**Table S1. Summarized description of the genetic linkage map of the PR 255 x PB 217 F1 population.**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Linkage Group  (LG) | Length  (cM) | Number of SSR markers | Number of SNP markers | Total number of markers | Average distance between markers (cM) |
| 1 | 182.4 | 25 | 11 | 36 | 5.21 |
| 2 | 228.5 | 21 | 9 | 30 | 7.88 |
| 3 | 206.7 | 22 | 5 | 27 | 7.95 |
| 4 | 126.9 | 11 | 8 | 19 | 7.05 |
| 5 | 220.5 | 22 | 10 | 32 | 7.11 |
| 6 | 180.5 | 18 | 13 | 31 | 6.02 |
| 7 | 182.8 | 20 | 9 | 29 | 6.53 |
| 8 | 235.0 | 25 | 4 | 29 | 8.39 |
| 9 | 155.7 | 15 | 7 | 22 | 7.41 |
| 10 | 302.6 | 35 | 12 | 47 | 6.58 |
| 11 | 200.6 | 10 | 10 | 20 | 10.56 |
| 12A | 181.5 | 13 | 6 | 19 | 10.08 |
| 12B | 19.1 | 0 | 3 | 3 | 9.55 |
| 13 | 188.2 | 18 | 5 | 23 | 8.55 |
| 14 | 285.4 | 28 | 14 | 42 | 6.96 |
| 15 | 168.5 | 18 | 5 | 23 | 7.66 |
| 16 | 166.8 | 18 | 3 | 21 | 8.34 |
| 17 | 115.4 | 13 | 5 | 18 | 6.79 |
| 18A | 159.3 | 16 | 5 | 21 | 7.97 |
| 18B | 10.8 | 6 | 0 | 6 | 2.17 |
| 19 | 3.1 | 0 | 2 | 2 | 3.10 |
| 20 | 3.1 | 0 | 3 | 3 | 3.10 |
| 21 | 1.8 | 0 | 2 | 2 | 1.80 |
|  |  |  |  |  |  |
| **Total** | **3,525.2** | **354** | **151** | **505** | **7.44** |

**Table S2. Different variance-covariance structures for the genetic matrix related to height, circumference, and latex production traits.**

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Trait | Genetic matrix | Tested model | AIC | | | | | | |
| SH1 | SH2 | TSH | WH1 | WH2 | TWH | TSWH |
| Height |  | ID ID | **27,832.90** | 29,905.16 | **33,249.39** | 24,302.48 | 26,748.81 | 29,108.17 | **33,641.59** |
|  |  | DIAG ID | 27,834.22 | 29,905.77 | 33,255.29 | 24,300.81 | **26,742.08** | 29,104.38 | 33,645.26 |
|  |  | CSHet ID | NC | NC | NC | NC | NC | NC | NC |
|  |  | FA ID | 27,838.93 | **29,899.30** | 33,261.55 | **24,295.00** | 26,748.08 | **29,100.80** | 33,644.82 |
|  |  | UNST ID | NC | NC | NC | NC | NC | NC | NC |
|  |  |  |  |  |  |  |  |  |  |
|  |  |  | SC1 | SC2 | SC3 | SC4 | SC5 | TSC |  |
| Circumfer. |  | ID ID | 19,380.01 | **23,166.45** | **24,445.07** | 27,782.71 | 20,735.00 | **30,688.38** |  |
|  |  | DIAG ID | **19,376.46** | 23,170.78 | 24,450.87 | **27,772.84** | 20,733.06 | 30,693.84 |  |
|  |  | CSHet ID | NC | NC | NC | NC | NC | NC |  |
|  |  | FA ID | 19,377.81 | NC | 24,454.63 | NC | **20,731.35** | NC |  |
|  |  | UNST ID | NC | NC | NC | NC | NC | NC |  |
|  |  |  |  |  |  |  |  |  |  |
|  |  |  | WC1 | WC2 | WC3 | WC4 | TWC | TSWC |  |
| Circumfer. |  | ID ID | **13,103.83** | 18,813.49 | 14,676.96 | 15,478.54 | **22,310.79** | **31,350.97** |  |
|  |  | DIAG ID | 13,109.42 | **18,807.09** | **14,649.24** | 15,477.64 | 22,311.81 | 31,355.49 |  |
|  |  | CSHet ID | NC | NC | NC | NC | NC | NC |  |
|  |  | FA ID | NC | 18,808.06 | 14,653.52 | **15,475.84** | NC | NC |  |
|  |  | UNST ID | NC | NC | NC | NC | NC | NC |  |
|  |  |  |  |  |  |  |  |  |  |
|  |  |  | TLP |  |  |  |  |  |  |
| Latex Prod. |  | DIAG ID | 31,317.74 |  |  |  |  |  |  |
|  |  | CSHet ID | 31,318.36 |  |  |  |  |  |  |
|  |  | AR1Het  ID | **31,314.53** |  |  |  |  |  |  |
|  |  | FA ID | NC |  |  |  |  |  |  |
|  |  | UNST ID | 31,321.39 |  |  |  |  |  |  |

**Table S3. Different variance-covariance structures for the residual matrix related to height, circumference, and latex production traits.**

