Supplementary Table 2. Evaluation summary of introgression lines (ILs) from the AA genome wild relatives of rice and upland rice in Dianjingyou 1 background

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Trait | *O. barthii* | | | *O. glumaepatula* | | | *O. meridionalis* | | | *O. nivara* | | | *O. rufipogon* | | | Upland rice | | | | Total |
| No. of the donors | No. of ILs | Generation | No. of the donors | No. of ILs | Generation | No.of the donors | No. of ILs | Generation | No. of the donors | No. of ILs | Generation | No. of the donors | No. of ILs | Generation | No. of the donors | | No. of ILs | Generation |
| Spreading panicle | 4 | 16 | BC3F7 | 1 | 5 | BC3F7 | 3 | 28 | BC3F7 | 12 | 109 | BC2-BC3 | 3 | 16 | BC2-BC3 | 46 | 103 | | BC2F8 | 277 |
| Erect panicle | 2 | 2 | BC3F7 | 1 | 1 | BC3F7 | 2 | 4 | BC3F7 | 2 | 4 | BC2-BC3 |  |  | BC3F7 | 5 | 10 | | BC2F8 | 21 |
| Dense panicle |  |  |  |  |  |  |  |  |  | 1 | 1 | BC2-BC3 |  |  |  | 5 | 13 | | BC2F8 | 14 |
| Lax panicle |  |  |  |  |  |  |  |  |  | 5 | 10 | BC2-BC3 | 2 | 2 | BC2-BC3 | 2 | 2 | | BC2F8 | 14 |
| Awn | 2 | 5 | BC3F7 | 2 | 4 | BC3F7 | 4 | 10 | BC3F7 | 11 | 41 | BC2-BC3 | 2 | 4 | BC2-BC3 | 6 | 9 | | BC2F8 | 73 |
| Prostrate growth | 1 | 3 | BC3F7 |  |  | BC3F7 | 1 | 5 | BC3F7 | 6 | 19 | BC2-BC3 |  |  |  | 2 | 2 | | BC2F8 | 29 |
| Plant height | 2 | 2 | BC3F7 | 2 | 2 | BC3F7 | 3 | 5 | BC3F7 | 16 | 53 | BC2-BC3 | 6 | 10 | BC3F7 | 33 | 50 | | BC2F8 | 123 |
| Pericarp color | 2 | 2 | BC3F7 |  |  |  |  |  |  | 6 | 12 | BC2-BC3 | 1 | 1 | BC2-BC3 | 4 | 4 | | BC2F8 | 19 |
| Kernel color |  |  |  |  |  |  | 1 | 1 | BC3F7 | 6 | 15 | BC2-BC3 |  |  |  | 9 | 16 | | BC2F8 | 32 |
| Glabrous hull |  |  |  |  |  |  |  |  |  |  |  | BC2-BC3 |  |  |  | 20 | 93 | | BC2F8 | 93 |
| Grain length | 4 | 19 | BC3F7 | 2 | 15 | BC3F7 | 10 | 37 | BC3F7 | 24 | 204 | BC2-BC3 | 10 | 44 | BC2-BC3 | 62 | 368 | | BC2F8 | 687 |
| Grain width | 4 | 7 | BC3F7 | 4 | 12 | BC2-BC3 | 7 | 17 | BC3F7 | 22 | 114 | BC2-BC3 | 8 | 26 | BC2-BC3 | 49 | 113 | | BC2F8 | 289 |
| 1,000-grain weight | 7 | 18 | BC3F7 | 4 | 22 | BC3F7 | 9 | 72 | BC3F7 | 26 | 242 | BC2-BC3 | 9 | 32 | BC2-BC3 | 125 | 695 | | BC2F8 | 1081 |
| Drought-resistance |  |  |  |  |  |  |  |  |  |  |  |  |  |  | BC3F7 | 32 | 35 | | BC2F8 | 35 |
| Aerobic adaption |  |  |  |  |  |  |  |  |  |  |  |  |  |  | BC3F7 | 32 | 48 | | BC2F8 | 48 |
| Total |  | 74 |  |  | 61 |  |  | 179 |  |  | 824 |  |  | 135 |  |  | 1561 | |  | 2834 |

