**Supplemental File S2:**

**Molecular Dissection of Quantitative Variation in Bermudagrass Hybrids (*Cynodon dactylon* x *transvaalensis*): Morphological Traits**

**G3: Genes | Genomes | Genetics**

**Sameer Khanal1 · Jeffrey C. Dunne2 · Brian M. Schwartz3 · Changsoo Kim1,4 · Susana Milla-Lewis2 · Paul L. Raymer5 · Wayne W. Hanna3 · Jeevan Adhikari1 · Susan A. Auckland1 · Lisa Rainville1 · Andrew H. Paterson1**

*1 Plant Genome Mapping Laboratory, University of Georgia, Athens, GA 30606, 2 Crop Science Department, North Carolina State University, Raleigh, NC 27695, 3 Department of Crop and Soil Sciences, University of Georgia, Tifton, GA 31794, 4 Chungnam National University, 99 Daehak-ro, Yuseong-gu, Daejeon 34134, South Korea, 5 Department of Crop and Soil Sciences, University of Georgia, Griffin, GA 30224*

* \*Corresponding author. E-mail: paterson@uga.edu

File S2.1. Detailed methodology and results of single marker analysis (SMA).

*Methodology.* A Bonferroni corrected significance threshold [1] would be too stringent (*P* = 4.7 x 10-6), considering a total of 588 markers tested against 18 single environment phenotypes for the five traits (i.e., HT, ILEN, LLS, LLEN, and LW). We thus chose a threshold of 0.005, acknowledging that, some significant associations could be artifactual (i.e., false positives) depending upon the estimated number of virtual independent markers in the parental linkage maps. Specifically, given total recombinational length estimates of 1,181.1 cM of *C. transvaalensis* (T574) and 3,105.8 cM of *C. dactylon* (T89) monoploid maps [2] and with an assumption that independently segregating loci are separated by 30 cM, 40 (of 171) and 104 (of 349) markers are expected to be virtually independent in the respective maps. At *P* = 0.005, we could expect ~4 (40x18x0.005) and 10 (104x18x0.005) false positive associations in the respective maps. The expected number of artifactual associations range between two to six (in T574) and six to 14 (in T89) if 50 cM and 20 cM separate independently segregating loci. Similar SMA technique has been employed for exploratory QTL study in sugarcane [3]. Significant associations at contiguous and closely linked markers could either result from an effect of a single QTL in the region or from multiple QTL - both necessitate subjective criterion for selective retention of non-redundant set of QTL (i.e., deduced QTL). In case of contiguously significant markers, the most significant association was recorded as deduced QTL. Given that parental linkage maps were built at maximum recombination fraction of 40 cM, discrete and significant associations (i.e., at *P =* 0.005) separated by that distance can be recorded as different QTL for a given trait within a CG; after all, few linkages extended beyond 30 cM [2].

A less stringent modified threshold (i.e., *P =* 0.05) was employed to identify recurring marker-trait associations, which were reported as ‘putative QTL’ given that they were also significant at *P ≤* 0.005 in at least one other environment. The percentage of total phenotypic variance explained (*R*2), QTL effect (i.e., average effect of an allele substitution) at each significant association, and multiple regression statistic (i.e., statistic to determine overall variation explained by multiple QTL detected for single environment phenotypes of each trait) were obtained using JMP.

*Results.* Based on the *methodology* discussed, eight to twenty of the 98 associations identified could be artifactual based on estimate parameters. The 98 associations corresponded to 68 different marker alleles, 21 from T574 and 47 from T89. Further, eight (of 14) T574 CGs and 18 (of 34) T89 CGs carried 15 and 39 markers associated with the traits, respectively. T574 and T89 also contributed significant associations with two unlinked biparental and five and six unlinked simplex markers, respectively. A single marker was associated with the trait(s) for four and 10 CGs of T574 and T89, whereas several were significant (two to seven) for the remaining four and eight CGs, respectively.

Only six pairs of markers discretely scattered (i.e., separated by 40 cM) within the same CG showed significant association with the same trait i.e., T5742B11a/TC55531-1400 (T89 1a/b) for HT at Griffin (2010), RZ140b/T5742D06a (T574 9 and 11) for ILEN at Tifton (2011), T5742F09c/PCD142 (T89 4c/d-I and 18) and CA162523-100/T5741D01a (T89 3c/d and 16) for LLEN at Tifton (2012), and CA265902-300/T5741D01ab (T89 3c/d and 16) and RZ543a/CA265902-300 (T89 3c/d and 16) for LW at Tifton (2012) and Griffin (2012), respectively. For the first five cases, QTL effects were in the same direction (i.e., reducing trait values), corresponding markers were in coupling phase, and complementary alleles (i.e., in repulsion phase) of two of the markers (RZ140b and T5741D01a) showed effects opposite to their counterparts. For the sixth pair (i.e., RZ543a/CA265902-300), QTL effects were in the opposite direction and markers were in repulsion linkage. Based on these observations, the presence of single large effect QTL in the corresponding CGs cannot be ruled out, but discrete distribution of significant effects within the CGs necessitated their identification as distinct QTL.

For single environment phenotypes, the number of S-QTL varied from 0-3 for T574 and 0-7 for T89; and percent variation explained by a single marker (*R*2) ranged from eight to 22%. More than 50% of associations exhibiting *R*2 of more than 11% (20/34) of the total phenotypic variance were significant at *P =* 0.001 while only three of 39 associations explaining *R*2 ≤ 11% were significant at that threshold.

Among the 74 putative S-QTL detected, 14 and 44 could be assigned to seven and 15 linkage groups (LGs) of T574 and T89, while 16 (five T574, 10 T89, and one biparental) were associated with unlinked markers. Further, QTL were mapped to eight of nine putative homology groups (HGs) with two to 18 QTL in each HG. Only HG 8 did not contribute any S-QTL.

Most S-QTL from both parental sources conditioned a decrease in trait values (12 T574 and 34 T89) while fewer alleles conditioned an increase in trait value (four T574 and 13 T89). QTL at six pairs of complementary alleles (i.e., alleles of a codominant marker in repulsion phase) underlying nine S-QTL showed effects that are equal in magnitude, but opposite in direction.

Multiple regression involving up to four SMA-derived QTL (i.e., S-QTL and D-QTL) explained 11.7-42.2% of phenotypic variance for HT in different environments (Supplemental Table 3). Similarly, five SMA-derived QTL explained 17.8-56.0% of phenotypic variance for ILEN and three SMA-derived QTL explained 10.5-31.7% for LLS. For the leaf traits, five SMA-detected QTL explained 28.9-42.2% of phenotypic variances for LLEN and up to four SMA-derived QTL explained 25.7-69.4% for LW.

References

[1] Rice WR (1989) Analyzing Tables of Statistical Tests. Evolution 43:223-225

[2] Khanal S, Kim C, Auckland SA, Rainville LK, Adhikari J, Schwartz BM, Paterson AH (2017b) SSR-enriched genetic linkage maps of bermudagrass (Cynodon dactylon x transvaalensis), and their comparison with allied plant genomes. Theor Appl Genet. doi:10.1007/s00122-017-2854-z

[3] Hoarau JY, Grivet L, Offmann B, Roboin LM, Diorflar JP, Payet J, Hellmann M, D’Hont A, Glaszmann JC (2002) Genetic dissection of a modern sugarcane cultivar (Saccharum spp.).II. Detection of QTLs for yield components. Theor Appl Genet 105(6-7):1027-1037

Supplementary Table S2.1. Correlation coefficients of five bermudagrass morphological traits in *C. dactylon* (T89) x *transvaalensis* (T574) F1 population.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Trait | Env.a | Height | | | | |  | Internode length | | | |  | Length of the longest stolon | | | |  | Leaf length | |  | Leaf width | | | |
| (HT; cm) | | | | |  | (ILEN; mm) | | | |  | (LLS; mm) | | | |  | (LLEN; mm) | |  | (LW; mm) | | | |
| G10 | T10 | T11 | G12 | T12 |  | G11 | T11 | G12 | T12 |  | G10-T1 | T10-T1 | G10-T2 | T10-T2 |  | G12 | T12 |  | T11 | G12 | T12 |
| HT | G10 | 1 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | |
|  | T10 | 0.61\*\*\*\* | 1 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | |
|  | T11 | 0.16NS | 0.23\* | 1 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | |
|  | G12 | 0.06NS | 0.22\* | 0.41\*\*\*\* | 1 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | |
|  | T12 | 0.32\*\*\* | 0.17NS | 0.53\*\*\*\* | 0.25\*\* | 1 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | |
|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | |
| ILEN | G11 | 0.21\* | 0.33\*\*\* | 0.12NS | 0.14NS | 0.13NS |  | 1 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | |
|  | T11 | 0.05NS | 0.07NS | 0.20\* | -0.03NS | 0.14NS |  | 0.51\*\*\*\* | 1 |  |  |  |  |  |  |  |  |  |  |  |  |  |  | |
|  | G12 | 0.24\* | 0.21\* | 0.31\*\* | 0.07NS | 0.36\*\*\* |  | 0.51\*\*\*\* | 0.57\*\*\*\* | 1 |  |  |  |  |  |  |  |  |  |  |  |  |  | |
|  | T12 | 0.10NS | 0.14NS | 0.49\*\*\*\* | 0.29\*\* | 0.40\*\*\*\* |  | 0.32\*\*\* | 0.39\*\*\*\* | 0.39\*\*\*\* | 1 |  |  |  |  |  |  |  |  |  |  |  |  | |
|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | |
| LLS | G10-T1 | 0.03NS | 0.10NS | 0.19NS | 0.14NS | 0.22\* |  | 0.33\*\*\* | 0.40\*\*\*\* | 0.38\*\*\*\* | 0.26\*\* |  | 1 |  |  |  |  |  |  |  |  |  |  | |
|  | T10-T1 | 0.10NS | 0.29\*\* | 0.10NS | 0.09NS | 0.06NS |  | 0.28\*\* | 0.23\* | 0.31\*\* | 0.05NS |  | 0.60\*\*\*\* | 1 |  |  |  |  |  |  |  |  |  | |
|  | G10-T2 | 0.08NS | 0.14NS | 0.23\* | 0.19\* | 0.17NS |  | 0.42\*\*\*\* | 0.46\*\*\*\* | 0.46\*\*\*\* | 0.30\*\* |  | 0.84\*\*\*\* | 0.61\*\*\*\* | 1 |  |  |  |  |  |  |  |  | |
|  | T10-T2 | 0.02NS | 0.38\*\*\*\* | 0.00NS | 0.16NS | 0.00NS |  | 0.42\*\*\*\* | 0.27\*\* | 0.28\*\* | 0.14NS |  | 0.51\*\*\*\* | 0.75\*\*\*\* | 0.53\*\*\*\* | 1 |  |  |  |  |  |  |  | |
|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | |
| LLEN | G12 | 0.08NS | 0.07NS | 0.32\*\*\* | 0.54\*\*\*\* | 0.40\*\*\*\* |  | 0.15NS | 0.05NS | 0.15NS | 0.35\*\*\* |  | 0.08NS | 0.00NS | 0.09NS | -0.01NS |  | 1 |  |  |  |  |  | |
|  | T12 | 0.26\*\* | 0.24\* | 0.47\*\*\*\* | 0.35\*\*\* | 0.70\*\*\*\* |  | 0.27\*\* | 0.29\*\* | 0.38\*\*\*\* | 0.50\*\*\*\* |  | 0.12NS | 0.04NS | 0.19NS | -0.01NS |  | 0.54\*\*\*\* | 1 |  |  |  |  | |
|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | |
| LW | T11 | 0.03NS | 0.06NS | 0.23\* | 0.13NS | 0.24\* |  | 0.18NS | 0.34\*\*\* | 0.24\* | 0.20\* |  | 0.09NS | -0.12NS | 0.13NS | 0.02NS |  | 0.22\* | 0.30\*\* |  | 1 |  |  | |
|  | G12 | 0.13NS | 0.06NS | 0.28\*\* | 0.07NS | 0.41\*\*\*\* |  | 0.16NS | 0.30\*\* | 0.24\* | 0.17NS |  | 0.07NS | -0.04NS | 0.09NS | 0.01NS |  | 0.28\*\* | 0.35\*\*\* |  | 0.41\*\*\*\* | 1 |  | |
|  | T12 | -0.05NS | -0.01NS | 0.26\*\* | 0.18NS | 0.36\*\*\* |  | 0.07NS | 0.21\* | 0.13NS | 0.24\* |  | -0.02NS | -0.06NS | -0.01NS | 0.00NS |  | 0.27\*\* | 0.40\*\*\*\* |  | 0.40\*\*\*\* | 0.53\*\*\*\* | 1 | |

a Single environment phenotypes for *HT* height (5 environments), *ILEN* internode length (4 environments), *LLS* length of the longest stolon (4 environments), *LLEN* leaf length (2 environments), and *LW* leaf width (3 environments). Environment identified with prefixes G, Griffin and T, Tifton followed by *10* (2010), *11* (2011), *12* (2012) and T1 (1st date), or T2 (2nd date). *NS* not significant

