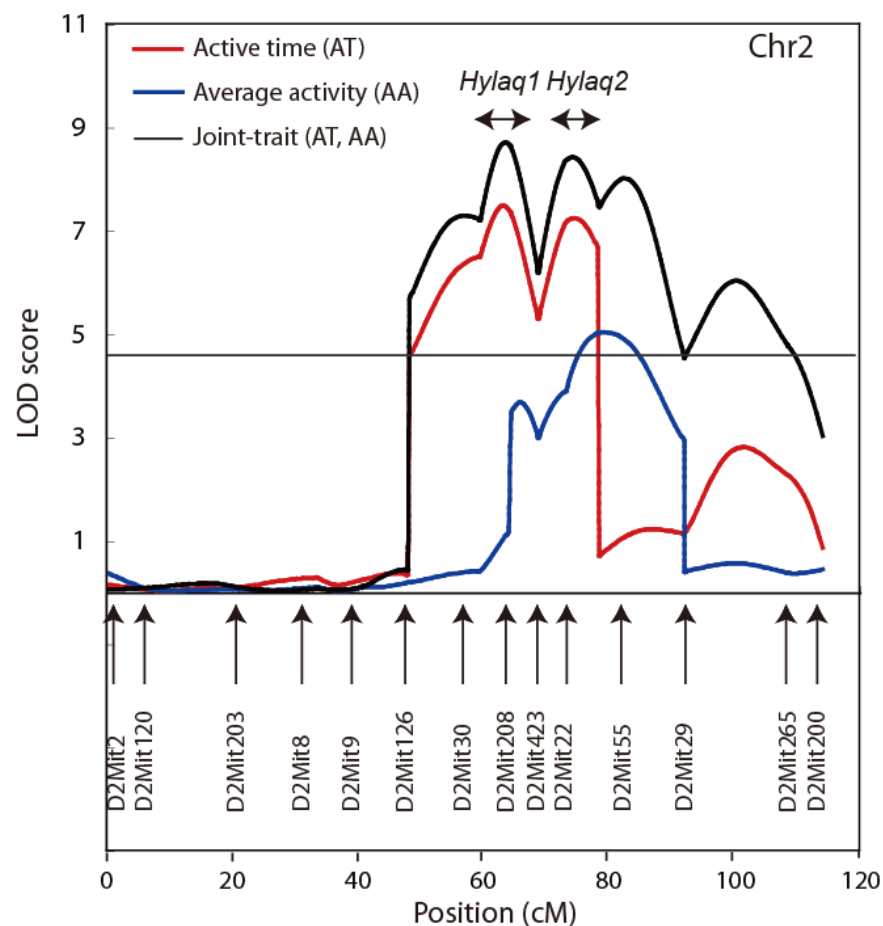


Additional file 6 – Multiple traits analysis using AT and AA.

Multiple traits analysis also supports that there are at least two loci, *Hylaq1* and *Hylaq2*, located close to each other on Chr 2. The joint-trait showed two peaks corresponding to the peaks of AT and AA. Another significant peak was appeared at the distal side of these peaks.



Method: Multiple traits analysis was conducted using QTL Cartographer version 2.5. AT and AA were used as multiple traits. Genome-wide thresholds for significant ($P < 0.05$) QTLs were determined based on 1,000 permutations.