Table S1 Chromosome assignment and length of linkage groups, and marker density of the maps based on the population of Fleet/AWCS799

| Chromosome | Number of markers | Length (cM) | Marker density (cM/Marker) | |
|------------|-------------------|-------------|-------------------------------|--|
| 1H | 84 | 256.3 | 3.1 | |
| 2H | 105 | 324.1 | 3.1 | |
| 3H | 165 | 356.7 | 2.2 | |
| 4H | 82 | 222.0 | 2.7 | |
| 5H | 134 | 343.8 | 2.6 | |
| 6H | 95 | 199.3 | 2.1 | |
| 7H | 76 | 262.5 | 3.5 | |
| Total | 741 | 1964.7 | 2.7 | |

Table S2 Table S2 A linkage map of barley based on the population of Fleet/AWCS799

Table S3 Primer sequences of the maker linked with Qcrs.caf-6H

| Marker ID | Primer sequences | Product length (bp) | Motif / Number ^a | Tm (°C) |
|------------------|---------------------------------|---------------------|-----------------------------|---------|
| 6H_SSR_497772849 | 5'-GCATTAGTTGTCATAGTAGGTAGCA-3' | 242 | C / 10 | 60 |
| | 5'-TTCAAGACCACGACCTTGGG-3' | | | |

^a The difference of motif number between two alleles.

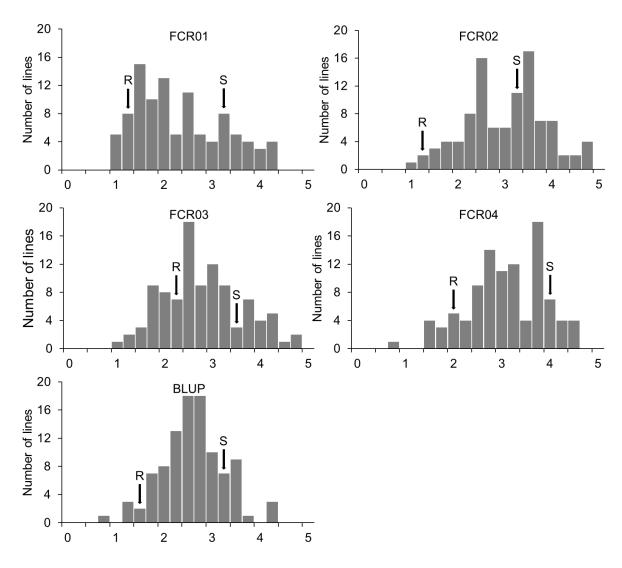


Fig. S1 Distribution of disease index (DI) values for the four FCR severity tests and the BLUP data from the mapping population Fleet/AWCS799. "S" stand for susceptible parent Fleet and "R" for resistant parent AWCS799.

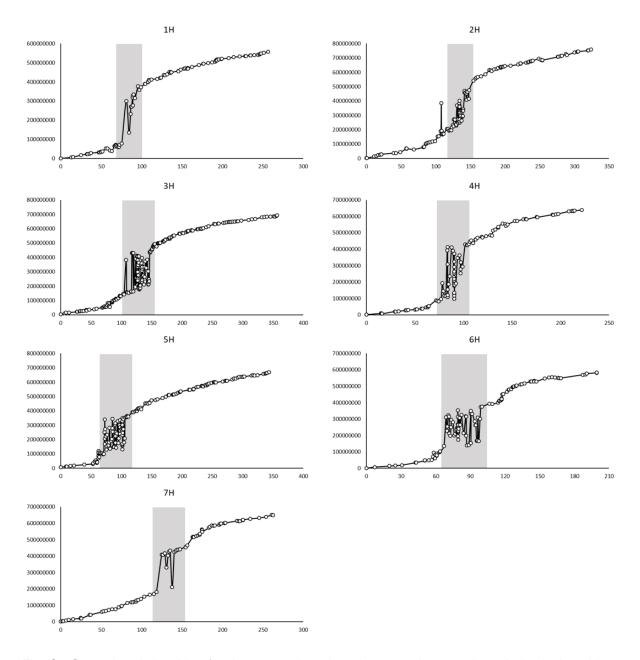


Fig. S2 Syntenic relationships for the mapped markers between the genetic and physical positions. Horizontal-axis represents genetic distance (cM) and vertical-axis represent physical distances (base pairs). Peri-centromeric regions were highlighted in gray shadow.