Supplementary Table 3. Evaluation summary of introgression lines from *O. glaberrima* in Dianjingyou 1 background

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Trait | No. of Donors | No. of ILs | Generation | Total |
|  |  |  |  |  |
| Spreading panicle | 7 | 15 | BC4F9 | 17 |
|  | 2 | 2 | BC6F7 |  |
| Erect panicle | 1 | 1 | BC3F10 | 1 |
| Dense panicle | 2 | 4 | BC4F9 | 4 |
| Lax panicle | 2 | 8 | BC4F9 | 8 |
| Panicle length | 3 | 6 | BC4F9 | 18 |
|  | 1 | 3 | BC2F11 |  |
|  | 2 | 4 | BC4F9 |  |
|  | 2 | 5 | BC5F8 |  |
| Awn | 1 | 4 | BC2F11 | 4 |
| Prostrate growth | 1 | 2 | BC2F11 | 2 |
| Plant height | 1 | 1 | BC4F9 | 10 |
|  | 1 | 3 | BC5F8 |  |
|  | 1 | 6 | BC2F11 |  |
| Tiller number | 2 | 4 | BC4F9 | 6 |
|  | 1 | 2 | BC5F8 |  |
| Pericarp color | 1 | 1 | BC4F11 | 1 |
| Glabrous hull | 1 | 2 | BC3F10 | 8 |
|  | 1 | 6 | BC4F9 |  |
| Long empty glume | 1 | 2 | BC3F10 | 6 |
|  | 1 | 2 | BC4F9 |  |
|  | 1 | 2 | BC6F7 |  |
| Grain length | 2 | 2 | BC2F17 | 99 |
|  | 1 | 2 | BC4F9 |  |
|  | 2 | 5 | BC5F8 |  |
|  | 1 | 2 | BC6F7 |  |
|  | 1 | 12 | BC2F11 |  |
|  | 5 | 32 | BC3F10 |  |
|  | 8 | 35 | BC4F9 |  |
|  | 3 | 9 | BC6F7 |  |
| Grain width | 2 | 2 | BC4F9 | 5 |
|  | 1 | 3 | BC5F8 |  |
| 1,000-Grain weight | 1 | 2 | BC2F11 | 57 |
|  | 4 | 18 | BC3F10 |  |
|  | 4 | 13 | BC4F9 |  |
|  | 3 | 7 | BC5F8 |  |
|  | 1 | 2 | BC2F11 |  |
|  | 2 | 5 | BC3F10 |  |
|  | 3 | 8 | BC4F9 |  |
|  | 1 | 2 | BC5F8 |  |
| Seed shattering | 1 | 2 | BC3F10 | 2 |
| Senescence | 1 | 1 | BC5F8 | 1 |
| Total |  |  |  | 251 |

Supplementary Table 4. Evaluation summary of introgression lines from the AA genome wild relatives of rice and upland rice in Yundao 1 background