\**p* < 0.05, \*\**p* < 0.01, \*\*\**p* < 0.001, \*\*\*\**p* < 0.0001

Supplementary Table S2.2. Marker-trait associations following single marker analysis and QTL correspondence between bermudagrass and allied species.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| *Cynodon* marker-trait associations | | | | | | | | | QTL correspondencea | | | | | | | | |
| Markerb | Source LG (HG) | | Env.c | | *R2* | | Effectd | | Species | | Chr. | | QTL/gene namee | | Trait name | | Referencef |
| **Canopy height (HT)** | |  | |  | |  | |  | |  | |  | |  | |  | |
| CA093658-240 | T574 1a/b (HG 01) | | T10 | | 8.3 | | +1.09\*\*\* | | *Oryza* | | 3 | | qHEJ-3 | | seedling height | | [1] |
|  |  | |  | |  | |  | | *Sorghum* | | 4 | | PTHT.4b-1 | | plant height | | [18] |
| PAP07C04a | T574 3a/b and 12 (HG 03) | | T10 | | 16.0 | | -1.39\*\*\* | | *Sorghum* | | 3 | | HtAvg-3-1, PTHT-3-1, PTHT-3-2 | | plant height | | [13], [16] |
|  |  | |  | |  | |  | | *Saccharum* | | - | | PTHT.32\_2-1 | | plant height | | [15] |
| CF574110-150 | T89 12 (HG03) | | T11 | | 14.7 | | +3.68\*\*\*\*\* | | *Sorghum* | | 1 | | HtAvg-1-1 | | plant height | | [13] |
|  |  | | G12 | | 12.9 | | +1.38\*\*\*\* | | *Saccharum* | | - | | PLHT.11\_3-1 | | plant height | | [15] |
| PAP02D11 | T89 12 (HG 03) | | T11 | | 11.1 | | -3.36\*\*\* | | *Oryza* | | 1 | | Fh1-2, qPHT-1, sd-1, ph1 | | plant height | | [3], [7], [12], [22], [23] |
|  |  | |  | |  | |  | | *Oryza* | | 1 | | fll1 | | flag leaf length | | [22] |
|  |  | |  | |  | |  | | *Sorghum* | | 3 | | HtAvg-3-1, PTHT-3-1, PTHT-3-2 | | plant height | | [13], [16] |
|  |  | |  | |  | |  | | *Saccharum* | | - | | PTHT.32\_2-1 | | plant height | | [15] |
| CA186643-90 | T89 3c/d and 16 (HG 03) | | T12 | | 10.8 | | +2.03\*\*\* | | *Sorghum* | | 1 | | PTHT.1-1 | | plant height | | [18] |
| T5741A10a | T89 5a/b and 15 (HG 05) | | T12 | | 19.2 | | -2.79\*\*\*\*\* | | *Oryza* | | 2 | | qPH-2 | | plant height | | [14] |
| CA100438-215 | T89 20 (HG 07) | | T10 | | 15.0 | | -1.47\*\*\*\*\*\* | | *Sorghum* | | 9 | | HtM-9-1 | | plant height | | [13] |
| PAP06F11a | T89 20 (HG 07) | | T10 | | 11.2 | | +1.31\*\*\* | | *Sorghum* | | 9 | | PTHT-9-1 | | plant height | | [2] |
| TC55531-1400 | T89 1a/b (HG 09) | | G10 | | 9.7 | | -0.82\*\*\* | | *Oryza* | | 1 | | qFLL-1 | | first leaf length | | [17] |
| **T5748C04c** | T89 3a/b (HG 02) | | T12 | | 14.1 | | -2.37\*\*\* | |  | |  | |  | |  | |  |
| CA125611-160 | T89 4a/b (HG 02) | | G10 | | 10.9 | | -0.73\*\*\* | |  | |  | |  | |  | |  |
| T5748F06a | T89 12 (HG 03) | | T11 | | 10.0 | | -3.36\*\*\* | |  | |  | |  | |  | |  |
| CA162523-100 | T89 3c/d and 16 (HG 03) | | T11 | | 10.3 | | -3.32\*\*\* | |  | |  | |  | |  | |  |
|  |  | | T12 | | 13.5 | | -2.29\*\*\*\*\* | |  | |  | |  | |  | |  |
| CA265902-300 | T89 3c/d and 16 (HG 03) | | T12 | | 8.8 | | -1.80\*\*\* | |  | |  | |  | |  | |  |
| RZ543a | T89 3c/d and 16 (HG 03) | | T11 | | 10.1 | | +3.22\*\*\* | |  | |  | |  | |  | |  |
|  |  | | T12 | | 12.7 | | +2.24\*\*\*\* | |  | |  | |  | |  | |  |
| **T5742F05** | T89 8a/b (HG 05) | | T12 | | 13.4 | | +2.38\*\*\* | |  | |  | |  | |  | |  |
| RZ900 | T89 7a/b and 11 (HG 06) | | T12 | | 14.0 | | -2.55\*\*\* | |  | |  | |  | |  | |  |
| TC66673-270 | T89 11 (HG 06) | | T12 | | 10.8 | | -2.01\*\*\* | |  | |  | |  | |  | |  |
| T5742B11a | T89 1a/b (HG 09) | | G10 | | 10.3 | | -0.88\*\*\* | |  | |  | |  | |  | |  |
| T5741G04a | T574 Unlinked (*na*) | | T10 | | 12.5 | | -1.37\*\*\* | |  | |  | |  | |  | |  |
| CA097696-520 | T574/T89 Unlinked (*na*) | | T11 | | 12.3 | | -3.89\*\*\* | |  | |  | |  | |  | |  |
| **T5741E11b** | T89 Unlinked (*na*) | | G10 | | 12.2 | | -0.99\*\*\* | |  | |  | |  | |  | |  |
|  |  | | T10 | | 15.7 | | -1.67\*\*\* | |  | |  | |  | |  | |  |
| PCD053c | T89 Unlinked (*na*) | | T11 | | 15.3 | | +3.89\*\*\*\*\*\* | |  | |  | |  | |  | |  |
| T5746E05 | T89 Unlinked (*na*) | | T12 | | 14.1 | | -2.12\*\*\*\*\* | |  | |  | |  | |  | |  |
| **Internode length (ILEN)** | |  | |  | |  | |  | |  | |  | |  | |  | |
| T5748G02b | T89 4c/d-I and 18 (HG 01) | | G11 | | 10.3 | | +2.44\*\*\* | | *Oryza* | | 7 | | Ph7a | | plant height | | [20] |
| T5745D06c | T89 4c/d-II (HG 01) | | G12 | | 12.4 | | -2.29\*\*\* | | *Oryza* | | 3 | | qHEJ-3 | | seedling height | | [1] |
|  |  | |  | |  | |  | | *Oryza* | | 2 | | qPH-2 | | plant height | | [14] |
|  |  | |  | |  | |  | | *Sorghum* | | 1 | | HtAvg-1-1 | | plant height | | [13] |
|  |  | |  | |  | |  | | *Saccharum* | | - | | PLHT.11\_3-1 | | plant height | | [15] |
| TC48763-210 | T89 4c/d-1 and 18 (HG 01) | | G12 | | 8.6 | | -2.18\*\*\* | | *Sorghum* | | 3 | | PTHT-3-1 | | plant height | | [2] |
| T5746E10b | T89 3c/d and 16 (HG 03) | | G11 | | 16.0 | | -3.52\*\*\* | | *Oryza* | | 1 | | qFLL-1 | | first leaf length | | [17] |
|  |  | | T11 | | 18.5 | | -3.23\*\*\* | |  | |  | |  | |  | |  |
| CA186643-90 | T89 3c/d and 16 (HG 03) | | G11 | | 9.3 | | +2.47\*\*\* | | *Sorghum* | | 1 | | PTHT.1-1 | | plant height | | [18] |
| TC62910-300 | T89 1c/d (HG 06) | | G12 | | 9.4 | | +2.17\*\*\* | | *Sorghum* | | 6 | | PTHT-6-1, PTHT-F-2, PTHT.6b-1 | | plant height | | [2], [11], [19] |
| RZ545 | T89 7a/b and 11 (HG 06) | | G11 | | 15.9 | | +3.17\*\*\*\* | | *Oryza* | | 3 | | qLEI3 | | lowest elongated internode | | [5], [6] |
| CA182108-410 | T574 6a/b (HG 06) | | G12 | | 11.5 | | -2.44\*\*\*\* | | *Sorghum* | | 1 | | PTHT-1-1 | | plant height | | [16] |
| RZ140bc | T574 9 and 11 (HG 09) | | T11 | | 11.1 | | -2.55/+2.55\*\*\* | | *Oryza* | | 6 | | ph6 | | plant height | | [21] |
| Marker | Source LG (HG) | | Env. | | *R2* | | Effect | | Species | | Chr. | | QTL/gene name | | Trait name | | Reference |
| CA078136-1500 | T574 Unlinked (*na*) | | G12 | | 9.1 | | +2.15\*\*\* | | *Oryza* | | 1 | | Fh1-2, qPHT-1, qPHT1-1, sd-1, ph1 | | plant/seedling height | | [3], [7], [8], [12], [22], [23] |
|  |  | |  | |  | |  | | *Oryza* | | 1 | | fll1 | | flag leaf length | | [22] |
| T5743D12e | T89 4c/d-I and 18 (HG 01) | | G11 | | 10.3 | | +2.59\*\*\* | |  | |  | |  | |  | |  |
| PCD021b | T89 4c/d-1 and 18 (HG 01) | | G11 | | 9.4 | | +2.45\*\*\* | |  | |  | |  | |  | |  |
| CA162523-100 | T89 3c/d and 16 (HG 03) | | G11 | | 13.9 | | -2.99\*\*\*\*\* | |  | |  | |  | |  | |  |
|  |  | | T11 | | 12.7 | | -2.62\*\*\*\* | |  | |  | |  | |  | |  |
| CA265902-300 | T89 3c/d and 16 (HG 03) | | G11 | | 18.1 | | -3.37\*\*\*\*\*\* | |  | |  | |  | |  | |  |
|  |  | | T11 | | 15.3 | | -2.82\*\*\*\*\*\* | |  | |  | |  | |  | |  |
| T5741D01ab | T89 3c/d and 16 (HG 03) | | G11 | | 8.5 | | +2.32/-2.32\*\*\* | |  | |  | |  | |  | |  |
|  |  | | T12 | | 12.5 | | +2.11\*\*\*\*\* | |  | |  | |  | |  | |  |
| RZ543a | T89 3c/d and 16 (HG 03) | | G11 | | 9.3 | | +2.39\*\*\* | |  | |  | |  | |  | |  |
| PCD131f | T574 3a/b and 12 (HG 03) | | T11 | | 13.0 | | -2.69\*\*\*\*\* | |  | |  | |  | |  | |  |
| T5746F06 | T574 3a/b and 12 (HG 03) | | T11 | | 22.4 | | -3.48\*\*\*\*\*\* | |  | |  | |  | |  | |  |
| T5743D06b | T574 3a/b and 12 (HG 03) | | T11 | | 12.6 | | +2.51\*\*\* | |  | |  | |  | |  | |  |
| PCD137ab | T89 7a/b and 11 (HG 06) | | T12 | | 12.8 | | -2.11/+2.11\*\*\*\* | |  | |  | |  | |  | |  |
| PCD145b | T89 2a/b/c (HG 09) | | G12 | | 11.2 | | -2.42\*\*\* | |  | |  | |  | |  | |  |
| T5742D06a | T574 9 and 11 (HG 09) | | T11 | | 16.1 | | -2.96\*\*\* | |  | |  | |  | |  | |  |
| T5743A03 | T89 1a/b (HG 09) | | G11 | | 18.5 | | +3.98\*\*\* | |  | |  | |  | |  | |  |
| T5743D06c | T574 14 (UN) | | G11 | | 18.6 | | -3.86\*\*\* | |  | |  | |  | |  | |  |
| PCD101 | T574 14 (UN) | | G11 | | 19.0 | | +3.37\*\*\* | |  | |  | |  | |  | |  |
| T5745B07 | T89 24 (UN) | | G12 | | 8.8 | | +2.22\*\*\* | |  | |  | |  | |  | |  |
| TC66673 | T574 Unlinked (*na*) | | G11 | | 9.7 | | -2.48\*\*\* | |  | |  | |  | |  | |  |
| T5742E03c | T89 Unlinked (*na*) | | G11 | | 8.5 | | -2.30\*\*\* | |  | |  | |  | |  | |  |
| **PCD145a** | T89 Unlinked (*na*) | | T11 | | 12.2 | | +2.57\*\*\*\* | |  | |  | |  | |  | |  |
| **T5741C01** | T89 Unlinked (*na*) | | G12 | | 9.2 | | +2.52\*\*\* | |  | |  | |  | |  | |  |
| **T5741E08** | T89 Unlinked (*na*) | | G11 | | 12.8 | | -3.56\*\*\* | |  | |  | |  | |  | |  |
|  |  | | G12 | | 19.2 | | -4.01\*\*\*\*\*\* | |  | |  | |  | |  | |  |
| T5746E05 | T89 Unlinked (*na*) | | T12 | | 11.3 | | -1.99\*\*\* | |  | |  | |  | |  | |  |
| PCD065c | T89 Unlinked (*na*) | | G11 | | 11.0 | | +2.74\*\*\* | |  | |  | |  | |  | |  |
| **Length of the longest stolon (LLS)** | |  | |  | |  | |  | |  | |  | |  | |  | |
| CF573608-150 | T574 1a/b (HG 01) | | TT2 | | 8.2 | | +6.08\*\*\* | | *Sorghum* | | 4 | | PTHT.4b-1 | | plant height | | [18] |
| CA100438-215 | T89 20 (HG 07) | | TT1 | | 14.6 | | -4.59\*\*\*\*\* | | *Sorghum* | | 9 | | HtM-9-1 | | plant height | | [13] |
|  |  | | TT2 | | 22.4 | | -19.14\*\*\*\*\*\* | |  | |  | |  | |  | |  |
| RZ140bc | T574 9 and 11 (HG 09) | | GT1 | | 11.0 | | -4.39/+4.39\*\*\* | | *Oryza* | | 6 | | ph6 | | plant height | | [21] |
| TC48809-240 | T89 Unlinked (*na*) | | TT1 | | 8.7 | | +4.84\*\*\* | | *Sorghum* | | 3 | | HtAvg-3-1, PTHT-3-1, PTHT-3-2 | | plant height | | [13], [16] |
|  |  | |  | |  | |  | | *Saccharum* | | - | | PTHT.32\_2-1 | | plant height | | [15] |
| CA193820-505/510 | T89 14 and 27 (HG 04) | | TT2 | | 14.6 | | -8.29/+8.29\*\*\*\*\* | |  | |  | |  | |  | |  |
|  |  | | TT2 | | 11.7 | | +8.33\*\*\* | |  | |  | |  | |  | |  |
| **T5746F07** | T89 1c/d (HG 06) | | TT1 | | 12.2 | | +4.98\*\*\* | |  | |  | |  | |  | |  |
| T5746H09 | T89 1c/d (HG 06) | | TT1 | | 8.2 | | -3.46\*\*\* | |  | |  | |  | |  | |  |
| T5742C01a | T89 20 (HG 07) | | TT2 | | 10.4 | | -7.33\*\*\* | |  | |  | |  | |  | |  |
| T5746C08 | T89 1a/b (HG 09) | | GT1 | | 9.8 | | -4.07\*\*\* | |  | |  | |  | |  | |  |
| **Leaf length (LLEN)** | |  | |  | |  | |  | |  | |  | |  | |  | |
| CA186643-90 | T89 3c/d and 16 (HG 03) | | T12 | | 8.6 | | +3.15\*\*\* | | *Sorghum* | | 1 | | PTHT.1-1 | | plant height | | [18] |
| TC56094-130 | T574 3a/b and 12 (HG 03) | | G12 | | 9.4 | | -3.08\*\*\* | | *Sorghum* | | 1 | | PTHT.1-1 | | plant height | | [18] |
| T5741A10a | T89 5a/b and 15 (HG 05) | | T12 | | 14.5 | | -4.28\*\*\* | | *Oryza* | | 2 | | qPH-2 | | plant height | | [14] |
| T5742F09c | T89 4c/d-I and 18 (HG 01) | | T12 | | 12.4 | | -3.76\*\*\*\*\* | |  | |  | |  | |  | |  |
| PCD142 | T89 4c/d-I and 18 (HG 01) | | T12 | | 16.6 | | -4.42\*\*\* | |  | |  | |  | |  | |  |
| CA162523-100 | T89 3c/d and 16 (HG 03) | | T12 | | 13.8 | | -3.92\*\*\*\*\* | |  | |  | |  | |  | |  |
| RZ543a | T89 3c/d and 16 (HG 03) | | T12 | | 11.4 | | +3.78\*\*\* | |  | |  | |  | |  | |  |
| T5741D01ab | T89 3c/d and 16 (HG 03) | | T12 | | 10.2 | | -3.51/+3.51\*\*\* | |  | |  | |  | |  | |  |
| Marker | Source LG (HG) | | Env.b | | *R2* | | Effectc | | Species | | Chr. | | QTL/gene name | | Trait name | | Reference |
| TC67261-150/230 | T89 14 and 27 (HG 04) | | T12 | | 10.1 | | -3.34/+3.34\*\*\* | |  | |  | |  | |  | |  |
| RZ900- | T89 7a/b and 11 (HG 06) | | T12 | | 11.6 | | -3.80\*\*\* | |  | |  | |  | |  | |  |
| CA173231-220 | T574 9 and 11 (HG 09) | | G12 | | 10.6 | | -3.20\*\*\* | |  | |  | |  | |  | |  |
| T5745B07 | T89 24 (UN) | | T12 | | 10.8 | | +3.74\*\*\* | |  | |  | |  | |  | |  |
| TC67261-390 | T574 Unlinked (*na*) | | T12 | | 9.8 | | -3.29\*\*\* | |  | |  | |  | |  | |  |
| PCD053c | T89 Unlinked (*na*) | | T12 | | 8.9 | | +3.13\*\*\* | |  | |  | |  | |  | |  |
| T5746E05 | T89 Unlinked (*na*) | | T12 | | 12.7 | | -3.84\*\*\*\*\* | |  | |  | |  | |  | |  |
| **Leaf width (LW)** | |  | |  | |  | |  | |  | |  | |  | |  | |
| TC62694-450 | T89 3a/b (HG 02) | | T12 | | 13.3 | | -0.12\*\*\*\*\* | | *Oryza* | | 2 | | - | | shoot length | | [9] |
| CA078499-800 | T574 7a-2/b-I and 5a/b (HG 05) | | T11 | | 10.1 | | -0.12\*\*\* | | *Oryza* | | 3 | | qHEJ-3 | | seedling height | | [1] |
|  |  | |  | |  | |  | | *Saccharum* | | - | | PLHT.11\_3-1 | | plant height | | [15] |
| T5743B10b | T89 21 (HG 07) | | T12 | | 14.7 | | -0.11\*\*\* | | *Oryza* | | 1 | | Fh1-2, qPHT-1, qPHT1-1, sd-1, ph1 | | plant/seedling height | | [3], [7], [8], [12], [22], [23] |
|  |  | |  | |  | |  | | *Oryza* | | 1 | | qFLL-1 | | first leaf length | | [17] |
|  |  | |  | |  | |  | | *Oryza* | | 1 | | qRIE 1 | | rate (internodal elongation) | | [10] |
| CA146239-450/460 | T574 13 (HG UN) | | T11 | | 8.6 | | -0.11/+0.11\*\*\* | | *Oryza* | | 3 | | qLT3-1 | | length (third seedling leaf) | | [4] |
| RZ543a | T89 3c/d and 16 (HG 03) | | G12 | | 17.1 | | +0.15\*\*\*\*\*\* | |  | |  | |  | |  | |  |
|  |  | | T12 | | 9.8 | | +0.10\*\*\* | |  | |  | |  | |  | |  |
| CA162523-100 | T89 3c/d and 16 (HG 03) | | T12 | | 10.6 | | -0.11\*\*\* | |  | |  | |  | |  | |  |
| CA265902-300 | T89 3c/d and 16 (HG 03) | | T12 | | 9.5 | | -0.10\*\*\* | |  | |  | |  | |  | |  |
| T5741D01ab | T89 3c/d and 16 (HG 03) | | T12 | | 10.7 | | -0.11/+0.11\*\*\*\* | |  | |  | |  | |  | |  |
| T5743E08 | T89 12 (HG 03) | | T12 | | 9.0 | | +0.09\*\*\* | |  | |  | |  | |  | |  |
| T5748F03b | T574 5a/b (HG 05) | | G12 | | 14.4 | | -0.16\*\*\* | |  | |  | |  | |  | |  |
| **T5745F03** | T89 1a/b (HG 09) | | T11 | | 15.7 | | -0.16\*\*\*\* | |  | |  | |  | |  | |  |
| T5745A06a | T574 Unlinked (*na*) | | G12 | | 14.9 | | -0.13\*\*\* | |  | |  | |  | |  | |  |
| T5743G05c | T89 Unlinked (*na*) | | G12 | | 13.0 | | -0.13\*\*\* | |  | |  | |  | |  | |  |
| T5742D02 | T89 Unlinked (*na*) | | T12 | | 9.4 | | -0.09\*\*\* | |  | |  | |  | |  | |  |
| T5746E05 | T89 Unlinked (*na*) | | T11 | | 9.3 | | -0.11\*\*\* | |  | |  | |  | |  | |  |
|  |  | | T12 | | 16.0 | | -0.12\*\*\*\*\*\* | |  | |  | |  | |  | |  |
| **PCD115** | T89 Unlinked (*na*) | | T12 | | 21.6 | | +0.19\*\*\* | |  | |  | |  | |  | |  |
| **T5748B12** | T89 Unlinked (*na*) | | T11 | | 13.4 | | +0.20\*\*\* | |  | |  | |  | |  | |  |
| **T5742C01b** | T89 Unlinked (*na*) | | G12 | | 8.9 | | -0.11\*\*\* | |  | |  | |  | |  | |  |

