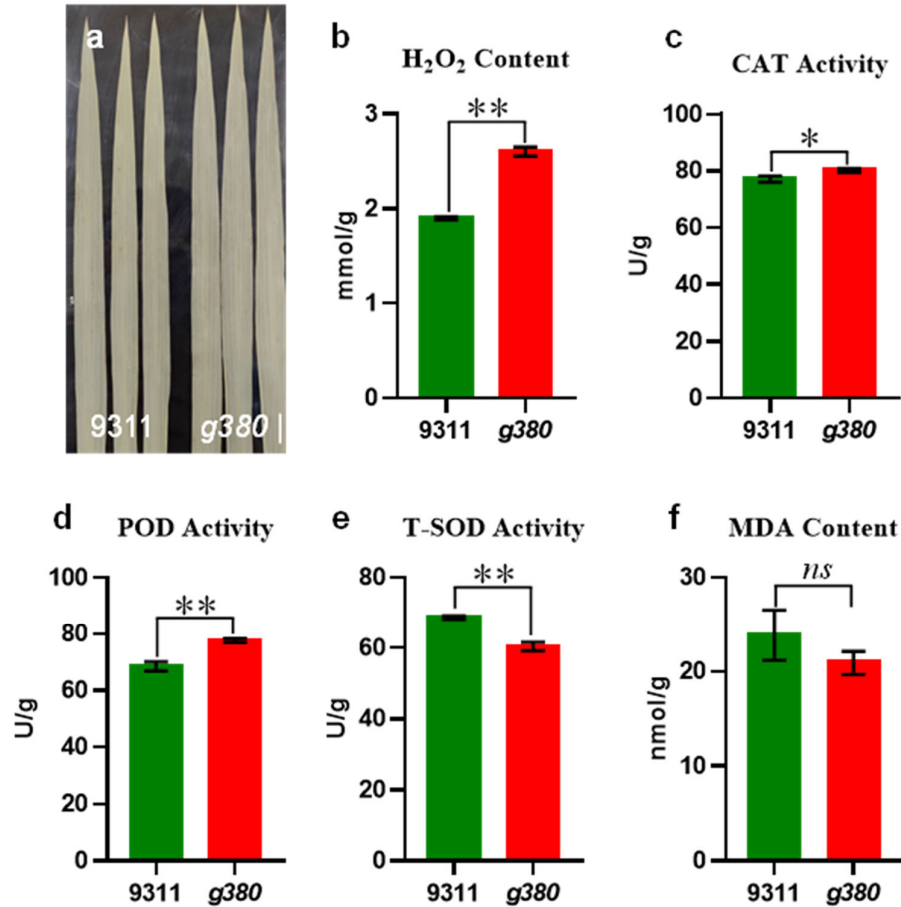
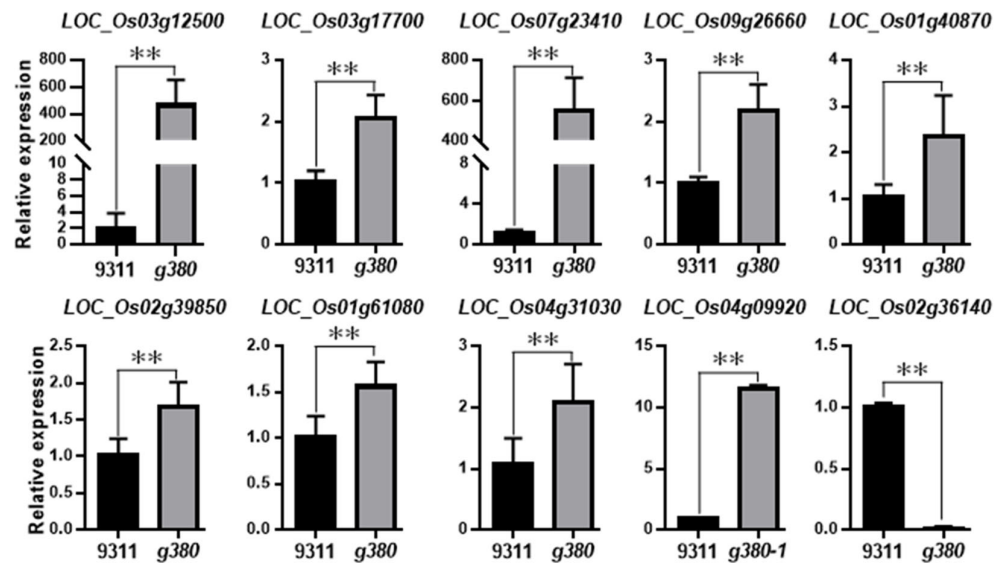


