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| **Table S1. Genome wide association hits for resistance to gray leaf spot.** Functionally annotated genome wide association hits. A 10 Kilobase window on either side of the GWA hit was screened for genes. Chr=Chromosome; BPP=Bootstrap posterior probability. |
| Chr | Marker Position | allele | effect | BPP | Gene | Functional Annotation |
| 1 | 2,030,770  | T/C | 0.62 | 7 | GRMZM2G164696 | Maize for beta 1 tubulin |
| 1 | 9,931,873  | C/G | 0.71 | 10 | GRMZM2G178571 | *Zea mays* 1-deoxy-D-xylulose 5-phosphate synthase 1 |
| 1 | 21,532,972  | G/A | -0.52 | 8 | GRMZM2G086604 | *Zea mays* retrotransposon Cinful-1 |
| 1 | 21,557,348  | G/T | 0.93 | 7 | Intergenic |  |
| 1 | 26,273,179  | C/T | 1.47 | 8 | Intergenic |  |
| 1 | 64,986,440  | C/G | -0.51 | 10 | GRMZM2G127181 | uncharacterized |
| 1 | 74,843,220  | T/C | -0.36 | 6 | Intergenic |  |
| 1 | 75,268,439  | G/A | -0.60 | 14 | Intergenic |  |
| 1 | 173,110,701  | G/A | -2.00 | 8 | Intergenic |  |
| 1 | 180,262,819  | C/T | -1.39 | 16 | Intergenic |  |
| 1 | 183,969,702  | G/T | -0.70 | 12 | GRMZM2G080746 | uncharacterized |
| 1 | 186,614,192  | T/C | -1.01 | 35 | AC205695.3\_FG008 | uncharacterized |
| 1 | 187,927,685  | G/A | -1.87 | 26 | Intergenic |  |
| 1 | 198,970,183  | T/C | 0.74 | 7 | Intergenic |  |
| 1 | 199,579,946  | A/G | -0.85 | 7 | Intergenic |  |
| 1 | 201,295,476  | G/A | -0.63 | 12 | Intergenic |  |
| 1 | 207,120,463  | --/CC | -0.77 | 7 | GRMZM2G303157 | *Zea mays* T cytoplasm male sterility restorer factor 2  |
| 1 | 284,043,464  | G/A | 0.43 | 6 | Intergenic |  |
| 1 | 284,048,249  | C/A | 0.49 | 6 | GRMZM2G069772 | *Zea mays* rust resistance protein rp3-1  |
| 1 | 284,837,740  | A/G | 0.30 | 9 | Intergenic |  |
| 1 | 284,841,425  | G/T | 0.46 | 8 | Intergenic |  |
| 1 | 284,892,880  | A/C | 0.34 | 13 | Intergenic |  |
| 1 | 286,994,723  | G/A | 0.63 | 8 | GRMZM2G371210 | phytoene synthase (PSY1)  |
| 1 | 293,630,563  | -------/GCCACAT | -2.93 | 7 | GRMZM2G068117 | *Zea mays* putative pol protein  |
| 2 | 13,580,508  | C/G | -0.59 | 11 | cDNA |  |
| 2 | 17,397,612  | G/T | -0.66 | 7 | Intergenic |  |
| 2 | 17,422,032  | A/T | -0.75 | 8 | GRMZM2G057131 | rust resistance protein rp3-1 (rp3-1)  |
| 2 | 20,029,416  | C/G | -0.66 | 10 | Intergenic |  |
| 2 | 20,639,672  | CTAGC/----- | -0.70 | 7 | Intergenic |  |
| 2 | 20,971,563  | C/A | -0.80 | 7 | Intergenic |  |
| 2 | 21,542,600  | G/C | -0.95 | 9 | GRMZM2G425211 | uncharacterized |
| 2 | 22,215,570  | C/A | -0.58 | 7 | GRMZM2G545802 | putative growth-regulating factor 1 |
