**Supplementary Table S1.** Details and primer sequences of the reference gene and target genes used in qRT-PCR.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Gene name | Cucumber genes ID | Gene annotation | Forward primer | Reverse primer |
| Defense-related genes | |  |  |  |
| *PLP2* | XM\_004152747.2 | PREDICTED: *Cucumis sativus* patatin-like protein 2 (LOC101220557), mRNA | AGTGTCGACGTTGGATGAGG | TCCGAAGTCTGGAAGATGCC |
| *RGA2* | XM\_011661129.1 | PREDICTED: *Cucumis sativus* disease resistance protein RGA2-like (LOC101213334), transcript variant X1, mRNA | CTGTACTTCGTGATGCAGAGC | CGTCTCCCAACTTTTCGAGC |
| *N* | XM\_011657984.1 | PREDICTED: *Cucumis sativus* TMV resistance protein N-like (LOC101204125), mRNA | TGCGTTGACAAAAGTTGGCG | GTCGATGCTAGCGGCTTCAA |
| *CHIT-1* | *CHIT-1* | Chitinase 1 | TGGTCACTGCAACCCTGACA | AGTGGCCTGGAATCCGACT |
| *β-1,3-Glucanase* | *β-1,3-Glucanase* | β-1,3-Glucanase | TCAATTATCAAAACTTGTTCGATGC | AACCGGTCTCGGATACAACAAC |
| *PR-1* | *PR-1* | Pathogenesis-related protein 1 | TGCTCAACAATATGCGAACC | TCATCCACCCACAACTGAAC |
| *PAL-1* | *PAL-1* | Phenylalanine ammonia-lyase 1 | ATGGAGGCAACTTCCAAGGA | CCATGGCAATCTCAGCACCT |
| *LOX-1* | *LOX-1* | Lectin-like, oxidised low-density lipoprotein receptor-1 | CTCTTGGGTGGTGGTGTTTC | TGGTGGGATTGAAGTTAGCC |
| *J1-2* | XM\_011656233.1 | PREDICTED: *Cucumis sativus* defensin J1-2-like (LOC105435412), mRNA | TCCAAGCCATCGCTTCAAGG | CGTGAAAGCCCTCCGTTTTG |
| *RGA1* | XM\_011661132.1 | PREDICTED: *Cucumis sativus* putative disease resistance protein RGA1 (LOC101212849), transcript variant X1, mRNA | AGGCATAGGTGGAGGAAGGA | GTCCATTCAAGATGGCACCC |
| *RGA3* | XM\_011652803.1 | PREDICTED: *Cucumis sativus* putative disease resistance protein RGA3 (LOC101215544), mRNA | TCAAGGAAAGAGCATCGGCA | TGGAATGCCTCCAAACTGCT |
| *TLP* | XM\_004147408.2 | PREDICTED: *Cucumis sativus* thaumatin-like protein (LOC101221868), mRNA | GGTTGGGGTAGTGGAGATGC | AAACCGATCCACATCACGCT |
| *ARF* | XM\_004135929.2 | PREDICTED: *Cucumis sativus* ADP-ribosylation factor (LOC101217563), mRNA | CCGGTGAAGGGCTGTATGAA | AGCAATCCCAGCTCGAAAGAA |
| *GST* | XM\_004134341.2 | PREDICTED: *Cucumis sativus* probable glutathione S-transferase (LOC101207387), mRNA | GAGTTCCCTCAGGTGTGTGG | CCATCATGGGGTTCCAGTCC |
| *RLK\_HSL1* | XM\_011660382.1 | PREDICTED: *Cucumis sativus* receptor-like protein kinase HSL1 (LOC101208240), mRNA | TGGGGAGTTGCCTTTACGAC | TCCCGTCAAGTGGTTCATGG |
| *ZAT10* | XM\_004141237.2 | PREDICTED: *Cucumis sativus* zinc finger protein ZAT10 (LOC101221218), mRNA | TCACTACGACGACCCAAACC | CCACGTGGACGCTTAGTTCT |
| *TD* | XM\_004143241.2 | PREDICTED: *Cucumis sativus* threonine dehydratase biosynthetic, chloroplastic (LOC101205445), mRNA | TCGCCGGTGTTGCTTCTTAT | TGCATCATATGGCTCCACCC |
