**Table S3.** QTLs identified for morphological and yield traits under DS and WW conditions and root architectural traits under ABA conditions with IciMapping

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Trait name** | **QTLs** | **Chromo-****some** | **LOD** | **PVE (%)** | **Peak Marker** | **Position (cM)** | **Candidate gene position (bp)** | **Number of genes within 25 kb of the marker closest to the QTL peak** | **Gene annotation** |
| PHC | *qPHC1.1* | 1 | 10.57 | 4.85 | KZ14152 | 43 | 38480787 | 9 | Protein phosphorylation |
| PHC | *qPHC2.1* | 2 | 24.42 | 13.81 | KZ23918 | 546 | 27023516 | 7 | Transport.Major\_Intrinsic\_Proteins.PIP |
| PHC | *qPHC2.2* | 2 | 17.19 | 8.63 | KZ24204 | 552 | 29443430 | 11 | Protein phosphorylation |
| RL\_ABA3 | *qRLA3-2.3* | 2 | 28.85 | 0.61 | KZ24639 | 236 | 33179587 | 5 | Stress.abiotic.heat |
| RL\_ABA5 | *qRLA5-2.2* | 2 | 20.72 | 0.59 |
| BYD | *qBYD3.1* | 3 | 10.57 | 6.48 | KZ35574 | 19 | 32079708 | 6 | Signaling.receptor\_kinases.leucine\_rich\_repeat\_XI |
| RL\_ABA3 | *qRLA3-3.1* | 3 | 32.94 | 0.61 |
| RL\_ABA5 | *qRLA5-3.1* | 3 | 24.79 | 0.59 |
| PPBC | *qPPBC4.1* | 4 | 4.73 | 10.34 | KZ44474 | 137 | 436771 | 7 | PS.photorespiration.hydroxypyruvate\_reductase |
| BYC | *qBYC4.2* | 4 | 3.58 | 2.78 | KZ45735 | 226 | 26174168 | 7 | PS.lightreaction.photosystem\_II.PSII\_polypeptide\_subunits |
| RL\_ABA3 | *qRLA3-4.2* | 4 | 22.34 | 0.61 |
| RL\_ABA5 | *qRLA5-4.2* | 4 | 14.21 | 0.59 |
| PLD | *qPLD4.2* | 4 | 2.70 | 6.08 | KZ44511 | 286 | 1233282 | 7 | ERF domain containing protein. (Os04t0649100-02);APETALA2 transcription factor, Seed shattering through abscission zone (AZ) development (Os04t0649100-03) |
| FGC  | *qFGC5.1* | 5 | 5.74 | 1.12 | KZ57234 | 481 | 28101481 | 12 | Drought-responsive ethylene response factor 10, drought-responsive ERF 10, ethylene response factor 84, APETALA2/ethylene-responsive element binding protein 97 |
| FGD | *qFGD5.1* | 5 | 2.53 | 4.74 |
| RL\_ABA3 | *qRLA3-5.1* | 5 | 25.08 | 0.61 |
| RL\_ABA5 | *qRLA5-5.1* | 5 | 16.95 | 0.59 |

**Table S3.** QTLs identified for morphological and yield traits under DS and WW conditions and root architectural traits under ABA conditions with IciMapping (Continued)