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Trait | Genetic matrix | Tested model | AIC1 | | | | | | |
| SH1 | SH2 | TSH | WH1 | WH2 | TWH | TSWH |
| Height |  | DIAG ID | **27,688.11** | 29,952.79 | 33,009.46 | 24,348.41 | 26,795.09 | **29,062.68** | **33,465.93** |
|  |  | DIAG DIAG | NC | NC | NC | NC | NC | NC | NC |
|  |  | ID DIAG | 27,840.46 | 29,941.95 | 33,091.15 | 24,302.28 | 26,808.75 | 29,138.13 | 33,562.72 |
|  |  | AR1 ID | 27,833.83 | 29,900.67 | 33,251.35 | **24,290.68** | **26,744.08** | 29,099.31 | 33,643.55 |
|  |  | AR1Het ID | 27,688.20 | 29,954.22 | 33,011.14 | 24,340.44 | 26,797.09 | 29,063.49 | 33,467.91 |
|  |  | DIAG AR1 | 27,689.62 | 29,952.84 | **33,007.47** | 24,350.25 | 26,796.59 | 29,064.56 | 33,465.99 |
|  |  | DIAG AR1Het | NC | NC | NC | NC | NC | NC | NC |
|  |  | AR1 AR1 | 27,834.67 | **29,900.20** | 33,251.18 | 24,292.61 | 26,745.55 | 29,100.77 | 33,644.32 |
|  |  | AR1 AR1Het | 27,842.23 | 29,942.17 | 33,092.62 | 24,302.35 | 26,812.28 | 29,138.86 | 33,565.60 |
|  |  | AR1Het AR1 | 27,690.00 | 29,953.59 | 33,009.45 | 24,342.35 | 26,798.56 | 29,065.13 | 33,467.75 |
|  |  | AR1Het AR1Het | NC | NC | NC | NC | NC | NC | NC |
|  |  |  |  |  |  |  |  |  |  |
|  |  |  | SC1 | SC2 | SC3 | SC4 | SC5 | TSC |  |
| Circumfer. |  | DIAG ID | 19,245.46 | 23,200.12 | 24,535.06 | 27,710.71 | 20,768.06 | 30,757.96 |  |
|  |  | DIAG DIAG | NC | NC | NC | NC | NC | NC |  |
|  |  | ID DIAG | 19,289.66 | 23,201.78 | 24,476.16 | 27,743.68 | 20,737.99 | 30,744.88 |  |
|  |  | AR1 ID | 19,375.51 | **23,168.15** | 24,443.31 | 27,764.11 | 20,724.93 | **30,685.71** |  |
|  |  | AR1Het ID | **19,244.76** | 23,202.03 | 24,533.55 | **27,705.92** | 20,764.22 | 30,755.80 |  |
|  |  | DIAG AR1 | 19,247.09 | 23,200.40 | 24,532.04 | 27,712.66 | 20,761.13 | 30,759.19 |  |
|  |  | DIAG AR1Het | NC | NC | NC | NC | NC | NC |  |
|  |  | AR1 AR1 | 19,376.47 | 23,168.61 | **24,441.25** | 27,766.10 | 20,718.53 | 30,687.02 |  |
|  |  | AR1 AR1Het | 19,289.79 | 23,204.47 | 24,472.71 | 27,735.85 | **20,718.50** | 30,744.83 |  |
|  |  | AR1Het AR1 | 19,246.03 | 23,202.40 | 24,532.25 | 27,707.73 | 20,752.78 | 30,755.91 |  |
|  |  | AR1Het AR1Het | NC | NC | NC | NC | NC | NC |  |
|  |  |  |  |  |  |  |  |  |  |
|  |  |  |  |  |  |  |  |  |  |

**Table S3. Different variance-covariance structures for the residual matrix related to height, circumference, and latex production traits (continued).**

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Trait | Genetic matrix | Tested model | AIC1 | | | | | | |
| WC1 | WC2 | WC3 | WC4 | TWC | TSWC |  |
| Circumfer. |  | DIAG ID | **13,082.74** | **18,791.80** | 14,095.60 | 15,473.86 | 22,339.97 | 31,405.34 |  |
|  |  | DIAG DIAG | NC | NC | NC | NC | NC | NC |  |
|  |  | ID DIAG | 13,176.17 | 18,835.40 | 14,615.21 | 15,481.02 | 22,346.58 | 31,410.52 |  |
|  |  | AR1 ID | 13,104.94 | 18,807.47 | 14,639.45 | 15,473.99 | **22,303.26** | 31,346.40 |  |
|  |  | AR1Het ID | 13,083.99 | 18,793.35 | 14,096.11 | **15,472.29** | 22,333.32 | 31,400.67 |  |
|  |  | DIAG AR1 | 13,084.18 | 18,793.13 | **14,083.79** | 15,475.75 | 22,341.92 | 31,405.44 |  |
|  |  | DIAG AR1Het | NC | NC | NC | NC | NC | NC |  |
|  |  | AR1 AR1 | 13,106.88 | 18,809.44 | 14,594.16 | 15,475.08 | 22,305.25 | **31,346.33** |  |
|  |  | AR1 AR1Het | 13,179.00 | 18,838.57 | 14,562.36 | 15,481.43 | 22,340.99 | 31,407.39 |  |
|  |  | AR1Het AR1 | 13,085.62 | 18,794.86 | 14,085.58 | 15,473.70 | 22,335.15 | 31,398.60 |  |
|  |  | AR1Het AR1Het | NC | NC | NC | NC | NC | NC |  |
|  |  |  |  |  |  |  |  |  |  |
|  |  |  | TLP |  |  |  |  |  |  |
| Latex Prod. |  | DIAG ID | 31,343.36 |  |  |  |  |  |  |
|  |  | ID DIAG | 31,306.16 |  |  |  |  |  |  |
|  |  | DIAG DIAG | NC |  |  |  |  |  |  |
|  |  | AR1 ID | 31,298.66 |  |  |  |  |  |  |
|  |  | AR1Het ID | 31,328.17 |  |  |  |  |  |  |
|  |  | DIAG AR1 | 31,341.71 |  |  |  |  |  |  |
|  |  | DIAG AR1Het | NC |  |  |  |  |  |  |
|  |  | AR1 AR1 | 31,297.25 |  |  |  |  |  |  |
|  |  | AR1 AR1Het | **31,288.75** |  |  |  |  |  |  |
|  |  | AR1Het AR1 | 31,329.16 |  |  |  |  |  |  |
|  |  | AR1Het AR1Het | NC |  |  |  |  |  |  |

