

Table S1. Number of panicles scored according to their size of lesion of Panicle Blast according to the method proposed by Ou (Ou, S.H., 1965). “0” is for without any evidence of infection; “1” for a lesion smaller than 0.5 mm of diameter with no sporulation; “2” is for the lesion ranges between 0.5 to 1 mm and brown in color and without sporulation; “3” is when lesion takes a round or elliptical shape and ranges between 1-3 mm in diameter, having grey colored center and brown margins, these type of lesions are capable of sporulation; “4” is for proper necrotic grey centered with brown margin lesions, length varies from 3 mm or above, and are capable of sporulation; and “5” in this the lesion is of same as in described in 4 but with more area covered. Genotypes with scoring of lesions around 0 to 3 were considered as resistant reaction, and those with 4 to 5 were considered as susceptible reaction against the blast disease.

| Scoring | HP2216 | | | | Tetep | | | |
|---------|--------|--------|--------|--------|-------|--------|--------|--------|
| | Mock | 48 hpi | 72 hpi | 96 hpi | Mock | 48 hpi | 72 hpi | 96 hpi |
| 0 | 25 | 0 | 0 | 0 | 25 | 16 | 15 | 15 |
| 1 | 0 | 6 | 0 | 0 | 0 | 9 | 10 | 10 |
| 2 | 0 | 4 | 2 | 0 | 0 | 0 | 0 | 0 |
| 3 | 0 | 7 | 5 | 1 | 0 | 0 | 0 | 0 |
| 4 | 0 | 8 | 6 | 2 | 0 | 0 | 0 | 0 |
| 5 | 0 | 0 | 12 | 22 | 0 | 0 | 0 | 0 |

Table S2. Mapping of RNA-Seq Reads Obtained from Tetep and HP2216 against *Oryza sativa* Nipponbare (MSU release 7). R1: Biological replicate 1, R2: Biological replicate 2; hpi: hours post infection.

| Sample | Total Raw Reads | Total Preprocessed Reads (Left+Right) | Total Reads Aligned | Multi Aligned Reads (Left + Right) | Total Reads Aligned % | Total Unaligned Reads % |
|-------------------------|-----------------|---------------------------------------|---------------------|------------------------------------|-----------------------|-------------------------|
| Susceptible line | | | | | | |
| HP2216_48 hpi R1 | 22,996,818 | 22,815,936 | 19,386,788 | 593,518 | 85 | 3.1 |
| HP2216_48 hpi R2 | 21,230,382 | 20,216,986 | 14,205,622 | 568,932 | 70.3 | 4 |
| HP2216_72 hpi R1 | 42,404,536 | 42,235,521 | 37,181,937 | 4,609,385 | 88 | 12.4 |
| HP2216_72 hpi R2 | 23,142,268 | 22,273,058 | 17,608,583 | 1,876,575 | 79.1 | 10.7 |
| HP2216_96 hpi R1 | 45,546,236 | 45,257,792 | 39,341,401 | 4,778,432 | 86.9 | 12.1 |
| HP2216_96 hpi R2 | 21,701,598 | 20,963,602 | 17,771,260 | 2,713,392 | 84.8 | 15.3 |
| HP2216_Mock R1 | 47,109,206 | 46,768,736 | 41,225,139 | 957,667 | 88.1 | 2.3 |
| HP2216_Mock R2 | 21,392,421 | 20,672,630 | 17,704,067 | 2,709,972 | 85.6 | 15.3 |
| Resistant Line | | | | | | |
| Tetep_48 hpi R1 | 42,034,770 | 41,756,080 | 36,732,185 | 670,900 | 88 | 1.8 |
| Tetep_48 hpi R2 | 21,946,596 | 20,813,520 | 13,841,691 | 259,150 | 66.5 | 1.9 |
| Tetep_72 hpi R1 | 42,194,552 | 41,880,774 | 36,958,832 | 673,142 | 88.2 | 1.8 |
| Tetep_72 hpi R2 | 22,017,790 | 20,952,144 | 15,876,148 | 312,849 | 75.8 | 2 |
| Tetep_96 hpi R1 | 46,289,178 | 45,940,760 | 40,544,425 | 755,308 | 88.3 | 1.9 |
| Tetep_96 hpi R2 | 22,198,855 | 21,537,207 | 18,169,151 | 332,915 | 84.4 | 1.8 |
| Tetep_Mock R1 | 44,181,464 | 43,800,508 | 39,189,039 | 930,869 | 89.5 | 2.4 |
| Tetep_Mock R2 | 23,327,572 | 22,570,334 | 19,217,509 | 421,213 | 85.1 | 2.2 |
| Average | 31,857,140 | 31,278,474 | 26,559,611 | 1,447,764 | 83.4 | 5.7 |
| In million | 31.857140 | 31.278474 | 26.559611 | 1.447764 | 83.35 | 5.69 |

Table S3. Details of primers used for quantitative real time PCR validation.

| Locus_id | Annotation | Forward Primer | Reverse Primers |
|----------------|--|-----------------------------|--------------------------|
| LOC_Os01g62480 | laccase precursor protein, putative, expressed | GAACAACACCAACGTGAA-GAC | CTTGCCGATCACGAAGAA |
| LOC_Os02g43790 | ethylene-responsive transcription factor, putative, expressed | CCGAGGACATGGTCGTGTA | AGGAAGCTGCCGATGGA |
| LOC_Os03g16960 | cysteine-rich repeat secretory protein 55 precursor, putative, expressed | CAACTAC- CAATCCGACTCAAGA | CTGCACGTTCAACAAGAATCAC |
| LOC_Os03g17200 | plant-specific domain TIGR01589 family protein, expressed | GTGCAGCACCTGATAGA-GAAA | TCTCCAGCTCCTCCATACT |
| LOC_Os03g46860 | helix-loop-helix DNA-binding protein, putative, expressed | AGGATCCACGGCGAGAATAA | TGACATTGGTGTGCGTGATG |
| LOC_Os04g56430 | cysteine-rich receptor-like protein kinase, putative, expressed | GCACTTTGCTCGTTCTCCT | CAGGTTCAGGAGGTTGTTCTC |
| LOC_Os04g59150 | peroxidase precursor, putative, expressed | GCATCATTCTTGCCTCTTG | CGTAGTGATTGGAAGATGG-TAGG |
| LOC_Os05g07820 | leucine-rich repeat receptor protein kinase EXS precursor, putative, expressed | GATCAGCTCCTCCATT-GTTCTT | GTGGCAGATGTTGTGTCTACT |
| LOC_Os06g08360 | ethylene-responsive element-binding protein, putative, expressed | GCAACTGCAACCACTTCTG | GGATGACGCAGGTGAAGA |
| LOC_Os06g09860 | expressed protein | CGCTCAAGGTGTTTCGACAT | ACGTAGCAGAGGTACTGGTT |
| LOC_Os06g12210 | helix-loop-helix DNA-binding domain containing protein, expressed | GATCAAC- GAGCTCATCTCCAA | GGTGCAGGCTCTTGATGTA |
| LOC_Os08g43700 | OsSAUR36 - Auxin-responsive SAUR gene family member, expressed | CGGTGATGGAG-TATGTCATGTG | CATCACAATGGAAGTGAAGGAG |