Table S5 Genome-wide detection and functional annotation of selective sweep regions in the *tej* subgroup based on a combination of three methods.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Chr. | Interval start (Mb) | Interval  end (Mb) | Peak (Mb) | Functional annotation | Known genes |
| 1 | 2.20 | 2.37 | 0.17 |  |  |
| 1 | 30.91 | 31.60 | 0.69 | plant architecture, | *THIS1*, |
| 1 | 35.49 | 36.01 | 0.52 | Flowering time, plant architecture, | *OsHAP3A*, *OsCCT01*, *LAX1*, |
| 1 | 38.13 | 38.62 | 0.49 | plant architecture, | *sd1*, *OsPH1*, *OsNAC6*, |
| 2 | 0.88 | 0.99 | 0.11 |  |  |
| 2 | 7.97 | 8.25 | 0.28 | Grain type, | *OsUBP15*, *GW2*, |
| 2 | 10.70 | 11.08 | 0.38 | temperature stress tolerance, | *OsVTE1*, |
| 2 | 15.17 | 15.53 | 0.36 | blast disease, | *OsWRKY42*, |
| 2 | 28.55 | 28.91 | 0.36 | Grain type, | *GS2*, |
| 2 | 31.96 | 32.20 | 0.24 | Grain quality, flowering time | *SSIIB*, *OsMADS22*, |
| 3 | 11.71 | 11.96 | 0.25 | plant architecture, blast disease, | *WOX6*, *OsWRKY55*, |
| 3 | 12.71 | 12.81 | 0.10 |  |  |
| 3 | 24.71 | 28.52 | 3.81 | blast disease, plant architecture, flowering time, temperature stress tolerance, phosphate transporter, grain quality, | *TLP*, *SLR1*, *RGG1*, *OsTBP2*, *OsTB1*, *OsSWAP70A*, *OsRZ3*, *OsNLA2*, *OsGRF9*, *OsCR4*, *FLO6*, |
| 3 | 30.68 | 30.81 | 0.13 | blast disease, | *OsWRKY13*, |

Table S5 continued

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Chr. | Interval start (Mb) | Interval  end (Mb) | Peak (Mb) | Functional annotation | Known genes |
| 3 | 33.82 | 35.93 | 2.11 | Flowering time, grain type, plant architecture, temperature stress tolerance, grain yield, seed germination, grain quality, | *SPIN1*, *qTGW3*, *PTOX*1, *OsRZ1*, *OsIDS1*, *OsGATA12*, *OsABA2*, *GPA3*, *CRT*, |
| 4 | 8.69 | 10.11 | 1.42 | Grain quality, | *OsSUS7, OsCTR1*, |
| 4 | 23.60 | 25.51 | 1.91 | blast disease, temperature stress tolerance, nitrate transporter, plant architecture, | *Rymv1*, *RML1*, *OsV4*, *OsOxi1*, *OsNAR2.2*, *FCP1*, *DAO*, |
| 4 | 25.72 | 27.53 | 1.81 | Grain color, grain type, plant architecture, | *OsYSL9*, OsYSL12, OsYSL13, OsYSL16, OsYABBY5, OsINV2, *OsGA2ox6*, *LABA1*, |
| 4 | 28.26 | 28.84 | 0.68 | Flowering time | *ROC4*, |
| 4 | 29.95 | 30.35 | 0.40 | blast disease, temperature stress tolerance, | *RAVL1*, *OsMYB511*, *OsCDPK7*, *COLD1* |
| 4 | 34.60 | 34.90 | 0.30 |  | *sh4*, |
| 5 | 4.91 | 5.40 | 0.49 | blast disease, grain type, | *qSW5*, *OsWRKY67*, |

Table S5 continued

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Chr. | Interval start (Mb) | Interval  end (Mb) | Peak (Mb) | Functional annotation | Known genes |
| 5 | 29.62 | 29.79 | 0.17 |  |  |
| 6 | 1.69 | 1.86 | 0.17 | Grain quality, | *Waxy*, |
| 6 | 2.97 | 3.28 | 0.31 | Grain size, flowering time | *HGW*, *Hd3a*, *RFT1* |
| 6 | 7.80 | 9.05 | 1.25 | plant architecture, flowering time, | *OsGSR1*, *OsCOL16*, |
| 6 | 16.06 | 17.57 | 1.51 | Flowering time, plant architecture, grain size, | *OsMFT1*, *NOC3*, |
| 6 | 22.71 | 22.81 | 0.1 |  |  |
| 6 | 28.48 | 30.82 | 2.34 | blast disease, plant architecture, | *OsRRK1*, *OsLRR-RLK1*, *OsARF19*, *FON1*, |
| 7 | 2.71 | 3.07 | 0.16 | plant architecture, blast disease, | *Prog1*, *OsTCP21*, |
| 7 | 5.28 | 5.52 | 0.24 |  | *Rc* |
| 7 | 11.59 | 13.75 | 2.16 | Grain quality, | *OsGBSSII*, |
| 7 | 28.25 | 28.36 | 0.11 |  |  |
| 8 | 3.08 | 3.42 | 0.36 | Flowering time, Nitrate Transporter, | *OsNRT1.1A*, *OsLHY*, |
| 8 | 22.60 | 23.91 | 1.31 | Grain size, | *AL8*, |
| 9 | 8.62 | 8.80 | 0.18 |  |  |
| 9 | 21.48 | 21.69 | 0.21 | plant architecture, | *SAUR39*, |
| 12 | 27.00 | 27.63 | 0.63 | Grain quality, Nitrate Transporter, | *OsSUT2*, *OsNPF2.2*, |