

Table 1 Suppl. Primers used in real time quantitative reverse transcription PCR analysis.

| Gene_ID   | Sense primers            | Anti-sense primers       |
|-----------|--------------------------|--------------------------|
| Bra017544 | TGGCTTCTTCTTATTCTTCATC   | TCTTGCGGACATCTTCTC       |
| Bra025290 | TAAGTGTTCAACAAGTCAAG     | GTTCCGAAGCATAATAAGC      |
| Bra010588 | ACTGAATCTCGCTTATTG       | CTCTTGAATGTCTGTTGA       |
| Bra022850 | AATCTCTACAGGCTAAGTAA     | TCTCTACAGGATAGTTCAC      |
| Bra027866 | GTTATGCTTCCTCTACCTA      | ACTCCAATGCTGTTATCT       |
| Bra015597 | TTGTTGGAGGAAGTTATC       | AGTTCTTGATTCTTGGTAT      |
| Bra010496 | GTTCTTGATGATGTGGAT       | CCTTGTGAATATGGTTGA       |
| Bra018810 | AGGAAACAGAAGAGAAGAAATCAT | CTACCTCGTCCACAGAT        |
| Bra035126 | GAGGTTGGAGATAACATAG      | AGGTAACAGAGTCTTGAT       |
| Bra009882 | TATTCCTAACACGCCTCTC      | GCCAACTACTTCAATTACGATT   |
| Bra012116 | CTAAAGTGGCAGAAAGAAAA     | ATTGACATTGACGGTAGC       |
| Bra001175 | AACGTCTCTGATTCTAT        | GAGTCATCTGGTAGTCA        |
| Bra000497 | GATGTGAAGGAAGGTCAT       | TTAGTGGGACAACAAATCT      |
| Bra000682 | GGCTCACCTAATAAGAT        | ATGAGAAGTCAGGAACAT       |
| Bra016606 | CCTTACATGCTTAGTTCCAA     | TCGTGAAGTTCGTTGATG       |
| Bra017680 | :CCATCATCAACAACAAC       | CTCTTCTTCTCCAATCCT       |
| Bra023406 | CGAGCAAGAATGTAGTAA       | ATCTATATTGACACCTATGG     |
| Bra001473 | AGTACGGTTACGAACAGAA      | GAAGCGACTCCATGATTC       |
| Bra001634 | TACAATACGAACATAGAGACAAGA | TGGAAGGAGAGGAATGGT       |
| Bra032503 | GGAAGGATTCTAACGGCTAA     | ATGGTGAGAGGAGGAAGA       |
| Bra035185 | ATGTTTCAGGGTGTAGTAA      | CCTCGTAAGTTGCCATAA       |
| Bra023406 | CGAGCAAGAATGTAGTAA       | ATCTATATTGACACCTATGG     |
| Bra032876 | CGATGATGATGATGATGCT      | ACCTGTGAATGTAGTAATGAC    |
| Bra013950 | ATGGAGATACAGGAGATTG      | GATGTGGAAGAAGAGGAA       |
| Bra013416 | ACTGCTTACTCGTATGGAA      | ACCTCTGAACAAGATGGAA      |
| Bra025093 | GCATCTATTCTCCAAGTG       | GAACATTCTCAACAAGTG       |
| Bra000910 | AGGATTTCTCTCACTGTAT      | CATTCTCTTCTCTTGCTC       |
| Bra032601 | TAGTGCCATTAAGACCAT       | TTCTTGCTTCTTGATACG       |
| Bra019131 | GAACGATATGGTTACACTAAT    | GGTCATTAAGCCTATCCT       |
| Bra024267 | GTCGTAGTTATACCTTAC       | ATCTATTGCCATAATACC       |
| Bra032477 | TTCTTCTGAGCGTTATTG       | ACATACTGAACGTGTGGTA      |
| Bra033040 | TAACCACCGACTTCTACT       | ATTTGTTTGCTGGAGATTG      |
| Bra037877 | GCGTTCCTCTTCATCTTCT      | CTTAGTTGAGCGTGAGACA      |
| Bra014550 | AGCGTCATTCACTTAACAG      | CGTCACCAACCAACATAA       |
| Bra019179 | AGGAATCTAGTGATGATACAG    | TTGCGTAAGAAGACAGAG       |
| Bra028617 | TTACAAGACGGTTCAAGA       | TACACTCCTTCGCTAATC       |
| Bra039694 | ATAATGAAAGACATCGGAATC    | TTGGTAGTAGACGGAGAA       |
| Bra001652 | CTGAGCGACAAGGTAGAT       | AGCCAAGAAGTTCATCA        |
| Bra002257 | CGTTCGTGTCGTCATCAA       | TTATCTGCTCCTTCTCCTTCTA   |
| Bra016362 | ATACGAGAGGATTGATGA       | GCCTTAGACATAAGCATT       |
| Bra011925 | GGAACCATTACAATAGTC       | TAGGAGAAGAACAATCAT       |
| Bra007947 | TATCATCGTCTGGAAC         | GAGATCACCTTCTATAACC      |
| Bra026176 | ACTCTCACGGCACCATT        | CATCTCTATCATCTCCTTGAACAT |
| Bra015870 | TTCTCCAGTGCTCTCATT       | GCTGTTCTGTAAAGTGAAGA     |
| Bra033975 | TGATGATGCTGTAAAGAC       | GTAATGAAGGATGCTAAGA      |
| Bra000310 | TTCGGTCTTCCATATCAA       | TGTCGCAATAGTCTTCAG       |
| Bra027940 | ATCGGTCAGTAGCATTGT       | AAGAGTCGTGAGTGTAGAAT     |
