

Table S1. Phenotypic correlation coefficients between resistance traits to halo blight races 1, 5, 7 and 9 in the UI3A52 and UI3T F₂ populations (above and below the diagonal, respectively).

| Trait ¹ | Race 1 | | | | | Race 5 | | | | | Race 7 | | | | | Race 9 | | | | | | | | |
|--------------------|---------|--------|------|--------|-------|--------|---------|------|--------|-------|--------|---------|--------|------|--------|--------|------|--------|---------|------|--------|-------|------|------|
| | PLAUDPC | PLAREA | PDC | PAUDPC | PAREA | PLDC | PLAUDPC | PDC | PAUDPC | PAREA | PLDC | PLAUDPC | PLAREA | PDC | PAUDPC | PAREA | PLDC | PLAREA | PLAUDPC | PDC | PAUDPC | PAREA | | |
| Race 1 | PLDC | 0.96 | 0.63 | 0.32 | 0.35 | | | | | | 0.84 | 0.84 | | 0.39 | 0.39 | | | | | 0.38 | 0.41 | | | |
| | PLAUDPC | | 0.65 | 0.35 | 0.37 | | | | | | 0.86 | 0.85 | | 0.42 | 0.43 | 0.28 | | | | 0.42 | 0.44 | 0.29 | | |
| | PLAREA | | | 0.26 | | | | | | | 0.54 | 0.52 | | 0.35 | 0.31 | | | | | 0.25 | 0.25 | | | |
| | PDC | | | | 0.98 | 0.62 | | | | | 0.32 | 0.29 | 0.38 | 0.89 | 0.87 | 0.57 | | | | 0.89 | 0.86 | 0.65 | | |
| | PAUDPC | | | 0.96 | | 0.64 | | | | | 0.36 | 0.33 | 0.39 | 0.87 | 0.87 | 0.53 | | | | 0.88 | 0.85 | 0.62 | | |
| Race 5 | PAREA | | 0.63 | | | | | | | | | | 0.48 | 0.62 | 0.60 | 0.60 | | | | 0.62 | 0.53 | 0.52 | | |
| | PLDC | | | | | | | | | | | | | | | | | | | | | | | |
| | PLAUDPC | | | | | 0.99 | | | | | | | | | | | | | | | | | | |
| | PDC | | 0.93 | 0.87 | 0.78 | | | | | | 0.99 | | | | | | | | | | | | | |
| | PAUDPC | | 0.96 | 0.90 | 0.74 | | | 0.99 | | | | | | | | | | | | | | | | |
| Race 7 | PAREA | | 0.78 | 0.63 | 0.73 | | | 0.81 | 0.83 | | | | | | | | | | | 0.41 | 0.42 | 0.32 | | |
| | PLDC | | | | | | | | | | 0.99 | | | 0.41 | 0.43 | 0.26 | | | | | | | | |
| | PLAUDPC | | | | | | | | | | | 0.99 | | | 0.38 | 0.39 | 0.25 | | | | 0.39 | 0.4 | 0.30 | |
| | PLAREA | | | | | | | | | | | | 0.99 | | | 0.31 | 0.29 | 0.41 | | | | 0.40 | 0.33 | 0.40 |
| | PDC | | | 0.78 | | | 0.62 | | | | | | | 0.99 | | | 0.99 | 0.63 | | | | 0.88 | 0.87 | 0.65 |
| Race 9 | PAUDPC | | | 0.81 | | | 0.68 | 0.61 | | | | | | 0.99 | | | 0.99 | 0.61 | | | | 0.88 | 0.87 | 0.63 |
| | PAREA | | | | | | | | | | | | | | | | | | | 0.61 | 0.58 | 0.75 | | |
| | PLDC | | | | | 0.99 | 0.98 | | | | | | | | | 0.63 | | | | | | | | |
| | PLAUDPC | | | | | 0.99 | 0.98 | | | | | | | | | 0.63 | | | | | | | | |
| | PLAREA | | | | | 0.67 | 0.72 | | | | | | | | | | | | | | | | | |
| Race 9 | PDC | | 0.87 | 0.81 | 0.78 | | | 0.91 | 0.92 | 0.84 | | | | | | 0.65 | 0.66 | | | | 0.96 | 0.71 | | |
| | PAUDPC | | 0.94 | 0.88 | 0.70 | | | 0.93 | 0.96 | 0.86 | | | | | | | | | | 0.98 | | 0.70 | | |
| | PAREA | | | 0.62 | 0.68 | 0.65 | 0.66 | 0.74 | | | | | | | | 0.67 | | 0.69 | 0.70 | 0.72 | 0.69 | | | |
| | | | | | | | | | | | | | | | | | | | | | | | | |

¹Correlations significant at $P \leq 0.05$ are shown. UI3T = races 1, 5, 7 and 9 were evaluated in pod; races 5 and 9 were evaluated in primary leaf. UI3A52 = races 1, 7 and 9 were evaluated in pod; races 1 and 7 were evaluated in primary leaf. PDC = pod disease score, PAUDPC = pod area under the disease progress curve, PAREA = size of the lesion on pods, PLDC = primary leaf disease score, PLAUDPC = primary leaf area under the disease progress curve, PLAREA = size of the lesion on primary leaves.