1AIC values correspond to the mixed models with the most likely genetic matrix and the tested residual matrix.

**Table S4. Selected models for the genetic and residual matrices related to height, circumference, and latex production traits.**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Trait | Genetic matrix | Selected model | Residual matrix | Selected model | Number of parameters | AIC |
| SH1 |  | ID ID |  | DIAG ID | 83 | 27,688.11 |
| SH2 |  | FA ID |  | ID ID | 10 | 29,899.30 |
| TSH |  | ID ID |  | DIAG AR1 | 84 | 33,007.47 |
| WH1 |  | FA ID |  | AR1 ID | 11 | 24,290.68 |
| WH2 |  | DIAG ID |  | ID ID | 6 | 26,742.08 |
| TWH |  | FA ID |  | DIAG ID | 90 | 29,062.68 |
| TSWH |  | ID ID |  | DIAG ID | 83 | 33,465.93 |
|  |  |  |  |  |  |  |
| SC1 |  | DIAG ID |  | AR1Het  ID | 87 | 19,244.76 |
| SC2 |  | ID ID |  | ID ID | 3 | 23,166,45 |
| SC3 |  | ID ID |  | AR1 AR1 | 5 | 24,441.25 |
| SC4 |  | DIAG ID |  | AR1Het  ID | 87 | 27,705.92 |
| SC5 |  | FA ID |  | AR1 AR1Het | 68 | 20,718.50 |
| TSC |  | ID ID |  | AR1 ID | 4 | 30,685.71 |
| WC1 |  | ID ID |  | DIAG ID | 83 | 13,082.74 |
| WC2 |  | DIAG ID |  | DIAG ID | 86 | 18,791.80 |
| WC3 |  | DIAG ID |  | DIAG AR1 | 87 | 14,083.79 |
| WC4 |  | FA ID |  | AR1Het  ID | 91 | 15,472.29 |
| TWC |  | ID ID |  | AR1 ID | 4 | 22,303.26 |
| TSWC |  | ID ID |  | AR1 AR1 | 5 | 31,346.33 |
|  |  |  |  |  |  |  |
| TLP |  | AR1Het ID |  | AR1 AR1Het | 98 | 31,288.75 |

These models were selected according to the lowest value of the AIC, which were calculated using both genetic and residual matrices in the statistical model.

**Table S5.** Characteristics of the 111 QTLs mapped for all phenotypic traits: *R²*, LOD score, additive and dominance effects, segregation type.

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| QTL | Trait | Flanking Markers | Linkage Group (LG) | Position  in cM | Global LOD | *R2* | αPR 255  (LOD) | αPB 217  (LOD) | δPR 255 x PB 217  (LOD) | Segregation |
| 1 | TWH | sHbUNI0515\_S | 1 | 0.00 | 5.365 | 2.363 | 3.149  (4.363) | 2.193  (2.358) | 3.055  (4.162) | 3:1 |
|  | TWC | sHbUNI0515\_S | 1 | 0.00 | 4.016 | 1.161 | 1.246  (1.889) | 1.753  (3.202) | 1.841  (3.604) | 3:1 |
|  | SC1 | sHbUNI0515\_S – g01A2746 | 1 | 2.00 | 3.629 | 0.932 | -1.169  (2.538) | -0.993  (0.829) | 0.188  (0.151) | 1:1 |
| 2 | WC1 | Hb\_seq\_06\_2 | 1 | 30.32 | 14.344 | 1.799 | -0.642  (7.286) | -0.800  (8.310) | 0.509  (8.769) | 1:1:1:1 |
| 3 | SC3 | HBE110 | 1 | 49.73 | 4.463 | 3.394 | -0.658  (0.712) | -0.792  (1.183) | 1.202  (2.471) | 1:2:1 |
| 4 | TLP | HBE225 | 1 | 59.00 | 7.735 | 4.219 | 10.956  (1.331) | 22.548  (6.015) | -11.302  (1.446) | 1:1:1:1 |
| 5 | SC4 | A2419 | 2 | 3.96 | 10.870 | 13.699 | -1.847  (4.793) | 0.139  (0.029) | -2.077  (5.918) | 1:2:1 |
| 6 | WH1 | A2348 – HB\_seq\_38\_2 | 2 | 18.00 | 10.890 | 1.805 | 5.318  (8.483) | 5.865  (9.658) | 6.309  (10.581) | 3:1 |

**Table S5.** Characteristics of the 111 QTLs mapped for all phenotypic traits: *R²*, LOD score, additive and dominance effects, segregation type.