## Supplementary materials

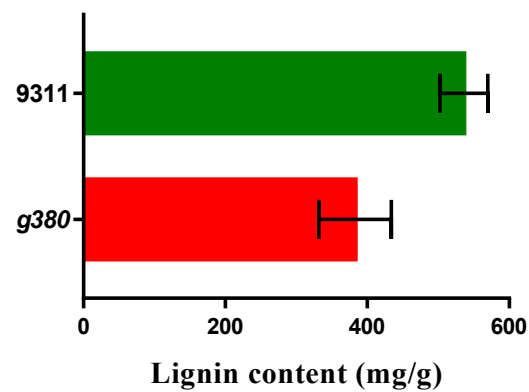
**Supplementary Figure S1.** ROS accumulation in *g380* before the lesions formation. (a) DAB staining of *9311* and *g380* leaves. (b-f) The ROS related physiological-biochemical indexes of *9311* and *g380* leaves. Bar=1 cm in (a). Values are mean  $\pm$  SD ( $n = 3$ ). \*\* indicates significant differences at  $p < 0.01$  level by Welch's *t*-test, \* indicates significant differences at  $p < 0.05$  level by Welch's *t*-test, *ns* indicates  $p > 0.05$  level by Welch's *t*-test.



**Supplementary Figure S2.** Upregulated genes enriched the phenylpropanoid biosynthesis (dosa00940) pathway.



Supplementary Figure S3. Lignin content of 9311 and *g380* before *g380* lesion formed.



**Supplementary Table S1.** Summary of RNA-seq data production.

Sample	Raw reads	Raw bases	Clean reads	Clean bases	Clean data rate	Reads mapped to genome	Mapping rate
g380_1	109,394,138	10,939,413,800	102,335,692	10,012,335,791	91.53%	79,424,324	77.61%
g380_2	99,866,956	9,986,695,600	93,789,966	9,195,128,262	92.07%	72,140,490	76.92%
g380_3	103,030,918	10,303,091,800	97,158,506	9,535,482,959	92.55%	73,454,724	75.60%
9311_1	112,525,000	11,252,500,000	103,597,194	10,141,888,103	90.13%	81,316,532	78.49%
9311_2	102,858,738	10,285,873,800	97,198,894	9,547,028,366	92.82%	70,210,316	72.23%
9311_3	116,315,728	11,631,572,800	109,122,984	10,710,401,300	92.08%	83,746,156	76.74%

**Supplementary Table S2.** Differentially expressed *PR* genes.

<i>gene_symbol</i>	MSU_ID	log <sub>2</sub> FC	<i>P</i> Value	FDR
<i>OsPR1b</i>	LOC_Os01g28450	6.09	2.76E-09	9.66E-07
<i>OsPR1a</i>	LOC_Os07g03710	8.18	3.72E-12	2.45E-09
<i>PR5</i>	LOC_Os12g43430	5.14	5.03E-14	4.34E-11
<i>PR1c</i>	LOC_Os01g28500	2.89	3.91E-06	7.30E-04
<i>PR1</i>	LOC_Os07g03730	5.43	8.42E-09	2.72E-06
<i>Gns5</i>	LOC_Os01g71340	5.07	7.58E-09	2.51E-06
<i>Gns6</i>	LOC_Os01g71350	4.28	8.73E-14	7.41E-11
<i>OsCHIT8</i>	LOC_Os06g51060	3.52	3.88E-05	5.36E-03
<i>OsCHIT14</i>	LOC_Os10g39680	3.54	5.00E-05	6.62E-03
<i>OsCHIT17</i>	LOC_Os05g33130	6.94	9.61E-14	8.03E-11
<i>OsPR4a</i>	LOC_Os11g37970	3.94	1.62E-09	5.94E-07
<i>OsPR4c</i>	LOC_Os11g37950	7.41	2.74E-14	2.48E-11
<i>TLP</i>	LOC_Os03g46070	4.27	4.86E-17	6.80E-14
<i>BBTI-7</i>	LOC_Os01g03390	5.42	1.40E-09	5.21E-07
<i>BBTI-12</i>	LOC_Os01g04050	2.56	3.51E-05	4.92E-03
<i>Oschib1</i>	LOC_Os10g28080	5.09	5.20E-18	9.40E-15
<i>OsPR10</i>	LOC_Os12g36880	5.54	1.01E-15	1.16E-12
<i>PR10B</i>	LOC_Os12g36850	5.51	2.47E-15	2.61E-12
<i>RSOsPR10</i>	LOC_Os12g36830	5.44	2.07E-10	9.20E-08
<i>OsGLP8-7</i>	LOC_Os08g09010	3.39	4.50E-04	4.34E-02