a BLASTn against CSGRqtl [25] or Q-TARO [26]. b Marker names and size of the alleles for SSR amplicons; names in *bold* are double dose markers c Single environment phenotypes for *HT* height (5 environments), *ILEN* internode length (4 environments), *LLS* length of the longest stolon (4 environments), *LLEN* leaf length (2 environments), and *LW* leaf width (3 environments). Environment identified with prefixes G, Griffin and T, Tifton followed by *10* (2010), *11* (2011), *12* (2012) and T1 (1st date), or T2 (2nd date). d *-ve* and *+ve* signs correspond to a decrease or increase in trait values; \*\*\**p* ≤ 0.005, \*\*\*\**p* ≤ 0.001, \*\*\*\*\**p* ≤ 0.0005, \*\*\*\*\*\**p* ≤ 0.0001. e QTL identifiers follow names provided in the databases - *Sorghum* and *Saccharum* QTL names originally include *Q.* followed by *first author name* and *date of* *publication*. For example, PTHT.4b-1 is identified as Q.Shiringani2010.PTHT.4b-1 in CSGRqtl. *na* not available.

f References

[1] Abdelkhalik AF, Shishido R, Nomura K, Ikehashi H (2005) QTL-based analysis of heterosis for grain shape traits and seedling characteristics in an indica-japonica hybrid in rice (Oryza sativa L.). Breeding Science 55:41-48

[2] Brown PJ, Klein PE, Bortiri E, Acharya CB, Rooney WL, Kresovich RS (2006) Inheritance of infloriscence architecture in sorghum. Theoretical and Applied Genetics 113(5):931-942

[3] Cao G, Zhu J, He C, Gao Y, Yan J, Wu P (2001) Impact of epistasis and QTL×environment interaction on the developmental behavior of plant height in rice (Oryza sativa L.). Theoretical and Applied Genetics 103:153-160

[4] Cui K, Peng S, Xing Y, Xu C, Yu S, Zhang Q (2002) Molecular dissection of seedling-vigor and associated physiological traits in rice. Theoretical and Applied Genetics 105:745-753

[5] Hattori Y, Miura K, Asano K, Yamamoto E, Mori H, Kitano H, Matsuoka M, Ashikari M A major QTL confers rapid internode elongation in response to water rise in deepwater rice

[6] Hattori Y, Nagai K, Mori H, Kitano H, Matsuoka M, Ashikari M Mapping of three QTLs that regulate internode elongation in deepwater rice

[7] Hittalmani S, Huang N, Courtois B, Venuprasad R, Shashidhar HE, Zhuang J-Y, Zheng K-L, Liu G-F, Wang G-C, Sidhu JS, Srivantaneeyakul S, Singh VP, Bagali PG, Prasanna HC, McLaren G, Khush GS (2003) Identification of QTL for growth- and grain yield-related traits in rice across nine locations of Asia. Theoretical and Applied Genetics 107:679-690

[8] Hittalmani S, Shashidhar HE, Bagali PG, Huang N, Sidhu JS, Singh VP, Khush GS (2002) Molecular mapping of quantitative trait loci for plant growth, yield and yield related traits across three diverse locations in a doubled haploid rice population. Euphytica 125:207-214

[9] Huang Z, Yu T, Su L, Yu SB, Zhang ZH, Zhu YG (2004) Identification of chromosome regions associated with seeling vigor in rice. Yi Chuan Xue Bao 31:596-603

[10] Kawano R, Mochizuki T, Yasui H, Doi K, Yoshimura A (2003) QTL analysis for floating ability in rice. Rice Genetics Newsletter 20:74-77

[11] Kebede H, Subudhi PK, Rosenow DT, Nguyen HT (2001) Quantitative trait loci influencing drought tolerance in grain sorghum (*Sorghum bicolor* L. Moench). Theoretical and Applied Genetics 103(2):266-276

[12] Li ZK, Yu SB, Lafitte HR, Huang N, Courtois B, Hittalmani S, Vijayakumar CH, Liu GF, Wang GC, Shashidhar HE, Zhuang JY, Zheng KL, Singh VP, Sidhu JS, Srivantaneeyakul S, Khush GS (2003) QTL x environment interactions in rice. I. heading date and plant height. Theoretical and Applied Genetics 108:141-13

[13] Lin YR, Schertz KF, Paterson AH (1995) Comparative analysis of QTLs affecting plant height and maturity across the Poaceae, in reference to an interspecific sorghum population. Genetics 141(1):391-411

[14] Mao BB, Cai WJ, Zhang ZH, Hu ZL, Li P, Zhu LH, Zhu YG (2003) Characterization of QTLs for harvest index and source-sink charaters in a DH population of rice (*Oryza sativa* L.). Yi Chuan Xue Bao 30:1118-1126

[15] Ming R, Del Monte TA, Hernandez E, Moore PH, Irvine JE, Paterson AH (2002) Comparative analysis of QTLs affecting plant height and flowering among closely-related diploid and polyploid genomes. Genome 45(5):794-803

[16] Ritter KB, Jordan DR, Chapman SC, Godwin ID, Mace ES, McIntyre CL (2008) Identification of QTL for sugar-related traits in a sweet x grain sorghum (Sorghum bicolor L. Moench) recombinant inbred population. Molecular Breeding 22(3):367-384

[17] Shen B, Zhuang JY, Zhang KQ, Xia QQ, Sheng CX, Zheng KL (2003) QTLs mapping of leaf traits and root vitality in a recombinant inbred line population of rice. Yi Chuan Xue Bao 30:1133-1139

[18] Shiringani AL, Frisch M, Friedt W (2010) Genetic mapping of QTLs for sugar-related traits in a RIL population of *Sorghum bicolor* L. Moench. Theoretical and Applied Genetics 121(2):323-336

[19] Srinivas G, Satish K, Madhusudhana R, Reddy RN, Mohan SM, Setharama N (2009) Identification of quantitative trait loci for agronomically important traits and their association with genic-microsatellite markers in sorghum. Theoretical and Applied Genetics 118(8)1439-1454

[20] Tan ZB, Shen LS, Kuang HG, Lu CF, Chen Y, Zhou KD, Zhu LH (1996) Identification of QTLs for lengths of the top internodes and other traits in rice and analysis of their genetic effects. Acta Genet Sinica 23:439-446

[21] Xiao J, Li J, Yuan L, Tanksley SD (1996) Identification of QTLs affecting traits of agronomic importance in a recombinant inbred population derived from a subspecific rice cross. Theoretical and Applied Genetics 92:230-244

[22] Yan J, Zhu J, He C, Benmoussa M, Wu P (1999) Molecular marker-assisted dissection of genotype x environment interaction for plant type traits in rice (*Oryza sativa* L.). Crop Science 39:538-544

[23] Yu SB, Li JX, Xu CG, Tan YF, Li XH, Zhang Q (2002) Identification of quantitative trait loci and epistatic interactions for plant height and heading date in rice. Theoretical and Applied Genetics 104(4):619-625

Supplementary Table S2.3. Summary statistics of marker-trait associations (i.e., total number of associations, deduced S-QTAs, and D-QTAs) following single marker analysis (SMA) and results of multiple regression based on deduced QTAs.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Trait | Canopy height  (HT; cm) | | | | |  | Stolon internode length  (ILEN; mm) | | | |  | Length of the longest stolon  (LLS, mm) | | | |  | Leaf length  (LLEN, mm) | |  | Leaf width  (LW; mm) | | |
| Env.a | G10 | T10 | T11 | G12 | T12 |  | G11 | T11 | G12 | T12 |  | G10-T1 | T10-T1 | G10-T2 | T10-T2 |  | G12 | T12 |  | T11 | G12 | T12 |
| Associations detected |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Simplex markersb | 29(3)[0] | 14(4)[1] | 15(5)[2] | 7(0)[1] | 18(4)[3] |  | 16(14)[2] | 16(4)[4] | 26(6)[1] | 12(1)[2] |  | 12(2)[0] | 25(1)[1] | 13(0)[0] | 11(10)[2] |  | 15(2)[0] | 9(10)[3] |  | 19(2)[0] | 12(3)[1] | 17(6)[3] |
| Simplex markers common between different locations in same yearc | 10(2)[0] |  |  | 2(0)[1] |  |  | 4(3)[2] |  | 2(3)[1] |  |  | 8(1)[0] |  | 7(0)[0] |  |  | 7(4)[2] |  |  |  | 4(5)[2] |  |
| Simplex markers common between different years in same locationd | 2(0)[0] | 4(3)[5] |  |  |  |  | 6(7)[2] | 4(1)[2] |  |  |  | 6(2)[0] | 14(3)[2] |  |  |  |  |  |  | 1(4)[1] |  |  |
| Simplex markers common between years and locationse | 31--4--3 |  |  |  |  |  | 22--10--1 |  |  |  |  | 19--8--2 |  |  |  |  | 14 |  |  | 10--4 |  |  |
|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Deduced S-QTAsf | 4(3)[0] | 2(3)[1] | 1(2)[2] | 1(0)[1] | 2(2)[2] |  | 4(7)[1] | 4(2)[2] | 3(6)[1] | 4(1)[2] |  | 1(2)[0] | 3(1)[1] | 3(0)[0] | 3(1)[2] |  | 7(2)[0] | 0(8)[3] |  | 4(2)[0] | 3(4)[1] | 2(5)[2] |
| Deduced S-QTAs common between different locations in same yearg | 0(2)[0] |  |  | 1(0)[0] |  |  | 3(2)[1] |  | 0(3)[2] |  |  | 0(2)[0] |  | 3(0)[0] |  |  | 0(5)[2] |  |  |  | 0(4)[1] |  |
| Deduced S-QTAs common between different years in same locationh | 0(0)[0] | 0(0)[5] |  |  |  |  | 1(4)[1] | 2(0)[2] |  |  |  | 1(2)[0] | 1(2)[2] |  |  |  |  |  |  | 0(4)[1] |  |  |
| Deduced S-QTAs common between years and locationsi | 8--1--0--0 |  |  |  |  |  | 4--5--0 |  |  |  |  | 4--1--2 |  |  |  |  | 6 |  |  | 3--4 |  |  |
|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| D-QTAsj | 1(1)[0] | 3(1)[0] | 1(0)[0] | 2(0)[0] | 1(2)[0] |  | 2(1)[0] | 0(0)[1] | 1(1)[1] | 0(0)[0] |  | 0(0)[0] | 0(1)[0] | 0(0)[0] | 0(1)[0] |  | 0(0)[0] | 0(0)[0] |  | 0(1)[1] | 1(1)[0] | 2(1)[0] |
| D-QTAs common between different locations in same yeark | 1(1)[0] |  |  | 0(1)[0] |  |  | 0(0)[0] |  | 0(0)[0] |  |  | 0(0)[0] |  | 0(0)[0] |  |  | 0(0)[0] |  |  |  | 0(1)[0] |  |
| D-QTAs common between different years in same locationl | 0(0)[0] | 2(1)[0] |  |  |  |  | 1(1)[1] | 0(0)[0] |  |  |  | 0(0)[0] | 0(1)[0] |  |  |  |  |  |  | 0(0)[1] |  |  |
| D-QTAs common between years and locationsm | 1--1--0--0 |  |  |  |  |  | 2--0--0 |  |  |  |  | 1--0--0 |  |  |  |  | 0 |  |  | 2--0 |  |  |
|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Multiple regressionn |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Number of deduced QTAs fit the model | 3 | 2 | 4 | 1 | 3 |  | 3 | 2 | 5 | 2 |  | 2 | 3 | 2 | 2 |  | 5 | 5 |  | 2 | 4 | 4 |
| *R*2 of multiple regression | 31.3 | 21.4 | 42.2 | 11.7 | 31.9 |  | 42.9 | 48.3 | 56.0 | 17.8 |  | 16.2 | 19.7 | 10.5 | 31.7 |  | 28.9 | 42.2 |  | 27.2 | 69.4 | 33.5 |
|  | (45) | (46) | (54) | (82) | (42) |  | (34) | (40) | (41) | (58) |  | (68) | (79) | (68) | (80) |  | (54) | (76) |  | (61) | (16) | (76) |

