

Table S2 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 composite interval mapping (CIM) procedure.

Trait	90%	95%	99%	100%
Yield (YD)	17.63537	20.31503	24.36029	27.97551
Tiller number (TP)	17.54152	18.97397	22.94701	30.24515
Grain number (GN)	16.59045	19.05533	23.75548	32.35316
K grain weight (KGW)	17.42943	19.34218	23.52755	30.84495
Grain length (GL)	17.79907	19.47785	23.77882	28.63580
Grain width (GW)	17.40540	19.40530	24.15972	28.06567
Heading date (HD)	17.38699	19.07095	23.6893	30.38192
Apicule color (OsC1)	17.93634	20.54178	2730.653	2773.310
Mean threshold	17.46557	19.52280	23.74545	29.78602
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.