

Table S1. Pearson's correlation coefficients among traits of different environments in the Yangmai 12/Yanzhan 1 population.

| Trait | Env ^a | Grain width | | | | | Grain length | | | | |
|--------------|------------------|-------------|---------|---------|---------|---------|--------------|---------|---------|---------|------|
| | | E1 | E2 | E3 | E4 | BLUE | E1 | E2 | E3 | E4 | Blue |
| Grain width | E1 | 1 | | | | | | | | | |
| | E2 | 0.592** | 1 | | | | | | | | |
| | E3 | 0.562** | 0.557** | 1 | | | | | | | |
| | E4 | 0.602** | 0.583** | 0.562** | 1 | | | | | | |
| | BLUE | 0.843** | 0.868** | 0.813** | 0.854** | 1 | | | | | |
| Grain length | E1 | 0.299** | 0.220* | 0.226* | 0.236* | 0.279** | 1 | | | | |
| | E2 | 0.199* | 0.277** | 0.229* | 0.249* | 0.258** | 0.730** | 1 | | | |
| | E3 | 0.224* | 0.205* | 0.275** | 0.246* | 0.263** | 0.650** | 0.680** | 1 | | |
| | E4 | 0.238* | 0.233* | 0.231* | 0.261** | 0.259** | 0.669** | 0.702** | 0.725** | 1 | |
| | BLUE | 0.275** | 0.273** | 0.280** | 0.268** | 0.308** | 0.902** | 0.902** | 0.863** | 0.883** | 1 |

^aE1, Yangzhou Experimental Station of 2020; E2, Sihong Experimental Station of 2020; E3, Yangzhou Experimental Station of 2021; E4, Sihong Experimental Station 2021; BLUE represents best linear unbiased estimator. *: significant at $P < 0.05$, **: significant at $P < 0.01$

Table S2. Primers for Kompetitive Allele Specific PCR markers KASP_2D, KASP_4B, and KASP_5A

| KASP | SNP Marker | Forward primer 1 (5'-3') ^a | Forward primer 2 (5'-3') ^a | Common reverse primer (5'-3') |
|---------|-------------|--|--|-------------------------------|
| KASP_2D | AX109059601 | <u>GAAGGTGACCAAGTTCATGCT</u> gtgaagagcatg gtgaaggcG | <u>GAAGGTCGGAGTCAACGGATT</u> tgaagagcatg gtgaaggcC | gctctcgggtgtagttcca |
| KASP_4B | AX108819885 | <u>GAAGGTGACCAAGTTCATGCT</u> gcgtttgtgtgt gccctC | <u>GAAGGTCGGAGTCAACGGATT</u> gcgtttgtgtgt gccctG | atgattggtgcgaattggc |
| KASP_5A | AX109365651 | <u>GAAGGTGACCAAGTTCATGCT</u> cccagatgtcgtgtttggaatG | <u>GAAGGTCGGAGTCAACGGATT</u> cccagatgtcgtgtttggaatA | gaaagatgtgtccaaatgtcagtt |

^aThe tails for competitive primers are underlined and capital

Table S3. Distribution of detected QTL related with grain width and grain length in 117 cultivars and advanced lines planted in the yield evaluation nursery

| Cultivars/lines | Wheat zone ^a | Genotype ^b | | | Phenotype ^c | |
|-----------------|-------------------------|-----------------------|---------|---------|------------------------|---------|
| | | KASP_2D | KASP_4B | KASP_5A | GW (mm) | GL (mm) |
| Huaichuanmai 16 | YRVWZ | B | A | A | 3.49 | 6.81 |
| Huaimai 1403 | YRVWZ | B | A | A | 3.48 | 6.94 |
| Huaimai 1558 | YRVWZ | B | A | A | 3.29 | 7.18 |
| Huaimai 21 | YRVWZ | B | B | B | 3.39 | 6.45 |
| Huaimai 25 | YRVWZ | B | A | A | 3.46 | 6.84 |
| Huaimai 302 | YRVWZ | B | A | A | 3.39 | 7.02 |
| Huaimai 36 | YRVWZ | B | B | B | 3.38 | 7.06 |
| Huaimai 38 | YRVWZ | B | A | B | 3.39 | 7.06 |
| Huaimai 39 | YRVWZ | B | A | B | 3.39 | 6.76 |
| Huaimai 40 | YRVWZ | B | A | B | 3.34 | 6.78 |
| Jimai 1290 | YRVWZ | A | B | B | 2.99 | 6.53 |
| Jimai 1291 | YRVWZ | B | B | B | 3.38 | 6.88 |
| Jimai 1302 | YRVWZ | B | A | A | 3.44 | 6.77 |
| Jimai 1303 | YRVWZ | B | B | B | 3.34 | 6.58 |
| Jimai 1306 | YRVWZ | B | A | A | 3.39 | 6.93 |
| Jimai 1309 | YRVWZ | B | A | A | 3.51 | 7.02 |
| Jimai 1312 | YRVWZ | A | B | A | 3.04 | 6.52 |
| Jimai 1316 | YRVWZ | A | B | A | 3.18 | 6.39 |
| Jimai 1324 | YRVWZ | B | B | B | 3.51 | 6.41 |
| Jimai 1328 | YRVWZ | B | A | A | 3.48 | 7.01 |
| Jimai 1329 | YRVWZ | A | B | A | 3.15 | 6.44 |
| Jimai 1330 | YRVWZ | B | B | B | 3.47 | 6.99 |