Table S2. Distribution of molecular markers on the linkage map constructed from the F₂ UI3T population.

| LG | Map length (cM) | Nº markers | Marker density (cM/marker) | Marker types | | | | |
|--------------|--------------------|------------|-------------------------------|------------------|----------|------------------|-----------|-----------|
| | | | | SSR ^a | Fin | PFC ^b | Pse-race1 | Pse-race5 |
| 1 | 40.45 | 7 | 5.8 | 6 | 1 | | | |
| 2 | 97.82 | 11 | 8.9 | | 11 | | | |
| 3 | 86.93 | 12 | 7.2 | | 12 | | | |
| 4 | 38.24 | 5 | 7.7 | | 5 | | | |
| 5 | 45.56 | 5 | 9.1 | | 5 | | | |
| 6 | 126.28 | 11 | 11.5 | 10 | | 1 | | |
| 7 | 10.91 | 2 | 5.5 | | 2 | | | |
| 8 | 79.76 | 10 | 8.0 | | 10 | | | |
| 9 | 113.64 | 13 | 8.7 | | 13 | | | |
| 10 | 48.80 | 10 | 4.9 | 7 | | 1 | 1 | 1 |
| 11 | 62.42 | 5 | 12.5 | 5 | | | | |
| Total | 750.81 | 91 | 89.8 | 86 | 1 | 1 | 1 | 1 |

^aSSR: Simple sequence repeat. ^bPFC: flower colour marker.**Table S3.** Distribution of molecular markers on the linkage map constructed from the F₂ UI3A52 population.

| LG | Map length (cM) | Nº markers | Marker density (cM/marker) | Marker types | | | | |
|--------------|--------------------|------------|-------------------------------|------------------|----------|------------------|-----------|-----------|
| | | | | SSR ^a | Fin | PFC ^b | Pse-race1 | Pse-race7 |
| 1 | 45.92 | 5 | 9.2 | 4 | 1 | | | |
| 2 | 92.62 | 15 | 6.2 | | 15 | | | |
| 3 | 50.90 | 12 | 4.2 | | 12 | | | |
| 4 | 84.40 | 9 | 9.4 | | 9 | | | |
| 5 | 51.55 | 4 | 12.9 | | 4 | | | |
| 6 | 91.83 | 12 | 7.7 | 11 | | 1 | | |
| 7 | 41.12 | 3 | 13.7 | | 3 | | | |
| 8 | 65.85 | 8 | 8.2 | | 8 | | | |
| 9 | 87.20 | 14 | 6.2 | | 14 | | | |
| 10 | 45.45 | 10 | 4.5 | 8 | | | 1 | 1 |
| 11 | 69.75 | 7 | 10.0 | 7 | | | | |
| Total | 726.59 | 99 | 92.2 | 95 | 1 | 1 | 1 | 1 |

^aSSR: Simple sequence repeat. ^bPFC: flower colour marker.

Table S4. The annotated potential candidate genes identified on QTL intervals, their chromosome (Chr) location (start and end), the putative predicted function resulting from Phytozome and TAIR functional annotations and their homologs in Arabidopsis.