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Trait name** | **QTLs** | **Chromo-****some** | **LOD** | **PVE (%)** | **Peak Marker** | **Position (cM)** | **Candidate gene position (bp)** | **Number of genes within 25 kb of the marker closest to the QTL peak** | **Gene annotation** |
| FGC  | *qFGC6.2* | 6 | 3.71 | 0.87 | KZ68491 | 230 | 29755505 | 9 | Control of rice architecture via BR signaling (Os06t0704300-01)\_Tetrapyrrole biosynthetic process |
| BYC | *qBYC6.2* | 6 | 3.01 | 2.66 |
| RL\_ABA3 | *qRLA3-6.1* | 6 | 26.24 | 0.61 |
| RL\_ABA5 | *qRLA5-6.1* | 6 | 18.12 | 0.59 |
| FGC | *qFGC7.1* | 7 | 3.06 | 1.27 | KZ79333 | 283 | 28219138 | 10 | Lipid\_metabolism.lipid\_degradation.lipases |
| SPC | *qSPC7.1* | 7 | 2.58 | 9.88 |
| SPC | *qSPC7.2* | 7 | 4.62 | 6.37 | KZ79821 | 91 | 9822937 | 7 | Protein of unknown function DUF594 domain containing protein. (Os07t0269400-00) |
| SPD | *qSPD7.1* | 7 | 4.85 | 2.12 | KZ77844 | 265 | 912849 | 9 | Stress biotic\_Endoplasmic reticulum protein, Regulation of sugar partitioning in carbon-demanding young leaves and developing leaf sheaths (Os07t0116300-01) |
| PLC | *qPLC7.1* | 7 | 5.05 | 9.62 | KZ78019 | 107 | 11608339 | 13 | Regulation of nutrient metabolism and endosperm development (Os07t0296900-01) |
| PPBC | *qPPBC7.1* | 7 | 2.91 | 6.27 |
| SPC | *qSPC8.1* | 8 | 3.40 | 5.75 | KZ90034 | 115 | 26147631 | 11 | Embryo and endosperm development (Os08t0525500-01)\_carbohydrate metabolic process\_UDP-glucuronic acid 4-epimerase 2 |
| PPBC | *qPPBC8.1* | 8 | 2.66 | 7.25 |
| FGD  | *qFGD8.1* | 8 | 2.78 | 3.79 | KZ89547 | 357 | 3507836 | 6 | RNA.processing.RNA\_helicase\_DEAD-box RNA helicase, Pre-mRNA splicing under cold stress (Os08t0159900-01) |
| RL\_ABA3 | *qRLA3-8.1* | 8 | 24.48 | 0.61 |
| RL\_ABA5 | *qRLA5-8.1* | 8 | 16.35 | 0.59 |

**Table S3.** QTLs identified for morphological and yield traits under DS and WW conditions and root architectural traits under ABA conditions with IciMapping (Continued)

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Trait name** | **QTLs** | **Chromo-****some** | **LOD** | **PVE (%)** | **Peak Marker** | **Position (cM)** | **Candidate gene position (bp)** | **Number of genes within 25 kb of the marker closest to the QTL peak** | **Gene annotation** |
| BYD | *qBYD9.1* | 9 | 3.37 | 2.24 | KZ101571 | 341 | 4220164 | 7 | Carbohydrate metabolic process (GO:0005975) |
| RL\_ABA5 | *qRLA5-9.1* | 9 | 13.57 | 0.59 |
| SPD  | *qSPD10.1* | 10 | 3.03 | 0.98 | KZ102164 | 300 | 12048509 | 6 | Intracellular protein transport (GO:0006886) |
| RL\_ABA3 | *qRLA3-10.1* | 10 | 20.11 | 0.61 |
| BYC | *qBYC10.1* | 10 | 7.25 | 5.09 | KZ102869 | 112 | 3205210 | 10 | RNA.transcription |
| BYD | *qBYD10.2* | 10 | 6.71 | 4.31 | KZ102866 | 118 | 3156402 | 5 | MYB transcription factor |
| RL\_ABA3 | *qRLA3-10.3* | 10 | 23.86 | 0.61 |
| BYD | *qBYD10.3* | 10 | 21.82 | 8.49 | KZ102900 | 302 | 3719254 | 10 | Similar to Chalcone and stilbene synthases, N-terminal domain containing protein. (Os10t0158400-00) |
| BYD | *qBYD12.2* | 12 | 3.19 | 6.34 | KZ105668 | 412 | 953389 | 10 | Late embryogenesis abundant protein, LEA-14 (IPR004864) |