**Supplementary Table S3.** Differentially expressed *WRKY* genes.

<i>gene_symbol</i>	MSU_ID	log <sub>2</sub> FC	<i>P</i> Value	FDR
<i>OsWRKY14</i>	LOC_Os01g53040	3.04	1.38E-04	1.64E-02
<i>OsWRKY24</i>	LOC_Os01g61080	2.44	1.20E-04	1.44E-02
<i>OsWRKY32</i>	LOC_Os02g53100	4.79	3.06E-05	4.42E-03
<i>OsWRKY19</i>	LOC_Os05g49620	4.59	8.63E-16	1.03E-12
<i>OsWRKY28</i>	LOC_Os06g44010	3.71	7.77E-11	3.99E-08
<i>OsWRKY69</i>	LOC_Os08g29660	2.70	3.96E-05	5.44E-03
<i>OsWRKY72</i>	LOC_Os11g29870	3.21	1.15E-07	2.97E-05

**Supplementary Table S4.** Upregulated genes enriched the phenylpropanoid biosynthesis (dosa00940) pathway.

<i>gene_symbol</i>	<i>MSU_ID</i>	<i>log<sub>2</sub>FC</i>	<i>P Value</i>	<i>FDR</i>
<i>prx15</i>	LOC_Os01g22352	4.47	6.40E-12	3.89E-09
<i>prx16</i>	LOC_Os01g22370	1.65	2.60E-04	2.74E-02
<i>OsALDH2C1</i>	LOC_Os01g40870	2.37	3.77E-11	2.03E-08
<i>prx22</i>	LOC_Os01g73200	2.09	4.88E-05	6.49E-03
<i>Os4CL3</i>	LOC_Os02g08100	1.81	3.38E-05	4.79E-03
<i>OsCAD2</i>	LOC_Os02g09490	3.21	2.07E-08	6.36E-06
<i>OsHCT2</i>	LOC_Os02g39850	2.12	6.60E-09	2.20E-06
<i>OsPAL1</i>	LOC_Os02g41630	3.44	3.40E-09	1.18E-06
<i>OsPAL2</i>	LOC_Os02g41650	2.43	8.77E-06	1.52E-03
<i>OsPAL4</i>	LOC_Os02g41680	3.47	5.76E-12	3.58E-09
<i>OsBGLU1</i>	LOC_Os03g53800	2.70	1.38E-06	2.91E-04
<i>OsHCT1</i>	LOC_Os04g42250	1.77	1.34E-06	2.85E-04
<i>prx61</i>	LOC_Os04g59190	4.63	9.48E-07	2.07E-04
<i>prx117</i>	LOC_Os08g02110	4.55	7.56E-17	1.01E-13
<i>OsCOMT</i>	LOC_Os08g06100	2.58	9.99E-08	2.68E-05
<i>OsCCR20</i>	LOC_Os08g34280	2.65	2.31E-07	5.61E-05
<i>Os9BGlu31</i>	LOC_Os09g33680	1.05	3.37E-04	3.42E-02
<i>OsF5H1</i>	LOC_Os10g36848	4.20	2.04E-17	3.31E-14

