# Table S1. Marker, chromosome (Chr), Map position (cM) based on the IBM 4 map and physical position based on B73 version 3 map (V3\_POS)

|  |  |  |  |
| --- | --- | --- | --- |
| **Marker** | **Chr** | **cM** | **V3\_POS** |
| PHM13360-13 | 2 | 98.62 | 111456119 |
| PHM13420-11 | 3 | 92.11 | 158556508 |
| PHM14412-4 | 2 | 127.4 | 203610640 |
| PHM14618-11 | 4 | 117 | 181259942 |
| PHM1745-16 | 3 | 85.92 | 143928532 |
| PHM3457-6 | 2 | 96.4 | 63555891 |
| PHM4185-13 | 1 | 113.04 | 83790877 |
| PHM4495-14 | 9 | 59.01 | 26832690 |
| PHM4586-12 | 2 | 79.29 | 30307725 |
| PHM4677-11 | 8 | 90.36 | 153401883 |
| PHM4720-12 | 9 | 44.98 | 17007768 |
| PHM4757-14 | 8 | 89.8 | 152292467 |
| PHM4880-179 | 2 | 98.5 | 107819754 |
| PHM5480-17 | 1 | 169.08 | 204802481 |
| PHM5805-19 | 8 | 71 | 121753452 |
| PHM9635-30 | 4 | 96.04 | 165703732 |
| PHM9914-11 | 3 | 95.07 | 161300790 |
| PZA00060-2 | 9 | 114.49 | 129272199 |
| PZA00379-2 | 8 | 59.45 | 66897042 |
| PZA00485-2 | 2 | 99.07 | 124688681 |
| PZA00492-26 | 4 | 91.78 | 161102050 |
| PZA00637-4 | 2 | 106.37 | 173044019 |
| PZA00667-1 | 3 | 96.67 | 162786508 |
| PZA01886-1 | 9 | 114.68 | 134140227 |
| PZA01926-1 | 4 | 90.25 | 159099990 |
| PZA02209-2 | 5 | 124.04 | 181262867 |
| PZA02519-7 | 10 | 91.95 | 141609305 |
| PZA02731-1 | 2 | 125.76 | 200742661 |
| PZA02969-9 | 10 | 97.93 | 143487977 |
| PZA03577-1 | 2 | 195.72 | 237178781 |

**Table S2**. Results of single marker analysis. Population, marker, marker location (bin), traits previously associated with the marker (Lopez-Zuniga 2016), markers that were selected to represent the introgression in cases where more than one marker was used (Selected), marker p-value for GLS (GLS p-value), marker p-value for SLB (SLB p-value), marker p-value for NLB (NLB p-value).

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Population | Bin | Marker | Previous | Selected | GLS  p-value | SLB  p-value | NLB  p-value |
| H100\_DRIL32.090 | 2.05 | PHM3457-6 | MDR | X | 0.0148 | 0.048 | 0.0014 |
| PZA00485-2 |  |  | 0.047 | 0.0677 | 0.0003 |
| PZA00637-4 | SLB |  | 0.944 | 0.2505 | 0.3225 |
| 8.03 | PZA00379-2 | MDR, SLB | X | 0.1161 | 0.0418 | 0.0021 |
| PHM4757-14 | MDR, GLS, NLB |  | 0.0841 | 0.1566 | 0.005 |
| H100\_DRIL32.095 | 3.04 | PHM1745-16 | MDR |  | 0.0759 | 0.3306 | 0.4362 |
| 9.04 | PZA01886-1 | MDR, SLB |  | 0.1608 | 0.0021 | 0.2098 |
| H100\_DRIL32.134 | 2.05 | **PHM3457-6** | MDR |  | 0.0067 | 0.1091 | 0.0586 |
| PZA00485-2 |  | X | 0.0002 | 0.0569 | 0.0727 |
| 8.03 | PHM4757-14 | MDR, GLS, NLB |  | 0.064 | 0.7353 | <.0001 |
| H100\_DRIL32.191 | 9.03 | PHM4495-14 | MDR, SLB |  | 0.7377 | 0.1658 | 0.0472 |
| 9.04 | PZA01886-1 | MDR, SLB |  | 0.0984 | 0.4386 | 0.6653 |
| H100\_DRIL52.055 | 2.07 | **PZA03577-1** | MDR |  | 0.8099 | 0.0199 | 0.2669 |
| 9.03 | PHM4720-12 | SLB |  | 0.8869 | 0.2741 | 0.6136 |
| 9.04 | PZA00060-2 | MDR |  | 0.465 | 0.0224 | 0.02 |
| 10.04 | PZA02519-7 | MDR, SLB |  | 0.977 | 0.1484 | 0.6371 |
| PZA02969-9 | GLS |  | 0.4391 | 0.3221 | 0.8482 |
| H100\_DRIL52.157 | 1.05 | PHM4185-13 | MDR, SLB, NLB |  | 0.6451 | 0.4918 | 0.7396 |
| PHM5480-17 | SLB |  | 0.1304 | 0.9009 | 0.8308 |

