|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **S2 Table**. **QTLs for atherosclerosis at the aortic root in F2 Mice from intercross between DBA-apoE and B6-apoE mice.**   |  |  |  |  |  |  |  |  |  |  |  |  |  |  | | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | |  | Chr | Peak  (cM) | CI  (cM) | Peak  (Mb) | CI  (Mb) | LOD | Significance | a | d | d /a | High  allele | Mode | % | | Root | | | | | | | | | | | | | | | F+M | 2 | 74 | 58-103 | 149 | 114-181 | 2.9 | Suggestive | 47 | 40 | 0.8 | DBA | Dominant | 6.8 | |  | 7 | 37 | 23-48 | 68 | 37-84 | 3.0 | Suggestive | -49 | 7 | 0.1 | B6 | Additive | 5.0 | |  | 14 | 22 | 7-32 | 40 | 16-61 | 2.6 | Suggestive | -49 | -31 | 0.6 | B6 | Recessive | 4.9 | | F | 7 | 42 | 23-52 | 71 | 37-89 | 2.8 | Suggestive | -49 | 47 | 1.0 | B6 | Dominant | 8.0 | |  | 16 | 58 | 3-58 | 94 | 56-94 | 2.7 | Suggestive | 62 | 18 | 0.3 | DBA | Additive | 7.6 | | M | 2 | 102 | 57-103 | 189 | 131-193 | 2.9 | Suggestive | 67 | -4 | 0.1 | DBA | Additive | 13.4 |   F, female; M, male; Chr, chromosome; CI, 95% credible interval; LOD, logarithm of odds; LOD score for sex-combined scan shown in Table was determined in single locus scan using sex as additive; for each QTL, model of inheritance was determined according to allelic effect at the nearest marker of a QTL by performing Haley-Knott regression using the additive and dominant/recessive models; ratio (d/a) was used to determine mode of inheritance [11, 12]: 0.5 <│ d/a │< 1.5 –dominant or recessive;  d/a = 0 - pure additive; │ d/a │≤ 0.5-additive; │ d/a │≥1.5 - overdominant or overrecessive; % variance indicates the percentage of the total F2 phenotypic variance. |  |