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| QTL | Trait | Flanking Markers | Linkage Group (LG) | Position  in cM | Global LOD | *R2* | αPR 255  (LOD) | αPB 217  (LOD) | δPR 255 x PB 217  (LOD) | Segregation |
| 6 | WC1 | A2348 – HB\_seq\_38\_2 | 2 | 18.00 | 18.689 | 1.972 | 1.106  (15.647) | 1.187  (17.313) | 1.249  (18.190) | 3:1 |
| 7 | SC5 | sHbCIR0100 | 2 | 32.70 | 4.623 | 6.877 | -0.929  (3.038) | -0.757  (2.564) | -0.314  (0.371) | 1:2:1 |
|  | WC4 | sHbCIR0100 | 2 | 32.70 | 8.636 | 7.221 | -0.454  (4.998) | -0.388  (5.179) | -0.242  (1.723) | 3:1 |
| 8 | SC3 | A2419 | 2 | 39.59 | 11.116 | 0.472 | -2.102  (7.578) | 0.236  (0.108) | -1.604  (4.336) | 1:2:1 |
|  | TSC | A2419 | 2 | 39.59 | 17.732 | 14.426 | -7.189  (11.365) | 0.174  (0.007) | -6.086  (7.687) | 1:2:1 |
|  | SC3 | A2419 – sHbUNI0513 | 2 | 40.00 | 11.081 | 0.537 | -2.087  (7.486) | 0.244  (0.114) | -1.619  (4.368) | 1:2:1 |
|  | SC2 | A2419 – sHbUNI0513 | 2 | 43.00 | 5.125 | 5.567 | -0.712  (1.802) | 0.251  (0.228) | -0.989  (3.075) | 1:2:1 |
| 9 | WC3 | g02T2607 | 2 | 84.58 | 5.541 | 4.515 | 0.227  (4.490) | 0.125  (1.409) | -0.017  (0.026) | 1:2:1 |

**Table S5.** Characteristics of the 111 QTLs mapped for all phenotypic traits: *R²*, LOD score, additive and dominance effects, segregation type.

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| QTL | Trait | Flanking Markers | Linkage Group (LG) | Position  in cM | Global LOD | *R2* | αPR 255  (LOD) | αPB 217  (LOD) | δPR 255 x PB 217  (LOD) | Segregation |
| 9 | TWH | g02T2607 – Hb\_seq\_138 | 2 | 88.00 | 5.369 | 5.539 | -2.313  (4.185) | 1.001  (0.699) | -0.578  (0.224) | 1:1 |
| 10 | TLP | g02t182 – SSH197 | 2 | 159.00 | 7.637 | 4.391 | 21.299  (4.084) | 19.744  (3.535) | -12.484  (1.321) | 3:1 |
| 11 | WC2 | EHBc92 | 2 | 205.38 | 4.742 | 2.565 | 0.057  (0.026) | 0.304  (0.496) | 0.801  (4.412) | 1:1 |
| 12 | SC4 | g10a262 – HBE134 | 3 | 93.00 | 7.034 | 2.394 | 2.263  (3.516) | 1.576  (4.046) | -1.121  (1.084) | 3:1 |
| 13 | TLP | EHBp23a | 3 | 101.13 | 5.268 | 1.416 | 14.598  (2.398) | -12.227  (1.673) | 10.678  (1.272) | 3:1 |
|  | WC2 | HB180 | 3 | 105.44 | 5.592 | 3.473 | 0.566  (2.923) | -0.361  (1.245) | -0.544  (2.722) | 3:1 |
| 14 | WC1 | HB24 – sHbUNI0502 | 3 | 116.00 | 5.900 | 4.451 | 0.382  (4.927) | -0.102  (0.367) | -0.284  (2.264) | 1:2:1 |
|  | TWC | HB24 – sHbUNI0502 | 3 | 117.00 | 5.445 | 4.828 | 1.508  (4.499) | -0.434  (0.285) | -1.120  (2.087) | 1:2:1 |

**Table S5.** Characteristics of the 111 QTLs mapped for all phenotypic traits: *R²*, LOD score, additive and dominance effects, segregation type.

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| QTL | Trait | Flanking Markers | Linkage Group (LG) | Position  in cM | Global LOD | *R2* | αPR 255  (LOD) | αPB 217  (LOD) | δPR 255 x PB 217  (LOD) | Segregation |
| 15 | SH2 | HB176 – EHBc57 | 3 | 164.00 | 3.665 | 4.169 | -1.028  (0.708) | -0.174  (0.023) | 2.200  (3.092) | 1:1 |
| 16 | WC4 | EHBc57 | 3 | 170.95 | 5.930 | 6.413 | 0.260  (2.399) | -0.032  (0.038) | 0.320  (3.662) | 1:2:1 |
| 17 | SC3 | HBE121 – A2749 | 3 | 184.00 | 8.542 | 0.255 | -0.573  (0.566) | 0.711  (0.889) | 2.066  (6.848) | 1:1:1:1 |
|  | SC3 | HBE121 – A2749 | 3 | 185.00 | 8.502 | 0.210 | -0.576  (0.558) | 0.699  (0.857) | 2.093  (6.814) | 1:1:1:1 |
|  | TSC | HBE121 – A2749 | 3 | 186.00 | 4.940 | 3.555 | -1.503  (0.468) | -0.524  (0.060) | 5.010  (4.571) | 1:1 |
| 18 | WH2 | g04A2402 – sHbCIR0057 | 4 | 86.00 | 3.485 | 2.826 | 0.549  (1.105) | 0.441  (0.770) | 0.746  (1.771) | 1:2:1 |
| 19 | TLP | sHbCIR0057 | 4 | 97.15 | 13.252 | 8.678 | 14.391  (2.077) | -32.543  (12.118) | 8.657  (0.772) | 1:1:1:1 |
| 20 | TWH | g04a385 | 4 | 109.97 | 4.056 | 3.425 | 1.765  (2.502) | 1.467  (1.739) | 0.643  (0.337) | 1:2:1 |