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Traits | *O. barthii* | | *O. glumaepatula* | | *O. meridionalis* | | *O. nivara* | | *O. rufipogon* | | Upland rice | | Total |
| No. of the donors | No. of ILs | No. of the donors | No. of ILs | No. of the donors | No. of ILs | No. of the donors | No. of ILs | No. of the donors | No. of ILs | No .of the donors | No. of ILs |
| Spreading panicle | 3 | 6 | 1 | 6 | 4 | 14 | 4 | 22 | 6 | 21 | 13 | 25 | 94 |
| Erect panicle | 3 | 11 |  |  | 6 | 54 | 4 | 15 | 8 | 29 | 2 | 5 | 114 |
| Dense panicle |  |  |  |  |  |  | 1 | 2 |  |  | 12 | 55 | 57 |
| Lax panicle | 1 | 1 |  |  | 1 | 1 | 8 | 11 | 8 | 12 | 16 | 35 | 60 |
| Awn | 5 | 15 | 2 | 2 | 7 | 14 | 8 | 21 | 12 | 44 | 2 | 2 | 98 |
| Prostrate growth | 2 | 3 |  |  | 2 | 4 | 6 | 15 | 3 | 4 | 1 | 1 | 27 |
| Plant height | 4 | 12 | 2 | 6 | 9 | 25 | 14 | 52 | 19 | 60 | 13 | 27 | 182 |
| Pericarp color |  |  |  |  | 2 | 4 | 4 | 8 | 6 | 11 | 12 | 13 | 36 |
| Kernel color | 1 | 1 |  |  | 5 | 9 | 2 | 4 | 4 | 13 | 2 | 2 | 29 |
| Glabrous hull |  |  |  |  | 2 | 2 | 2 | 5 | 2 | 2 | 7 | 18 | 27 |
| Grain length | 6 | 27 | 2 | 6 | 5 | 62 | 10 | 91 | 17 | 111 | 20 | 67 | 364 |
| Grain width | 2 | 12 |  |  |  |  |  |  | 7 | 13 | 1 | 1 | 26 |
| 1,000-grain weight | 8 | 119 | 8 | 54 | 13 | 331 | 21 | 448 | 26 | 506 | 83 | 460 | 1918 |
| Drought-resistance | 3 | 3 |  |  | 1 | 6 | 1 | 8 | 2 | 7 | 34 | 67 | 91 |
| Aerobic adaption | 5 | 34 | 3 | 11 | 6 | 21 | 8 | 12 | 10 | 25 | 27 | 47 | 150 |
| Total |  | 244 |  | 85 |  | 547 |  | 714 |  | 858 |  | 825 | 3273 |

Note: BC3F7 ILs derived from the wild relatives of rice as the donor were developed，and BC2F8 ILs derived from the upland rice as the donor were built.

Supplementary Table 5. Evaluation summary of introgression lines from *O. longistaminata* in RD23 background

|  |  |  |  |
| --- | --- | --- | --- |
| Traits | No.of ILs | Generations | Total |
| Plant height | 4 | BC2F10 | 10 |
|  | 6 | BC3F9 |  |
| Awn | 4 | BC2F10 | 17 |
|  | 8 | BC3F9 |  |
|  | 5 | BC4F8 |  |
| Kernel color | 1 | BC3F14 | 2 |
|  | 1 | BC4F9 |  |
| Grain length | 14 | BC2F10 | 25 |
|  | 6 | BC3F9 |  |
|  | 5 | BC4F8 |  |
| Grain width | 14 | BC2F10 | 81 |
|  | 41 | BC3F9 |  |
|  | 22 | BC4F8 |  |
|  | 4 | BC5F11 |  |
| 1,000-grain weight | 45 | BC2F10 | 126 |
|  | 17 | BC3F9 |  |
|  | 43 | BC4F8 |  |
|  | 6 | BC1F21 |  |
|  | 15 | BC5F11 |  |
| Blast-resistance | 4 | BC3F14 | 4 |
| Total |  |  | 265 |

Supplementary Table 7. Chromosome coverage of substituted segments in introgression lines from the donor of *O. barthii*

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Chr | Length | Times | Coverage length | Coverage rate (%) |
| 1 | 129.64 | 2.99 | 37.40 | 86.44 |
| 2 | 75.14 | 2.09 | 25.45 | 70.82 |
| 3 | 176.11 | 4.83 | 36.41 | 100.00 |
| 4 | 110.55 | 3.11 | 27.06 | 76.22 |
| 5 | 72.67 | 2.42 | 25.16 | 83.98 |
| 6 | 83.48 | 2.67 | 25.61 | 81.95 |
| 7 | 85.04 | 2.86 | 27.34 | 92.06 |
| 8 | 113.56 | 3.99 | 28.44 | 100.00 |
| 9 | 84.59 | 3.67 | 23.01 | 100.00 |
| 10 | 29.31 | 1.26 | 19.83 | 85.45 |
| 11 | 34.84 | 1.20 | 11.36 | 39.14 |
| 12 | 46.50 | 1.68 | 15.98 | 58.04 |
| Genome | 1041.42 | 2.79 | 303.07 | 81.19 |