| Bra036701 | GCTGGTCTCTTCATTATTC      | CTTGCTCTCTTCACTCATC      |
| Bra007071 | CCTTGATAGTAATCATTCTA     | CAATAGTCTGAAGTGTTA       |
| Bra015390 | AATCCTTGATACTCCTAAGAT    | ATTGCCATGAAGTGAGAA       |
| Bra038095 | GTTTCGTAGCCATTACTTCGTA   | AACAGGAGCACCGTCTAT       |
| Bra040814 | TTGTGGAAGAGTTGGTTA       | GCCTTATGTGTAGATGGT       |
| Bra040685 | CAGTAACGAATGAGAACA       | AAGCAGGAGATATAAGGT       |
| Bra009196 | CACCGATGATGATGTAATC      | TTAGCCTGTCCTATGTTT       |
| Bra021105 | GGTTCCTCTCCATTATCAA      | CATCCTCCATCTCATAGC       |
| Bra035819 | TGAATGGGTACCAAGGAAAT     | TCTTAGTCGGAGGAGCAG       |
| Bra039295 | ATTACAAGGTGGATACAA       | CGAAGATTCATCAACATT       |

| Gene_ID   | Sense primers            | Anti-sense primers       |
|-----------|--------------------------|--------------------------|
| Bra000407 | AGTCCTACATCTGGCTTA       | CATACAACCTCTTGACATATC    |
| Bra012213 | GCACATTCTCTGAACATC       | TTCTTCCGCATCTGTATA       |
| Bra026084 | GGACTATACCTTCTGAACCTTGAC | TTCCAGTAAGATTGTTGTTGTAGA |
| Bra015047 | GGCTCCTCTTAATCCTGA       | TGTCCTTCTGAACCTCTT       |
| Bra024699 | ATGTCTGGTGGTAAAGGA       | GGTCATGTTGCCATACTC       |
| Bra018725 | CACAGACTACCATTGAGATTG    | CGAACCTAGCACGAGTAA       |
| Bra001457 | GAAGAACAAGATTACCAT       | CTCATATTATACGCATAGT      |
| Bra035909 | ACCACTATTGAGATTGACT      | GCTCCATACACTTCCTAA       |
| Bra009415 | GTATTCAATGTTCCCTCAGA     | ACCTTATCAGCCATAGTT       |
| Bra002966 | ATCCATACCGAAGACAAG       | GCTTAAGAACCTCCAGAA       |
| Bra003079 | ATAAGAGGATGAAGACAGA      | GGATTACAAGGAGGAGTA       |
| Bra003501 | GACATCAACAACGCTTAT       | GACCTTCTTCACCATACT       |
| bra024651 | ATAAGAAGGATGTTAGTG       | GAATCAATCTCAATAGTC       |
| bra002354 | CCTAAGCAAGAAGATGAA       | TGTATGAAGCAATGAGTT       |
| bra021868 | CCTAAGCAAGAAGATGAA       | TGTATGAAGCAATGAGTT       |
| bra019877 | GGTGGAAGAAGACAAGAA       | CTGTTACTAATGCTGTACTC     |
| bra037014 | GGTCTCCATATTCTCAAT       | TATTAGCAATCCAAGTCA       |
| bra016611 | ACAACCACAGATGAAGAGAAG    | GCAATTAAGCACCAGTATAACC   |
| bra030878 | AAGCACGATCACAATTCT       | CCACTTCCTCCGACTATA       |
| bra002898 | CAAGGACTGAGATACTAC       | GAACTATTGATGTGATGAG      |
| Bra001996 | CCAATCACACTTCTCAAC       | CTTCGTTACATCCTCCTT       |
| Bra015796 | CGATTGATTACATTGAGTT      | ATTCCATACTGTGTCATC       |
| Bra017696 | TACAACCTGGTCATCAAGGA     | CAAACAAAGTCACGAGGT       |
| Bra000881 | GACAAGTGTTACATTATCTCA    | TTCCAACCTCATCATCTC       |

Table 2 Suppl. Comparison of the methylation ratio in different gene elements in plants infected by *Turnip mosaic virus* (*TuMV*) and in control (CK) plants. UTR - untranslated region, CDS - coding sequence, CGI - cytosine-phosphate-avidin island).

| Plants      | Upstream 2k        | Five-UTR | CDS                | Intron              | Intergenic          | CGIs               | Repeats            | Three-UTR |
|-------------|--------------------|----------|--------------------|---------------------|---------------------|--------------------|--------------------|-----------|
| <i>TuMV</i> | 7.377<br>(62.32 %) | 0        | 4.090<br>(91.35 %) | 21.544<br>(11.85 %) | 12.826<br>(74.54 %) | 3.871<br>(33.79 %) | 13.285<br>(2.66 %) | 0         |
| CK          | 4.889<br>(53.89 %) | 0        | 3.219<br>(92.52 %) | 16.723<br>(8.23 %)  | 10.119<br>(79.88 %) | 3.814<br>(41.32 %) | 7.870<br>(3.10 %)  | 0         |

Table 3 Suppl. The detailed information of resistance genes of *Brassica rapa* associated with plant pathogen interaction, salicylic acid, auxin signaling, and cell wall biosynthesis pathways.