| 2 | 172,704,846  | A/T | 0.46 | 7 | GRMZM2G000601 | ubiquitin-conjugating enzyme E2-17 kDa |
| 2 | 225,963,000  | C/A | -1.49 | 26 | Intergenic |  |
| 2 | 228,976,174  | C/A | -1.72 | 7 | Intergenic |  |
| 2 | 229,145,253  | G/A | -1.35 | 39 | GRMZM2G041642 | rust resistance protein rp3-1 (rp3-1)  |
| 2 | 229,637,503  | C/G | -2.41 | 7 | Intergenic |  |
| 2 | 229,862,946  | T/G | -0.93 | 16 | GRMZM2G391164 | uncharacterized |
| 2 | 230,414,321  | C/T | -1.18 | 6 | GRMZM2G152258 | tropinone reductase 2 |
| 2 | 230,584,153  | A/G | -1.89 | 7 | GRMZM2G513206 | ramosa 2 (ra2)  |
| 2 | 230,615,501  | T/G | -0.88 | 10 | GRMZM2G052403 | Tha8 (tha8)  |
| 2 | 230,898,848  | T/A | -0.53 | 7 | GRMZM2G082302 | uncharacterized |
| 3 | 163,420,613  | G/A | 0.84 | 12 | Intergenic |  |
| 3 | 163,875,247  | T/G | 1.21 | 16 | Intergenic |  |
| 3 | 163,888,333  | G/A | 0.81 | 35 | Intergenic |  |
| 3 | 165,031,510  | T/C | 1.08 | 9 | Intergenic |  |
| 3 | 165,509,907  | G/T | 0.82 | 7 | GRMZM2G444541 | *Zea mays* cultivar B73 chloroplast |
| 3 | 165,792,180  | T/A | 0.84 | 16 | Intergenic |  |
| 3 | 167,576,843  | C/- | 0.57 | 7 | Intergenic |  |
| 3 | 202,841,878  | C/T | -0.70 | 43 | AC207628.4\_FG011 | *Zea mays* see2a for putative legumain |
| 3 | 206,959,629  | C/G | -0.53 | 9 | GRMZM2G028568 | phytoene synthase (Y1)  |
| 3 | 217,329,015  | G/A | 0.61 | 8 | Intergenic |  |
| 4 | 11,272,990  | C/T | -1.46 | 13 | GRMZM2G068330 | *Zea mays* protein dimerisation region containing protein |
| 4 | 12,987,147  | G/A | -1.19 | 6 | GRMZM2G124593 | uncharacterized |
| 4 | 39,437,101  | C/T | -0.49 | 22 | Intergenic |  |
| 4 | 93,594,993  | T/G | -1.28 | 28 | Intergenic |  |
| 4 | 137,271,558  | T/G | -0.84 | 11 | Intergenic |  |
| 4 | 140,210,546  | C/T | -1.66 | 81 | Intergenic |  |
| 4 | 143,945,947  | C/T | -0.57 | 33 | Intergenic |  |
| 4 | 147,941,545  | ---/GTC | 1.05 | 10 | Intergenic |  |
| 4 | 149,532,029  | A/T | -0.61 | 9 | Intergenic |  |
| 4 | 160,911,650  | C/A | -0.70 | 7 | Intergenic |  |
| 4 | 161,434,924  | G/A | -0.70 | 6 | GRMZM2G137696 | *Zea mays* discolored-1 (mutant allele dsc1-Ref::Mu1)  |
| 4 | 245,875,432  | C/A | -0.87 | 11 | Intergenic |  |
| 5 | 4,244,452  | C/T | -0.33 | 12 | GRMZM2G007063 | *Zea mays* opaque-2 heterodimerizing protein 1b (ohp1b) |
| 5 | 4,294,169  | A/C | -0.52 | 12 | GRMZM5G801939 | uncharacterized |
| 5 | 4,669,956  | G/C | -0.52 | 11 | GRMZM2G027495 | *Zea mays* B73 acc oxidase (ACO35)  |
| 5 | 6,369,752  | C/T | -1.26 | 7 | GRMZM2G176042 | uncharacterized |
| 5 | 6,418,770  | A/G | -1.01 | 10 | GRMZM2G077404 | *Zea mays* arginine N-methyltransferase 2 |
