**Table S3** FourQTL regions exhibit opposite effects in different NAM RIL subpopulations.

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Order** | **Subpopulation** | **Marker** | **Chr** | **Genetic1 (cM)** | **Physical2 (Mb)** | **LOD** | **Confidence Interval (Mb)** | **Effect3** |
| 1 | IL14H | PZA03551.1 | 1 | 24.4 | 12.2 | 3.6 | 6.2 - 77.2 | 1.17 |
| MS71 | PZA02094.9 | 1 | 31.7 | 15.8 | 4.9 | 11 - 26.2 | -0.69 |
| KI11 | PZA01030.1 | 1 | 36.3 | 17.7 | 5 | 15 - 28.4 | -1.08 |
| CML103 | PZB01957.1 | 1 | 47.2 | 26.2 | 6.4 | 22.6 - 34.7 | -0.86 |
| B97 | PZA02490.1 | 1 | 52.7 | 32.6 | 3.3 | 26.2 - 45.5 | -0.68 |
| KI3 | PZA02490.1 | 1 | 53.7 | 32.6 | 3.6 | 22.9 - 50.1 | 0.9 |
| 2 | CML322 | PZA02014.3 | 1 | 124.2 | 213.2 | 5.7 | 204.3 - 223 | -0.82 |
| OH43 | PZA01039.1 | 1 | 125.6 | 213.7 | 4.3 | 204.8 - 217.6 | 0.83 |
| M162W | PZA00658.21 | 1 | 132.9 | 225.1 | 4.6 | 204.8 - 231.7 | -0.58 |
| 3 | CML69 | PZA01530.1 | 5 | 58.3 | 38.5 | 4 | 11.5 - 58.6 | 0.43 |
| P39 | PHM12992.5 | 5 | 58.4 | 39.2 | 5.2 | 15.1 - 58.2 | 1.05 |
| CML322 | PZA02207.1 | 5 | 60.6 | 49.9 | 5 | 38.5 - 60.8 | -0.5 |
| CML322 | PZA01303.1 | 5 | 66 | 73.1 | 5.2 | 60.8 - 84.3 | -0.82 |
| KY21 | PZA02862.3 | 5 | 66.8 | 75.9 | 4.2 | 49.9 - 84.3 | 0.79 |
| 4 | IL14H | PHM4341.42 | 10 | 46.7 | 117.6 | 4.1 | 98.7 - 130.1 | -1.02 |
| CML322 | PZA01141.1 | 10 | 47.6 | 120.8 | 3.3 | 72.8 - 130.1 | 1 |
| CML247 | PZA01005.1 | 10 | 49.2 | 124.9 | 4.6 | 111.8 - 132.6 | 0.62 |
| MO18W | PZA00647.9 | 10 | 52.2 | 130.1 | 3.7 | 124.5 - 140 | 0.78 |
| CML333 | PZA02320.1 | 10 | 56.1 | 132.6 | 14.1 | 124.5 - 136.3 | 1.37 |
| M162W | PZB01111.8 | 10 | 61.4 | 134.4 | 3.5 | 124.9 - 142.2 | 0.67 |

1 Genetic positions according to IBM31 and NAM32 genetic map.

2 Physical positions according to B73 RefGen\_v2.

3 QTL effects were calculated by using B73 subtracting non-B73 alleles.