| <i>B. rapa</i> gene ID | Chromosome position   | Gene definition                                              | Log2 (fold change) | <i>A. thaliana</i> ID |
|------------------------|-----------------------|--------------------------------------------------------------|--------------------|-----------------------|
| Bra017544              | A09:12891490-12896998 | "disease resistance protein (TIR-NBS-LRR class), putative"   | 0.986143112        | AT5G46470             |
| Bra025290              | A06:21287841-21295738 | "disease resistance protein (CC-NBS-LRR class), putative"    | 1.023781459        | AT5G66900             |
| Bra010588              | A08:14567383-14576139 | "disease resistance protein (TIR-NBS-LRR class), putative"   | 0.955346426        | AT2G14080             |
| Bra022850              | A03:7403727-7407409   | "disease resistance protein (TIR-NBS-LRR class), putative"   | 0.980950673        | AT5G18360             |
| Bra027866              | A09:9803317-9806303   | "disease resistance protein (CC-NBS-LRR class), putative"    | 0.944565137        | AT1G58410             |
| Bra015597              | A10:274524- 277168    | "disease resistance protein (CC-NBS-LRR class), putative"    | 1.033370336        | AT1G12280             |
| Bra010496              | A08:14044537-14048704 | "disease resistance protein (TIR-NBS-LRR class), putative"   | 0.980950673        | AT5G11250             |
| Bra018810              | A06:1827511-1829099   | "disease resistance protein (CC-NBS-LRR class), putative"    | -0.01537768        | AT5G43730             |
| Bra035126              | A07:25571050-25577376 | "disease resistance protein (TIR-NBS-LRR class), putative"   | -2.003479639       | AT5G17680             |
| Bra009882              | A06:18463567-18466415 | "disease resistance protein (CC-NBS-LRR class), putative"    | -2.017604826       | AT5G66900             |
| Bra012116              | A07:12146015-12150753 | "disease resistance protein (CC-NBS-LRR class), putative"    | -5.014806445       | AT5G66900             |
| Bra001175              | A03:15145899-15152027 | "nucleotide binding (NBS)"                                   | -1.063965479       | AT5G46270             |
| Bra000497              | A03:11443867-11444241 | auxin-responsive family protein                              | 0.000547523        | AT2G28085             |
| Bra000682              | A03:12451397-12451693 | auxin-responsive family protein                              | 0.945164681        | AT4G09530             |
| Bra016606              | A08:18490276-18490668 | auxin-responsive family protein                              | -1.031861307       | AT1G17345             |
| Bra017680              | A03:29781844-29786584 | auxin-responsive protein-related                             | -4.015600518       | AT4G34800             |
| Bra023406              | A02:2222157-2225853   | auxin-responsive GH3 family protein                          | -2.163508412       | AT5G13370             |
| Bra001473              | A03:16542902-16543282 | auxin-responsive family protein                              | -2.000605586       | AT3G12830             |
| Bra001634              | A03:17624668-17625966 | IAA26;                                                       | -0.033802986       | AT3G16500             |
