**Table S6. Distribution across donor parents of NILs with introgressions across the five significant genomic regions identified via genome wide association analysis and stepwise regression. NILs are distributed based on donor and labelled as being resistant (R), susceptible (S), or not significantly different from B73 (ns). If the NIL has the same significant allelic effect as that identified from joint linkage mapping of NLB QTL in the maize nested association mapping population, it is in bold. More than one NIL with a similar effect is noted in brackets.**

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| QTL bin | Chr | SNP | # of NILs | CML103 | CML228 | CML247 | CML277 | CML322 | CML333 | CML52 | CML69 | Ki11 | Ki3 | M162W | Mo17 | Mo18W | NC350 | NC358 | Oh43 | Tx303 | Tzi8 |
| 1.06 | 1 | 191,522,802 | 21 | **R**;ns | R(2) | - | R | ns | ns | - | R; ns | R | S; ns | R; ns | ns | - | - | ns | - | R(2); ns | **S(2)** |
| 2.01/2.02 | 2 | 4,263,855 | 8 | - | - | - | - | S | **S** | **ns(2)** | - | - | - | **ns(2)** | - | **ns** | - | - | S | - | - |
| 5.05 | 5 | 193,652,476 | 19 | **ns** | - | - | S(2) | **S** | - | ns | S | - | S | - | S(2); ns(2) | ns | - | ns | S(2) | S(2) | ns(2) |
| 6.05 | 6 | 141,836,653 | 16 | R; **ns** | **ns** | R | - | - | **R**; ns | - | - | ns | **R** | ns | R | ns(2) | **R** | - | ns | - | R(2) |
| 8.05 | 8 | 138,561,937 | 26 | ns(3) | ns(2) | ns | ns | - | ns | ns(2) | - | R | R | **R(2)** | - | ns | ns(2) | R | - | R(2); ns(4) | **R**; ns |