| Gene Name | Chromosome | Gene Start...End (bp) | Description Pyrozoome | Arabidopsis Homolog | Description TAIR |
|--------------------------|------------|-----------------------|---|---------------------|--|
| <i>Phnl.008G.098500</i> | Chr08 | 10319464...10323106 | Flavonol synthase | AT5c05600 | Encodes a protein with similarity to flavonol synthases |
| <i>Phnl.008G.120600</i> | Chr08 | 10505620...10509420 | Serine/Treonine protein kinase | AT5c02290 | Protein kinase NAK |
| <i>Phnl.008G.109001</i> | Chr08 | 10681885...10685563 | Esterase | AT5c02210 | SGNH hydrolase-type esterase protein |
| <i>Phnl.008G.103900</i> | Chr08 | 11325850...11327548 | Zinc finger C3HC4 type | AT4c3431 | UDP-glucosyl transferase 73B3 |
| <i>Phnl.008G.104900</i> | Chr08 | 11539614...11542822 | Glycosyltransferase | AT5c01520 | RING/U-box protein |
| <i>Phnl.008G.105300</i> | Chr08 | 11594380...11609778 | Serine/Treonine protein kinase | AT3c09010 | Protein kinase |
| <i>Phnl.008G.105600</i> | Chr08 | 11643663...11646782 | NL-like protein | AT3c05750 | Leucine-rich repeat protein kinase |
| <i>Phnl.008G.105700</i> | Chr08 | 11650196...11651706 | Galactosyl transferase | AT2c38150 | 14-glycosyltransferase protein |
| <i>Phnl.008G.105900</i> | Chr08 | 11661123...11665557 | Pentatricopeptide repeat family (PPR) | AT4c28010 | Tetratricopeptide repeat (TR)-like protein |
| <i>Phnl.008G.106400</i> | Chr08 | 11726822...11728705 | Aquaporin | AT4c00430 | Plasma membrane intrinsic protein |
| <i>Phnl.008G.106500</i> | Chr08 | 11754183...11760972 | NL-like protein | AT4c08850 | Leucine-rich repeat receptor-like protein |
| <i>Phnl.008G.106600</i> | Chr08 | 11766828...11771697 | Serine/Treonine protein kinase | AT4c08850 | Leucine-rich repeat receptor-like protein |
| <i>Phnl.008G.106700</i> | Chr08 | 11833930...11837425 | Glycerol transferase | AT2c38110 | Glycerol-3-phosphate acyltransferase 6 |
| <i>Phnl.008G.107400</i> | Chr08 | 11938397...11941731 | Pentatricopeptide repeat family (PPR) | AT3c09060 | Pentatricopeptide repeat (PPR) protein |
| <i>Phnl.008G.108400</i> | Chr08 | 12155232...12159861 | NL-like protein | AT4c08850 | Receptor like protein 13 |
| <i>Phnl.008G.108500</i> | Chr08 | 12177794...12182886 | NL-like protein | AT4c74170 | Receptor like protein 13 |
| <i>Phnl.008G.109000</i> | Chr08 | 12247176...12250708 | Pectinase | AT4c58190 | Receptor like protein 9 |
| <i>Phnl.008G.109100</i> | Chr08 | 12255903...12260296 | Serine/Treonine protein kinase | AT4c74190 | Receptor like protein 15 |
| <i>Phnl.008G.109200</i> | Chr08 | 12298571...12300950 | Pectinase | AT4c58190 | Receptor like protein 9 |
| <i>Phnl.008G.109300</i> | Chr08 | 12306228...12312248 | NL-like protein | AT4c74180 | Receptor like protein 14 |
| <i>Phnl.008G.109600</i> | Chr08 | 12386198...12388610 | NL-like protein | AT4c58380 | E3 ligase involved in membrane trafficking and salt stress |
| <i>Phnl.008G.111100</i> | Chr08 | 12599137...12601627 | Zinc finger C3HC4 type | AT5c49290 | Receptor like protein 56 |
| <i>Phnl.008G.111600</i> | Chr08 | 12621658...12629777 | NL-like protein | AT4c58190 | Receptor like protein 9 |
| <i>Phnl.008G.111700</i> | Chr08 | 12704332...12705729 | Pectinase | AT4c58190 | Receptor like protein 9 |
| <i>Phnl.008G.111800</i> | Chr08 | 12731112...12735272 | NL-like protein | AT5c05630 | RING/FYVE/PHD zinc finger protein |
| <i>Phnl.008G.112400</i> | Chr08 | 12920518...12923637 | Zinc finger C3HC4 type | AT3c53990 | AT1SP, UNIVERSAL STRESS PROTEIN |
| <i>Phnl.008G.115500</i> | Chr08 | 13219256...13220618 | Universal stress protein | AT4c58270 | ATGSTU8, GLUTATHIONE S-TRANSFERASE TAU 8 |
| <i>Phnl.008G.115600</i> | Chr08 | 13221659...13223083 | Glutathione transferase | AT4c58270 | ATGSTU8, GLUTATHIONE S-TRANSFERASE TAU 8 |
| <i>Phnl.008G.115700</i> | Chr08 | 13237819...13238946 | Glutathione transferase | AT3c58380 | Bitunctional inhibitor/lipid-transfer protein |
| <i>Phnl.008G.115900</i> | Chr08 | 13258029...13259010 | Lipid transfer protein (LTP) | AT5c02070 | Protein kinase |
| <i>Phnl.008G.115800</i> | Chr08 | 13271112...12735272 | Serine/Treonine protein kinase | AT4c74180 | LH-like protein |
| <i>Phnl.008G.115900</i> | Chr08 | 13295713...13296184 | Zinc finger C3HC4 type | AT3c53990 | Myzus persicae-induced lpsase 1 |
| <i>Phnl.008G.115700</i> | Chr08 | 132995718...13299572 | Univer sal stress protein | AT4c58270 | Pathogenes-related thaumatin protein |
| <i>Phnl.008G.117900</i> | Chr08 | 13373819...13238946 | Glutathione transferase | AT4c58270 | LATERAL BRANCHING OXIDOREDUCTASE 1, LBO1 |
