Supplementary Figure 1 Population structure of DC1 and 8-way populations based on PCA.
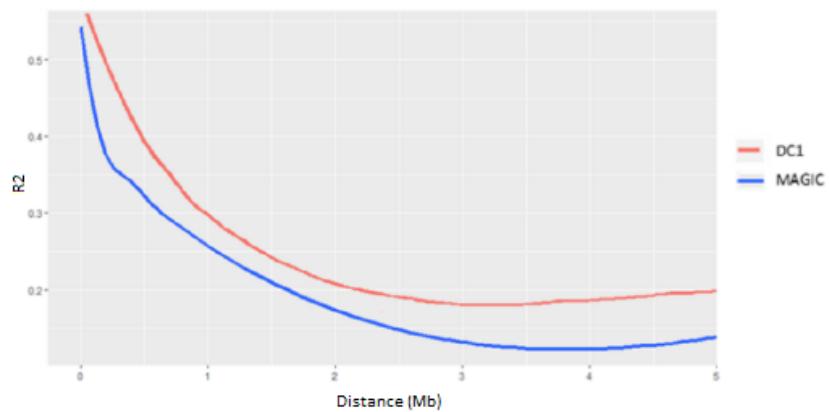
Supplementary Figure 2 Whole genome linkage disequilibrium decay of DC1 and 8-way populations.

| DC1 in Hainan 2017 | DC1 in Hainan 2018 | 8-way in IRRI 2017 | 8-way in Hainan 2018 | 8-way in Henan 2018 |