| 5 | 6,536,883  | G/C | -1.20 | 15 | GRMZM2G095185 | uncharacterized |
| 5 | 6,540,639  | A/T | -1.47 | 15 | GRMZM2G090432 | uncharacterized |
| 5 | 6,588,968  | A/T | -1.22 | 22 | Intergenic |  |
| 5 | 7,088,865  | A/G | -0.82 | 12 | Intergenic |  |
| 5 | 20,486,425  | --/TA | 0.77 | 6 | GRMZM2G080231 | uncharacterized |
| 5 | 21,974,701  | C/G | 0.81 | 9 | Intergenic |  |
| 5 | 25,824,240  | C/A | -1.00 | 13 | Intergenic |  |
| 5 | 40,275,106  | T/C | 0.93 | 16 | Intergenic |  |
| 5 | 56,244,216  | A/T | -1.03 | 6 | Intergenic |  |
| 5 | 181,353,895  | --/CT | 0.50 | 6 | Intergenic |  |
| 5 | 182,336,996  | C/T | 0.64 | 6 | Intergenic |  |
| 5 | 194,708,029  | C/G | 0.40 | 11 | GRMZM2G144097 | *Zea mays* folylpolyglutamate synthase (LOC100285702) |
| 5 | 197,017,506  | -/G | 0.57 | 7 | Intergenic |  |
| 5 | 204,100,563  | T/G | 0.59 | 26 | GRMZM2G029186 | uncharacterized |
| 5 | 205,473,574  | G/C | 0.82 | 22 | AC195458.3\_FG001 | uncharacterized |
| 6 | 96,317,088  | T/C | 0.37 | 9 | Intergenic |  |
| 6 | 96,520,306  | TGT/--- | 0.58 | 9 | GRMZM2G472187 | uncharacterized |
| 6 | 97,120,550  | G/C | 0.97 | 11 | GRMZM2G131020 | *Zea mays* CUE domain containing protein (LOC100282879) |
| 6 | 104,876,576  | G/T | -1.08 | 6 | Intergenic |  |
| 6 | 108,329,244  | C/G | -1.11 | 9 | GRMZM2G701063 | *Zea mays* transcriptional activator  |
| 6 | 109,996,701  | T/C | -0.55 | 11 | Intergenic |  |
| 6 | 110,193,339  | C/A | -0.76 | 9 | Intergenic |  |
| 6 | 110,249,748  | TC/-- | -0.66 | 11 | Intergenic |  |
| 6 | 129,925,381  | C/T | -0.42 | 12 | Intergenic |  |
| 6 | 138,425,664  | T/C | -0.42 | 6 | GRMZM2G117439 | uncharacterized |
| 6 | 143,322,264  | -----/GCTCG | -0.36 | 6 | Intergenic |  |
| 6 | 149,244,757  | T/C | -0.48 | 6 | Intergenic |  |
| 7 | 2,931,863  | G/C | -0.74 | 6 | Intergenic |  |
| 7 | 3,212,361  | -------/CTCGATT | -0.56 | 6 | Intergenic |  |
| 7 | 121,127,424  | ------/CTCCCA | -0.54 | 6 | Intergenic |  |
| 7 | 123,595,279  | G/A | -0.54 | 67 | GRMZM2G154752 | uncharacterized |
| 7 | 158,495,841  | C/A | 0.66 | 6 | Intergenic |  |
| 7 | 159,611,041  | -/A | -0.53 | 11 | GRMZM2G158452 | uncharacterized |
| 7 | 162,122,347  | T/A | -1.37 | 11 | Intergenic |  |
| 8 | 8,431,762  | T/A | 0.86 | 6 | Intergenic |  |
| 8 | 9,495,845  | C/T | 0.34 | 7 | GRMZM2G473485 | *Zea mays* rust resistance protein rp3-1 (rp3-1)  |
| 8 | 13,658,348  | G/T | 1.02 | 6 | AC187393.3\_FG001 | *Zea mays* heat shock factor-binding protein 1 (hsbp1)  |
| 8 | 20,706,941  | G/A | -0.64 | 7 | GRMZM2G080588 | Z.mays GapC2  |
| 8 | 26,104,142  | -/G | -0.64 | 9 | GRMZM2G154221 | *Zea mays* T cytoplasm male sterility restorer factor 2 (rf2a)  |
