**Supplemental File S2**

We performed a simulation study to demonstrate that the hypothesis test

: are QTLs of the same gene vs : is not true,

can be implemented by applying Test 1 on neighboring QTL pairs, where are the locations of input QTLs. The procedure of the test is as follows:

1. The *p-*­value from Test 1 was calculated for each neighboring pair , , where is the *i*th smallest QTL location, .
2. Hypothesis was rejected if any of these *p*-values was smaller than .

The type-I error rate for this test was estimated for input QTLs by the proportion of rejected in experiments, in which all s were generated from the same cluster or normal distribution. Without loss of generality, in each experiment the QTL locations were generated as independent realizations of a standard normal distribution. The type-I error rates were reported below in Table S2-1 and displayed in Figure S2-1. Our test remained conservative for any number of input QTLs since the type-I error rates were below for all .

Table S2-1. Type-I error rates for testing the hypothesis of multiple clusters given different number () of input QTLs.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | 2 | 3 | 4 | 5 | 6 | 7 |
| Type-I Error | 0.0499 | 0.0275 | 0.0141 | 0.0081 | 0.0052 | 0.0037 |

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| 8 | 9 | 10 | 15 | 20 | 25 | 30 |
| 0.0029 | 0.0022 | 0.0019 | 0.001 | 6.00E-04 | 4.00E-04 | 3.00E-04 |



Figure S2-1. Type-I error rates for testing the hypothesis of multiple clusters. The horizontal line indicates the desired type-I error rate