(A) Row A panels labeled with *qGL3.1*, *qGL3.2*, *qGL7*

(B) Row B panels labeled with *qGW5*, *qGW7*, *qGW8*

(C) Row C panels labeled with *qGLWR3*, *qGLWR5*, *qGLWR7*, *qGLWR8*

(D) Row D panels labeled with *qGT5*, *qGT1*, *qGT3*

(E) Row E panels labeled with *qTGW3.1*, *qTGW5*, *qTGW8.1*, *qTGW3.2*, *qTGW3*, *qTGW8.2*
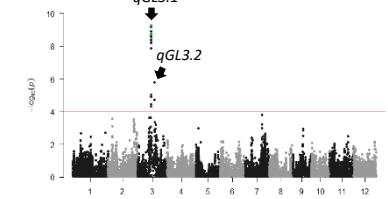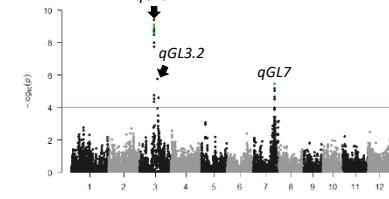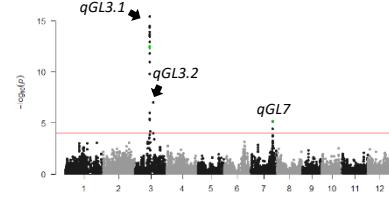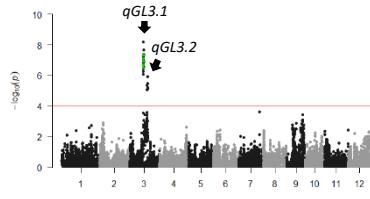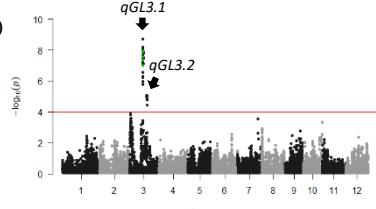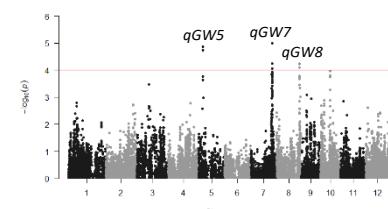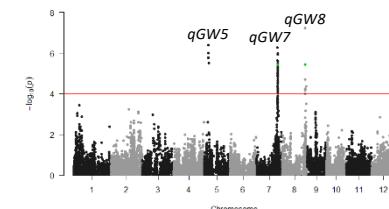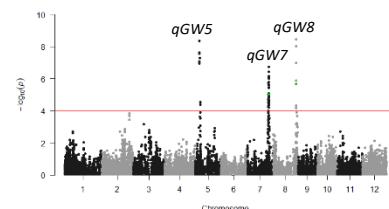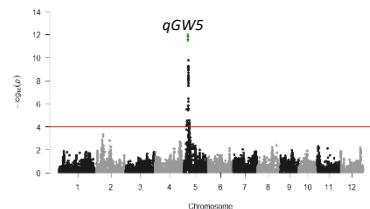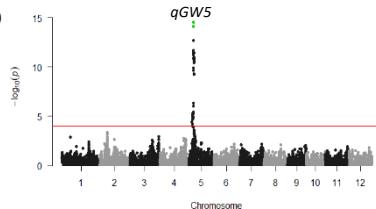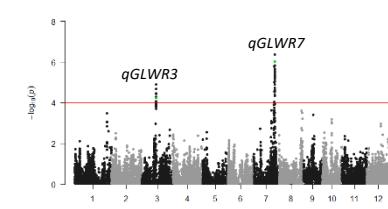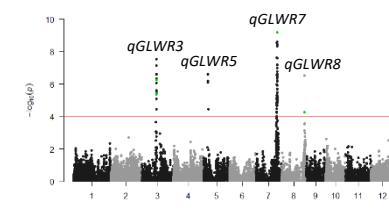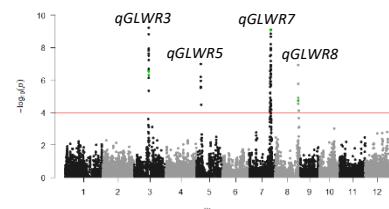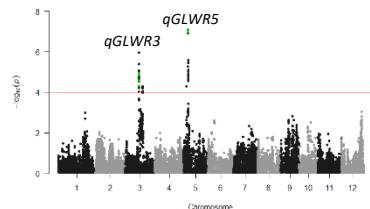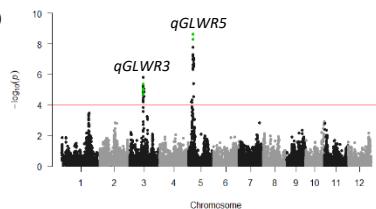