| <i>Phnl.008G.118000</i> | Chr08 | 13375819...13238946 | Lipase | AT5c02070 | Leucine-rich repeat protein kinase |
| <i>Phnl.008G.117700</i> | Chr08 | 13441681...14433497 | Serine/Treonine protein kinase | AT2c32180 | ABA and drought-induced RING-DUF1117 gene |
| <i>Phnl.008G.122900</i> | Chr08 | 14476637...14478004 | Pathogenesis related Thaumatin (PRTL P) | AT5c02140 | WRKY DNA-binding protein 49 |
| <i>Phnl.008G.118300</i> | Chr08 | 14495367...14495922 | Oxidoreductase | AT5c21420 | Pentatricopeptide repeat (PPR)-like protein |
| <i>Phnl.008G.118500</i> | Chr08 | 14548063...14548199 | Serine/Treonine protein kinase | AT3c47110 | Pentatricopeptide repeat (PPR)-like protein |
| <i>Phnl.008G.118600</i> | Chr08 | 14575781...14577231 | Zinc finger C3HC4 type | AT5c46620 | RING/U-box superfamily protein |
| <i>Phnl.008G.118400</i> | Chr08 | 14740208...14743290 | WRKY TF | AT5c43290 | F-box/RNF-like/FBD-like domains-containing protein |
| <i>Phnl.008G.101600</i> | Chr08 | 15045866...15411182 | Pentatricopeptide repeat family (PPR) | AT5c65560 | S-locus lectin protein in kinase family protein |
| <i>Phnl.008G.101200</i> | Chr08 | 15335624...15438955 | Pentatricopeptide repeat family (PPR) | AT5c16420 | Protein in kinase superfamily protein |
| <i>Phnl.008G.109400</i> | Chr08 | 16248222...16249847 | Zinc finger C3HC4 type | AT2c37580 | Protein kinase with octocosaapeptide/Phox/Bem1p |
| <i>Phnl.008G.109300</i> | Chr08 | 16271031...16271907 | NL-like protein | AT4c58270 | Transmembrane kinase-like 1 |
| <i>Phnl.008G.124400</i> | Chr08 | 16608575...16610205 | NL-like protein | AT4c58270 | Leucine-rich repeat transmembrane protein kinase |
| <i>Phnl.008G.124300</i> | Chr08 | 16672270...16675330 | Lipase | AT2c79130 | Lipase 1 |
| <i>Phnl.008G.124200</i> | Chr08 | 16755582...16757827 | Serine/Treonine protein kinase | AT5c48730 | FBD, F-box, Skp2-like and Leucine Rich Repeat protein |
| <i>Phnl.008G.122700</i> | Chr08 | 17085291...17103461 | Serine/Treonine protein kinase | AT3c24715 | Xyloglucan endotransglucosylase/hydrolase 2 |
| <i>Phnl.008G.122400</i> | Chr08 | 17352547...17357788 | Serine/Treonine protein kinase | AT3c24660 | S-locus lectin protein kinase |
| <i>Phnl.008G.122200</i> | Chr08 | 17397673...17401925 | Serine/Treonine protein kinase | AT5c48940 | F-box/RNF-like/FFB-like domains-containing protein |
| <i>Phnl.008G.12537</i> | Chr08 | 18554390...18558807 | Lipase | AT4c58270 | RING/U-box protein |
| <i>Phnl.008G.126700</i> | Chr08 | 18742319...18746922 | Pentatricopeptide repeat family (PPR) | AT5c48730 | Xyloglucan endotransglucosylase/hydrolase 2 |
| <i>Phnl.008G.124900</i> | Chr08 | 19421181...19423235 | NL-like protein | AT4c03340 | RPML interacting protein 4 (RIN4) |
| <i>Phnl.008G.124800</i> | Chr08 | 19448115...1945086 | Glycosyltransferase | AT2c19130 | F-box/RNF-like/FFB-like domains-containing protein |
| <i>Phnl.008G.1224500</i> | Chr08 | 19803079...19804421 | NL-like protein | AT4c26340 | Fatty acyl-ACP thioesterase |
| <i>Phnl.008G.1228400</i> | Chr08 | 20059106...20661492 | Zinc finger C3HC4 type | AT5c07120 | RING/U-box protein |
| <i>Phnl.008G.129100</i> | Chr08 | 20795642...20799197 | Glycosyltransferase | AT4c73090 | Fatty acyl-ACP thioesterase |
| <i>Phnl.008G.123900</i> | Chr08 | 20990182...20992380 | NL-like protein | AT5c22660 | Galactosyltransferase protein |
| <i>Phnl.008G.1239900</i> | Chr08 | 21029894...21032325 | Oxidoreductase | AT4c73090 | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase |
| <i>Phnl.008G.130600</i> | Chr08 | 21193569...21195702 | Esterase | AT3c25070 | Pentatricopeptide repeat (PPR) protein |
| <i>Phnl.008G.130800</i> | Chr08 | 21212388...21217383 | Galacturonosyl transferase | AT3c25110 | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase |
| <i>Phnl.008G.132200</i> | Chr08 | 21617510...21620576 | Galactosyl transferase | AT4c73090 | Pentatricopeptide repeat (PPR) protein |
| <i>Phnl.008G.133000</i> | Chr08 | 22089795...22092262 | Oxidoreductase | AT4c73090 | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase |
| <i>Phnl.008G.134100</i> | Chr08 | 22688822...2247056 | Pentatricopeptide repeat family (PPR) | AT4c74890 | Pentatricopeptide repeat (PPR) protein |
| <i>Phnl.008G.134600</i> | Chr08 | 22643571...22647076 | Lipid transfer protein (LTP) | AT4c74890 | Bifunctional inhibitor/lipid-transfer protein/seed storage |
| <i>Phnl.008G.137100</i> | Chr08 | 27792568...27793248 | Serine/Treonine protein kinase | AT2c32800 | Protein kinase |
| <i>Phnl.008G.1329200</i> | Chr08 | 29375892...29378417 | | | |