| 8 | 35,882,697  | G/C | -0.86 | 10 | Intergenic |  |
| 8 | 49,566,758  | G/A | -0.90 | 24 | Intergenic |  |
| 8 | 57,863,663  | G/A | -1.07 | 30 | Intergenic |  |
| 8 | 72,046,701  | ---/AAC | -0.77 | 7 | Intergenic |  |
| 8 | 105,554,753  | C/T | 0.80 | 6 | Intergenic |  |
| 8 | 141,605,883  | G/A | 1.08 | 8 | GRMZM2G015735 | *Zea mays* chloroplast phytoene synthase (Y1)  |
| 8 | 146,531,554  | -/G | 0.77 | 6 | Intergenic |  |
| 8 | 149,501,067  | A/T | 0.71 | 6 | Intergenic |  |
| 8 | 154,091,270  | A/G | 1.29 | 8 | Intergenic |  |
| 8 | 158,597,202  | C/T | 0.42 | 23 | Intergenic |  |
| 8 | 170,550,068  | T/C | 0.31 | 8 | Intergenic |  |
| 8 | 173,107,104  | C/A | -1.04 | 8 | GRMZM2G124365 | *Zea mays* B transcriptional activator (b1)  |
| 9 | 16,154,952  | G/C | -1.15 | 6 | Intergenic |  |
| 9 | 16,379,663  | CAG/--- | -0.87 | 13 | Intergenic |  |
| 9 | 16,620,539  | A/G | -0.82 | 14 | Intergenic |  |
| 9 | 18,225,380  | C/T | -0.93 | 6 | GRMZM5G899123 | *Zea mays* rust resistance protein rp3-1 (rp3-1)  |
| 9 | 99,711,027  | T/C | -1.17 | 10 | Intergenic |  |
| 9 | 128,943,719  | G/A | 0.85 | 11 | GRMZM2G045178 | uncharacterized |
| 9 | 133,801,705  | C/A | 1.38 | 10 | GRMZM2G134279 | *Zea mays* starch branching enzyme IIb (ae)  |
| 9 | 142,738,763  | A/G | -0.53 | 9 | GRMZM2G150598 | *Zea mays* starch synthase I (sS1)  |
| 9 | 142,906,275  | C/A | -0.54 | 40 | Intergenic |  |
| 9 | 143,305,297  | C/T | -0.51 | 7 | Intergenic |  |
| 9 | 150,278,166  | C/T | 0.75 | 31 | Intergenic |  |
| 10 | 1,429,820  | C/T | 0.39 | 20 | GRMZM2G048067 | uncharacterized |
| 10 | 1,529,739  | C/A | 0.47 | 20 | GRMZM2G098603 | *Zea mays* B73 pathosis-related protein 2  |
| 10 | 1,716,176  | C/T | 0.53 | 15 | GRMZM2G430780 | *Zea mays* NADPH-dependent reductase (a1)  |
| 10 | 1,888,649  | C/T | 0.80 | 14 | GRMZM2G022606 | uncharacterized |
| 10 | 1,918,857  | A/T | 0.51 | 14 | GRMZM2G104638 | uncharacterized |
| 10 | 1,922,550  | G/C | 0.36 | 14 | GRMZM2G104655 | Ribosome inactivating protein 1 (rip1)  |
| 10 | 3,691,250  | C/G | 0.53 | 6 | GRMZM2G143769 | *Zea mays* rust resistance protein (Rp1-D)  |
| 10 | 46,171,212  | G/A | -0.57 | 7 | Intergenic |  |
| 10 | 67,107,876  | C/T | -0.42 | 11 | Intergenic |  |
| 10 | 108,685,826  | A/G | -0.55 | 23 | Intergenic |  |
| 10 | 137,015,827  | G/T | -0.56 | 16 | GRMZM5G818664 | *Zea mays* latency associated nuclear anti |
| 10 | 138,301,336  | C/G | -0.42 | 12 | GRMZM2G105801 | uncharacterized |
| 10 | 144,243,105  | GT/-- | -0.77 | 6 | Intergenic |  |
| 10 | 144,489,188  | G/T | -0.62 | 15 | Intergenic |   |