Table S2 continued

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Population | Bin | Marker | Previous | Selected | GLS  p-value | SLB  p-value | NLB  p-value |
| H100\_DRIL52.268 | 2.07 | **PZA03577-1** | MDR |  | 0.0088 | 0.1047 | 0.6988 |
| 4.05 | PHM14618-11 | NLB |  | 0.8279 | 0.1815 | 0.5258 |
| 8.03 | PHM4757-14 | GLS |  | 0.0459 | 0.6461 | 0.6885 |
| H100\_DRIL62.030 | 3.04 | PHM13420-11 | MDR, GLS |  | 0.0069 | 0.9588 | 0.1513 |
| H100\_DRIL62.078 | 4.05 | PZA01926-1 | MDR, SLB |  | <.0001 | 0.3494 | 0.1194 |
| PZA00492-26 |  |  | 0.0001 | 0.1552 | 0.0148 |
| PHM9635-30 | GLS | X | 0.0005 | 0.0765 | 0.0045 |
| 5.04 | PZA02209-2 | MDR |  | 0.0388 | 0.0102 | 0.0049 |
| H100\_DRIL62.156 | 3.04 | PHM13420-11 | MDR, GLS | X | 0.0002 | <.0001 | 0.0005 |
| PZA00667-1 | SLB |  | 0.0013 | <.0001 | 0.0002 |
| 8.03 | PHM4677-11 | GLS |  | 0.4629 | 0.3404 | 0.9757 |
| H100\_DRIL72.061 | 2.05 | PHM4586-12 | GLS |  | 0.8148 | 0.7092 | 0.6987 |
| PHM14412-4 | MDR, GLS | X | <.0001 | 0.2839 | 0.4154 |
| 3.04 | PHM9914-11 | GLS |  | 0.8668 | 0.0006 | 0.0071 |
| PZA00667-1 | MDR | X | 0.388 | 0.0052 | 0.0015 |
| H100\_DRIL72.232 | 2.05 | PHM4586-12 | GLS |  | 0.2727 | 0.0609 | 0.0065 |