**Table S5.** Characteristics of the 111 QTLs mapped for all phenotypic traits: *R²*, LOD score, additive and dominance effects, segregation type.

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| QTL | Trait | Flanking Markers | Linkage Group (LG) | Position  in cM | Global LOD | *R2* | αPR 255  (LOD) | αPB 217  (LOD) | δPR 255 x PB 217  (LOD) | Segregation |
| 21 | WC3 | sHbCIR0066 | 5 | 17.42 | 3.449 | 2.730 | -0.086  (0.506) | 0.182  (2.776) | 0.043  (0.121) | 1:1 |
| 22 | WC4 | g05a390 | 5 | 86.99 | 9.921 | 8.525 | 0.497  (8.207) | 0.248  (2.537) | 0.012  (0.004) | 1:1:1:1 |
| 23 | TWC | HB190 | 5 | 93.59 | 5.554 | 5.128 | 1.409  (3.958) | 0.690  (0.979) | 0.795  (1.289) | 3:1 |
| 24 | WH1 | g05a491 | 5 | 148.29 | 5.423 | 1.728 | 0.992  (1.277) | 2.106  (4.156) | 0.382  (0.203) | 1:2:1 |
| 25 | SH2 | EHBmu5 | 5 | 161.15 | 5.243 | 3.235 | -1.619  (1.391) | 2.162  (4.722) | -1.842  (3.251) | 1:2:1 |
| 26 | TSH | g05A2723 | 5 | 212.22 | 6.604 | 5.143 | 2.760  (4.050) | 2.403  (3.118) | 1.067  (0.645) | 1:2:1 |
| 27 | SH1 | HB\_seq\_12 | 5 | 218.51 | 5.543 | 3.954 | 0.802  (1.099) | 1.356  (3.262) | 0.952  (1.488) | 3:1 |
| 28 | WH1 | EHBc48 | 6 | 33.78 | 6.748 | 1.386 | 0.401  (0.231) | -7.523  (6.104) | -0.826  (0.197) | 1:1 |

**Table S5.** Characteristics of the 111 QTLs mapped for all phenotypic traits: *R²*, LOD score, additive and dominance effects, segregation type.

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| QTL | Trait | Flanking Markers | Linkage Group (LG) | Position  in cM | Global LOD | *R2* | αPR 255  (LOD) | αPB 217  (LOD) | δPR 255 x PB 217  (LOD) | Segregation |
| 29 | SC5 | HBE122 – HBE53 | 6 | 50.00 | 5.646 | 3.477 | -1.081  (1.502) | -1.606  (3.781) | -0.291  (0.402) | 1:2:1 |
| 30 | SH1 | Hb\_seq\_19\_1 – g06T2449 | 6 | 131.00 | 6.389 | 6.751 | -1.569  (3.288) | -1.485 (3.232) | -0.160  (0.039) | 1:2:1 |
| 31 | TLP | g06T2449 – Hb\_seq\_128 | 6 | 139.00 | 6.717 | 1.172 | -5.454  (0.324) | 15.565  (2.427) | 25.484  (5.370) | 1:2:1 |
|  | SH2 | Hb\_seq\_128 | 6 | 142.76 | 4.915 | 3.453 | 1.992  (3.564) | -0.913  (0.657) | 0.823  (0.605) | 1:1 |
| 32 | WH2 | EHBp5 – sHbCIR0067 | 6 | 166.00 | 6.460 | 5.244 | 0.283  (0.338) | -1.004  (3.657) | -1.079  (3.826) | 1:2:1 |
| 33 | TSC | sHbCIR0262 – HBE49 | 6 | 174.00 | 4.161 | 2.895 | 4.085  (3.139) | -2.092  (0.640) | -0.987  (0.126) | 1:1 |
| 34 | SC2 | HBE49 | 6 | 180.49 | 6.021 | 4.900 | 1.236  (5.568) | -0.451  (0.344) | -0.195  (0.068) | 1:1 |
| 35 | WC2 | HBE116 | 7 | 9.59 | 3.731 | 2.731 | -0.141  (0.163) | 0.497  (2.117) | -0.434  (1.503) | 1:2:1 |

**Table S5.** Characteristics of the 111 QTLs mapped for all phenotypic traits: *R²*, LOD score, additive and dominance effects, segregation type.