Supplementary Table 8. Chromosome coverage of substituted segments in introgression lines from the donor of *O. glumaepatula*

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Chr | Length | Times | Coverage length | Coverage rate (%) |
| 1 | 89.97 | 2.07 | 30.92 | 71.45 |
| 2 | 49.25 | 1.37 | 24.10 | 67.05 |
| 3 | 289.86 | 7.96 | 36.41 | 100.00 |
| 4 | 60.00 | 1.68 | 26.84 | 75.58 |
| 5 | 51.27 | 1.71 | 14.27 | 47.62 |
| 6 | 75.55 | 2.41 | 28.62 | 91.60 |
| 7 | 28.18 | 0.94 | 17.93 | 60.37 |
| 8 | 18.63 | 0.65 | 15.83 | 55.66 |
| 9 | 81.52 | 3.54 | 21.40 | 92.99 |
| 10 | 41.76 | 1.79 | 22.23 | 95.80 |
| 11 | 32.07 | 1.10 | 17.47 | 60.19 |
| 12 | 25.58 | 0.92 | 16.88 | 61.31 |
| Genome | 843.65 | 2.26 | 272.91 | 73.11 |

Supplementary Table 9. Chromosome coverage of substituted segments in introgression lines from the donor of *O. meridionalis*

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Chr | Length | Times | Coverage length | Coverage rate (%) |
| 1 | 96.76 | 2.23 | 42.30 | 97.76 |
| 2 | 138.03 | 3.84 | 29.47 | 81.99 |
| 3 | 244.21 | 6.70 | 36.41 | 100.00 |
| 4 | 225.45 | 6.35 | 32.78 | 92.33 |
| 5 | 143.85 | 4.80 | 24.27 | 81.00 |
| 6 | 90.33 | 2.89 | 31.25 | 100.00 |
| 7 | 65.94 | 2.22 | 24.18 | 81.40 |
| 8 | 142.03 | 4.99 | 28.44 | 100.00 |
| 9 | 143.41 | 6.23 | 21.65 | 94.09 |
| 10 | 74.06 | 3.19 | 21.05 | 90.69 |
| 11 | 104.86 | 3.61 | 17.62 | 60.71 |
| 12 | 132.92 | 4.82 | 23.43 | 85.10 |
| Genome | 1601.86 | 4.29 | 332.86 | 89.17 |

Supplementary Table 10. Chromosome coverage of substituted segments in introgression lines from the donor of *O. nivara*

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Chr | Length | Times | Coverage length | Coverage rate (%) |
| 1 | 1200.24 | 27.73 | 43.27 | 100.00 |
| 2 | 996.39 | 27.72 | 31.16 | 86.70 |
| 3 | 1949.39 | 53.53 | 36.41 | 100.00 |
| 4 | 1045.16 | 29.43 | 35.50 | 100.00 |
| 5 | 905.14 | 30.21 | 28.66 | 95.65 |
| 6 | 1329.89 | 42.55 | 31.25 | 100.00 |
| 7 | 456.48 | 15.37 | 26.80 | 90.25 |
| 8 | 858.69 | 30.18 | 28.44 | 100.00 |
| 9 | 1062.76 | 46.18 | 23.01 | 100.00 |
| 10 | 459.32 | 19.79 | 23.21 | 100.00 |
| 11 | 590.07 | 20.33 | 29.02 | 100.00 |
| 12 | 889.97 | 32.32 | 25.95 | 94.26 |
| Genome | 11743.50 | 31.46 | 362.69 | 97.17 |

Supplementary Table 11. Chromosome coverage of substituted segments in introgression lines from the donor of *O. rufipogon*