**Table S3** Pairwise correlations between diseases by population. Correlation coefficient and sample number (n)

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Population** | **H100\_DRIL32.090** | | **H100\_DRIL32.095** | | **H100\_DRIL32.134** | | **H100\_DRIL32.191** | |
| Disease | SLB | GLS | SLB | GLS | SLB | GLS | SLB | GLS |
| NLB | 0.62\*\* | 0.33\*\* | 0.26\* | 0.28\* | 0.32\* | 0.32\* | 0.31\*\* | 0.18 |
| (n=58) | (n=63) | (n=77) | (n=84) | (n=57) | (n=60) | (n=78) | (n=82) |
| GLS | 0.44\*\* |  | 0.25\* |  | 0.53\*\* |  | 0.37\*\* |  |
| (n=65) |  | (n=77) |  | (n=58) |  | (n=82) |  |
| **Population** | **H100\_DRIL52.055** | | **H100\_DRIL52.157** | | **H100\_DRIL52.268** | | **H100\_DRIL62.030** | |
| Disease | SLB | GLS | SLB | GLS | SLB | GLS | SLB | GLS |
| NLB | 0.26\* | 0.003 | 0.08 | -0.04 | 0.2 | -0.09 | 0.32\*\* | 0.19 |
| (n=59) | (n=61) | (n=90) | (n=96) | (n=69) | (n=72) | (n=68) | (n=76) |
| GLS | 0.27\* |  | 0.14 |  | 0.29\* |  | 0.03 |  |
| (n=62) |  | (n=93) |  | (n=73) |  | (n=74) |  |
| **Population** | **H100\_DRIL62.078** | | **H100\_DRIL62.156** | | **H100\_DRIL72.061** | | **H100\_DRIL72.232** | |
| Disease | SLB | GLS | SLB | GLS | SLB | GLS | SLB | GLS |
| NLB | 0.31\*\* | 0.19 | 0.38\*\* | 0.5\*\* | 0.13 | 0.13 | 0.01 | 0.17 |
| (n=68) | (n=76) | (n=54) | (n=58) | (n=72) | (n=75) | (n=53) | (n=55) |
| GLS | 0.03 |  | 0.21 |  | 0.19 |  | 0 |  |
| (n=74) |  | (n=56) |  | (n=74) |  | (n=56) |  |

\*\* Significant at the *P*=0.001 level

\* Significant at the *P*=0.05 level

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**Table S4**. Variance components estimates and their standard errors for random effects, and F-tests and their associated p-values for fixed effects for standardized area under disease progress curve (sAUDPC) of (A) GLS (B) NLB and (C)SLB. p-values for random effects are derived from Wald tests. Of the three diseases, GLS was the only disease that was trialed in more than one location so a location (loc) term is included. The two NLB replications were planted in different (though neighboring) fields so range and column effect are nested within replication (rep). Both SLB replications were in the same field so nesting range and column effect within replication was not necessary in this case.

**A**.GLS

|  |  |  |  |
| --- | --- | --- | --- |
| **Cov Parm** | **Estimate** | **Standard Error** | **Pr > Z** |
| loc | 0.010 | 0.021 | 0.314 |
| rep(loc) | 0.003 | 0.007 | 0.356 |
| range(loc) | 0.037 | 0.009 | <.0001 |
| column(loc) | 0.023 | 0.005 | <.0001 |
| Residual | 0.170 | 0.006 | <.0001 |
| **Fixed Effect** | **F Value** | **Pr > F** |  |
| line | 2.76 | <.0001 |  |

**B.** NLB

|  |  |  |  |
| --- | --- | --- | --- |
| **Cov Parm** | **Estimate** | **Standard Error** | **Pr > Z** |
| rep | 89.86 | 127.27 | 0.2401 |
| range(rep) | 1.50 | 0.39 | <.0001 |
| column(rep) | 4.33 | 0.80 | <.0001 |
| Residual | 4.15 | 0.21 | <.0001 |
| **Fixed Effect** | **F Value** | **Pr > F** |  |
| DTA | 66.88 | <.0001 |  |
| line | 2.59 | <.0001 |  |

**C.**SLB

|  |  |  |  |
| --- | --- | --- | --- |
| **Cov parameter** | **Estimate** | **Standard Error** | **Pr > Z** |
| rep | 0.127 | 0.182 | 0.243 |
| range | 0.043 | 0.012 | 0.0002 |
| column | 0.061 | 0.015 | <.0001 |
| Residual | 0.169 | 0.009 | <.0001 |
| **Fixed Effect** | **F Value** | **Pr > F** |  |
| DTA | 35.57 | <.0001 |  |
| line | 2.64 | <.0001 |  |