a Environment: *G* Griffin, *T* Tifton, *10* (2010), *11* (2011), *12* (2012) and *T1* (1st date) or *T2* (2nd date). bfj Total number of marker-trait associations detected with simplex markers (i.e., segregating in 1:1 ratio), deduced S-QTAs (see “Materials and methods”), and duplex markers (i.e., segregating at 3:1 or 5:1 ratio) and significant at *P* = 0.05 or (0.005) or [0.001]. cgk Number of common marker-trait associations between Griffin and Tifton in the same year (or time in case of LLS). dhl Number of common marker-trait associations between different years (or times in case of LLS) at Griffin and Tifton. eim Total number of common markers between 2 -- 3 -- 4 or -- 5 environments (i.e., locations and/or year or time) given that in at least one of the environments, deduced association is significant at *P* = 0.005 for the given trait. f A subset of deduced QTAs fitted multiple regression models (degrees of freedom in parenthesis) that explained certain percentage of total phenotypic variation (i.e., *R*2).

Supplementary Table S2.4. Significant marker-trait associations (deduced S-QTAs and D-QTAs) and their genomic affiliations following single marker analysis (SMA) of bermudagrass morphological traits.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **HG**  Origina LGb | Markerc | Position (cM)d | Height (cm) | | | |  | Internode length (cm) | | | |  | Length of the longest stolon (cm) | | | |  | Leaf length (cm) | | | |  | Leaf width (cm) | | | |
| Env.e | *P*f | *R*2 | Effect |  | Env.e | *P*f | *R*2 | Effect |  | Env.e | *P*f | *R*2 | Effect |  | Env.e | *P*f | *R*2 | Effect |  | Env.e | *P*f | *R*2 | Effect |
| **HG 1** |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| T574 1a/b | CA093658-240+ | 0.0 | T10 | \*\*\* | 8% | +1.09 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|  | CF573608-150+ | 25.5 |  |  |  |  |  |  |  |  |  |  | TT1 | \* | 6% | +2.97 |  |  |  |  |  |  |  |  |  |  |
|  |  |  |  |  |  |  |  |  |  |  |  |  | TT2 | \*\*\* | 8% | +6.09 |  |  |  |  |  |  |  |  |  |  |
| T89 4c/d-I | T5742F09c- | 96.2 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | G12 | \*\* | 7% | -2.53 |  |  |  |  |  |
| and 18 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | T12 | \*\*\*\*\* | 12% | -3.77 |  |  |  |  |  |
|  | T5748G02b- | 136.4 |  |  |  |  |  | G11 | \*\*\* | 10% | +2.44 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|  | PCD142- | 206.6 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | T12 | \*\*\* | 17% | -4.43 |  |  |  |  |  |
|  | PCD021b- | 23.6 |  |  |  |  |  | G11 | \*\*\* | 9% | +2.46 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|  | TC48763-210+ | 34.7 |  |  |  |  |  | G12 | \*\*\* | 9% | -2.19 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| T89 4c/d-II | T5745D06c- | 141.4 |  |  |  |  |  | G12 | \*\*\* | 12% | -2.30 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **HG 2** |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| T89 3a/b | **T5748C04c+** | 64.7 | T12 | \*\*\* | 14% | -2.37 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|  | TC62694-450+ | 95.7 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | T12 | \*\*\* | 13% | -0.12 |
| T89 4a/b | CA125611-160- | 13.8 | G10 | \*\*\*\* | 11% | -0.74 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **HG 3** |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| T574 3a/b | TC56094-130+ | 38.7 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | G12 | \*\*\* | 9% | -3.08 |  |  |  |  |  |
| and 12\* | T5746F06+ | 94.0 |  |  |  |  |  | T11 | \*\*\*\*\*\* | 22% | -3.48 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|  | PAP07C04a- | 100.7 | G10 | \*\* | 14% | -0.78 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|  |  |  | T10 | \*\*\* | 16% | -1.40 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| T89 3c/d | RZ543a+ | 41.4 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | G12 | \*\*\*\*\*\* | 17% | +0.15 |
| and 16 | CA162523-100- | 51.1 | T11 | \*\*\* | 10% | -3.2 |  |  |  |  |  |  |  |  |  |  |  | T12 | \*\*\*\*\* | 14% | -3.93 |  |  |  |  |  |
|  |  |  | T12 | \*\*\*\*\* | 14% | -2.30 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|  | CA265902-300- | 59.9 |  |  |  |  |  | G11 | \*\*\*\*\*\* | 18% | -3.37 |  |  |  |  |  |  |  |  |  |  |  | G12 | \*\*\* | 8% | -0.11 |
|  |  |  |  |  |  |  |  | T11 | \*\*\*\*\*\* | 15% | -2.83 |  |  |  |  |  |  |  |  |  |  |  | T11 | \* | 5% | -0.08 |
|  |  |  |  |  |  |  |  | G12 | \*\* | 8% | -1.94 |  |  |  |  |  |  |  |  |  |  |  | T12 | \*\*\* | 9% | -0.10 |
|  | *T5741D01ab* | 98.4 |  |  |  |  |  | T12 | \*\*\*\*\* | 12% | -2.11/+2.11 | | |  |  |  |  | T12 | \*\*\* | 10% | -3.51/+3.51 |  | T12 | \*\*\*\* | 11% | -0.11/+0.11 |
|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| T89 12\* | CF574110-150- | 10.2 | G12 | \*\*\*\* | 13% | +1.38 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|  |  |  | T11 | \*\*\*\*\* | 15% | +3.67 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|  |  |  | T12 | \* | 5% | +1.36 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|  | T5743E08- | 102.6 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | G12 | \* | 4% | +0.08 |
|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | T11 | \*\* | 7% | +0.10 |
|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | T12 | \*\*\* | 9% | +0.09 |
|  | CA097696-520+ | 112.0 | T11 | \*\*\* | 10% | -3.36 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|  |  |  | T12 | \* | 7% | -1.90 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **HG 4** |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| T89 14 | *TC67261-150/230* | 0.0 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | G12 | \* | 6% | -2.45/+2.45 |  |  |  |  |  |
| and 27\* |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | T12 | \*\*\* | 10% | -3.34/+3.34 |  |  |  |  |  |
|  | *CA193820-505/510* | 0.0 |  |  |  |  |  |  |  |  |  |  | TT1 | \* | 6% | -2.96/+2.96 |  |  |  |  |  |  |  |  |  |  |
|  |  |  |  |  |  |  |  |  |  |  |  |  | TT2 | \*\*\*\*\* | 15% | -8.29/+8.29 |  |  |  |  |  |  |  |  |  |  |
|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **HG**  Origina LGb | Markerc | Position  (cM)d | Height (cm) | | | |  | Internode length (cm) | | | |  | Length of the longest stolon (cm) | | | |  | Leaf length (cm) | | | |  | Leaf width (cm) | | | |
| Env.e | *P*f | *R*2 | Effect |  | Env.e | *P*f | *R*2 | Effect |  | Env.e | *P*f | *R*2 | Effect |  | Env.e | *P*f | *R*2 | Effect |  | Env.e | *P*f | *R*2 | Effect |
| **HG 5** |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| T574 7a-2/b-I | CA078499-430/600 | 133.7 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | T11 | \*\*\* | 10% | -0.12 |
| and 5a/b |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | T12 | \* | 6% | -0.09 |
|  | T5748F03b- | 35.5 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | G12 | \*\*\* | 14% | -0.16 |
| T89 5a/b | T5741A10a- | 84.4 | T11 | \* | 7% | -2.61 |  |  |  |  |  |  |  |  |  |  |  | G12 | \* | 7% | -2.72 |  |  |  |  |  |
| and 15 |  |  | T12 | \*\*\*\*\* | 19% | -2.79 |  |  |  |  |  |  |  |  |  |  |  | T12 | \*\*\* | 14% | -4.28 |  |  |  |  |  |
| T89 8a/b | **T5742F05** | 77.4 | G12 | \* | 9% | +1.47 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|  |  |  | T11 | \* | 9% | +3.4 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|  |  |  | T12 | \*\*\* | 13% | +2.38 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **HG 6** |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| T574 6a/b | CA182108-410+ | 0.0 |  |  |  |  |  | G12 | \*\*\*\* | 11% | -2.44 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| T89 1c/d | TC62910-300+ | 31.8 |  |  |  |  |  | G12 | \*\*\* | 9% | +2.18 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|  |  |  |  |  |  |  |  | T12 | \*\* | 7% | +1.57 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|  | **T5746F07** | 115.8 |  |  |  |  |  |  |  |  |  |  | TT1 | \*\*\* | 12% | +4.99 |  |  |  |  |  |  |  |  |  |  |
|  |  |  |  |  |  |  |  |  |  |  |  |  | TT2 | \*\*\* | 12% | +8.34 |  |  |  |  |  |  |  |  |  |  |
|  | T5746H09- | 128.5 |  |  |  |  |  |  |  |  |  |  | TT1 | \*\*\* | 8% | -3.47 |  |  |  |  |  |  |  |  |  |  |
|  |  |  |  |  |  |  |  |  |  |  |  |  | TT2 | \* | 4% | -4.45 |  |  |  |  |  |  |  |  |  |  |
| T89 7a/b | RZ545+ | 26.1 |  |  |  |  |  | G11 | \*\*\*\* | 16% | +3.18 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| and 11 |  |  |  |  |  |  |  | T11 | \* | 7% | +1.72 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|  |  |  |  |  |  |  |  | T12 | \* | 7% | +1.62 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|  | *PCD137ab* | 52.7 |  |  |  |  |  | G12 | \* | 6% | +1.78/-1.78 | | |  |  |  |  |  |  |  |  |  |  |  |  |  |
|  |  |  |  |  |  |  |  | T12 | \*\*\*\* | 13% | +2.11/-2.11 | | |  |  |  |  |  |  |  |  |  |  |  |  |  |
|  | RZ900- | 90.2 | G10 | \* | 7% | -0.74 |  |  |  |  |  |  |  |  |  |  |  | T12 | \*\*\* | 12% | -3.81 |  |  |  |  |  |
|  |  |  | T12 | \*\*\* | 14% | -2.56 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|  | TC66673-270- | 66.9 | T12 | \*\*\* | 11% | -2.01 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **HG 7** |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| T89 20\* | CA100438-215+ | 24.7 | T10 | \*\*\*\*\*\* | 15% | -1.47 |  |  |  |  |  |  | TT1 | \*\*\*\*\* | 15% | -4.59 |  |  |  |  |  |  |  |  |  |  |
|  |  |  |  |  |  |  |  |  |  |  |  |  | TT2 | \*\*\*\*\*\* | 22% | -10.14 |  |  |  |  |  |  |  |  |  |  |
| T89 21\* | T5743B10b- | 43.2 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | G12 | \*\* | 11% | -0.11 |
|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | T11 | \* | 8% | -0.11 |
|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | T12 | \*\*\* | 15% | -0.11 |
|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **HG 9** |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| T574 9 | *RZ140bc* | 0.0 |  |  |  |  |  | T11 | \*\*\* | 11% | -2.55/+2.55 | | GT1 | \*\*\* | 11% | -4.39/+4.39 |  |  |  |  |  |  |  |  |  |  |
| and 11\* |  |  |  |  |  |  |  |  |  |  |  |  | GT2 | \* | 6% | -4.50/+4.50 |  |  |  |  |  |  |  |  |  |  |
|  |  |  |  |  |  |  |  |  |  |  |  |  | TT2 | \* | 6% | -5.49/+5.49 |  |  |  |  |  |  |  |  |  |  |
|  | T5742D06a+ | 122.7 |  |  |  |  |  | T11 | \*\*\* | 16% | -2.96 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|  | CA173231-220+ | 0.0 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | G12 | \*\*\* | 11% | -3.20 |  |  |  |  |  |
| T89 2a/b/c | PCD145b+ | 0.0 |  |  |  |  |  | G11 | \* | 8% | -2.06 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|  |  |  |  |  |  |  |  | T11 | \* | 5% | -1.51 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|  |  |  |  |  |  |  |  | G12 | \*\*\* | 11% | -2.42 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| T89 1a/b | T5746C08- | 35.8 |  |  |  |  |  |  |  |  |  |  | GT1 | \*\*\* | 10% | -4.07 |  |  |  |  |  |  |  |  |  |  |
|  |  |  |  |  |  |  |  |  |  |  |  |  | TT1 | \* | 7% | -3.07 |  |  |  |  |  |  |  |  |  |  |
|  |  |  |  |  |  |  |  |  |  |  |  |  | GT2 | \*\* | 8% | -5.63 |  |  |  |  |  |  |  |  |  |  |
|  | **T5745F03** | 48.2 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | T11 | \*\*\*\*\*\* | 16% | -0.15 |
|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | T12 | \* | 6% | -0.08 |
|  |  |  |  | | | |  |  | | | |  |  | | | |  |  | | | |  |  | | | |
| **HG**  Origina LGb | Markerc | Position  (cM)d | Height (cm) | | | |  | Internode length (cm) | | | |  | Length of the longest stolon (cm) | | | |  | Leaf length (cm) | | | |  | Leaf width (cm) | | | |
| Env.e | *P*f | *R*2 | Effect |  | Env.e | *P*f | *R*2 | Effect |  | Env.e | *P*f | *R*2 | Effect |  | Env.e | *P*f | *R*2 | Effect |  | Env.e | *P*f | *R*2 | Effect |
|  | T5742B11a- | 84.0 | G10 | \*\*\* | 10% | -0.88 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|  |  |  | T12 | \* | 6% | -1.49 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|  | TC55531-1400- | 142.1 | G10 | \*\*\* | 10% | -0.83 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **Unassigned** |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| T574 13\* | CA146239-450/460 | 0.0 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | T11 | \*\*\* | 8% | -0.11/+0.11 |
| T574 14\* | PCD101+ | 0.0 |  |  |  |  |  | G11 | \*\*\* | 19% | +3.37 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|  |  |  |  |  |  |  |  | G12 | \* | 12% | +2.61 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| T89 24\* | T5745B07+ | 30.8 |  |  |  |  |  | G12 | \*\*\* | 9% | +2.23 |  |  |  |  |  |  | G12 | \* | 5% | +2.28 |  |  |  |  |  |
|  |  |  |  |  |  |  |  | T12 | \* | 6% | +1.51 |  |  |  |  |  |  | T12 | \*\*\* | 11% | +3.75 |  |  |  |  |  |
|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **Unlinked** |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| T574 | CA078136-1500 |  |  |  |  |  |  | G11 | \* | 5% | +1.68 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|  |  |  |  |  |  |  |  | G12 | \*\*\* | 9% | +2.15 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|  |  |  |  |  |  |  |  | T12 | \* | 7% | +1.51 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|  | TC66673-118 |  |  |  |  |  |  | G11 | \*\*\* | 10% | -2.49 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|  |  |  |  |  |  |  |  | T11 | \*\* | 8% | -2.07 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|  |  |  |  |  |  |  |  | T12 | \* | 5% | -1.33 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|  | T5745A06a |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | G12 | \*\*\* | 15% | -0.14 |
|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | T11 | \* | 10% | -0.13 |
|  | TC67261-390 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | G12 | \* | 6% | -2.40 |  |  |  |  |  |
|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | T12 | \*\*\* | 10% | -3.29 |  |  |  |  |  |
|  | T5741G04a |  | G10 | \* | 7% | -0.78 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|  |  |  | T10 | \*\*\* | 12% | -1.37 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Biparental | TC48809 |  |  |  |  |  |  |  |  |  |  |  | TT1 | \*\*\* | 9% | +4.84 |  |  |  |  |  |  |  |  |  |  |
|  |  |  |  |  |  |  |  |  |  |  |  |  | TT2 | \* | 4% | +6.01 |  |  |  |  |  |  |  |  |  |  |
| T89 | PCD053c |  | T11 | \*\*\*\*\*\* | 15% | +3.88 |  |  |  |  |  |  |  |  |  |  |  | T12 | \*\*\* | 9% | +3.13 |  |  |  |  |  |
|  |  |  | T12 | \*\* | 8% | +1.64 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|  | T5742E03c |  |  |  |  |  |  | G11 | \*\*\* | 9% | -2.31 |  |  |  |  |  |  |  |  |  |  |  | T12 | \*\*\* | 9% | -0.09 |
|  | T5743G05c |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | G12 | \*\*\* | 13% | -0.13 |
|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | T12 | \* | 8% | -0.08 |
|  | T5746E05 |  |  |  |  |  |  | T12 | \*\*\* | 11% | -2.00 |  |  |  |  |  |  | G12 | \* | 7% | -2.52 |  | G12 | \* | 5% | -0.08 |
|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | T12 | \*\*\*\*\* | 13% | -3.84 |  | T11 | \*\*\* | 9% | -0.12 |
|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | T12 | \*\*\*\*\*\* | 16% | -0.12 |
|  | PCD065c |  |  |  |  |  |  | G11 | \*\*\* | 11% | +2.74 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|  | **T5748B12** |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | T11 | \*\*\* | 13% | +0.20 |
|  | **T5741E08** |  |  |  |  |  |  | G11 | \*\*\* | 13% | -3.56 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|  |  |  |  |  |  |  |  | G12 | \*\*\*\*\*\* | 19% | -4.01 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|  | **PCD145a** |  |  |  |  |  |  | T11 | \*\*\*\* | 12% | +2.57 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|  | **T5742C01b** |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | G12 | \*\*\* | 9% | -0.12 |
|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | T12 | \* | 5% | -0.08 |
|  | **T5741C01** |  |  |  |  |  |  | G11 | \* | 5% | +1.96 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|  |  |  |  |  |  |  |  | G12 | \*\*\* | 9% | +2.53 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|  | **PCD115** |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | T12 | \*\*\* | 22% | +0.19 |
|  | **T5741E11b** |  | **G10** | \*\*\* | 12% | -0.99 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|  |  |  | **T10** | \*\*\* | 16% | -1.67 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |

