**Table S1 Biometrical parameters of QTLs affecting fiber quality traits by single-marker analysis**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Trait** | **Chrom.** | **Locusa** | **Trait** | **Position（cM）** | **R²(%)b** | **Ac** |
| UHM | 3 | BNL3267\*¶¶ | UHM13 | 28.1 | 16.23 | -0.65 |
|  | 4 | BNL530\* | UHM11 | 21.5 | 18.28 | -0.37 |
|  | 4 | DPL0494\* | UHM11 | 41.5 | 20.88 | -0.19 |
|  | 5c | CICR529\*¶ | UHM11 | 0.0 | 21.21 | -1.03 |
|  | 19a | CIR224¶ | UHM11 | 6.5 | 16.63 | -1.00 |
|  | 22 | NAU3093\* | UHM11 | 146.1 | 18.91 | -0.89 |
| STR | 3 | BNL3267 | STR11 | 28.1 | 16.23 | -1.45 |
|  | 5c | CICR529¶ | STR12 | 0.0 | 19.83 | -2.19 |
|  | 9 | BNL2750 | STR11 | 114.6 | 16.69 | -1.15 |
|  | 11 | DPL0253\* | STR12 | 94.9 | 41.3 | -2.25 |
|  | 18 | MUSS603 | STR12 | 44.1 | 20.10 | -2.14 |
|  | 19a | DPL0444¶ | STR12 | 263.8 | 20.10 | -2.14 |
|  | 19c | MUSS118\*¶¶ | STR13 | 59.7 | 25.59 | -2.71 |
|  | 21 | NTU208 | STR12 | 229.7 | 27.3 | -2.19 |
| MIC | 3 | CICR597\* | MIC11 | 51.1 | 12.78 | 0.42 |
|  | 3 | NAU5443b | MIC11 | 0.0 | 16.18 | -0.25 |
|  | 11 | BNL1552 | MIC11 | 154.8 | 16.33 | -0.31 |
|  | 11 | DPL0253\* | MIC12 | 94.9 | 29.6 | 0.40 |
|  | 14 | NTU182\* | MIC12 | 103.5 | 21.55 | 0.37 |
|  | 15 | CICR420¶ | MIC12 | 73.2 | 21.79 | 0.77 |
|  | 18 | CICR316 | MIC11 | 0.0 | 20.49 | 0.25 |
|  | 19c | NTU152\*¶ | MIC12 | 81.0 | 19.2 | 0.51 |
|  | 21 | NAU2954 | MIC12 | 249.7 | 22.36 | 0.28 |
|  | 21 | NTU208 | MIC12 | 229.7 | 12.73 | 0.32 |
|  | 23 | NTU179 | MIC11 | 46.7 | 12.87 | 0.66 |
|  | 24 | CICR204¶ | MIC12 | 96.6 | 23.37 | 0.59 |
|  | 25 | CICR313¶¶ | MIC12 | 61.6 | 20.73 | 0.51 |
|  | 25 | DPL0520¶ | MIC11 | 95.6 | 15.33 | 0.61 |
| UI | 3 | CICR597\* | UI11 | 51.1 | 24.1 | 1.05 |
|  | 21 | NAU3074 | UI11 | 52.2 | 16.00 | 0.49 |
|  | 22 | CICR438? | UI11 | 177.3 | 20.22 | 0.90 |
|  | 23 | DPL0378¶¶ | UI11 | 50.5 | 16.38 | 1.57 |
| ELO | 5a | CICR479¶ | ELO11 | 5.4 | 20.77 | -0.43 |
|  | 18 | CICR316\*¶ | ELO11 | 0.0 | 16.76 | -0.15 |
|  | 19a | CICR632\*¶ | ELO11 | 18.1 | 19.08 | -0.43 |
|  | 19c | CICR520¶ | ELO11 | 0.0 | 16.63 | 0.35 |
|  | 21 | NAU5505¶ | ELO13 | 213.3 | 13.87 | 0.23 |
|  | 23 | DPL0378 | ELO11 | 50.5 | 15.77 | -0.52 |
|  | 23 | NTU179 | ELO11 | 46.7 | 14.87 | -0.45 |
|  | 24 | CICR204¶¶ | ELO11 | 96.6 | 20.86 | -0.30 |

a: \* The QTL also detected by CIM.: ¶ A QTL was also identified on the same chromosome in our previous studies. ¶¶ A QTL was also identified on the same chromosome regions (either associated with the same SSR marker or overlapped by common markers) in our previous studies.

b: R2, percentage of phenotypic variation explained by the marker genotype at the corresponding marker.

c: A, additive effect, a positive number indicates that the alleles from the *G. hirsutum* parent increase trait values; a negative number indicates that the alleles from the *G. mustelinum* parent increase trait values.