Table S3 Genome-wide detection and functional annotation of selective sweep regions in the *ind* subgroup based on a combination of three methods.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Chr. | Interval start (Mb) | Interval  end (Mb) | Peak (Mb) | Functional annotation | Known genes |
| 1 | 22.41 | 22.51 | 0.10 |  |  |
| 1 | 40.14 | 42.36 | 2.22 | blast and leaf blight diseases, flowering time, grain length and awn development | *OsSSI2*, *OsMADS51*, *An-1* |
| 2 | 1.52 | 2.06 | 0.54 | grain length, grain weight and grain number per panicle | *OsSGL* |
| 3 | 14.65 | 14.87 | 0.22 |  |  |
| 3 | 25.47 | 26.43 | 0.96 |  |  |
| 3 | 28.66 | 28.76 | 0.10 | Flowering time, grain filling | *OsCOL10*, *GF14f* |
| 4 | 16.70 | 17.14 | 0.44 |  |  |
| 4 | 21.63 | 21.80 | 0.17 | grain filling rate | *OsACOT* |
| 4 | 33.41 | 33.56 | 0.15 |  |  |
| 4 | 33.82 | 34.62 | 0.50 | Shattering, inflorescence architecture | *sh4*, *OsLG1* |
| 5 | 4.90 | 5.10 | 0.20 | blast and bacteria blight resistance | *OsWRKY67* |
| 5 | 5.17 | 5.41 | 0.24 | Grain Size | *qSW5*, *GSE5* |
| 6 | 2.42 | 2.53 | 0.11 |  |  |
| 6 | 5.42 | 5.56 | 0.14 | Stigma color | *OsC1*, *S5* |
| 6 | 22.85 | 22.96 | 0.11 |  |  |
| 6 | 27.79 | 27.90 | 0.11 |  |  |
| 7 | 2.66 | 3.08 | 0.42 | Plant type | *Prog1* |
| 7 | 4.88 | 4.99 | 0.11 |  |  |
| 7 | 4.88 | 4.99 | 0.11 |  |  |

Table S3 continued

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Chr | Interval start (Mb) | Interval  end (Mb) | Peak (Mb) | Functional annotation | Known genes |
|  |  |  |  |  |  |
| 7 | 28.20 | 28.40 | 0.20 |  |  |
| 8 | 23.61 | 24.14 | 0.53 | germination and seedling growth, grain size | *SnRK1B*, *AL8* |
| 8 | 24.77 | 24.87 | 0.10 |  |  |
| 9 | 22.72 | 22.83 | 0.11 |  |  |
| 11 | 4.13 | 4.33 | 0.20 |  |  |
| 12 | 2.56 | 2.86 | 0.30 |  |  |
| 12 | 24.82 | 26.27 | 1.45 | seed germination | *OsLOL1* |