| *TSB1* | XM\_004142510.2 | PREDICTED: *Cucumis sativus* tryptophan synthase beta chain 1 (LOC101220286), mRNA | GAAAGTACGTCCCCGAGACC | TGAAAGTCTTGGTCCCCAGC |
| *RLP12* | XM\_004153584.2 | PREDICTED: *Cucumis sativus* receptor-like protein 12 (LOC101213157), mRNA | TTGGGTGCGCCATCAAGTTA | ACATGGCCTTGTCCTTGGTC |
| *PARG1* | XM\_004138898.2 | PREDICTED: *Cucumis sativus* poly(ADP-ribose) glycohydrolase 1-like (LOC101210832), transcript variant X1, mRNA | CGAAATACCGACCAGCTTGC | GCCCCAATCAACTCCTGACT |
| *At3g47110* | XM\_004150177.2 | PREDICTED: *Cucumis sativus* putative receptor-like protein kinase At3g47110 (LOC101208746), mRNA | CTGCGTGGAGAAGAACCACA | GATCCAAAGCTCCCTCGACC |
| *At4g27190* | XM\_011650710.1 | PREDICTED: *Cucumis sativus* disease resistance protein At4g27190-like (LOC101219523), mRNA | TGCAACTGTTGGACAAGCCT | TACTGGGTTCGCCAGGAAAC |
| *At2g42960* | XM\_011650579.1 | PREDICTED: *Cucumis sativus* probable receptor-like protein kinase At2g42960 (LOC101217212), transcript variant X1, mRNA | GGGCCAAGTTGCTAGAATGC | AAGTGGTAGCAGGGAGGTGT |
| Signal-transduction-related genes | |  |  |  |
| *ATM* | XM\_011658620.1 | PREDICTED: *Cucumis sativus* serine/threonine-protein kinase ATM (LOC101208785), transcript variant X2, mRNA | CATGGACAGGGAAGAGGCTG | CCACAATGAAACACTCTCACGTC |
| *GSO1* | XM\_011653820.1 | PREDICTED: *Cucumis sativus* LRR receptor-like serine/threonine-protein kinase GSO1 (LOC101206116), mRNA | ATGGCACGGCGTAACTTGTA | ACCCCCAAGAGTTCCGTAGA |
| *NINJA6* | XM\_011651915.1 | PREDICTED: *Cucumis sativus* ninja-family protein 6-like (LOC101203065), mRNA | CCGCTTCTGCTGCAAAAAGT | CGAATGGTTTCCTTGCGTGG |
| *XLG1* | XM\_011659520.1 | PREDICTED: *Cucumis sativus* extra-large guanine nucleotide-binding protein 1 (LOC101221850), transcript variant X2, mRNA | CTCTCACCTAAACAGTGCGGT | AGCTTCAGCAATCTGGAAAATCC |
| *CDL1* | XM\_011659037.1 | PREDICTED: *Cucumis sativus* serine/threonine-protein kinase CDL1 (LOC101217131), transcript variant X2, mRNA | GCCACCGAACGCAATCCATA | TTAGCGGAGAGTGGCTCCT |
| *Myo6* | XM\_004140536.2 | PREDICTED: *Cucumis sativu*s myosin-6-like (LOC101208630), mRNA | CAAAAGGGAAGGAGGCGGAT | AGCTCCGCAGCAGTTCTAAG |
| *HSL1* | XM\_004148350.2 | PREDICTED: *Cucumis sativus* receptor-like protein kinase HSL1 (LOC101219431), mRNA | TCTCACAACCCTACTCCCTG | GCAAGATGGCCTGGTCTACA |
| *FBL3* | XM\_011658883.1 | PREDICTED: *Cucumis sativus* F-box/LRR-repeat protein 3-like (LOC101204734), transcript variant X3, mRNA | ACTTGAAGCAGATGTTGGTCT | GTCAAGCCAGCCAAATGCAA |
| *At3g51990* | XM\_004149682.2 | PREDICTED: *Cucumis sativus* serine/threonine-protein kinase-like protein At3g51990 (LOC101219273), mRNA | GTCTAACCGTGTCGGGTCTC | AGCATGCCAACTCTTCCACA |