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| QTL | Trait | Flanking Markers | Linkage Group (LG) | Position  in cM | Global LOD | *R2* | αPR 255  (LOD) | αPB 217  (LOD) | δPR 255 x PB 217  (LOD) | Segregation |
| 36 | SC2 | g07A2429 | 7 | 121.73 | 4.233 | 3.207 | 0.532  (1.017) | -0.461  (0.788) | 0.834  (2.652) | 1:2:1 |
| 37 | SH2 | Hb\_seq\_161 | 8 | 10.04 | 5.758 | 3.279 | 1.373  (1.494) | -1.636  (2.807) | -1.671  (3.059) | 3:1 |
| 38 | TWH | g08A2442 | 8 | 24.92 | 4.852 | 3.849 | 2.056  (0.939) | 2.125  (3.248) | 0.032  (0.000) | 1:2:1 |
| 39 | WC4 | Hb\_seq\_171 | 8 | 57.95 | 4.150 | 4.620 | -0.128  (0.491) | 0.118  (0.452) | 0.291  (3.016) | 1:1 |
|  | WC3 | Hb\_seq\_171 – g08A66 | 8 | 60.00 | 4.936 | 4.705 | -0.221  (3.709) | -0.126  (1.285) | -0.023  (0.037) | 1:2:1 |
|  | TWC | Hb\_seq\_171 – g08A66 | 8 | 60.00 | 5.505 | 3.654 | -1.259  (3.063) | -0.730  (1.081) | 1.269  (2.883) | 3:1 |
| 40 | SC4 | g08Opr | 8 | 189.38 | 6.205 | 4.342 | 0.883  (1.012) | -0.853  (1.079) | -1.637  (3.353) | 3:1 |
| 41 | TSH | HBE140 | 8 | 215.73 | 3.612 | 4.101 | -2.434  (2.914) | -1.459  (0.649) | -0.086  (0.002) | 1:1 |

**Table S5.** Characteristics of the 111 QTLs mapped for all phenotypic traits: *R²*, LOD score, additive and dominance effects, segregation type.

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| QTL | Trait | Flanking Markers | Linkage Group (LG) | Position  in cM | Global LOD | *R2* | αPR 255  (LOD) | αPB 217  (LOD) | δPR 255 x PB 217  (LOD) | Segregation |
| 41 | SC2 | HBE140 – g08T2587 | 8 | 219.00 | 3.625 | 3.941 | -0.545  (0.956) | -0.782  (1.469) | -0.693  (0.979) | 3:1 |
|  | SC3 | HBE140 – g08T2587 | 8 | 219.00 | 6.848 | 7.267 | 0.431  (0.301) | -1.888  (4.226) | -1.037  (1.194) | 1:2:1 |
| 42 | TSC | g08T2587 | 8 | 235.01 | 6.361 | 5.525 | 1.568  (0.537) | -5.927  (3.138) | -4.467  (2.109) | 1:2:1 |
| 43 | WC4 | g09TAs2547 – g09A2682 | 9 | 30.00 | 3.578 | 1.321 | -0.870  (2.202) | 0.350  (1.230) | -0.109  (0.427) | 1:1:1:1 |
| 44 | SH2 | g09A2682 | 9 | 39.08 | 4.794 | 3.655 | -1.542  (2.526) | 1.520  (2.387) | 0.059  (0.004) | 1:2:1 |
| 45 | SH1 | HBE77 | 9 | 99.63 | 4.171 | 1.297 | -1.618  (3.659) | 1.099  (0.735) | -1.679  (1.061) | 1:2:1 |
| 46 | TLP | EHBp21 | 9 | 109.04 | 4.768 | 2.614 | -21.560  (4.768) | – | – | 1:1 |
| 47 | SC1 | g10a129 | 10 | 0.00 | 3.623 | 6.449 | 0.579  (2.006) | -0.881  (1.811) | 0.377  (0.376) | 1:2:1 |

**Table S5.** Characteristics of the 111 QTLs mapped for all phenotypic traits: *R²*, LOD score, additive and dominance effects, segregation type.

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| QTL | Trait | Flanking Markers | Linkage Group (LG) | Position  in cM | Global LOD | *R2* | αPR 255  (LOD) | αPB 217  (LOD) | δPR 255 x PB 217  (LOD) | Segregation |
| 48 | TWC | A2767 | 10 | 27.30 | 3.406 | 1.912 | 0.393  (0.285) | -0.704  (0.816) | -1.327  (2.951) | 1:1 |
| 49 | WC4 | g10A2438 – HBE204 | 10 | 123.00 | 3.867 | 2.987 | -0.066  (0.146) | -0.194  (1.280) | 0.279  (2.433) | 1:2:1 |
| 50 | WC3 | HB135 | 10 | 200.40 | 4.211 | 2.629 | -0.115  (1.162) | -0.134  (1.336) | 0.154  (2.252) | 3:1 |
| 51 | WH2 | HB186 | 10 | 215.90 | 4.500 | 4.832 | -0.861  (3.183) | 0.174  (0.133) | 0.470  (0.716) | 1:1 |
| 52 | WC2 | EHBc46 – HB170 | 10 | 262.00 | 7.710 | 0.589 | 0.823  (3.743) | 0.644  (3.136) | 0.337  (1.059) | 1:1:1:1 |
|  | WC2 | EHBc46 – HB170 | 10 | 263.00 | 7.755 | 0.504 | 0.833  (3.847) | 0.656  (3.188) | 0.353  (1.154) | 3:1 |
| 53 | WH1 | sHbUNI0518\_S | 10 | 302.22 | 5.735 | 4.510 | -1.762  (4.080) | 0.795  (0.874) | -1.631  (3.385) | 3:1 |
| 54 | TSC | TAs2173 – g11A2535 | 11 | 87.00 | 3.993 | 2.990 | 1.171  (0.270) | 4.570  (3.768) | 1.685  (0.505) | 1:1 |

**Table S5.** Characteristics of the 111 QTLs mapped for all phenotypic traits: *R²*, LOD score, additive and dominance effects, segregation type.