a Source of a QTA: either T89, T574 or biparental. b Linkage map nomenclature. c *-ve* and *+ve* signs correspond to linkage phase (complementary alleles in *italic*; M-QTLs in *bold* font).

d Marker position in an LG. e Environment: *G* Griffin, *T* Tifton, *10* (2010), *11* (2011), *12* (2012) and *T1* (1st date) or *T2* (2nd date).

f \*0.05, \*\*0.01, \*\*\*0.005, \*\*\*\*0.001, \*\*\*\*\*0.0005, \*\*\*\*\*\*0.0001

Supplementary Table S2.5. Summary statistics of genotype matrix mapping (GMM) showing significant marker-trait associations or combination of loci (i.e., digenic or trigenic) putatively involved in epistatic interactions.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Traita | Sourceb | Env.c | Search Range | F value | Corresponding individualsd | |  | Other individuals | |  | Effecte | PVE (*R*2) | No. of  interacting loci | Significant locus/allele combinationf |
| # plants | Mean |  | # plants | Mean |  |
| HT | Intragenomic (T574) | G10 | 6.17 | 59.26 | 3 | 8.11 |  | 46 | 3.58 |  | 4.53 | 0.54 | 3 | RZ401b(a-) TC61023\_180(a-) CA182108\_410(a-) |
| HT | Intragenomic (T574) | G10 | 6.17 | 61.68 | 2 | 8.83 |  | 48 | 3.45 |  | 5.38 | 0.54 | 3 | CA172041b(b-) T5745H10d(a-) RZ140c(b-) |
| HT | Intragenomic (T89) | G10 | 9.63 | 78.14 | 2 | 8.92 |  | 43 | 3.39 |  | 5.52 | 0.63 | 3 | CA100438\_215(--) T5741E11c(a-) RZ588(a-) |
| HT | Intragenomic (T574) | G10 | 2.99 | 29.93 | 7 | 5.26 |  | 46 | 3.36 |  | 1.91 | 0.33 | 2 | T5742A10b(a-) CA093658\_240(a-) |
| HT | Intragenomic (T89) | G10 | 4.92 | 45.69 | 6 | 3.53 |  | 17 | 2.93 |  | 0.60 | 0.16 | 2 | RZ717(a-) RZ900(--) |
| HT | Intragenomic (T89) | G10 | 4.92 | 49.20 | 2 | 8.92 |  | 38 | 3.61 |  | 5.31 | 0.54 | 2 | T5742B11b(a-) T5746E07a(--) |
| HT | T89 | G10 | 1.16 | 11.63 | 45 | 3.30 |  | 50 | 4.03 |  | -0.73 | 0.09 | 1 | CA125611\_160(a-) |
| HT | T574 | G10 | 1.18 | 11.76 | 26 | 3.10 |  | 24 | 3.88 |  | -0.78 | 0.11 | 1 | PAP07C04a(a-) |
| HT | Intragenomic (T574) | G12 | 3.56 | 32.15 | 2 | 7.17 |  | 14 | 10.98 |  | -3.81 | 0.46 | 3 | PAP07G03a(--) T5741C03a(a-) PAP05H08(a-) |
| HT | Intragenomic (T574) | G12 | 3.56 | 35.60 | 5 | 15.73 |  | 30 | 11.64 |  | 4.09 | 0.47 | 3 | T5743B10a(--) CA191677\_260(--) PCD132d(--) |
| HT | Intragenomic (T574) | G12 | 3.56 | 35.60 | 5 | 15.73 |  | 30 | 11.64 |  | 4.09 | 0.47 | 3 | T5743B10a(--) CA294786\_220(a-) PCD132d(--) |
| HT | Intragenomic (T574) | G12 | 3.56 | 35.60 | 5 | 15.73 |  | 30 | 11.64 |  | 4.09 | 0.47 | 3 | T5743B10a(--) PCD132d(--) CA093658\_240(--) |
| HT | Intragenomic (T89) | G12 | 4.41 | 42.96 | 6 | 15.28 |  | 14 | 11.09 |  | 4.18 | 0.65 | 3 | T5746E01b(a-) T5745A04c(a-) T5742C08b(a-) |
| HT | Intergenomic | G12 | 2.55 | 25.33 | 17 | 10.12 |  | 44 | 12.67 |  | -2.56 | 0.27 | 2 | T5743G01d(a-) T5741A08a(a-) |
| HT | Intergenomic | G12 | 2.55 | 25.50 | 7 | 14.33 |  | 28 | 11.76 |  | 2.57 | 0.35 | 2 | CA158542\_300(b-) RZ717(a-) |
| HT | Intragenomic (T89) | G12 | 2.57 | 25.70 | 8 | 9.58 |  | 35 | 12.70 |  | -3.11 | 0.34 | 2 | T5748D07b(a-) CA243036\_600(b-) |
| HT | T89 | G12 | 1.22 | 12.17 | 41 | 12.58 |  | 42 | 11.20 |  | 1.38 | 0.11 | 1 | CF574110\_150(a-) |
| HT | Intergenomic | T10 | 5.18 | 50.76 | 7 | 10.81 |  | 34 | 6.89 |  | 3.91 | 0.54 | 3 | PCD132d(a-) CA100438\_215(--) PAP04A06b(a-) |
| HT | Intragenomic (T574) | T10 | 3.70 | 34.10 | 8 | 10.27 |  | 31 | 7.05 |  | 3.22 | 0.43 | 3 | PCD017(--) T5742F09b(a-) TC62694\_270(--) |
| HT | Intragenomic (T574) | T10 | 3.70 | 34.16 | 5 | 11.60 |  | 34 | 7.09 |  | 4.51 | 0.44 | 3 | PCD101(a-) T5741D06a(--) T5746E04b(--) |
| HT | Intragenomic (T574) | T10 | 3.70 | 37.01 | 4 | 11.54 |  | 29 | 7.21 |  | 4.33 | 0.50 | 3 | CA146239a(--) PCD132d(a-) PAP10A04a(a-) |
| HT | Intragenomic (T574) | T10 | 3.70 | 35.15 | 3 | 12.11 |  | 12 | 6.92 |  | 5.19 | 0.67 | 3 | PCD132d(a-) T5743G01d(--) CA106832\_90(a-) |
| HT | Intragenomic (T89) | T10 | 5.18 | 48.79 | 8 | 10.85 |  | 54 | 6.74 |  | 4.12 | 0.43 | 3 | CA100438\_215(--) TC48763\_210(--) T5741C03c(--) |
| HT | Intragenomic (T89) | T10 | 5.18 | 47.31 | 6 | 10.47 |  | 33 | 6.69 |  | 3.79 | 0.54 | 3 | CA093674\_230(a-) T5742G03a(a-) CA100438\_215(--) |
| HT | Intragenomic (T89) | T10 | 5.18 | 51.80 | 5 | 10.63 |  | 26 | 6.34 |  | 4.29 | 0.61 | 3 | T5743C12d(a-) T5742G03a(a-) CA100438\_215(--) |
| HT | Intragenomic (T89) | T10 | 5.18 | 51.80 | 5 | 10.63 |  | 26 | 6.34 |  | 4.29 | 0.61 | 3 | T5743C12d(a-) T5742G03a(a-) CA255151\_190(a-) |
| HT | Intragenomic (T89) | T10 | 8.99 | 82.44 | 5 | 10.63 |  | 19 | 6.54 |  | 4.10 | 0.77 | 3 | **T5748B07c(a-)** PAP06F11a(a-) T5741A04a(a-) |
| HT | Intergenomic | T10 | 3.11 | 31.07 | 3 | 12.11 |  | 15 | 6.82 |  | 5.29 | 0.61 | 2 | RZ717(a-) T5743G01d(--) |
| HT | Intragenomic (T574) | T10 | 2.45 | 24.54 | 7 | 10.29 |  | 46 | 7.02 |  | 3.26 | 0.30 | 2 | T5742A10b(a-) CA093658\_240(a-) |
| HT | Intragenomic (T574) | T10 | 3.01 | 30.14 | 10 | 9.00 |  | 19 | 6.35 |  | 2.65 | 0.49 | 2 | T5743B05(a-) PAP07C04a(--) |
| HT | Intragenomic (T89) | T10 | 3.11 | 28.56 | 15 | 9.51 |  | 60 | 6.92 |  | 2.59 | 0.26 | 2 | TC58936\_120(--) PAP06F11a(a-) |
| HT | Intragenomic (T89) | T10 | 2.98 | 28.95 | 16 | 9.43 |  | 60 | 6.90 |  | 2.52 | 0.26 | 2 | TC48176\_260(a-) PAP06F11a(a-) |
| HT | Intragenomic (T89) | T10 | 3.11 | 29.79 | 16 | 9.45 |  | 60 | 6.90 |  | 2.55 | 0.27 | 2 | TC66108\_180(a-) PAP06F11a(a-) |
| HT | Intragenomic (T89) | T11 | 5.92 | 54.98 | 9 | 25.20 |  | 17 | 16.49 |  | 8.71 | 0.63 | 3 | T5743C12b(a-) T5746F07(a-) T5742B11b(--) |
| HT | Intergenomic | T11 | 3.16 | 28.70 | 5 | 26.58 |  | 20 | 16.78 |  | 9.79 | 0.50 | 2 | T5742D05a(a-) T5748B02c(--) |
| HT | Intragenomic (T574) | T11 | 2.61 | 26.13 | 2 | 31.28 |  | 30 | 17.38 |  | 13.90 | 0.42 | 2 | T5746G05(--) PCD017(--) |
| HT | Intragenomic (T89) | T11 | 3.16 | 31.62 | 14 | 23.54 |  | 64 | 16.71 |  | 6.83 | 0.27 | 2 | CF574110\_150(a-) PCD022a(a-) |
| HT | Intragenomic (T574) | T12 | 5.06 | 50.63 | 2 | 17.34 |  | 12 | 10.47 |  | 6.86 | 0.74 | 3 | T5743D06c(--) T5742A12(--) T5742A10b(a-) |
| HT | Intragenomic (T574) | T12 | 5.06 | 50.63 | 2 | 17.34 |  | 12 | 10.47 |  | 6.86 | 0.74 | 3 | T5743D06c(--) T5742A12(--) T5741B04(--) |
| HT | Intergenomic | T12 | 2.97 | 27.11 | 17 | 14.02 |  | 28 | 10.82 |  | 3.20 | 0.33 | 2 | T5745B06a(a-) PCD142(--) |
| HT | Intragenomic (T574) | T12 | 2.11 | 20.95 | 22 | 10.49 |  | 26 | 12.94 |  | -2.45 | 0.21 | 2 | T5745B06a(--) PAP07G03a(a-) |
| HT | Intragenomic (T574) | T12 | 2.11 | 21.11 | 11 | 9.04 |  | 53 | 12.96 |  | -3.93 | 0.22 | 2 | T5745B06a(--) T5741H06a(a-) |
| HT | Intragenomic (T89) | T12 | 2.97 | 27.45 | 14 | 15.38 |  | 56 | 11.50 |  | 3.88 | 0.26 | 2 | RZ543a(a-) T5746G11b(a-) |
| HT | Intragenomic (T89) | T12 | 2.97 | 29.68 | 15 | 15.44 |  | 48 | 11.39 |  | 4.06 | 0.30 | 2 | RZ543a(a-) T5741A10a(--) |
|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Traita | Sourceb | Env.c | Search Range | F value | Corresponding individualsd | |  | Other individuals | |  | Effecte | PVE (*R*2) | No. of  interacting loci | Significant locus/allele combinationf |
| # plants | Mean |  | # plants | Mean |  |
| HT | T89 | T12 | 1.60 | 14.61 | 55 | 11.71 |  | 36 | 13.83 |  | -2.12 | 0.12 | 1 | T5746E05(a-) |
| ILEN | Intergenomic | G11 | 6.00 | 59.97 | 6 | 31.75 |  | 23 | 24.26 |  | 7.49 | 0.65 | 3 | RZ455(a-) T5741A04a(a-) CA188502\_270(--) |
| ILEN | Intergenomic | G11 | 6.00 | 54.09 | 7 | 31.23 |  | 13 | 24.24 |  | 6.99 | 0.68 | 3 | T5746D06(--) T5743D12b(a-) CA188502\_270(--) |