**Supplementary Table S5.** Upregulated genes enriched the plant-pathogen interaction (dosa04626) pathway.

<i>gene_symbol</i>	<b>MSU_ID</b>	<b>log<sub>2</sub>FC</b>	<b>P Value</b>	<b>FDR</b>
<i>OsPR1b</i>	LOC_Os01g28450	6.09	2.76E-09	9.66E-07
<i>PRB1-2</i>	LOC_Os01g28500	2.89	3.91E-06	7.30E-04
<i>OsWRKY24</i>	LOC_Os01g61080	2.44	1.20E-04	1.44E-02
<i>KCS</i>	LOC_Os02g11070	2.59	3.63E-09	1.25E-06
<i>OsCEBiP</i>	LOC_Os03g04110	1.32	3.49E-04	3.52E-02
<i>OsMPK3</i>	LOC_Os03g17700	2.51	4.70E-07	1.09E-04
<i>OsRIN4</i>	LOC_Os04g31030	1.56	2.16E-04	2.36E-02
<i>OsCML21</i>	LOC_Os05g24780	3.81	5.52E-08	1.59E-05
<i>OsPR1a</i>	LOC_Os07g03710	8.18	3.72E-12	2.45E-09
<i>Osrbmh7</i>	LOC_Os09g26660	2.71	2.10E-04	2.32E-02
<i>OsPR1-101</i>	LOC_Os10g11500	4.34	3.05E-04	3.15E-02
<i>OsCML36</i>	LOC_Os11g04560	3.10	4.78E-07	1.10E-04



**Supplementary Table S6.** Sequences of primers for linkage analysis and chromosome walking.

Primer ID	Forward (5'-3')	Reverse (5'-3')
RM341	CAAGAAACCTCAATCCGAGC	CTCCTCCCGATCCCAATC
C2-9	TTTTTATCTCGAGGTACGGTAGTAG	TGAGAATTAGTGTTTCATTTGTAGATTC
C2-10	GGCTGGCTGTTGCTCATC	AAAAATCCCAACCCTGCTG
RM13611	CTCTTGAACGGCTGCACGAAAGG	CGCGAGAATGGTAGGTGGATCG
RM3850	AAGTTGAGAATGAGGGACAA	TTCGGAAGTGAAAAGGTAAT
L24	CCTCCTCTGAAAATCCA	GTACCACCTCGTCGTCGC
L26	GAGGTTTGTGATTGGTCG	ATCGTTGCTTGAAGTTGA
L39	CTATTCCTATTCCACCAGC	TCGTGCGATAACACTAAA
L45	GCAAGTTTAAAGTACGATC	TACAGTTGTGAACACCCA
L46	AGCGACCGAATTGAAGAG	TAAGCCGTGGCAAGGAAC
L4	GCGATTTGACCGTCCTTT	GACTTCCCGACACCTGCT
L6	GCTTACTACCGTACCACAT	AGGCTCCATTCTTCATA
L7	ACTGTACCCCTGATTTC	GCTGCCTAAGTGATTATTTTC
L9	CTCGCTAAGTATGAGATTTG	GGTCTTGATTACGGAGG
L10	TGGCTGTTTGCTTGATC	GAAATGCTGTAAGCGAGA
L12	GAGCGTAGGAGCAAACAG	TGAGATAGAACTCAGGGAG
L14	CAGTGACCGTTGTTGTT	GGATTATTAGGTTGGCTTTT
L15	CCCTAGACACGTACAAAA	CAAACCTATTCAAGCAGAT
L16	GCCACTGCCCAAATCCTC	TTGCCCCTCGTTTTACCA
L27	TAAGTAATTGTGGCTTCCTT	CCGTAGTTCTATAATATGGG
L28	TTTTCAAATAATGGTCT	TAAGAAGGTAGTGACAGC
L34	TGTGCTTGCTGTGCCTCT	GCCGATTTTGGGATTTGT
L36	TCTGGCTATGGTTGCT	TATTTGTACCGTGGGT
L37	TTTTCATAGTCGTTGGC	GCACTAGCATCTAGCGT
L38	ACGCTACTTTTCTTGCT	GACCGTCCGTCTTATT
L40	ATTGCCAGGCTATGTTTC	TGCGATATTGCATCTCAT
F11	TTCTAACCAGCACCAACAAT	GTAGCCATGACACAACCATCT
F12	GCATACTGAGATGGTTGTG	TGGTGGTAATGAATAGAG
F13	GTCTGGATGATGCAAGGGA	CCAACACGATAATGGGGAA
F4	GAAGATTGATTGTGTTGA	CTAGATGCTGTATGGTTGA
F5	ACCAATCAACCATAACAGCA	GAGCATCATCAGCATCACC
R8	ATGAGGTGAAAAAAGGAAAATG	TCTATAGGGTCCCAACCAAGGT
R9	TTGCGTCCTTCATTTTCCTATT	GCCATTTTCCTTTTTCACCTC
R10	AGAATACAAAAGGTAGCAAC	TCAATAGGAAAATGAAGGAC
R11	AGAAATACGGAGCCGACGGAAAT	AGGGGAAGAAGGAAGGTAGGGAG
R12	GCGGTTCACTAATGATAGAAAAG	CAATGGTAATAGAAACACGGATA