Table S4. Continued.

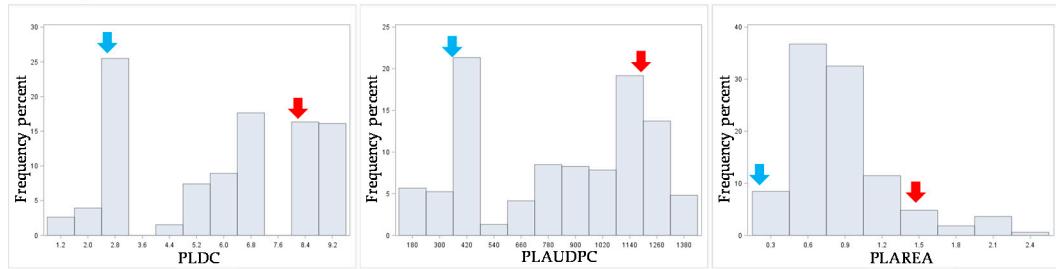
| Gene Name | Chromosome | Gene Start...End (bp) | Description Phytozome | Arabidopsis Homolog | Description TAIR |
|-------------------------|------------|-----------------------|---|---------------------|---|
| <i>Phvul.010G001300</i> | Chr10 | 1289816...1293978 | Glucosyl Transferase | AT1G22340 | UDP-glucosyl transferase 85A7 |
| <i>Phvul.010G001400</i> | Chr10 | 401790...407040 | Adenosyl-Methionine-dependent Methyltransferase | AT5G01470 | Sadenosyl-L-methionine-dependent methyltransferases protein |
| <i>Phvul.010G002000</i> | Chr10 | 453307...457549 | Zinc finger C3HC4 type | AT5G01520 | RING/U-box protein |
| <i>Phvul.010G002300</i> | Chr10 | 482796...483181 | Defensin-like protein (DEFL) | AT4G29273 | low-molecular-weight cysteine-rich 23 |
| <i>Phvul.010G002400</i> | Chr10 | 488355...488692 | Defensin-like protein (DEFL) | AT4G29273 | low-molecular-weight cysteine-rich 23 |
| <i>Phvul.010G002900</i> | Chr10 | 533958...537310 | Glucan glucosidase | AT5G01260 | Carbohydrate-binding-like fold |
| <i>Phvul.010G003100</i> | Chr10 | 552374...553612 | lactosyl ceramide galactosyl transferase | AT2G38150 | Alpha 1,4-glycosyltransferase family protein |
| <i>Phvul.010G004650</i> | Chr10 | 719323...722383 | Glycerol-3-phosphate 2-O-acyltransferase | AT2G38110 | Glycerol-3-phosphate acyltransferase 6 |
| <i>Phvul.010G005300</i> | Chr10 | 818028...824698 | Zinc finger C3HC4 type | AT5G05830 | RING/FYVE/PHD zinc finger protein |
| <i>Phvul.010G005500</i> | Chr10 | 849926...851704 | Lipid transferase | AT5G05960 | Bifunctional inhibitor/lipid transfer protein/seed storage 2S albumin protein |
| <i>Phvul.010G005800</i> | Chr10 | 875154...878597 | Lipase LTL1 | AT5G33370 | GDSL-like Lipase/Acylhydrolase protein |
| <i>Phvul.010G008700</i> | Chr10 | 1236830...1248545 | TIR-NL protein | AT5G36930 | Disease resistance protein (TIR-NBS-LRR class) |
| <i>Phvul.010G008900</i> | Chr10 | 1268630...1271183 | Universal stress protein family | AT3G53990 | Adenine nucleotide alpha hydrolases-like protein |
| <i>Phvul.010G009000</i> | Chr10 | 1282831...1287667 | Glucosyl Transferase | AT1G22340 | UDP-glucosyl transferase 85A7 |
| <i>Phvul.010G010300</i> | Chr10 | 1480675...1484047 | Serine/Threonine protein kinase | AT2G28930 | Protein kinase 1B |
| <i>Phvul.010G011400</i> | Chr10 | 1622170...1628245 | Serine/Threonine protein kinase | AT2G22970 | Serine carboxypeptidase-like 11 |
| <i>Phvul.010G012700</i> | Chr10 | 2089803...2092764 | Steroid 17alpha-monoxygenase | AT2G45570 | Cytochrome P450, family 76, subfamily C, polypeptide 2 |
| <i>Phvul.010G012800</i> | Chr10 | 2063963...2073914 | ABC Transporter Family member | AT3G62150 | P-glycoprotein 21 |
| <i>Phvul.010G012900</i> | Chr10 | 2037888...2039846 | Isoflavone 2'-hydroxylase / Isoflavone 2'-monooxygenase | AT4G37370 | Cytochrome P450, family 81, subfamily D, polypeptide 8 |
| <i>Phvul.010G013000</i> | Chr10 | 2027857...2029737 | Isoflavone 2'-hydroxylase / Isoflavone 2'-monooxygenase | AT4G37370 | Cytochrome P450, family 81, subfamily D, polypeptide 8 |
| <i>Phvul.010G013100</i> | Chr10 | 2020026...2021761 | Isoflavone 2'-hydroxylase / Isoflavone 2'-monooxygenase | AT4G37370 | Cytochrome P450, family 81, subfamily D, polypeptide 8 |
