



**Figure S3. QTL mapping of aggregation behavior and hermaphrodite mating frequency variation between N2 and HW**

As a control, variation in aggregation behavior between N2 and HW was mapped to a marker adjacent to *npr-1*. Using the same RILs, mating frequency mapped to two QTL, *mate-1* and *mate-2*, on chromosomes V and IV, respectively, but did not map to *npr-1*. In this analysis, aggregation was scored and mapped as a binary trait. Dotted line depicts significance threshold determined by permutation of the data.