**Supplementary Table S7.** Sequences of qRT-PCR primers.

Gene symbol/ID	Forward (5'-3')	Reverse (5'-3')
<i>Actin</i>	CAGGCCGTCCTCTCTGTGA	AAGGATAGCATGGGGGAGAG
<i>OsPR1a</i>	GGCCAATCTCCCTACTGATTAA	GCATAAACACGTAGCATAGCAT
<i>OsPR1b</i>	TACGCCAGCCAGAGGAGC	GCCGAACCCCAGAAGAGG
<i>OsPR10</i>	GGTGTGGGAAGCACATACAA	GTCTCCGTCGAGTGTGACTTG
<i>OsCPS2</i>	CATCTCCAAGTTTTGTTCGAG	TTTTCGCAGTCATCACTTTACG
<i>CYP76M6</i>	GGAAAGACTACGAGTACATCCC	AACTTCTCAGTCATGTCCATGT
<i>OsCPS4</i>	ATCTACCCTTTGGATGTGTACG	TGTCATCGATATCCTTTACCGG
<i>OsKSL4</i>	TTTGAGGTCTTTAGCGACAGAT	TATAGTTGGTCCCAATGCGAAT
<i>CYP99A2</i>	ATCATGGAGATAAACTCGGCAG	CTCTTCTTTGACGACGACTTG
<i>OsPAL1</i>	GACCCTGTATTTTCTTCGTTTCG	AGTAGCAATACTTTCACCCCAA
<i>OsPAL4</i>	GTGCTCTTTGAGGCTAACATTTC	CTTCTTGGCATGCTTCATGTAG
<i>OsF5H1</i>	TTCAACATCGGCGACTTCATC	ATGATCTTGTGCGATGAACCTGT
<i>OsROMT9</i>	GAAGAACCACTCCGTCATCATC	GAGGATCCACTTCATCAGGATG
<i>OsCCR20</i>	ATGGCGTACGTTAATTAGTTGC	TTTCCTTGCAGTAGTCAAGGTC
<i>OsCAD2</i>	GTACTGCAACAAGAGGATTTGG	GATCTTCACCACAAACTTCTGG
<i>LOC_Os03g12500</i>	AAGCTGCTGCAATACGTGTACTGG	CGACGAGCAACAGCCTTCCG
<i>LOC_Os03g17700</i>	TTACCTAGAGAGATTGCACGAC	TGGTGATTCAATCTAGTACCGG
<i>LOC_Os07g23410</i>	TACTTCTCGTGGAAATACACCC	TTGTACTTGTACACGTATGGGG
<i>LOC_Os09g26600</i>	GAGAGGAGCTCTACGACTTCT	CTGTACTTCCTCCCTCGTTATC
<i>LOC_Os01g40870</i>	GTGACCAAGAACCTCAACATTG	TGGTACATGGTACACTCTAGCT
<i>LOC_Os02g39850</i>	AGCCCACCAAGCTGTACT	GAAGATCACGTTGCCGAAGTAG
<i>LOC_Os01g61080</i>	GCCGACGACCAGCAGATCACC	ACGAGCCGACGCCGCCCTC
<i>LOC_Os04g31030</i>	CTACAGGATTGGAAGTCGCTAA	GCATTCTCAAACCTTCTGTGTGT
<i>LOC_Os04g09920</i>	CTCAAGTTCAGCAATGGGTTC	CCAGTATAATTGCCTTGACGTG
<i>LOC_Os02g36140</i>	CGAAGAATACATGGAAAGTGGC	GCCTGAACAACATCATCGTATTC