

Table 2 - QTLs for body weight

| QTL | Ch | Marker | Marker Dist | Cent. Dist | CI | LPR | % | <i>a</i> / <i>SD</i> | <i>d</i> / <i>SD</i> |
|---------------|----|--------------------|-------------|------------|--------|------|------|----------------------|----------------------|
| <i>WT1.1</i> | 1 | <i>rs3699304</i> | +4 | 97 | 67—115 | 2.80 | 4.82 | -0.26** | 0.27* |
| <i>WT11.1</i> | 11 | <i>mCV24434350</i> | +10 | 14 | 4—22 | 3.88 | 6.37 | -0.32** | 0.27* |
| <i>WT11.2</i> | 11 | <i>rs6370458</i> | +4 | 88 | 74—98 | 2.00 | 3.29 | -0.01 | 0.37** |
| <i>WT13.1</i> | 13 | <i>rs6329684</i> | +10 | 11 | 3—23 | 2.97 | 5.44 | 0.37** | -0.15 |
| <i>WT15.1</i> | 15 | <i>rs13482429</i> | +14 | 18 | 8—36 | 4.02 | 6.22 | -0.37** | 0.10 |
| <i>WT17.1</i> | 17 | <i>rs6309949</i> | 0 | 5 | 5—29 | 1.82 | 2.88 | 0.11 | 0.29* |
| <i>WT17.2</i> | 17 | <i>rs3660112</i> | 0 | 51 | 41—57 | 3.23 | 5.01 | 0.31** | -0.14 |

Shown are the locations, confidence intervals (CI), LPR scores ($\log_{10}\text{Prob}^{-1}$), percentage of the variation explained (%), and standardized additive (*a*) and dominance genotypic values (*d*) for QTLs on all chromosomes (Ch) significantly affecting body weight.

Locations are given as map distances from the nearest proximal marker (Marker Dist) and from the centromere (Cent. Dist), and confidence intervals are expressed from the centromere; all LPR values are significant at the 5% chromosome-wise level and those exceeding 3.80 are significant at the 5% experiment-wise level. * = $P < 0.05$; ** = $P < 0.01$.