| *ABA–PYR1* | XM\_004148430.2 | PREDICTED: *Cucumis sativus* abscisic acid receptor PYR1-like (LOC101218875), mRNA | TACGGAAGAGGATACGCGGT | CAGAATCAACGGCACGAACC |
| *ERS1* | XM\_011661069.1 | PREDICTED: *Cucumis sativus* ethylene response sensor 1 (LOC101205786), transcript variant X1, mRNA | CAATGGCCCCCTGATGAACT | GCTCCAACGGGATGGAGAAA |
| Growth-related genes | |  |  |  |
| *ARF6* | NM\_001305695.1 | *Cucumis sativus* auxin response factor 6 (LOC101210406), mRNA | GGATTTGTTGGGCTCTGGGT | TCGGAGACTTCATGCCACAG |
| *ACC* | XM\_004137238.2 | PREDICTED: *Cucumis sativus* 1-aminocyclopropane-1-carboxylate synthase 3-like (LOC101205326), mRNA | AGCGTTTGATCCCAACCACA | TAGAAGAAAGGCGTCGCCAG |
| *ABCG22* | XM\_004136488.2 | PREDICTED: *Cucumis sativus* ABC transporter G family member 22 (LOC101213089), mRNA | GTGGAGGCTTACGAGACGAG | CGTCTAGCGTCAGAGGTGTC |
| *AUX22B* | XM\_004150386.2 | PREDICTED: *Cucumis sativus* auxin-induced protein 22B-like (LOC101204324), mRNA | GAAATCTGGTCCGTCGGGAG | GTACTCCGGCGACAGTCATT |
| *PIN3* | NM\_001280786.1 | *Cucumis sativus* auxin efflux carrier component 3-like (CSPIN6), mRNA | AGAGAACTCTGCCGTTCAGC | AGACGAGGGCACAGTTTGAG |
| *AUX15A* | XM\_011659739.1 | PREDICTED: *Cucumis sativus* auxin-induced protein 15A (LOC101204027), transcript variant X2, mRNA | ACAAGTCTTTACTTGCGCGG | GAGCCCGACCCATTCAGATT |
| *PP2C* | XM\_004150268.2 | PREDICTED: *Cucumis sativus* probable protein phosphatase 2C 51 (LOC101214188), mRNA | CGGCGTCTCAGAGTTCGTAA | GTTGCGCTCAGTTTCCTGTG |
| *SPDS* | XM\_004150264.2 | PREDICTED: *Cucumis sativus* spermine synthase-like (LOC101212743), mRNA | GATCCTGTTGGTCCTGCACA | GGTCGTAGTGCTTGGGCTAT |
| *EG6* | XM\_004143821.2 | PREDICTED: *Cucumis sativus* endoglucanase 6-like (LOC101209379), mRNA | GCGACTCCAAATTCATCGCC | GAGGGTGTTGGGATCACTGG |
| *DHX16* | XM\_011662026.1 | PREDICTED: *Cucumis sativus* putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX16 (LOC101206270), mRNA | TTGGTGAAACTGGCTCTGGG | TCGCTTTGTGTACCCAGCTT |
| *LOX2* | XM\_004142190.2 | PREDICTED: *Cucumis sativus* lipoxygenase 2, chloroplastic-like (LOC101215837), mRNA | ACCTGCAGCTGCCATTAATTC | ATAGGACTCTGGTGGTGGGA |
| *ATHB-12* | XM\_004133744.2 | PREDICTED: *Cucumis sativus* homeobox-leucine zipper protein ATHB-12 (LOC101204509), mRNA | GGAAATACCGCCTGCAAAGG | TTCCAAACTGCACCCTGTCT |
| *ACO3* | NM\_001305743.1 | *Cucumis sativus* 1-aminocyclopropane-1-carboxylate oxidase 3 (LOC101204103), mRNA | AAAGTGCATGGAGCAGAGGT | GTGCTTTCCCAATCAGTGTCG |
| *ACA12* | XM\_004146914.2 | PREDICTED: *Cucumis sativus* calcium-transporting ATPase 12, plasma membrane-type (LOC101220140), mRNA | TTGCAGCTTCTCTCGGAACA | CGCCGTTCATTCACGACATC |
| *PUB18* | XM\_004152502.2 | PREDICTED: *Cucumis sativus* U-box domain-containing protein 19-like (LOC101221889), mRNA | ATTCCTGACGCCATAGCAGG | GCCCGAAGATGGCAACTACT |