| ILEN | Intragenomic (T574) | G11 | 3.82 | 34.98 | 9 | 30.64 |  | 29 | 24.02 |  | 6.62 | 0.46 | 3 | PCD101(a-) CA245812\_200(--) PCD148b(b-) |
| ILEN | Intragenomic (T574) | G11 | 3.82 | 36.18 | 9 | 30.64 |  | 30 | 24.00 |  | 6.64 | 0.46 | 3 | PCD101(a-) TC55445\_230(--) PCD148b(b-) |
| ILEN | Intragenomic (T574) | G11 | 3.82 | 36.18 | 9 | 30.64 |  | 30 | 24.00 |  | 6.64 | 0.46 | 3 | PCD101(a-) CA158542\_300(a-) PCD148b(b-) |
| ILEN | Intragenomic (T574) | G11 | 3.82 | 36.55 | 8 | 31.05 |  | 31 | 24.11 |  | 6.95 | 0.46 | 3 | PCD101(a-) TC56845\_500(--) PCD148b(b-) |
| ILEN | Intragenomic (T574) | G11 | 3.82 | 38.25 | 7 | 31.54 |  | 34 | 24.10 |  | 7.44 | 0.47 | 3 | PCD101(a-) T5745B06a(a-) PCD148b(b-) |
| ILEN | Intragenomic (T574) | G11 | 3.82 | 35.62 | 7 | 31.06 |  | 27 | 23.53 |  | 7.53 | 0.50 | 3 | PCD101(a-) RZ140c(b-) PCD148b(b-) |
| ILEN | Intragenomic (T89) | G11 | 5.10 | 51.00 | 6 | 31.94 |  | 33 | 24.91 |  | 7.03 | 0.52 | 3 | T5741A07(--) T5742A10a(a-) T5741G04c(b-) |
| ILEN | Intragenomic (T89) | G11 | 5.10 | 54.34 | 4 | 32.98 |  | 22 | 24.05 |  | 8.93 | 0.67 | 3 | RZ261c(--) T5745A04c(a-) T5741A04a(a-) |
| ILEN | Intergenomic | G11 | 3.66 | 33.00 | 6 | 30.54 |  | 17 | 23.22 |  | 7.32 | 0.57 | 2 | T5743D06c(--) T5743B10b(--) |
| ILEN | Intragenomic (T574) | G11 | 2.78 | 27.77 | 9 | 30.26 |  | 34 | 24.32 |  | 5.93 | 0.36 | 2 | PCD101(a-) CA145016\_350(a-) |
| ILEN | Intragenomic (T89) | G11 | 3.66 | 36.64 | 6 | 31.42 |  | 39 | 25.12 |  | 6.30 | 0.39 | 2 | TC52187\_250(a-) T5742A10a(a-) |
| ILEN | T89 | G11 | 2.06 | 20.62 | 46 | 26.90 |  | 49 | 23.54 |  | -3.37 | 0.16 | 1 | CA265902\_300(a-) |
| ILEN | Intergenomic | G12 | 3.69 | 36.90 | 2 | 24.11 |  | 4 | 17.26 |  | 6.85 | 0.78 | 2 | PAP07H09(--) T5741H06a(--) |
| ILEN | Intragenomic (T574) | G12 | 2.68 | 26.76 | 23 | 24.78 |  | 65 | 20.78 |  | 4.00 | 0.22 | 2 | T5741A08c(b-) CA182108\_410(--) |
| ILEN | Intragenomic (T574) | G12 | 2.68 | 25.24 | 9 | 26.13 |  | 28 | 20.23 |  | 5.90 | 0.38 | 2 | T5743D06c(--) T5745B01(--) |
| ILEN | Intragenomic (T89) | G12 | 2.93 | 29.28 | 29 | 19.32 |  | 57 | 23.20 |  | -3.89 | 0.24 | 2 | PCD021b(--) TC62910\_300(--) |
| ILEN | Intragenomic (T89) | G12 | 2.93 | 28.18 | 5 | 25.83 |  | 12 | 20.66 |  | 5.17 | 0.60 | 2 | RZ912(--) T5742B11a(a-) |
| ILEN | T89 | G12 | 1.02 | 10.22 | 41 | 20.73 |  | 42 | 23.15 |  | -2.42 | 0.09 | 1 | PCD145b(a-) |
| ILEN | T89 | G12 | 1.02 | 9.51 | 35 | 20.87 |  | 34 | 23.16 |  | -2.29 | 0.10 | 1 | T5745D06c(a-) |
| ILEN | T89 | G12 | 1.85 | 16.79 | 4 | 27.81 |  | 21 | 21.41 |  | -6.40 | 0.36 | 1 | **T5743C03b(a-)** |
| ILEN | T89 | G12 | 1.85 | 18.54 | 64 | 21.49 |  | 14 | 25.49 |  | -4.01 | 0.17 | 1 | **T5741E08(a-)** |
| ILEN | Intragenomic (T574) | T11 | 5.27 | 60.85 | 6 | 27.65 |  | 16 | 19.73 |  | 7.92 | 0.69 | 3 | T5746E03(a-) T5741H06a(--) T5748C08a(a-) |
| ILEN | Intragenomic (T574) | T11 | 3.09 | 28.23 | 10 | 25.29 |  | 24 | 21.04 |  | 4.25 | 0.27 | 2 | T5743C03e(a-) T5746D06(--) |
| ILEN | Intragenomic (T574) | T11 | 3.09 | 30.86 | 13 | 25.09 |  | 22 | 20.62 |  | 4.47 | 0.31 | 2 | T5746D06(--) RZ140c(b-) |
| ILEN | Intragenomic (T574) | T11 | 3.09 | 29.80 | 7 | 26.76 |  | 23 | 19.50 |  | 7.27 | 0.47 | 2 | T5746E03(a-) T5742D06a(--) |
| ILEN | T574 | T11 | 1.57 | 15.66 | 28 | 22.91 |  | 36 | 18.89 |  | -4.02 | 0.17 | 1 | T5746F06(a-) |
| ILEN | T89 | T11 | 0.83 | 8.05 | 46 | 21.57 |  | 49 | 19.22 |  | 2.34 | 0.06 | 1 | CA265902\_300(a-) |
| ILEN | T89 | T11 | 0.83 | 8.34 | 49 | 21.52 |  | 42 | 19.02 |  | -2.50 | 0.06 | 1 | TC60618\_150(a-) |
| ILEN | Intragenomic (T574) | T12 | 2.01 | 20.08 | 11 | 11.30 |  | 53 | 15.68 |  | -4.38 | 0.21 | 2 | T5745B06a(--) T5741H06a(a-) |
| ILEN | T89 | T12 | 1.38 | 13.79 | 61 | 14.43 |  | 39 | 16.79 |  | -2.35 | 0.10 | 1 | T5741D01b(a-) |
| LLS | Intergenomic | GT1 | 4.94 | 46.78 | 3 | 47.11 |  | 18 | 30.87 |  | 16.24 | 0.65 | 3 | T5746E07b(a-) RZ995(a-) PAP10A04b(a-) |
| LLS | Intergenomic | GT1 | 4.94 | 48.58 | 2 | 46.17 |  | 8 | 28.75 |  | 17.42 | 0.79 | 3 | T5741H11a(a-) RZ444b(a-) T5742D09(--) |
| LLS | Intragenomic (T574) | GT1 | 3.85 | 38.53 | 5 | 47.07 |  | 16 | 31.85 |  | 15.21 | 0.63 | 3 | T5746E07b(a-) RZ995(a-) T5743C03d(a-) |
| LLS | Intragenomic (T574) | GT1 | 3.85 | 35.36 | 4 | 46.50 |  | 13 | 31.62 |  | 14.89 | 0.66 | 3 | T5743B10a(a-) RZ455(--) RZ574(a-) |
| LLS | Intragenomic (T574) | GT1 | 3.85 | 35.36 | 4 | 46.50 |  | 13 | 31.62 |  | 14.89 | 0.66 | 3 | T5743B10a(a-) T5742A10b(--) RZ574(a-) |
| LLS | Intragenomic (T89) | GT1 | 3.89 | 37.38 | 8 | 45.71 |  | 64 | 34.35 |  | 11.35 | 0.33 | 3 | TC51780\_120(--) PCD131a(--) TC61478\_600(b-) |
| LLS | Intragenomic (T89) | GT1 | 3.89 | 35.92 | 3 | 39.00 |  | 17 | 30.16 |  | 8.84 | 0.38 | 3 | RZ575(a-) T5748C01a(--) PAP10A04b(a-) |
| LLS | Intragenomic (T89) | GT1 | 3.89 | 35.81 | 5 | 45.00 |  | 29 | 32.39 |  | 12.61 | 0.48 | 3 | T5748F05(a-) PCD070b(a-) PAP04A06b(--) |
| LLS | Intragenomic (T89) | GT1 | 3.89 | 38.92 | 3 | 49.00 |  | 19 | 32.54 |  | 16.46 | 0.62 | 3 | CA177713\_240(--) RZ912(--) T5748F05(a-) |
| LLS | Intragenomic (T89) | GT1 | 3.89 | 38.48 | 3 | 49.00 |  | 16 | 32.21 |  | 16.79 | 0.66 | 3 | CA177713\_240(--) RZ912(--) PCD070b(a-) |
| LLS | T89 | GT1 | 0.89 | 8.90 | 38 | 37.73 |  | 46 | 33.66 |  | 4.07 | 0.08 | 1 | T5746C08(a-) |
| LLS | T574 | GT1 | 1.01 | 9.57 | 46 | 37.36 |  | 33 | 32.97 |  | 4.39 | 0.09 | 1 | RZ140c(b-) |
| LLS | Intragenomic (T574) | GT2 | 3.56 | 33.96 | 3 | 68.00 |  | 11 | 46.30 |  | 21.70 | 0.70 | 3 | PAP07G03a(a-) RZ455(--) RZ574(a-) |
| LLS | Intragenomic (T89) | GT2 | 5.53 | 57.22 | 2 | 68.50 |  | 14 | 45.05 |  | 23.45 | 0.75 | 3 | PCD138(a-) T5745B05(--) T5741C07(--) |
| LLS | Intragenomic (T89) | GT2 | 2.75 | 27.54 | 5 | 62.93 |  | 19 | 53.51 |  | 9.43 | 0.29 | 2 | T5743A03(a-) T5748G02b(a-) |
|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Traita | Sourceb | Env.c | Search Range | F value | Corresponding individualsd | |  | Other individuals | |  | Effecte | PVE (*R*2) | No. of  interacting loci | Significant locus/allele combinationf |
| # plants | Mean |  | # plants | Mean |  |
| LLS | T89 | GT2 | 0.82 | 8.21 | 39 | 47.40 |  | 49 | 52.71 |  | 5.31 | 0.06 | 1 | PCD008(a-) |
| LLS | Intragenomic (T574) | TT1 | 3.85 | 49.11 | 5 | 41.53 |  | 10 | 31.03 |  | 10.50 | 0.68 | 3 | PCD132d(a-) PAP05H08(a-) T5743D12b(a-) |
| LLS | Intragenomic (T89) | TT1 | 4.21 | 40.43 | 13 | 30.90 |  | 30 | 40.38 |  | -9.48 | 0.47 | 3 | CA100438\_215(a-) T5746D05(a-) CA162523\_100(a-) |
| LLS | Intragenomic (T89) | TT1 | 4.21 | 42.14 | 7 | 45.71 |  | 28 | 35.77 |  | 9.94 | 0.53 | 3 | PCD132a(--) PCD131a(--) T5741A08a(a-) |
| LLS | Intragenomic (T89) | TT1 | 4.21 | 39.81 | 7 | 44.62 |  | 20 | 35.55 |  | 9.07 | 0.58 | 3 | CA193820\_510(a-) PCD068(a-) PCD132a(--) |
| LLS | Intergenomic | TT1 | 3.57 | 35.67 | 4 | 38.67 |  | 15 | 32.16 |  | 6.51 | 0.29 | 2 | RZ575(a-) PAP05H08(a-) |
| LLS | Intragenomic (T574) | TT1 | 2.10 | 19.02 | 18 | 33.13 |  | 68 | 39.54 |  | -6.41 | 0.16 | 2 | CA158542\_300(b-) TC56094\_130(a-) |
| LLS | Intragenomic (T574) | TT1 | 2.10 | 21.02 | 12 | 31.58 |  | 26 | 40.01 |  | -8.43 | 0.33 | 2 | T5743D06c(a-) CF573608\_150(--) |
| LLS | Intragenomic (T574) | TT1 | 2.10 | 19.46 | 6 | 45.61 |  | 16 | 36.60 |  | 9.01 | 0.42 | 2 | T5742A10b(--) RZ574(a-) |
| LLS | Intragenomic (T574) | TT1 | 2.10 | 19.76 | 7 | 44.38 |  | 15 | 36.27 |  | 8.11 | 0.43 | 2 | PAP07C04a(--) RZ574(a-) |
| LLS | Intragenomic (T574) | TT2 | 2.69 | 36.32 | 3 | 72.22 |  | 14 | 55.71 |  | 16.51 | 0.52 | 3 | T5743D06c(--) T5742D06a(a-) RZ140c(a-) |