| Bra032503              | A09:38106250-38108609 | IAA12;                                                       | -0.991221429       | AT1G04550             |
| Bra035185              | A07:25784617-25785520 | IAA15;                                                       | -2.365005253       | AT1G80390             |
| Bra023406              | A02:2222157-2225853   | auxin-responsive GH3 family protein                          | -2.002650263       | AT5G13370             |
| Bra032876              | A09:23374708-23377191 | auxin-responsive GH4 family protein                          | -1.154613227       | AT5G28130             |
| Bra013950              | A01:8661965-8664290   | NPR1 (NONEXPRESSER OF PR GENES 1)                            | 3.008738518        | AT1G64280             |
| Bra013416              | A01:5522324-5524313   | NPR4; NPR4 (NPR1-like protein 4)                             | 2.542866707        | AT4G19660             |
| Bra025093              | A06:24050595-24052584 | NPR3; NPR3 (NPR1-LIKE PROTEIN 3)                             | 3.053313255        | AT5G45110             |
| Bra000910              | A03:13883840-13884256 | systemic acquired resistance (SAR) regulator protein NIMIN-1 | 1.970089912        | AT4G01895             |
| Bra037235              | A09:5466769-5467275   | bZIP transcription factor                                    | 1.003721493        | AT2G18160             |
| Bra039631              | A07:1595491-1595997   | bZIP transcription factor                                    | 1.00115616         | AT2G18160             |
| Bra032601              | A09:38554377-38554820 | NIMIN1 (NIM1-INTERACTING 1)                                  | 0.984203339        | AT1G02450             |
| Bra019131              | A03:26200714-26201834 | "peroxidase, putative"                                       | 2.149874687        | AT4G26010             |
| Bra024267              | A06:15241117-15244088 | "peroxidase, putative"                                       | 1.007061958        | AT5G64100             |
| Bra032477              | A09:37999362-38000789 | "peroxidase, putative"                                       | 2.025197983        | AT1G05250             |
| Bra033040              | A02:22351170-22352129 | "peroxidase, putative"                                       | 1.029975256        | AT3G28200             |
| Bra037877              | A09:15213631-15217321 | "peroxidase, putative"                                       | -1.989557902       | AT4G08780             |
| Bra014550              | A04:1394980-1396856   | pectinesterase family protein                                | -2.004504204       | AT3G59010             |
| Bra019179              | A03:25874905-25875510 | pectin methylesterase inhibitor family protein               | -5.966116864       | AT4G25260             |
| Bra028617              | A02:1453080-1455117   | pectinesterase family protein                                | -1.034146118       | AT5G09760             |
| Bra039694              | A06:508113-510504     | pectinesterase                                               | -4.952253331       | AT1G53840             |
| Bra001652              | A03:17714000-17715425 | pectinesterase family protein                                | -1.077742006       | AT3G17060             |
| Bra002257              | A10:10694075-10696798 | pectinesterase family protein                                | 0.020740509        | AT5G19730             |