| <i>Phvul.010G013600</i> | Chr10 | 1903841...1907125 | NL-like protein | AT1G45616 | Receptor like protein 6 |
| <i>Phvul.010G013700</i> | Chr10 | 1892124...1895918 | NL-like protein | AT1G45616 | Receptor like protein 6 |
| <i>Phvul.010G013800</i> | Chr10 | 1821464...1855683 | Sterol Glucosyl Transferase | AT3G07020 | UDP-Glycosyltransferase protein |
| <i>Phvul.010G014000</i> | Chr10 | 1807165...1814966 | Glycosyl transferase | AT2G37585 | Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase protein |
| <i>Phvul.010G014101</i> | Chr10 | 1920411...1922933 | NL-like protein | AT1G45616 | Receptor like protein 6 |
| <i>Phvul.010G015100</i> | Chr10 | 2253323...2267345 | Serine/Threonine protein kinase | AT2G37840 | Protein kinase protein |
| <i>Phvul.010G015400</i> | Chr10 | 2305856...2316848 | Glutamate-5-semialdehyde dehydrogenase | AT2G39800 | delta1-pyrroline-5-carboxylate synthase 1 |
| <i>Phvul.010G015900</i> | Chr10 | 2350908...2357176 | Oxidoreductase | AT3G19010 | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase protein |
| <i>Phvul.010G018000</i> | Chr10 | 2633076...2636748 | Polygalacturonase / Pectinase | AT3G15720 | Pectin lyase-like protein |
| <i>Phvul.010G018300</i> | Chr10 | 2658302...2665822 | NL-like protein | AT5G48740 | Leucine-rich repeat protein kinase protein |
| <i>Phvul.010G018400</i> | Chr10 | 2689239...2693034 | TIR-NL protein | AT5G36930 | Disease resistance protein (TIR-NBS-LRR class) |
| <i>Phvul.010G019900</i> | Chr10 | 2884093...2885050 | Zinc finger C3HC4 type | AT3G25030 | RING/U-box protein |
| <i>Phvul.010G021001</i> | Chr10 | 3006260...3010587 | Lipase 5 | AT1G53920 | GDSL-motif lipase 5 |
| <i>Phvul.010G021200</i> | Chr10 | 3035922...3042052 | RPM1-interacting protein 4 (RIN4) | AT3G25070 | RPM1 interacting protein 4 |
| <i>Phvul.010G023100</i> | Chr10 | 3272172...3280327 | NL-like protein | AT5G63020 | Disease resistance protein (CC-NBS-LRR class) |
| <i>Phvul.010G023200</i> | Chr10 | 3283510...3296126 | NL-like protein | AT1G12280 | LRR and NB-ARC domains-containing disease resistance protein |
| <i>Phvul.010G023500</i> | Chr10 | 3306753...3310882 | NL-like protein | AT4G13020 | Protein kinase protein |
| <i>Phvul.010G023600</i> | Chr10 | 3315963...3326616 | Serine/Threonine protein kinase | AT4G13020 | Protein kinase protein |
| <i>Phvul.010G023800</i> | Chr10 | 3351907...3357035 | Glycosyl Hydrolase | AT3G07320 | O-Glycosyl hydrolases family 17 protein |
| <i>Phvul.010G024000</i> | Chr10 | 3382255...3384686 | NL-like protein | AT5G36930 | Disease resistance protein (TIR-NBS-LRR class) |
| <i>Phvul.010G024100</i> | Chr10 | 3388369...3391852 | TIR-NL protein | AT5G36930 | Disease resistance protein (TIR-NBS-LRR class) |
| <i>Phvul.010G024250</i> | Chr10 | 3412387...3416106 | TIR-NL protein | AT5G36930 | Disease resistance protein (TIR-NBS-LRR class) |
| <i>Phvul.010G024301</i> | Chr10 | 3434532...3438142 | TIR-NL protein | AT5G36930 | Disease resistance protein (TIR-NBS-LRR class) |
| <i>Phvul.010G024351</i> | Chr10 | 3445959...3449123 | NL-like protein | AT5G36930 | Disease resistance protein (TIR-NBS-LRR class) |
| <i>Phvul.010G024700</i> | Chr10 | 3484577...3492985 | Xyloglucan Glycosyl transferase | AT3G07330 | Cellulose-synthase-like C6 |

