**Supplemental File S2**

We performed a simulation study to demonstrate that the hypothesis test

$H\_{0}$:$ X\_{1},…, X\_{n}$ are QTLs of the same gene vs $H\_{1}$:$ H\_{0}$ is not true,

can be implemented by applying Test 1 on neighboring QTL pairs, where $X\_{1},…, X\_{n}$ are the locations of $n$ input QTLs. The procedure of the test is as follows:

1. The *p-*­value from Test 1 was calculated for each neighboring pair $\left(X\_{\left[i\right]}, X\_{\left[i+1\right]}\right)$, $i=1, …,n-1$, where $X\_{[i]}$ is the *i*th smallest QTL location, $i=1,…,n$.
2. Hypothesis $H\_{0}$ was rejected if any of these *p*-values was smaller than $α=0.05$.

The type-I error rate for this test was estimated for $n=2, …, 10, 15, 20, 25, 30$ input QTLs by the proportion of rejected $H\_{0}$ in $1,000,000$ experiments, in which all $X\_{i}$s were generated from the same cluster or normal distribution. Without loss of generality, in each experiment the QTL locations $X\_{1}, …, X\_{n}$ 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 $α=0.05$ for all $n$.

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

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| $$n$$ | 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 $α=0.05.$