| Bra016362              | A08:17277412-17277978 | pathogenesis-related protein                                 | 0.992342949        | AT1G70830             |
| Bra011925              | A07:13515145-13515900 | pathogenesis-related protein                                 | 2.959347725        | AT2G28790             |
| Bra007947              | A02:11049287-11050153 | pathogenesis-related protein                                 | 1.01677227         | AT1G70830             |
| Bra026176              | A06:5460739-5461381   | pathogenesis-related protein                                 | 2.788121605        | AT1G14960             |

| <i>B. rapa</i> gene ID | Chromosome position        | Gene definition                        | Log2 (fold change) | <i>A. thaliana</i> ID |
|------------------------|----------------------------|----------------------------------------|--------------------|-----------------------|
| Bra015870              | A07:23708862-23709708      | pathogenesis-related protein           | 2.015968641        | AT1G75050             |
| Bra033975              | A02:9508222-9516892        | "chitinase, putative"                  | 3.040729094        | AT1G67830             |
| Bra000310              | A03:10496406-10497525      | "chitinase, putative"                  | 1.971698761        | AT2G43570             |
| Bra027940              | A09:10434162-10435251      | "chitinase, putative"                  | 2.991422653        | AT2G43590             |
| Bra036701              | A09:5955829-5958544        | "chitinase, putative"                  | 1.976282005        | AT3G54420             |
| Bra007071              | A09:28668359-28669267      | "chitinase, putative"                  | -0.977218628       | AT1G14400             |
| Bra015390              | A10:1643145-1644134        | biquitin-protein ligase                | -0.008664131       | AT1G14400             |
| Bra038095              | A05:10684563-10686230      | ubiquitin-conjugating enzyme 26        | -2.003501893       | AT1G53020             |
| Bra040814              | A04:4017513-4022269        | ubiquitin-protein ligase               | 1.879873836        | AT1G53020             |
| Bra040685              | Scaffold000267:27674-30201 | ubiquitin-conjugating enzyme 26        | -3.949318876       | AT5G06460             |
| Bra009196              | A10:14872314-14875847      | ubiquitin activating enzyme            | 1.021998405        | AT3G15355             |
| Bra021105              | A01:23127661-23130248      | ubiquitin-conjugating enzyme 25        | -1.004606248       | AT3G20060             |
| Bra035819              | A05:18094674-18095990      | ubiquitin-conjugating enzyme19         | -1.002447128       | AT2G46030             |
| Bra039295              | A04:18825889-18827010      | ubiquitin-conjugating enzyme 6         | -1.019685745       | AT1G20140             |
| Bra012213              | A07:11498122-11498671      | SKP1-LIKE 4 ubiquitin-protein ligase   | -3.02702045        | AT2G45950             |
| Bra000407              | A03:10985040-10986810      | SKP1-LIKE20ubiquitin-protein ligase    | 2.009963036        | AT1G20140             |
| Bra012213              | A07:11498122-11498671      | SKP1-LIKE4 ubiquitin-protein ligase    | -2.000241279       | AT3G53090             |
| Bra026084              | A06:5912047-5913990        | heat shock protein 70;                 | -0.003735542       | AT1G16030             |
