-DNA insertion line genotyping |
| TAS3 LP2 (N432182 GABI-Kat) | CATGTGGAAACAAACGTATGAAG | 52.6 | T-DNA insertion line genotyping |
| GABI-Kat T-DNA primer 8474 | ATAATAACGCTGCGGACATCTACATTTT | 56.9 | T-DNA insertion line genotyping |
| EXL1 Geno Fwd (SALK\_010243C) | TCTATTACATTCGCGGCAATATTCG | 55.4 | T-DNA insertion line genotyping |
| EXL1 Geno Rev (SALK\_010243C) | GCTATACGTGTAGGGCTCATAAGAC | 56.5 | T-DNA insertion line genotyping |
| MEE39 Geno Fwd (SALK\_065070C) | ATGAAGAATCTTTGTTGGGTTTTTCTGTC | 56.4 | T-DNA insertion line genotyping |
| MEE39 Geno Rev (SALK\_065070C) | GAACGATCATAAACATCTTTCGGGTAC | 55.8 | T-DNA insertion line genotyping |
| RBC3B Geno Fwd (SALK\_117835) | AAAGATCTATGGCTTCCTCTATGCTCTCCTCCGC | 64.3 | T-DNA insertion line genotyping |
| RBC3B Geno Rev (SALK\_117835) | TTGGTACCAAGAAATTAAGCTTCGGTGAAGCTTGGGG | 65 | T-DNA insertion line genotyping |
| ABAH3 Geno Fwd (SALK\_078170) | AAGAGCTCATGGATTTCTCCGGTTTG | 59.1 | T-DNA insertion line genotyping |
| ABAH3 Geno Rev (SALK\_078170) | TTGGTACCCTATGGTTTTCGTTCCAAGG | 60.4 | T-DNA insertion line genotyping |
| NRT2.6 LP (SALK\_204101C) | CACCAAAGAGAGCTCCACAAG | 55.7 | T-DNA insertion line genotyping |
| NRT2.6 RP (SALK\_204101C) | GGCTCTATTGGAACCTCCTTG | 55.2 | T-DNA insertion line genotyping |
| CUP LP (SALK\_201444C) | CATCGTCACCACAATCTTTCC | 53.9 | T-DNA insertion line genotyping |
| CUP RP (SALK\_201444C) | GGACAAAAGTTTGCATATGGC | 52.8 | T-DNA insertion line genotyping |
| ATNTR2.1 Geno Fwd (SALK\_035429C) | GTTGGTTGCACATCATCATGGGAATCTTG | 60.1 | T-DNA insertion line genotyping |
| **Primer Name** | **Sequence (5’ to 3’)** | **Melting Temperature (oC)** | **Purpose** |
| ATNTR2.1 qPCR Rev (SALK\_035429C) | GGCGTCCACCCTCTGACTTG | 60.4 | T-DNA insertion line genotyping |
| OEP6 Geno Fwd (CS862774) | AAAGATCTATGGTGGAGAAGTCAGGAG | 57.5 | T-DNA insertion line genotyping |
| OEP6 Geno Rev (CS862774) | TCCTTAAGATTCTCACTCACCATATTCAGG | 57.6 | T-DNA insertion line genotyping |
| ESM1 LP (SALK\_150833C) | TGAACGTCTGTGAAGTTCACG | 55.2 | T-DNA insertion line genotyping |
| ESM1 RP (SALK\_150833C) | TGCCGGTTTTGTATTCTTGTC | 53.6 | T-DNA insertion line genotyping |
| RLD17 LP (SALK\_115776C) | CAAGAGCTGAAAGCCTCAAAC | 54.3 | T-DNA insertion line genotyping |
| RLD17 RP (SALK\_115776C) | TTACCAGGATGAGATGATCGG | 53.7 | T-DNA insertion line genotyping |