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Chr | Length | Times | Coverage length | Coverage rate (%) |
| 1 | 266.09 | 6.14 | 39.54 | 91.36 |
| 2 | 241.52 | 6.72 | 26.75 | 74.43 |
| 3 | 462.33 | 12.69 | 36.41 | 100.00 |
| 4 | 142.56 | 4.01 | 29.68 | 83.59 |
| 5 | 147.03 | 4.90 | 23.79 | 79.40 |
| 6 | 168.65 | 5.39 | 31.25 | 100.00 |
| 7 | 154.01 | 5.18 | 28.37 | 95.52 |
| 8 | 162.50 | 5.71 | 28.44 | 100.00 |
| 9 | 163.18 | 7.09 | 23.01 | 100.00 |
| 10 | 105.36 | 4.53 | 20.81 | 89.65 |
| 11 | 170.07 | 5.86 | 23.44 | 80.77 |
| 12 | 191.41 | 6.95 | 21.43 | 77.84 |
| Genome | 2374.71 | 6.36 | 332.92 | 89.19 |

Supplementary Table 12. Chromosome coverage of substituted segments in introgression lines from the donor of *O. glaberrima*

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Chr | Length | Times | Coverage length | Coverage rate (%) |
| 1 | 370.47 | 8.56 | 35.23 | 81.41 |
| 2 | 344.50 | 9.58 | 33.37 | 92.86 |
| 3 | 586.15 | 16.09 | 36.41 | 100.00 |
| 4 | 258.15 | 7.27 | 30.13 | 84.87 |
| 5 | 311.56 | 10.39 | 28.59 | 95.41 |
| 6 | 405.41 | 12.97 | 31.25 | 100.00 |
| 7 | 314.81 | 10.60 | 25.48 | 85.78 |
| 8 | 254.34 | 8.94 | 24.29 | 85.38 |
| 9 | 249.29 | 10.83 | 23.01 | 100.00 |
| 10 | 204.82 | 8.82 | 18.25 | 78.65 |
| 11 | 403.49 | 13.90 | 29.02 | 100.00 |
| 12 | 148.42 | 5.39 | 23.53 | 85.46 |
| Genome | 3851.42 | 10.31 | 338.56 | 90.70 |

Supplementary Table 13. Chromosome coverage of substituted segments in introgression lines from the donor of upland rice in *O. sativa*

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Chr | Length | Times | Coverage length | Coverage rate (%) |
| 1 | 5311.73 | 122.75 | 43.27 | 100.00 |
| 2 | 2822.51 | 78.53 | 35.94 | 100.00 |
| 3 | 4055.68 | 111.37 | 36.41 | 100.00 |
| 4 | 2950.88 | 83.11 | 35.50 | 100.00 |
| 5 | 3291.60 | 109.87 | 29.96 | 100.00 |
| 6 | 3387.60 | 108.40 | 31.25 | 100.00 |
| 7 | 2412.21 | 81.22 | 29.70 | 100.00 |
| 8 | 2639.73 | 92.80 | 28.44 | 100.00 |
| 9 | 3139.13 | 136.40 | 23.01 | 100.00 |
| 10 | 982.65 | 42.34 | 19.85 | 85.53 |
| 11 | 3317.60 | 114.31 | 29.02 | 100.00 |
| 12 | 1794.66 | 65.18 | 27.53 | 100.00 |
| Genome | 36105.97 | 96.73 | 369.89 | 99.10 |

Supplementary Table 14. The correlation of grain size in the different environments

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Traits |  | GL | | GW | | RLW | |
|  |  | E1 | E2 | E1 | E2 | E1 | E2 |
| GL | E1 | 1.00\*\* |  |  |  |  |  |
| E2 | 0.90\*\* | 1.00\*\* |  |  |  |  |
| GW | E1 | -0.12 | -0.11 | 1.00\*\* |  |  |  |
| E2 | -0.06 | -0.08 | 0.78\*\* | 1.00\*\* |  |  |
| RLW | E1 | 0.81\*\* | 0.74\*\* | -0.67\*\* | -0.49\*\* | 1.00\*\* |  |
| E2 | 0.71\*\* | 0.79\*\* | -0.55\*\* | -0.66\*\* | 0.85\*\* | 1.00\*\* |

Note:\* *P* < 0.05, \*\* *P* < 0.01