| LLS | Intragenomic (T89) | TT2 | 5.24 | 52.44 | 25 | 73.52 |  | 40 | 58.86 |  | 14.66 | 0.44 | 3 | **PCD131c(a-)** T5746F07(a-) CA100438\_215(--) |
| LLS | Intragenomic (T89) | TT2 | 5.24 | 52.02 | 25 | 73.52 |  | 36 | 58.82 |  | 14.69 | 0.45 | 3 | **PCD132c(a-)** T5746F07(a-) CA100438\_215(--) |
| LLS | Intragenomic (T89) | TT2 | 5.24 | 48.60 | 20 | 74.83 |  | 35 | 59.76 |  | 15.07 | 0.45 | 3 | **T5746F07(a-)** PAP06F11a(a-) CA100438\_215(--) |
| LLS | Intragenomic (T89) | TT2 | 6.00 | 59.96 | 3 | 75.78 |  | 8 | 52.25 |  | 23.53 | 0.80 | 3 | PAP07H09(--) T5743E12b(a-) PAP04A06b(--) |
| LLS | Intergenomic | TT2 | 2.96 | 26.60 | 24 | 72.49 |  | 65 | 60.93 |  | 11.55 | 0.22 | 2 | CA193820\_550(--) CA100438\_215(--) |
| LLS | Intergenomic | TT2 | 2.96 | 29.14 | 26 | 72.62 |  | 65 | 60.89 |  | 11.73 | 0.23 | 2 | CF573608\_150(a-) CA100438\_215(--) |
| LLS | Intergenomic | TT2 | 2.96 | 27.01 | 25 | 71.85 |  | 56 | 60.71 |  | 11.14 | 0.24 | 2 | PCD131d(a-) CA193820\_510a-) |
| LLS | Intergenomic | TT2 | 2.96 | 29.55 | 25 | 72.73 |  | 61 | 60.89 |  | 11.85 | 0.24 | 2 | PCD131d(a-) CA100438\_215(--) |
| LLS | Intergenomic | TT2 | 2.96 | 27.44 | 4 | 83.67 |  | 10 | 64.00 |  | 19.67 | 0.56 | 2 | RZ574(a-) PCD132a(--) |
| LLS | Intragenomic (T574) | TT2 | 2.15 | 20.08 | 28 | 71.21 |  | 60 | 61.42 |  | 9.79 | 0.17 | 2 | CA193820\_550(--) PCD131d(a-) |
| LLS | Intragenomic (T574) | TT2 | 2.15 | 21.51 | 25 | 72.05 |  | 65 | 61.67 |  | 10.38 | 0.18 | 2 | CA216782\_120(a-) PCD131d(a-) |
| LLS | Intragenomic (T574) | TT2 | 2.15 | 19.66 | 19 | 73.02 |  | 62 | 61.85 |  | 11.17 | 0.18 | 2 | T5743E09(--) CF573608\_150(a-) |
| LLS | Intragenomic (T89) | TT2 | 2.90 | 26.63 | 27 | 56.35 |  | 62 | 67.47 |  | -11.13 | 0.22 | 2 | CA100438\_215(a-) TC62910\_300(--) |
| LLS | Intragenomic (T89) | TT2 | 2.90 | 29.03 | 25 | 71.69 |  | 56 | 60.16 |  | 11.53 | 0.25 | 2 | CA100438\_215(--) CA193820\_510(a-) |
| LLS | T574 | TT2 | 1.18 | 11.11 | 17 | 65.53 |  | 35 | 59.27 |  | -6.26 | 0.07 | 1 | RZ801b(a-) |
| LLEN | Intragenomic (T574) | G12 | 4.90 | 49.04 | 2 | 44.22 |  | 12 | 29.74 |  | 14.48 | 0.77 | 3 | RZ455(a-) T5748A06(--) T5743G01d(a-) |
| LLEN | Intragenomic (T89) | G12 | 5.88 | 53.19 | 4 | 42.80 |  | 43 | 29.68 |  | 13.12 | 0.52 | 3 | RZ460b(a-) T5742E07(a-) CA211835\_70(--) |
| LLEN | Intragenomic (T89) | G12 | 5.88 | 58.75 | 2 | 44.22 |  | 12 | 28.95 |  | 15.27 | 0.80 | 3 | CA287747\_100(a-) RZ717(a-) T5748D07a(a-) |
| LLEN | Intragenomic (T574) | G12 | 2.02 | 18.46 | 22 | 35.02 |  | 65 | 30.08 |  | 4.94 | 0.16 | 2 | CA245812\_200(--) TC56094\_130(--) |
| LLEN | Intragenomic (T574) | G12 | 2.02 | 19.02 | 2 | 44.22 |  | 77 | 30.87 |  | 13.35 | 0.18 | 2 | TC61023\_180(--) T5748C08a(a-) |
| LLEN | Intragenomic (T574) | G12 | 2.02 | 20.17 | 19 | 35.63 |  | 62 | 30.09 |  | 5.54 | 0.18 | 2 | PAP06F11c(a-) TC56094\_130(--) |
| LLEN | Intragenomic (T574) | G12 | 2.02 | 18.35 | 10 | 37.76 |  | 50 | 30.75 |  | 7.01 | 0.20 | 2 | T5746E04b(--) TC66673\_70(a-) |
| LLEN | Intragenomic (T89) | G12 | 3.31 | 33.15 | 13 | 35.17 |  | 25 | 28.31 |  | 6.86 | 0.44 | 2 | RZ288(a-) RZ545(a-) |
| LLEN | T89 | G12 | 0.72 | 7.21 | 58 | 32.35 |  | 43 | 29.82 |  | -2.53 | 0.05 | 1 | T5742F09c(a-) |
| LLEN | T89 | G12 | 0.72 | 7.24 | 55 | 32.45 |  | 41 | 29.81 |  | -2.65 | 0.05 | 1 | CA243926\_280(a-) |
| LLEN | T574 | G12 | 1.09 | 10.91 | 43 | 29.64 |  | 51 | 32.84 |  | -3.20 | 0.09 | 1 | CA173231\_220(a-) |
| LLEN | Intragenomic (T89) | T12 | 4.49 | 44.21 | 11 | 32.46 |  | 56 | 23.13 |  | 9.32 | 0.39 | 3 | RZ543a(a-) PCD131b(--) T5743A08b(a-) |
| LLEN | Intragenomic (T89) | T12 | 4.49 | 47.21 | 7 | 30.22 |  | 28 | 20.47 |  | 9.75 | 0.50 | 3 | CA162523\_100(--) PCD132b(--) T5745B06d(a-) |
| LLEN | Intragenomic (T89) | T12 | 4.49 | 44.90 | 6 | 35.53 |  | 27 | 23.68 |  | 11.85 | 0.55 | 3 | T5741D01b(b-) T5743A03(a-) RZ588(a-) |
| LLEN | Intragenomic (T574) | T12 | 2.46 | 24.61 | 6 | 33.69 |  | 54 | 23.41 |  | 10.28 | 0.27 | 2 | CA097171\_280(a-) T5743A08a(a-) |
| LLEN | Intragenomic (T574) | T12 | 2.46 | 22.64 | 7 | 32.23 |  | 28 | 24.91 |  | 7.32 | 0.29 | 2 | T5743D06c(--) T5743D06b(b-) |
| LLEN | Intragenomic (T89) | T12 | 3.28 | 30.40 | 34 | 28.16 |  | 58 | 22.62 |  | 5.54 | 0.24 | 2 | T5742F09a(a-) T5742F09c(--) |
| LLEN | Intragenomic (T89) | T12 | 3.28 | 30.32 | 22 | 29.65 |  | 68 | 23.19 |  | 6.46 | 0.24 | 2 | T5745B07(a-) T5742F09c(--) |
| LLEN | Intragenomic (T89) | T12 | 3.28 | 30.61 | 18 | 30.24 |  | 48 | 23.29 |  | 6.95 | 0.29 | 2 | T5746E05(--) T5743B09a(a-) |
| LLEN | Intragenomic (T89) | T12 | 3.28 | 32.80 | 21 | 27.94 |  | 29 | 21.24 |  | 6.69 | 0.38 | 2 | PCD142(--) T5741A10a(--) |
| LW | Intergenomic | G12 | 5.64 | 61.98 | 4 | 1.94 |  | 17 | 1.61 |  | 0.34 | 0.71 | 3 | RZ995(a-) TC48809\_120(a-) T5746E10b(--) |
| LW | Intragenomic (T89) | G12 | 5.64 | 56.45 | 10 | 2.00 |  | 39 | 1.65 |  | 0.35 | 0.53 | 3 | T5743D12d(a-) T5742F09a(a-) T5742C08b(b-) |
|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Traita | Sourceb | Env.c | Search Range | F value | Corresponding individualsd | |  | Other individuals | |  | Effecte | PVE (*R*2) | No. of  interacting loci | Significant locus/allele combinationf |
| # plants | Mean |  | # plants | Mean |  |
| LW | Intragenomic (T574) | G12 | 2.39 | 23.86 | 8 | 1.85 |  | 14 | 1.59 |  | 0.26 | 0.47 | 2 | PCD101(--) PAP07C04a(--) |
| LW | Intragenomic (T89) | G12 | 3.11 | 30.66 | 16 | 1.93 |  | 69 | 1.67 |  | 0.25 | 0.25 | 2 | TC48402\_320(--) CA162523\_100(--) |
| LW | Intragenomic (T89) | G12 | 3.11 | 28.66 | 6 | 2.02 |  | 58 | 1.66 |  | 0.36 | 0.28 | 2 | RZ900(--) CA107430\_230(a-) |
| LW | Intragenomic (T89) | G12 | 3.11 | 31.06 | 9 | 1.96 |  | 55 | 1.65 |  | 0.31 | 0.30 | 2 | RZ900(--) TC65375\_150(a-) |
| LW | T89 | G12 | 1.82 | 18.15 | 33 | 1.81 |  | 56 | 1.66 |  | 0.15 | 0.15 | 1 | RZ543a(a-) |
| LW | T574 | G12 | 0.91 | 8.78 | 19 | 1.82 |  | 35 | 1.66 |  | -0.16 | 0.11 | 1 | T5748F03b(a-) |
| LW | Intragenomic (T89) | T12 | 5.13 | 51.31 | 6 | 2.13 |  | 19 | 1.84 |  | 0.28 | 0.65 | 3 | CA177713\_240(--) T5746E01a(a-) RZ460c(a-) |
| LW | Intergenomic | T12 | 3.08 | 28.27 | 20 | 2.02 |  | 66 | 1.84 |  | 0.18 | 0.23 | 2 | CA078499\_800(--) CA162523\_100(--) |
| LW | Intergenomic | T12 | 3.08 | 28.78 | 13 | 2.05 |  | 55 | 1.84 |  | 0.21 | 0.28 | 2 | T5743G06(--) RZ543a(a-) |
| LW | Intragenomic (T574) | T12 | 1.77 | 16.95 | 24 | 1.78 |  | 71 | 1.92 |  | -0.14 | 0.14 | 2 | TC57762\_290(a-) CA078499\_800(a-) |
| LW | Intragenomic (T574) | T12 | 1.77 | 16.37 | 26 | 1.79 |  | 64 | 1.92 |  | -0.13 | 0.14 | 2 | TC56094\_130(a-) CA078499\_800(a-) |
| LW | Intragenomic (T574) | T12 | 1.77 | 17.70 | 21 | 1.99 |  | 62 | 1.84 |  | 0.15 | 0.16 | 2 | CA094069\_210(--) CA078499\_800(--) |
| LW | Intragenomic (T574) | T12 | 1.77 | 17.49 | 15 | 1.99 |  | 44 | 1.85 |  | 0.15 | 0.21 | 2 | T5745D06a(--) CA078499\_800(--) |
| LW | Intragenomic (T89) | T12 | 3.08 | 27.87 | 28 | 1.79 |  | 57 | 1.94 |  | -0.15 | 0.23 | 2 | CA176859\_470(a-) T5743E08(--) |
| LW | Intragenomic (T89) | T12 | 3.08 | 29.44 | 19 | 2.03 |  | 65 | 1.84 |  | 0.19 | 0.25 | 2 | CA162523\_100(--) CA106603\_600(--) |
| LW | Intragenomic (T89) | T12 | 3.08 | 30.49 | 17 | 2.03 |  | 66 | 1.85 |  | 0.19 | 0.26 | 2 | CF574110\_150(a-) CA265902\_300(--) |
| LW | Intragenomic (T89) | T12 | 3.08 | 30.83 | 15 | 1.73 |  | 41 | 1.94 |  | -0.20 | 0.34 | 2 | T5743B10b(a-) CA177713\_260(a-) |
| LW | T89 | T12 | 2.07 | 20.72 | 55 | 1.84 |  | 36 | 1.96 |  | -0.12 | 0.17 | 1 | T5746E05(a-) |