| Bra015047              | A07:6193591-6195966        | heat shock protein 70;                 | 0.989945412        | AT5G42020             |
| Bra024699              | A09:24658241-24660418      | heat shock protein 70;                 | 0.990047455        | AT5G02500             |
| Bra018725              | A06:2311540-2312653        | heat shock protein 70;                 | 3.035300255        | AT5G02500             |
| Bra001457              | A03:16474528-16476872      | heat shock protein 70;                 | 1.095615768        | AT3G12580             |
| Bra035909              | A09:3556883-3559021        | heat shock protein 70;                 | -0.010067939       | AT5G02500             |
| Bra009415              | A10:15348271-15349916      | heat shock protein 20;                 | 1.003929227        | AT5G04890             |
| Bra002966              | A10:6457865-6458584        | heat shock protein 21;                 | 1.984234174        | AT5G54660             |
| Bra003079              | A10:5439378-5441507        | heat shock protein binding ,DnaJ       | 2.042747816        | AT5G53150             |
| Bra003501              | A07:16774795-16777119      | heat shock protein binding ,DnaJ       | 0.991512616        | AT3G62600             |
| bra024651              | A09:25033726-25037397      | leucine-rich repeat protein, putative" | 0.999271393        | AT1G27170             |
| bra002354              | A10:10190369-10192591      | leucine-rich repeat protein, putative" | 0.98850441         | AT5G21090             |
| bra021868              | A04:15050689-15053280      | leucine-rich repeat protein, putative" | -1.015964509       | AT2G33020             |
| bra019877              | A06:3925944-3928634        | leucine-rich repeat domain             | -2.090869902       | AT1G11170             |
| bra037014              | A03:29005679-29010457      | leucine-rich repeat domain             | 1.565162834        | AT4G33210             |
| bra016611              | A08:18508866-18510914      | leucine-rich repeat protein, putative" | -1.03489685        | AT1G17250             |
| bra030878              | A08:473766-474335          | disease resistance response            | 1.016321182        | AT1G55210             |
| bra002898              | A10:6942941-6947133        | leucine-rich repeat domain             | 0.004454613        | AT5G55540             |
| Bra001996              | A07:2758489-2761281        | serine/threonine protein kinase        | 2.03542614         | AT2G16750             |
| Bra015796              | A07:24106176-24108947      | serine/threonine protein kinase        | 1.570112038        | AT1G76040             |
| Bra017694              | A03:29864111-29864611      | serine/threonine protein kinase        | -6.340401681       | AT3G26940             |
| Bra000881              | A03:13697451-13699478      | serine/threonine protein kinase        | -6.127163506       | AT4G02420             |

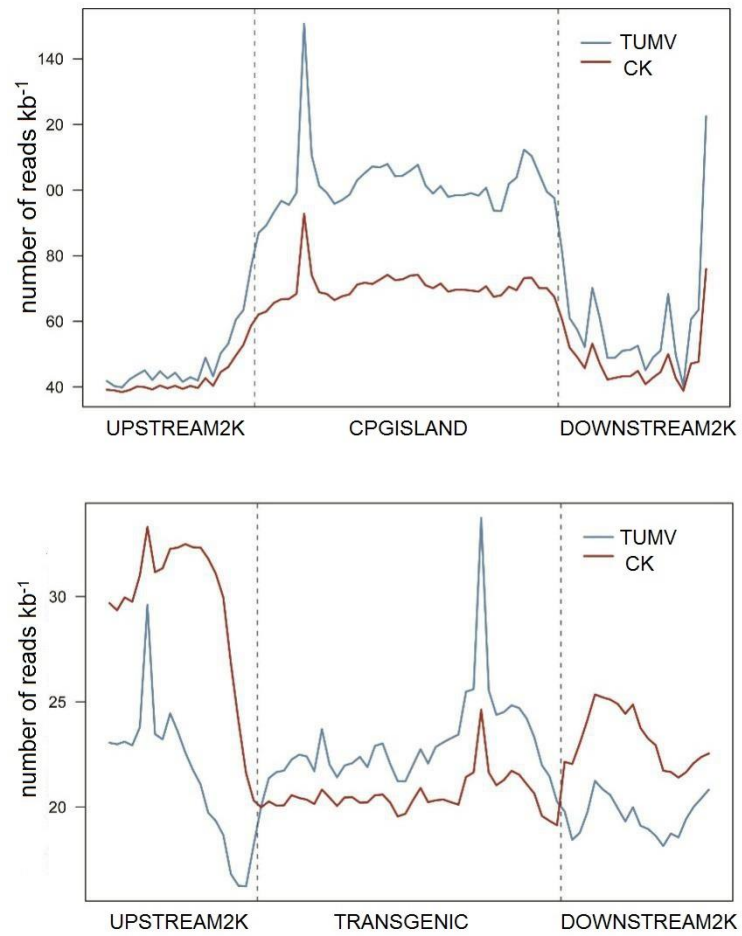


Fig. 1 Suppl. Distribution of reads around a gene body and cytosine-phosphate-avidin (CpG) island. The x-axis indicates the position around the gene body (the CpG island) and the y-axis indicates the normalized read number. This figure can reflect the methylation level around the gene body (the CpG island). Blue line - *Turnip mosaic virus* (TUMV), red line - control (CK).