**Table S2.** Epistatic analysis of F2 population derived from crosses between Di-17 and various wild-type or mutant lines.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Cross** | **Genotype a**  | **Plants obtained** | **HR b** | **R c**  | **S d** | **χ2** e |  P  |
| Di-17 x Col-0 | *HRT/-* | 129 | + | 29 | 100 | 0.43 | 0.50 |
| Di-17 x*cop1* | *HRT/- cop1**HRT/- COP1/-* | 35112 | -+ | 032 | 3580 | 11.60.76 | 0.0006 f0.38 |
| Di-17 x*drb1* | *HRT/- drb1**HRT/- DRB1/-* | 75255 | -+ | 770 | 68185 | 9.81.26 | 0.001 f0.26 |
| Di-17 x*drb2* | *HRT/- drb2**HRT/- DRB2/-* | 68247 | ++ | 255 | 66192 | 17.640.98 | 0.001 f0.32 |
| Di-17 x*drb3* | *HRT/- drb3**HRT/- DRB3/-* | 68201 | ++ | 046 | 68155 | 17.60.47 | 0.0001 f 0.48 |
| Di-17 x*drb5* | *HRT/- drb5**HRT/- DRB5/-* | 8177 | ++ | 021 | 873 | 2.661.37 | 0.100.24 |

a The genotype at *HRT* and various mutant loci was determined by CAPS analysis

b HR, hypersensitive response

c Resistant

d Susceptible

e One degree of freedom; based on segregation of 3 susceptible:1 resistant plants

f Statistically significant