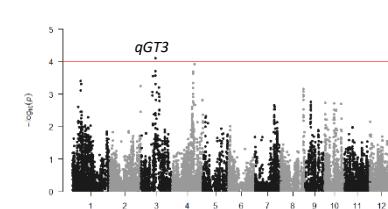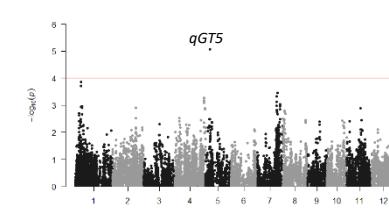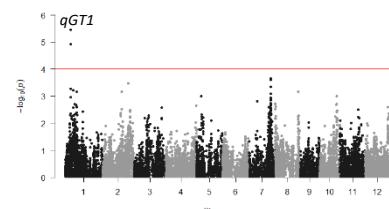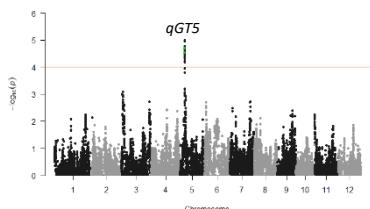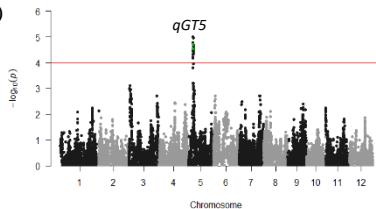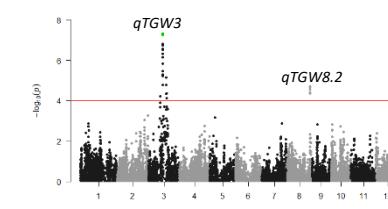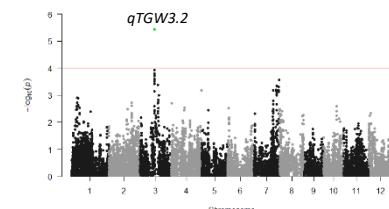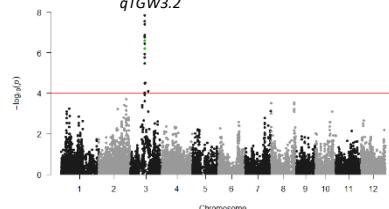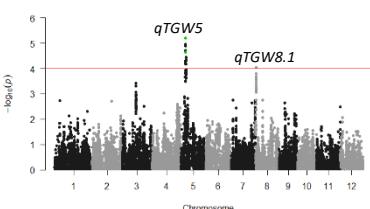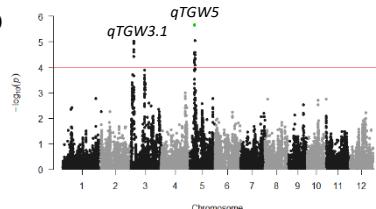
Supplementary Figure 3 Genome-wide Manhattan plots for (A) Grain length, (B) grain width, (C) grain length-width ratio, (D) grain thickness, and (E) thousand grain weight in DC1 and 8-way measured in different environments and across years. Dots in green color corresponds to SNPs of previously cloned genes (*GS3*, *GW5/qSW5, GL7*/*GW7*/*SLG7,* and *GW8/OsSPL16* on chromosomes 3, 5, 7 and 8, respectively).
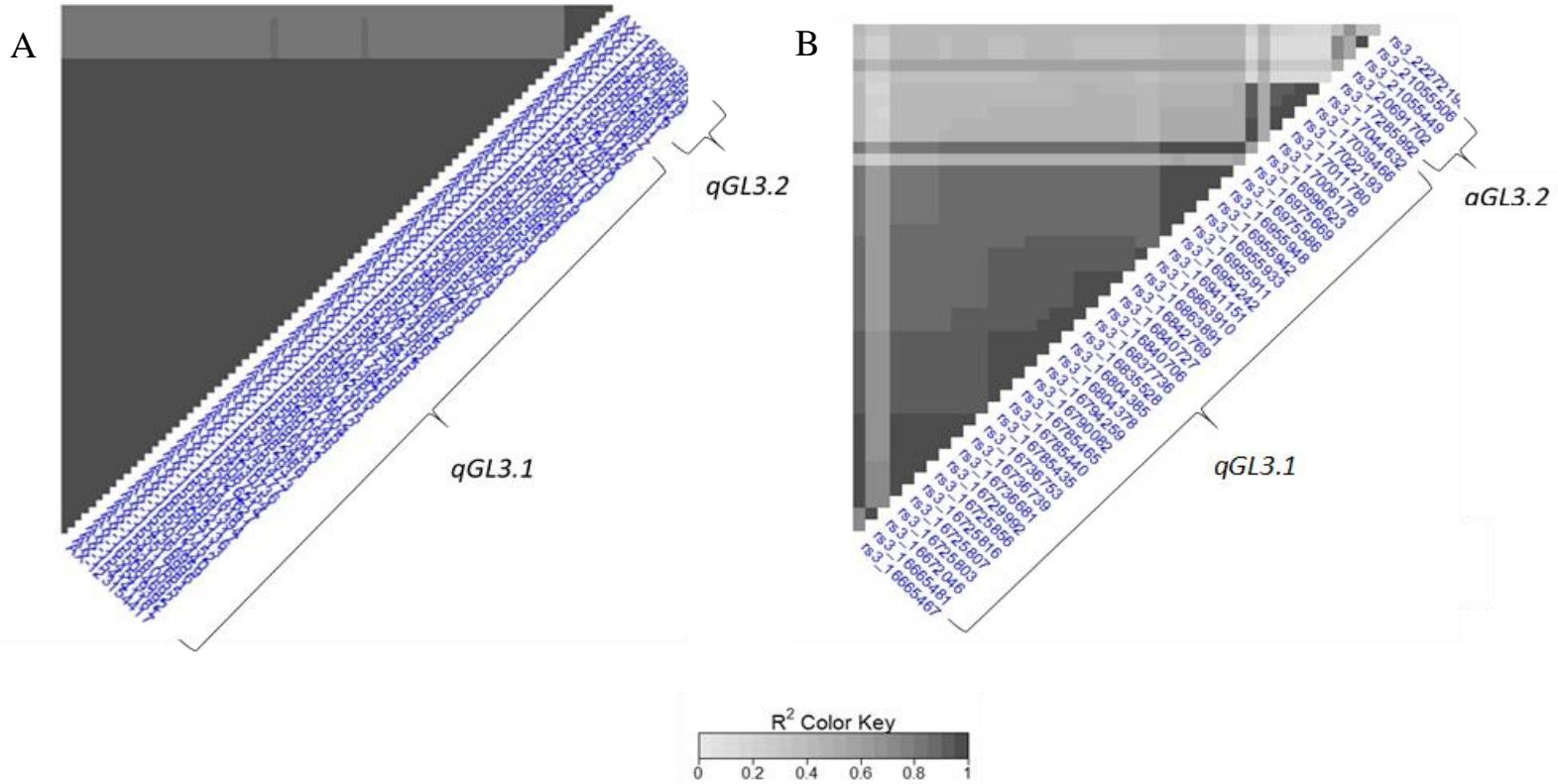
Supplementary Figure 4 LD blocks for *qGL3.1* and *qGL3.2* detected in (A) DC1 and (B) 8-way populations.