Table S4. Continued.

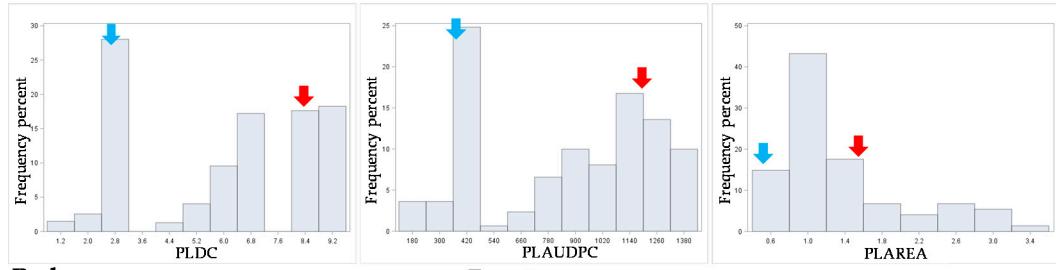
Table S4. Continued.

| Gene Name | Chromosome | Gene Start...End (bp) | Description Phytozome | Arabidopsis Homolog | Description TAIR |
|-------------------------|------------|-----------------------|--|---------------------|---|
| <i>Phvul.010G098200</i> | Chr10 | 36365007...363676239 | Esterase | AT1G01710 | Acyl-CoA thioesterase family protein |
| <i>Phvul.010G098400</i> | Chr10 | 36393060...36394219 | Oxidoreductase | AT4G23340 | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase protein |
| <i>Phvul.010G099700</i> | Chr10 | 36675257...36679613 | Glycerol transferase | AT1G01610 | Glycerol-3-phosphate acyltransferase 4 |
| <i>Phvul.010G100400</i> | Chr10 | 36793713...36796196 | Serine/Threonine protein kinase | AT4G00340 | RLK4 |
| <i>Phvul.010G100500</i> | Chr10 | 36801234...36804309 | Zinc finger C3HC4 type | AT4G00335 | RING-H2 finger B1A |
| <i>Phvul.010G100600</i> | Chr10 | 36814429...36816452 | Pentatricopeptide repeat family (PPR) | AT2G46050 | Pentatricopeptide repeat (PPR-like) protein |
| <i>Phvul.010G101100</i> | Chr10 | 36971142...36973192 | Zinc finger C3HC4 type | AT3G61460 | Brassinosteroid-responsive RING-H2 |
| <i>Phvul.010G101600</i> | Chr10 | 37068692...37070667 | Glucosyl transferase | AT4G34131 | UDP-glucosyl transferase 73B3 |
| <i>Phvul.010G101800</i> | Chr10 | 37085644...37087392 | Glucosyl transferase | AT4G34138 | UDP-glucosyl transferase 73B1 |
| <i>Phvul.010G103100</i> | Chr10 | 37208438...37212085 | Lipase | AT1G01540 | Protein kinase protein |
| <i>Phvul.010G104200</i> | Chr10 | 37414116...37415803 | WRKY TF | AT4G01250 | WRKY TF |
| <i>Phvul.010G104300</i> | Chr10 | 37472766...37482584 | NL-like protein | AT4G27190 | NB-ARC domain-containing disease resistance protein |
| <i>Phvul.010G104700</i> | Chr10 | 37598402...37599637 | WRKY TF | AT1G64000 | WRKY DNA-binding protein 56 |
| <i>Phvul.010G105200</i> | Chr10 | 37619151...37619723 | Zinc finger C3HC4 type | AT3G61550 | RING/U-box protein |
| <i>Phvul.010G105900</i> | Chr10 | 37677298...37683724 | Glycosyl transferase | AT4G01210 | Glycosyl transferase |
| <i>Phvul.010G108000</i> | Chr10 | 38056509...38057171 | Lipase | AT1G17420 | Lipoxygenase 3 |
| <i>Phvul.010G108700</i> | Chr10 | 38146639...38149457 | Zinc finger C3HC4 type | AT4G01130 | GDSL-like Lipase/Acylhydrolase superfamily protein |
| <i>Phvul.010G110500</i> | Chr10 | 38414889...38418585 | Natural Resistance Associated Macrophage protein (NRAMP) | AT1G47240 | NRAMP metal ion transporter 2 |
| <i>Phvul.010G110600</i> | Chr10 | 38420816...38422570 | Serine/Threonine protein kinase | AT5G56760 | Serine acetyltransferase 1;1 |
| <i>Phvul.010G111000</i> | Chr10 | 38509109...38512009 | Serine/Threonine protein kinase | AT1G64300 | Protein kinase protein |
| <i>Phvul.010G111900</i> | Chr10 | 38679128...38681765 | WRKY TF | AT4G23810 | WRKY family transcription factor |
| <i>Phvul.010G112400</i> | Chr10 | 38745119...38748532 | Pentatricopeptide repeat family (PPR) | AT4G01030 | Pentatricopeptide (PPR) repeat-containing protein |
| <i>Phvul.010G113700</i> | Chr10 | 38995279...38997358 | Zinc finger C3HC4 type | AT2G46495 | RING/U-box protein |
| <i>Phvul.010G114100</i> | Chr10 | 39045743...39062551 | Pentatricopeptide repeat family (PPR) | AT1G01320 | Tetratricopeptide repeat (TPR)-like protein |
| <i>Phvul.010G114900</i> | Chr10 | 39188392...39189333 | Ethylene responsive TF | AT1G01250 | Integrase-type DNA-binding protein |
| <i>Phvul.010G115600</i> | Chr10 | 39320406...39322691 | Zinc finger C3HC4 type | AT3G61850 | Dof-type zinc finger DNA-binding family protein |
| <i>Phvul.010G115800</i> | Chr10 | 39349541...39353600 | Serine/Threonine protein kinase | AT1G49160 | Protein kinase protein |
| <i>Phvul.010G116300</i> | Chr10 | 39389924...39392040 | Pentatricopeptide repeat family (PPR) | AT5G08510 | Pentatricopeptide repeat (PPR-like) protein |
| <i>Phvul.010G117600</i> | Chr10 | 39660323...39667705 | Serine/Threonine protein kinase | AT2G46700 | CDPK-related kinase 3 |
| <i>Phvul.010G118300</i> | Chr10 | 39752572...39758271 | Serine/Threonine protein kinase | AT1G01140 | CBL-interacting protein kinase 9 |
| <i>Phvul.010G119400</i> | Chr10 | 39958684...39970905 | Zinc finger C3HC4 type | AT4G00800 | Transducin protein |

