

Table S1 Threshold values of the LRT test statistic (one degree of freedom) under various genome-wide Type I error rates obtained from 1000 permuted samples for the interval mapping (IM) procedure.

| Trait | 90% | 95% | 99% | 100% |
|-----------------------|----------|----------|----------|----------|
| Yield (YD) | 13.42065 | 15.77650 | 18.62915 | 27.17197 |
| Tiller number (TP) | 13.19609 | 14.64264 | 19.48538 | 24.24969 |
| Grain number (GN) | 13.87269 | 15.80410 | 19.45575 | 25.80274 |
| K grain weight (KGW) | 14.05583 | 15.39363 | 18.51520 | 23.72287 |
| Grain length (GL) | 13.96338 | 15.56000 | 18.97977 | 27.83338 |
| Grain width (GW) | 14.04309 | 15.42061 | 18.30397 | 23.41500 |
| Heading date (HD) | 13.99390 | 15.58231 | 19.25128 | 27.55085 |
| Apicule color (OsC1) | 13.99859 | 15.43835 | 20.25753 | 25.67522 |
| Mean threshold | 13.81803 | 15.45227 | 19.10975 | 25.67771 |
| Theoretical threshold | 2.7055 | 3.8414 | 6.6349 | ∞ |

The $x\%$ percentile represents $\alpha = 1 - x\%$ Type I error rate. For example, the Chi-square threshold under 95% percentile gives the threshold used to control $\alpha = 1 - 95\% = 0.05$ genome-wide Type I error. The Chi-square threshold divided by $2\ln(10) \approx 4.61$ gives the LOD score threshold.