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| QTL | Trait | Flanking Markers | Linkage Group (LG) | Position  in cM | Global LOD | *R2* | αPR 255  (LOD) | αPB 217  (LOD) | δPR 255 x PB 217  (LOD) | Segregation |
| 54 | WC2 | TAs2173 – g11A2535 | 11 | 87.00 | 7.106 | 0.257 | 0.434  (1.586) | 0.775  (4.653) | 0.620  (2.934) | 3:1 |
|  | WC2 | TAs2173 – g11A2535 | 11 | 88.00 | 7.107 | 0.200 | 0.441  (1.594) | 0.784  (4.653) | 0.631  (2.980) | 3:1 |
| 55 | WC3 | EHBle3 – Hb\_seq\_197 | 11 | 141.00 | 4.060 | 3.859 | 0.178  (2.146) | 0.154  (2.065) | 0.073  (0.368) | 1:2:1 |
| 56 | SH1 | MnSOD | 11 | 174.08 | 8.063 | 6.479 | -1.390  (3.237) | -2.207  (5.511) | -0.609  (0.585) | 1:2:1 |
| 57 | TSH | HB\_seq\_29 | 12A | 36.28 | 4.205 | 2.485 | -1.809  (1.658) | 2.243  (2.603) | -0.604  (0.195) | 1:2:1 |
| 58 | WC3 | 512B5 | 13 | 140.77 | 3.416 | 3.223 | -0.200  (3.269) | 0.058  (0.117) | -0.036  (0.044) | 1:1 |
| 59 | TWH | g13A2757 – HBE98 | 13 | 174.00 | 4.368 | 4.625 | 1.474  (1.549) | 0.682  (0.349) | 1.994  (2.945) | 1:2:1 |
| 60 | WC3 | HBE156 | 14 | 30.16 | 7.451 | 1.078 | -0.230  (4.659) | -0.153  (2.124) | -0.065  (0.358) | 1:2:1 |

**Table S5.** Characteristics of the 111 QTLs mapped for all phenotypic traits: *R²*, LOD score, additive and dominance effects, segregation type.

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| QTL | Trait | Flanking Markers | Linkage Group (LG) | Position  in cM | Global LOD | *R2* | αPR 255  (LOD) | αPB 217  (LOD) | δPR 255 x PB 217  (LOD) | Segregation |
| 60 | WC3 | sHbCIR0076 | 14 | 30.30 | 7.419 | 1.054 | -0.230  (4.626) | -0.152  (2.121) | -0.066  (0.369) | 1:2:1 |
|  | SC3 | sHbCIR0268 – HB53 | 14 | 33.00 | 5.557 | 4.395 | -1.387  (3.624) | -0.555  (0.569) | 0.999  (1.629) | 1:2:1 |
| 61 | TLP | Hb\_seq\_187 – HB100 | 14 | 52.00 | 5.191 | 2.538 | -19.791  (4.110) | 6.118  (0.398) | 12.982  (1.575) | 1:2:1 |
| 62 | SH1 | EHBc99 | 14 | 75.83 | 4.352 | 3.989 | -0.312  (0.145) | -0.664  (0.670) | -1.552  (3.314) | 1:1 |
| 63 | WC4 | sHbCIR0079 – EHBc33 | 14 | 137.00 | 6.152 | 4.469 | 0.200  (1.293) | 0.352  (4.120) | -0.203  (1.262) | 3:1 |
| 64 | TWH | EHBc33 – sHbCIR0273 | 14 | 152.00 | 4.894 | 1.333 | -3.023  (2.589) | -0.645  (0.319) | 1.724  (1.768) | 1:2:1 |
| 65 | WH2 | g15TA2163 – HB81 | 15 | 44.00 | 4.594 | 2.943 | -0.327  (0.452) | 0.441  (0.806) | 0.994  (3.951) | 1:1 |
| 66 | SC5 | g15TAs2706 – HBE10 | 15 | 74.00 | 3.398 | 2.219 | -0.869  (3.059) | 0.181  (0.141) | 0.227  (0.191) | 1:1 |

**Table S5.** Characteristics of the 111 QTLs mapped for all phenotypic traits: *R²*, LOD score, additive and dominance effects, segregation type.