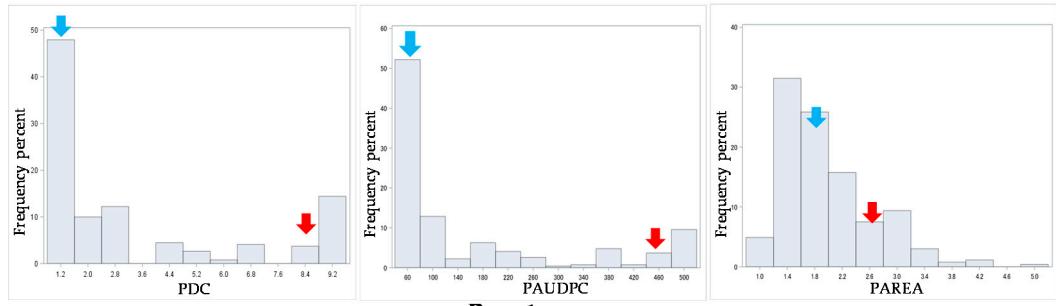
Primary leaf



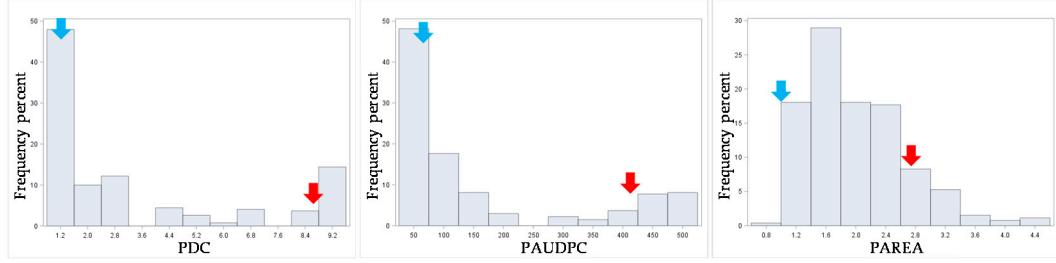
Race 5



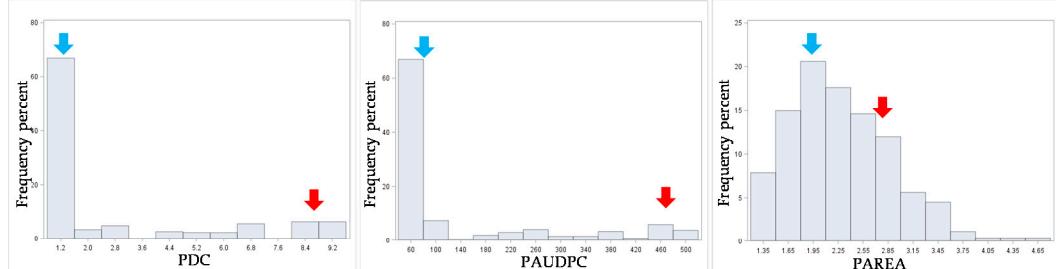
Race 9



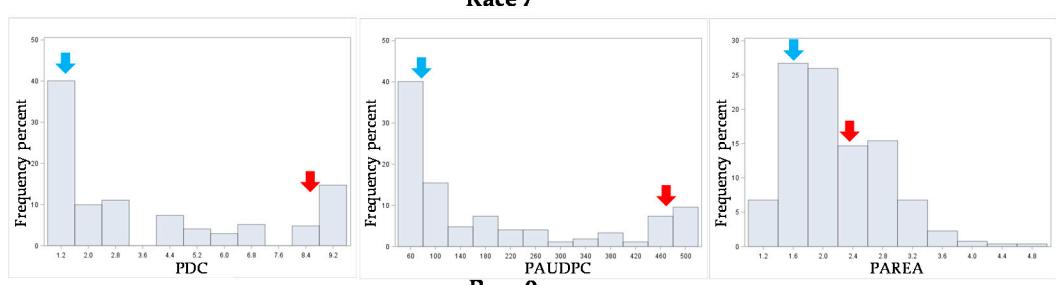
Race 1



Race 5



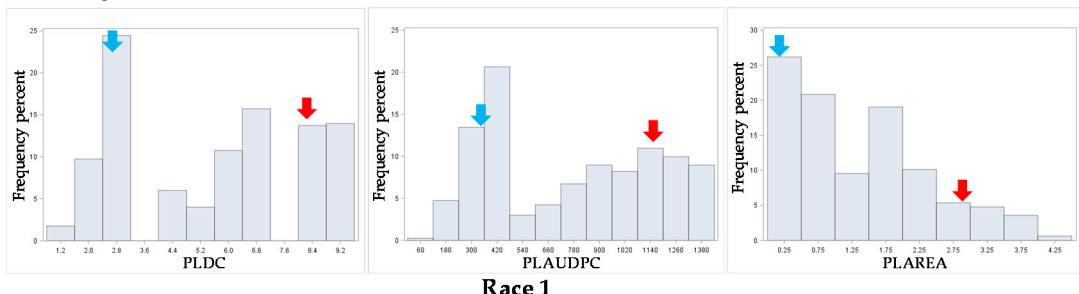
Race 7



Race 9

Figure S1. Frequency distribution for disease score (DC), area under the disease progress curve (AUDPC) and lesion (AREA) for primary leaf and pod resistance to halo blight races 1, 5, 7 and 9 of the F₂ UI3T population. Estimates of the two parents are indicated by blue (UI3) and red (Tendergreen) arrows. PDC = pod disease score; PAUDPC = pod area under the disease progress curve; PAREA = size of the lesion on pods; PLDC = primary leaf disease score; PLAUDPC = primary leaf area under the disease progress curve; PLAREA = size of the lesion on primary leaves. The two primary (unifoliate) leaves of bean plants were inoculated with races 5 and 9.

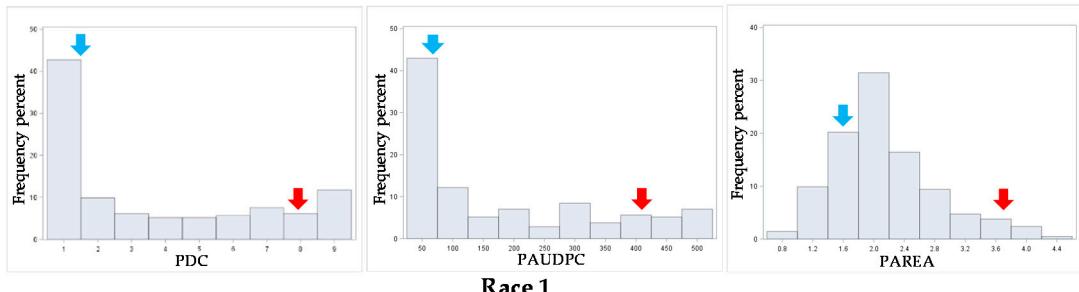
Primary leaf



Race 1

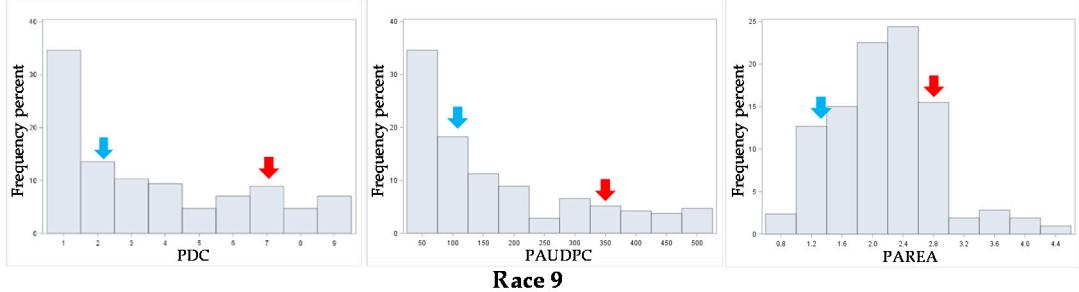
Race 7

Pod



Race 1

Race 7



Race 9

Figure S2. Frequency distribution for disease score (DC), area under the disease progress curve (AUDPC), and area lesion (AREA) in primary leaf and pod resistance to halo blight races 1, 7 and 9 of the F₂ UI3A52 population. Estimates of the two parents are indicated by blue (UI3) and red (A52) arrows. PDC = pod disease score; PAUDPC = pod area under the disease progress curve; PAREA = size of the lesion on pods; PLDC = primary leaf disease score; PLAUDPC = primary leaf area under the disease progress curve;

PLAREA = size of the lesion on primary leaves. The two primary (unifoliate) leaves of bean plants were inoculated with races 1 and 7.