| Binding and transport- related genes | |  |  |  |
| *ALB3L2* | XM\_004138848.2 | PREDICTED: *Cucumis sativus* ALBINO3-like protein 2, chloroplastic (LOC101218993), mRNA | TTGGCGATCTTGTCAGCAGT | GGCAAGTCGGCCTTGTTTTT |
| *ECA3* | XM\_011651259.1 | PREDICTED: *Cucumis sativus* calcium-transporting ATPase 3, endoplasmic reticulum-type (LOC101211345), mRNA | ACGAAGATGGTTCCACGACC | AGCCAGGCACCTAAGCATTT |
| *SPB1* | XM\_011650931.1 | PREDICTED: *Cucumis sativus* adoMet-dependent rRNA methyltransferase spb1 (LOC101209556), mRNA | ACCTAAAACCCTACAGCGCC | TGCTCTTTGGCAAGGCGATA |
| *MSH7* | XM\_004139382.2 | PREDICTED: *Cucumis sativus* DNA mismatch repair protein MSH7 (LOC101210755), mRNA | ACTGATGGCGCAATCTGACA | ATCTGCCCAAGCAACCTCTC |
| *ZC3H15* | XM\_004149550.2 | PREDICTED: *Cucumis sativus* zinc finger CCCH domain-containing protein 30-like (LOC101205376), mRNA | GGCGTGGGGATATGTGTGAA | CCATCCTTGCACAGACGAGT |
| *SLY1* | XM\_004140356.2 | PREDICTED: *Cucumis sativus* SEC1 family transport protein SLY1-like (LOC101220905), mRNA | GATGGCTTTGAACCTTCGCC | CCCGGCCGAAGTTGAGTTTA |
| Secondary-metabolism-related genes | |  |  |  |
| *SCPL20* | XM\_004148893.2 | PREDICTED: *Cucumis sativus* serine carboxypeptidase-like 20 (LOC101217226), mRNA | CCCTGGTTTCTCCGGTTCTC | CCTGCCGTGCTCCTTATTGA |
| *DYW9* | XM\_004152804.2 | PREDICTED: *Cucumis sativus* pentatricopeptide repeat-containing protein At4g30700 (LOC101215078), mRNA | GGATTCCACCGACAGGTGTT | CCTCACTCACCAAGCCAGAG |
| *rglB* | XM\_004143494.2 | PREDICTED: *Cucumis sativus* rhamnogalacturonate lyase B (LOC101206696), mRNA | AACACAACACAAAAAGCTTCGC | GCCATGGCAAGAGCTAAACC |
| *CHS2* | XM\_004145659.2 | PREDICTED: *Cucumis sativus* chalcone synthase 2 (LOC101205211), mRNA | GGTGGAGGCGAAACTAGGTC | CACGCGCTTGACATGTTACC |
| Transcriptional-factor-related genes | |  |  |  |
| *PRE3* | XM\_004152390.2 | PREDICTED: *Cucumis sativus* transcription factor PRE3 (LOC101213955), mRNA | ATTGCAGCAACTCCTGCCTG | TTGCAAGACCTTTGCTGCTG |
| *CAMTA1* | XM\_011658969.1 | PREDICTED: *Cucumis sativus* calmodulin-binding transcription activator 5 (LOC101211298), transcript variant X2, mRNA | GCCGGTGTTATTGGCTCCTA | ACGATGTGGATGGAAAATTCTCTTG |
| *MYB48* | XM\_004148168.2 | PREDICTED: *Cucumis sativus* transcription factor MYB48 (LOC101211775), transcript variant X1, mRNA | TGCAAAAGTTTCAGGATTGAATAGA | TCCCCATTTGGCGTGAAGTT |
| *MYB86* | XM\_011656422.1 | PREDICTED: *Cucumis sativus* transcription factor MYB86 (LOC105435439), mRNA | CTCGGACACTACTTGGCACA | CCCCATTTGAGGGCTAAGCA |
| *MYB24* | XM\_004147144.2 | PREDICTED: *Cucumis sativus* transcription factor MYB24-like (LOC101215779), mRNA | GCCAGACCTAAAGAGAGGGC | TACCCCATCTCGCATGAAGC |