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| QTL | Trait | Flanking Markers | Linkage Group (LG) | Position  in cM | Global LOD | *R2* | αPR 255  (LOD) | αPB 217  (LOD) | δPR 255 x PB 217  (LOD) | Segregation |
| 66 | WC4 | g15TAs2706 – HBE10 | 15 | 75.00 | 3.505 | 4.506 | -0.144  (0.633) | 0.022  (0.018) | 0.323  (3.117) | 1:1 |
| 67 | WC3 | HB\_seq\_02\_1 | 15 | 90.88 | 6.559 | 5.988 | -0.226  (4.350) | 0.089  (0.712) | -0.105  (1.022) | 1:2:1 |
| 68 | TWC | HB\_seq\_02\_1 – sHbUNI0327 | 15 | 97.00 | 6.842 | 6.746 | -1.833  (5.119) | 0.740  (0.574) | 0.424  (0.239) | 1:1 |
|  | WC2 | sHbUNI0327 | 15 | 100.28 | 4.413 | 5.550 | -0.745  (4.030) | 0.190  (0.234) | -0.049  (0.016) | 1:1 |
| 69 | SC4 | HBE192 – EHBc8 | 15 | 127.00 | 3.579 | 3.448 | -1.400  (2.166) | 0.015  (0.002) | -1.049  (1.112) | 1:2:1 |
| 70 | TSC | EHBc8 | 15 | 139.66 | 3.494 | 1.358 | -2.733  (1.745) | 3.981  (1.754) | 0.434  (0.045) | 1:2:1 |
| 71 | SH2 | g15A2697 – g15A2492 | 15 | 147.00 | 3.618 | 2.760 | -0.962  (0.870) | -1.840  (3.042) | 0.500  (0.219) | 1:2:1 |
| 72 | SC2 | HBE64 | 16 | 0.00 | 6.720 | 3.375 | 0.039  (0.005) | 1.792  (5.306) | 0.690  (1.719) | 1:1:1:1 |

**Table S5.** Characteristics of the 111 QTLs mapped for all phenotypic traits: *R²*, LOD score, additive and dominance effects, segregation type.

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| QTL | Trait | Flanking Markers | Linkage Group (LG) | Position  in cM | Global LOD | *R2* | αPR 255  (LOD) | αPB 217  (LOD) | δPR 255 x PB 217  (LOD) | Segregation |
| 72 | TSC | HBE64 – HBE84 | 16 | 4.00 | 5.137 | 3.932 | -1.531  (0.420) | 4.254  (3.789) | 1.722  (0.515) | 1:1 |
|  | TLP | HBE64 – HBE84 | 16 | 6.00 | 12.747 | 9.184 | -3.824  (0.163) | -32.267  (10.682) | -18.152  (3.223) | 1:1:1:1 |
| 73 | SC5 | HBE84 | 16 | 11.76 | 6.242 | 6.328 | 0.032  (0.005) | 1.135  (5.931) | 0.218  (0.218) | 1:1 |
| 74 | SC1 | g16a58 | 16 | 33.42 | 4.513 | 4.344 | -0.476  (1.593) | -0.620  (1.056) | 0.551  (2.159) | 3:1 |
| 75 | SC4 | g16a58 – g16t97 | 16 | 45.00 | 3.776 | 1.436 | -0.977  (1.315) | 0.621  (0.586) | 1.326  (2.525) | 1:2:1 |
|  | SC3 | g16t97 | 16 | 46.01 | 4.356 | 4.123 | -1.237  (2.783) | 0.109  (0.022) | 1.091  (2.186) | 1:2:1 |
| 76 | WC3 | EHBc97 – g17a78 | 17 | 14.00 | 4.009 | 3.361 | 0.110  (1.018) | -0.103  (0.750) | -0.199  (2.437) | 1:2:1 |
| 77 | SC3 | sHbUNI0517 | 17 | 72.63 | 6.071 | 4.157 | 1.019  (1.873) | -0.714  (0.878) | 2.257  (2.542) | 1:1:1:1 |

**Table S5.** Characteristics of the 111 QTLs mapped for all phenotypic traits: *R²*, LOD score, additive and dominance effects, segregation type.

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| QTL | Trait | Flanking Markers | Linkage Group (LG) | Position  in cM | Global LOD | *R2* | αPR 255  (LOD) | αPB 217  (LOD) | δPR 255 x PB 217  (LOD) | Segregation |
| 78 | TLP | Hb\_seq\_195 – Hb\_seq\_163 | 17 | 86.00 | 4.950 | 3.700 | 18.471  (3.425) | 15.336  (2.246) | -3.992  (0.153) | 1:2:1 |
| 79 | TSC | g18T2113 | 18A | 19.54 | 6.781 | 3.820 | -2.674  (1.696) | 0.438  (0.046) | 6.672  (4.782) | 1:1:1:1 |
| 80 | SC2 | Hb\_seq\_24 – HB49 | 18A | 27.00 | 3.684 | 2.437 | -0.393  (0.555) | 0.513  (0.923) | 0.788  (2.060) | 1:2:1 |
| 81 | SC5 | HB49 – HB15 | 18A | 33.00 | 3.808 | 5.534 | -0.855  (3.425) | -0.277  (0.358) | 0.218  (0.220) | 1:1 |
| 82 | TLP | Hb\_seq\_107 | 18A | 97.90 | 7.454 | 2.028 | 7.982  (0.878) | 69.677  (5.149) | -9.150  (1.311) | 1:2:1 |
| 83 | TLP | g10a288 | 18B | 4.02 | 6.310 | 4.150 | 1.445  (0.022) | -12.939  (1.679) | -19.952  (4.329) | 1:2:1 |
|  | WH2 | TAs2744\_1 | 18B | 8.34 | 4.141 | 2.564 | 0.861  (3.404) | -0.471  (0.845) | -0.048  (0.009) | 1:2:1 |