**S3 Table.** CNV overlapping effectors genes

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Order | Effector genes | Chr | Position | B2 | B51 | P28 | P29 | P3 | Py22.1 | Py5020 | T25 |
| 1 | BAS1\* | chr1 |  1,228,470  | % | % | % | % | % | % | % | % |
| 2 | AVR1-CO39# | chr2 |  7,253,033  | % | % | % | % | % | % | % | % |
| 3 | AVR-Pik | chr3 |  1,324,102  | % | % | % | % | % | % | % | % |
| 4 | PWL4 | chr3 |  388,420  | % | % | % | % | % | % | % | % |
| 5 | AVR-Pii | chr3 |  7,735,856  | NA | CNminus | & | % | NA | % | NA | % |
| 6 | AVR-Pi54 | chr4 |  1,079,049  | % | % | % | % | % | % | % | % |
| 7 | BAS2 | chr4 |  5,359,621  | % | % | % | % | % | % | % | % |
| 8 | BAS4 | chr5 |  17,696  | % | % | % | % | % | % | % | % |
| 9 | BAS3 | chr5 |  3,450,049  | % | % | % | % | % | % | % | % |
| 10 | PWT3# | chr5 |  3,632,010  | NA | CNplus | % | % | % | % | % | % |
| 11 | AVR-Pib | chr6 |  6,027,571  | CNplus | CNminus | % | CNplus | CNplus | CNplus | % | % |
| 12 | AVR-Pi9 | chr7 |  2,736,023  | % | % | % | % | % | % | % | % |
| 13 | AVRPiz-t | chr7 |  3,041,628  | % | % | % | % | % | % | % | % |
| 14 | AVR-Pita3 | chr7 |  344,264  | %\* | % | NA | CNminus | %\* | % | % | %\* |
| 15 | AVR-Pik\_km\_kp | chr7 | 3,846,519 | % | % | % | % | CNplus | % | % | % |
| 16 | PWL2 | scaf1 |  132,123  | & | & | % | CNminus | % | & | % | CNminus |
| 17 | BAS1\*\* | scaf1 |  134,228  | & | & | % | CNminus | % | & | % | CNminus |
| 18 | AVR-Pii | scaf1 |  29,460  | & | NA | NA | & | % | & | CNplus | & |

%: CNequal, conserved between the strain and B71

&: The CNV index was between CNequal and CNminus and was referred to as "polymorphic"

%\*: CNequal but partial genes were in polymorphic regions

NA: no CNV segments overlapping with gene regions of effectors

\*: 68% identity to 70-15 BAS1

\*\*: 99% identity to 70-15 BAS1

#: B71 has an insertion on the gene