| *MYB308* | XM\_004143899.2 | PREDICTED: *Cucumis sativus* myb-related protein 308-like (LOC101207994), mRNA | AGGCAACATAACAGCTGACGA | CGTTATCAGTTCGACCGGGG |
| *HSP15.4* | XM\_004145058.2 | PREDICTED: *Cucumis sativus* 15.4 kDa class V heat shock protein (LOC101212573), mRNA | ACTCTCATCTTTTCTCCGCCG | ACCGCGAATCTTCAACCTCC |
| *ATHB-40* | XM\_004143452.2 | PREDICTED: *Cucumis sativus* homeobox-leucine zipper protein ATHB-40 (LOC101216890), mRNA | CGGACGCCGACAACTCATTA | TCCCTCTCCCGTACCTTGTT |
| *HSFB2B* | XM\_004143882.2 | PREDICTED: *Cucumis sativus* heat stress transcription factor B-2b (LOC101203886), mRNA | AGATCTGGGAGAAGAGGCGA | CTGAGAATCTCCCGTTCCCG |
| *TINY* | XM\_004150241.2 | PREDICTED: *Cucumis sativus* ethylene-responsive transcription factor TINY-like (LOC101206242), mRNA | GGGGGAAATGGGTATCGGAA | TCGAGCAGCCATTTCAGGAC |
| Cell-death-related genes | |  |  |  |
| *AIFM2* | XM\_004134996.2 | PREDICTED: *Cucumis sativus* apoptosis-inducing factor 2-like (LOC101207218), mRNA | GGCCCTACTGGTGTTGAACT | TCTCGGCCCTCGGTGTATTA |
| *GCN1* | XM\_004152761.2 | PREDICTED: *Cucumis sativus* translational activator GCN1 (LOC101204332), mRNA | ATTCACTGGAGCATTGGCGA | CAGCACGTTGAACAGCTTCC |
| *lvsC* | XM\_011654285.1 | PREDICTED: *Cucumis sativus* BEACH domain-containing protein lvsC (LOC101204034), transcript variant X4, mRNA | TCCCAAACAGAAACAGAATCAGTC | CCAGACTCTGTGGAACAGCA |
| Oxidoreductase-related genes | |  |  |  |
| *LAC11* | XM\_004146508.2 | PREDICTED: *Cucumis sativus* laccase-11-like (LOC101218482), mRNA | GAAGTCCACACAGGATGGGG | GGAAGATCCTTTGGGGGTGG |
| *AOP1* | XM\_004152214.2 | PREDICTED: *Cucumis sativus* probable 2-oxoglutarate-dependent dioxygenase AOP1 (LOC101209158), mRNA | ACACTCTCCCCACCAAACAC | CCCACTTAGGACCCCCTGAT |
| *POX39* | XM\_004151830.2 | PREDICTED: *Cucumis sativus* peroxidase 39-like (LOC101213629), mRNA | GAATGCCCTGGAGTGGTCTC | AGTAAGGACCTCCTGTGGCT |
| *PER4* | XM\_004149318.2 | PREDICTED: *Cucumis sativus* peroxidase 4-like (LOC101204245), mRNA | TCATGTTTACCGGCAGCTCT | ACCGTGTTAAGGAGCTTGGG |
| *TKT2* | XM\_004134220.2 | PREDICTED: *Cucumis sativus* probable 1-deoxy-d-xylulose-5-phosphate synthase 2, chloroplastic (LOC101218190), mRNA | TGTTGGAGCTCTCAGCAGTG | GATGGTCTTTGCAGCTTCGC |
| Cell wall modification-related genes | |  |  |  |
| *EXT2* | XM\_011656029.1 | PREDICTED: *Cucumis sativus* extensin-2-like (LOC101208428), mRNA | CGCCAAGCTAAGGGTCAAGT | GGGAGGTGGGTAGTAAGGCT |
| *FH20* | XM\_011662036.1 | PREDICTED: *Cucumis sativus* formin-like protein 20 (LOC101215105), mRNA | TCCTTCATTGGCAGCGACTT | TTGGATGCACTTCGGTCACA |
| *PE* | XM\_004134704.2 | PREDICTED: *Cucumis sativus* pectinesterase (LOC101216377), mRNA | GTCGGAGCAGATCAATCGGT | TGGCGGTTGGAATGTGTGTA |
| Reference gene | |  |  |  |
| *EF 1-α* |  | Elongation factor 1-α | ACTGTGCTGTCCTCATTATTG | AGGGTGAAAGCAAGAAGAGC |