| PP2C LP (SALK\_104445) | CACCAATCTTCATGGAGATCG | 58.7 | T-DNA insertion line genotyping |
| PP2C RP (SALK\_104445) | GATTAATTTCGGCCAATGCTC | 52.4 | T-DNA insertion line genotyping |
| ADH1 LP (SALK\_052699) | CGATGGGTACACCGATTACTG | 55.1 | T-DNA insertion line genotyping |
| ADH1 RP (SALK\_052699) | AAAGATCGGCAACACATGATC | 53.4 | T-DNA insertion line genotyping |
| PIP2A (AT3G53420) -OE-BglII-Fwd | AAAGATCTATGGCAAAGGATGTGG | 55.2 | Cloning of overexpression lines |
| PIP2A (AT3G53420) -OE-EcoRI-Rev | AAGAATTCTTAGACGTTGGCAGCAC | 57.7 | Cloning of overexpression lines |
| FLA9 (AT1G03870) -OE-EcoRI-Fwd | AAGAATTCATGGCTACCACTCGTC | 56.9 | Cloning of overexpression lines |
| FLA9 (AT1G03870) -OE-BamHI-Rev | AAGGATCCTCAAAAGAGAAATTTCAAACATAAGAC | 57.6 | Cloning of overexpression lines |
| PERCB/34 (AT3G49120) -OE-EcoRI-Fwd | AAGAATTCATGCATTTCTCTTCGTCTTC | 55.9 | Cloning of overexpression lines |
| PERCB/34 (AT3G49120) -OE-BamHI-Rev | AAGGATCCTCACATAGAGCTAACAAAGTC | 57.8 | Cloning of overexpression lines |
| PIP1A (AT3G61430) -OE-EcoRI-Fwd | AAGAATTCATGGAAGGCAAGGAAGAAG | 57.5 | Cloning of overexpression lines |
| **Primer Name** | **Sequence (5’ to 3’)** | **Melting Temperature (oC)** | **Purpose** |
| PIP1A (AT3G61430) -OE-BamHI-Rev | AAGGATCCTTAGCTTCTGGACTTGAAGG | 59.7 | Cloning of overexpression lines |
| AGP31 (AT1G28290) -OE-BglII-Fwd | AAAGATCTATGGGTTTCATTGGTAAGAG | 55 | Cloning of overexpression lines |
| AGP31 (AT1G28290) -OE-BamHI-Rev | AAGGATCCTCATTTGGGGCAAGAC | 59.3 | Cloning of overexpression lines |
| HDT1/HDA3 (AT3G44750) -OE-EcoRI-Fwd | AAGAATTCATGGAGTTCTGGGGAATTG | 57.3 | Cloning of overexpression lines |
| HDT1/HDA3 (AT3G44750) -OE-BamHI-Rev | AAGGATCCTCACTTGGCAGCAGC | 61.7 | Cloning of overexpression lines |
| HDT3/HD2C (AT5G03740) -OE-BglII-Fwd | AAAGATCTATGGAGTTCTGGGGTG | 56.2 | Cloning of overexpression lines |
| HDT3/HD2C (AT5G03740) -OE-BamHI-Rev | AAGGATCCTCAAGCAGCTGCACTG | 61.4 | Cloning of overexpression lines |
| ROC2 (AT3G56070) -OE-EcoRI-Fwd | AAGAATTCATGGCGAATCCTAAAGTC | 55.5 | Cloning of overexpression lines |
| ROC2 (AT3G56070) -OE-BamHI-Rev | AAGGATCCTTATGAACTTGGGTTCTTGAG | 58.3 | Cloning of overexpression lines |
| ROC3 (AT2G16600) -OE-EcoRI-Fwd | AAGAATTCATGGCAACAAACCCTAAAG | 56.4 | Cloning of overexpression lines |
| ROC3 (AT2G16600) -OE-BamHI-Rev | AAGGATCCCTAAGAAATCTGACCACAATCAG | 59.5 | Cloning of overexpression lines |