a Traits under study: *HT* canopy height, *ILEN* internode length, *LLS* length of the longest internode, *LLEN* leaf length, and *LW* leaf width.

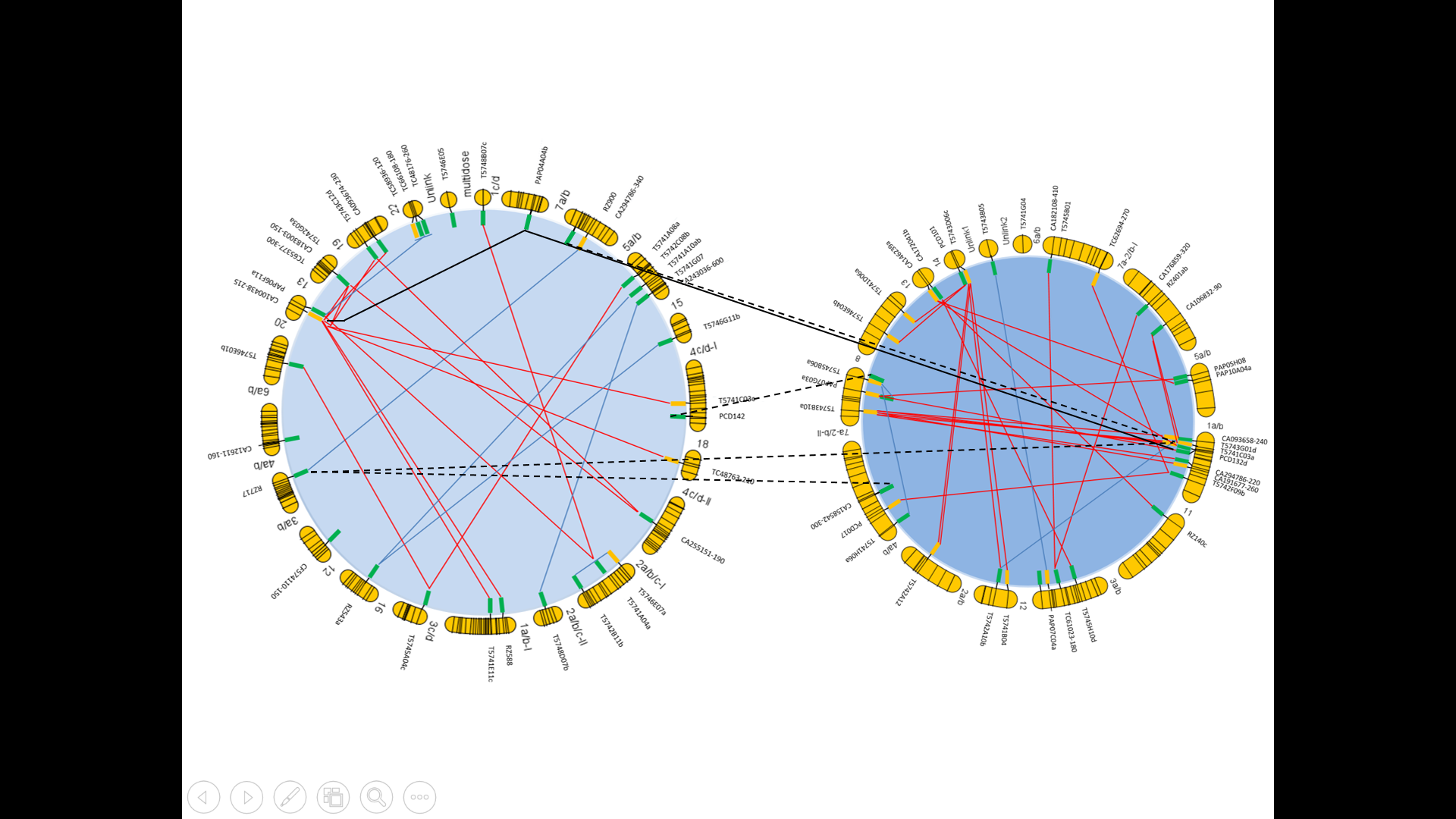
b Source of a significant marker-trait association or loci involved in epistatic interaction: intragenomic (i.e., within T89 or T574 loci) or intergenomic (between T89 and T574 loci).

c Environment: *G* Griffin, *T* Tifton, *10* (2010), *11* (2011), *12* (2012) and *T1* (1st date) or *T2* (2nd date).

d Number of corresponding plants with significant marker-trait association or combination of interacting loci and phenotypic means of corresponding individuals.

e Effect as a difference between phenotypic means of corresponding individuals *vs.* other individuals.

f *Blue* font (T89 locus) and *orange* font (T574 locus). In parenthesis: marker genotypes involved in significant association. (a-) or (b-) refers to heterozygosity at dominant marker locus and (--) refers to a lack of dominant marker allele at the locus.



a

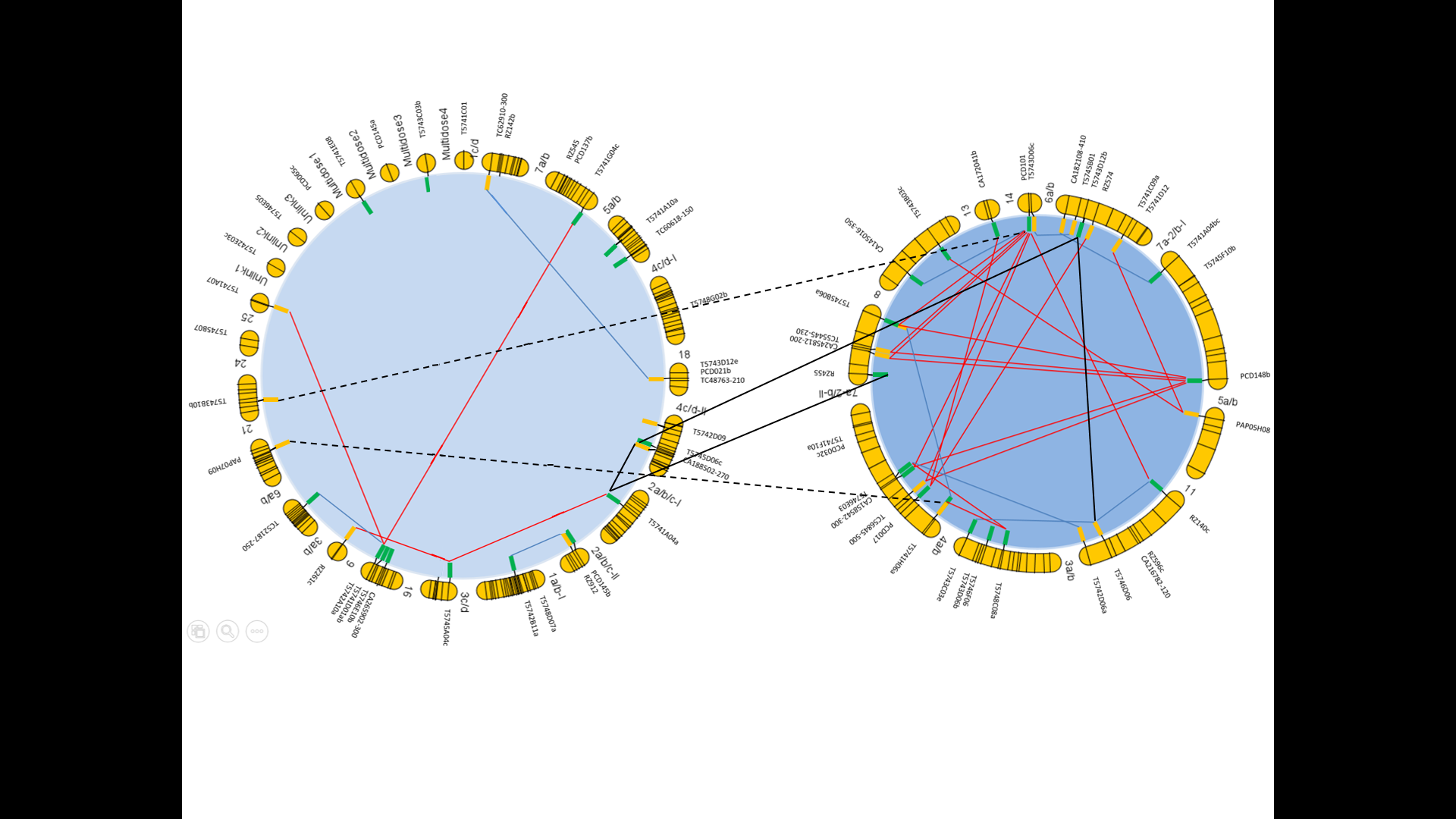
**T89**

**T574**

Supplemental Fig. S2.1 Loci involved in significant marker-trait associations identified by SMA and digenic and trigenic combinations detected by GMM. T89 and T574 cosegregating groups with significant loci detected for a. canopy height (HT), b. stolon internode length (ILEN), c. length of the longest stolon (LLS), and d. leaf length (LLEN) and leaf width (LW). Intragenomic combinations: digenic (*regular-blue* or *dashed -blue* lines) or trigenic (*regular-red* or *dashed-red* lines); Intergenomic combinations: digenic (*hashed-black* lines) or trigenic (*regular-black* lines). Digenic combination in LLEN (*regular-blue* lines); trigenic in LLEN (*regular-red* lines); digenic in LW (*hashed-blue* lines); trigenic in LW (*hashed-red* lines). *Rectangular* boxes in inner circle: *orange* (absence of dominant marker) and *green* (dominant marker genotype at marker locus).

**T574**

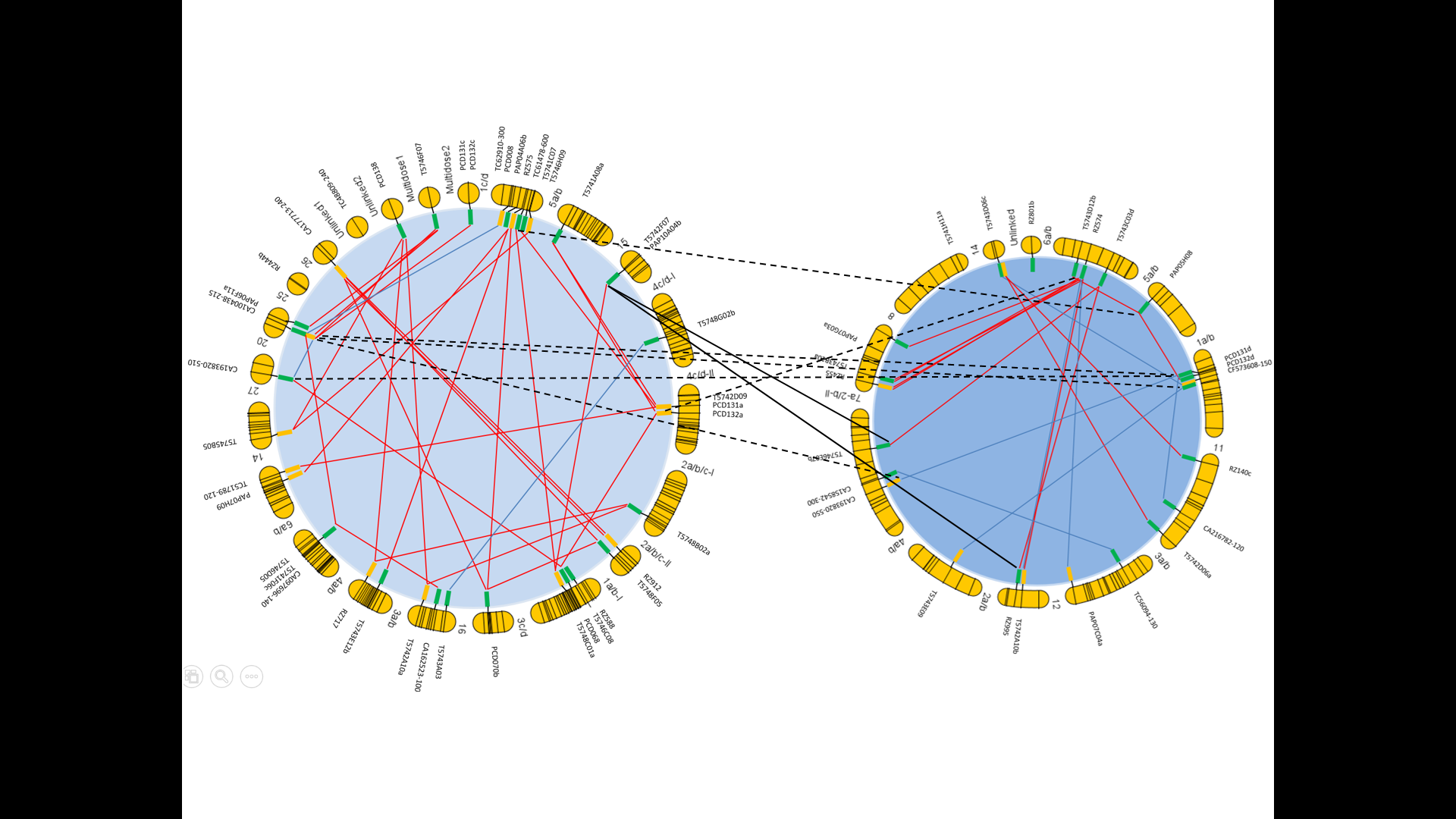
**T89**



b

**T89**

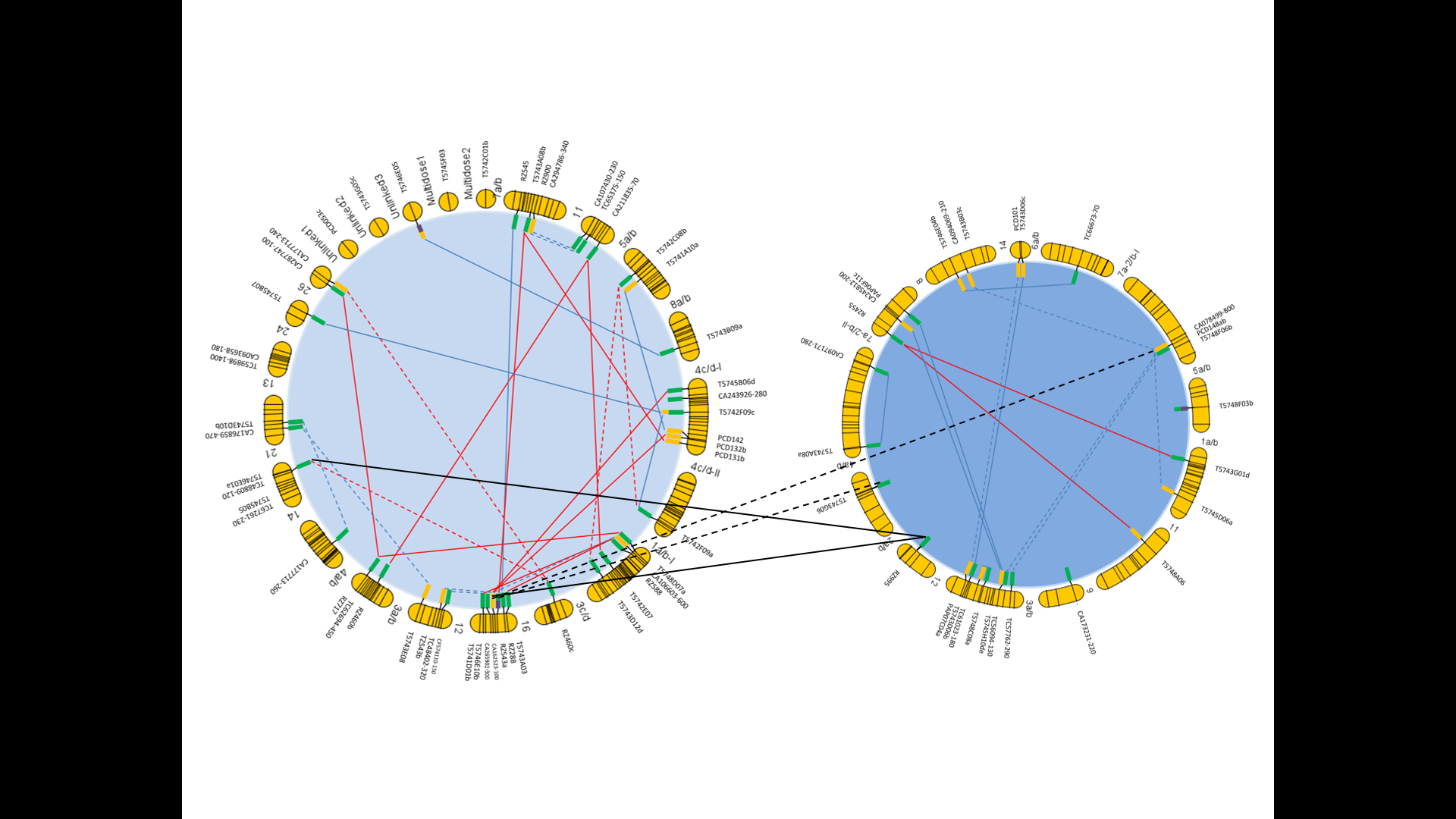
**T574**



c

**T89**

**T574**



d

**T89**

**T574**