**Table 3** Characteristics of the genetic linkage groups of the mapping population AA0769

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Linkage group | TM | SSR | DArT | SNP | SD (%) | ML | AMD |
| 1 | 143 | 2 | 91 | 50 | 17 (11.9%) | 153.18 | 1.07 |
| 2 | 220 | 2 | 121 | 96 | 4 (1.8%) | 187.11 | 0.85 |
| 3 | 144 | 3 | 82 | 59 | 27 (18.8%) | 143.12 | 0.99 |
| 4A | 50 | 2 | 29 | 19 | 1 (2%) | 79.97 | 1.60 |
| 4B | 42 | 0 | 28 | 14 | 13 (31%) | 56.40 | 1.34 |
| 5 | 97 | 2 | 47 | 48 | 1 (1%) | 144.96 | 1.49 |
| 6 | 120 | 2 | 64 | 54 | 5 (4.2%) | 129.62 | 1.08 |
| 7 | 73 | 2 | 53 | 18 | 6 (8.2%) | 111.04 | 1.52 |
| 8 | 80 | 4 | 38 | 38 | 10 (12.5%) | 100.12 | 1.25 |
| 9 | 64 | 2 | 36 | 26 | 11 (17.2%) | 85.58 | 1.34 |
| 10 | 54 | 3 | 37 | 14 | 1 (1.9%) | 91.91 | 1.70 |
| 11 | 108 | 2 | 51 | 55 | 17 (15.7%) | 85.74 | 0.79 |
| 12 | 61 | 0 | 29 | 32 | 9 (14.8%) | 49.75 | 0.82 |
| 13 | 83 | 2 | 32 | 49 | 6 (7.2%) | 103.26 | 1.24 |
| 14 | 53 | 2 | 39 | 12 | 4 (7.5%) | 62.82 | 1.19 |
| 15 | 68 | 2 | 27 | 39 | 1 (1.5%) | 93.80 | 1.38 |
| 16 | 6 | 0 | 3 | 3 | 0 | 42.23 | 7.04 |
| Total | **1466** | **32** | **807** | **626** | **133 (9.1%)** | **1720.61** | **-** |
| Mean | 86.24 | 1.88 | 47.47 | 36.82 | 7.82 (9.1%) | 101.21 | 1.17 |
| Min | 6 | 0 | 3 | 3 | 0 | 42.23 | 0.79 |
| Max | 220 | 4 | 121 | 96 | 27 (18.8%) | 187.11 | 7.04 |

TM = Total number of markers for each linkage group

SD (%) = Number of markers that have significant segregation distortion at *p*<0.05 level and percentage as compared to total number of markers in the group

ML = Map length in centiMorgans (cM)

AMD = Average marker density in cM