| | | | | | | |
|------------|-------|---|---|---|------|------|
| Jimai 1331 | YRVWZ | B | B | B | 3.38 | 6.92 |
| Jimai 1333 | YRVWZ | B | A | A | 3.44 | 7.15 |
| Jimai 1334 | YRVWZ | B | B | B | 3.39 | 6.55 |
| Jimai 1340 | YRVWZ | A | B | B | 3.21 | 6.68 |
| Jimai 1344 | YRVWZ | B | A | A | 3.59 | 7.14 |
| Jimai 1346 | YRVWZ | A | A | A | 3.29 | 6.57 |
| Jimai 1349 | YRVWZ | B | A | A | 3.55 | 7.11 |
| Jimai 1350 | YRVWZ | B | A | A | 3.51 | 6.82 |
| Jimai 1351 | YRVWZ | B | B | B | 3.55 | 6.59 |
| Jimai 1359 | YRVWZ | B | A | A | 3.57 | 6.99 |
| Jimai 1362 | YRVWZ | B | A | A | 3.52 | 6.84 |
| Jimai 1364 | YRVWZ | B | A | A | 3.43 | 7.16 |
| Jimai 1369 | YRVWZ | A | B | B | 3.15 | 6.55 |
| Jimai 1373 | YRVWZ | B | B | B | 3.42 | 6.81 |
| Jimai 1376 | YRVWZ | A | B | B | 3.03 | 6.52 |
| Jimai 1377 | YRVWZ | B | A | A | 3.49 | 7.21 |
| Jimai 1378 | YRVWZ | B | A | A | 3.47 | 6.74 |
| Jimai 1380 | YRVWZ | A | B | B | 2.95 | 6.64 |
| Jimai 1382 | YRVWZ | A | A | A | 3.27 | 6.71 |
| Jimai 1383 | YRVWZ | B | A | A | 3.46 | 6.95 |
| Jimai 19 | YRVWZ | A | A | A | 3.48 | 7.2 |
| Jimai 20 | YRVWZ | B | A | A | 3.5 | 6.97 |
| Jimai 23 | YRVWZ | B | A | A | 3.36 | 7.15 |
| Jimai 44 | YRVWZ | A | A | A | 3.26 | 6.68 |
| Jimai 52 | YRVWZ | B | A | A | 3.52 | 6.78 |
| Jinan 17 | YRVWZ | B | A | A | 3.41 | 7.22 |

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|---|--------|---|---|---|------|------|
| Lumai 14 | YRVWZ | B | A | A | 3.57 | 6.73 |
| Luyuan 502 | YRVWZ | B | A | A | 3.37 | 7.02 |
| Ningmai 11 | MLYVWZ | B | A | B | 3.58 | 6.79 |
| Ningmai 12 | MLYVWZ | B | B | A | 3.22 | 7 |
| Ningmai 13 | MLYVWZ | A | B | A | 3.31 | 6.57 |
| Ningmai 14 | MLYVWZ | A | A | A | 3.52 | 6.77 |
| Ningmai 15 | MLYVWZ | A | B | A | 3.43 | 6.65 |
| Ningmai 16 | MLYVWZ | A | B | A | 3.31 | 6.83 |
| Ningmai 18 | MLYVWZ | A | B | A | 2.93 | 6.54 |
| Ningmai 19 | MLYVWZ | A | B | A | 3.17 | 7.03 |
| Ningmai 21 | MLYVWZ | B | B | B | 3.4 | 6.55 |
| Ningmai 22 | MLYVWZ | B | B | B | 3.42 | 6.62 |
| Ningmai 24 | MLYVWZ | A | B | A | 3.43 | 6.83 |
| Ningmai 26 | MLYVWZ | A | B | B | 3.31 | 6.61 |
| Puxing 5 | YRVWZ | B | A | A | 3.58 | 6.99 |
| Shengxuan 3 | MLYVWZ | B | A | B | 3.53 | 6.78 |
| Shengxuan 6 | MLYVWZ | A | B | A | 3.36 | 6.38 |
| Sumai 3 | MLYVWZ | A | A | A | 3.41 | 6.35 |
| Taimai 198 | YRVWZ | B | A | A | 3.55 | 6.88 |
| Wangshuibai | MLYVWZ | A | B | A | 3.04 | 6.57 |
| Xinong 20 | YRVWZ | A | A | A | 3.28 | 6.84 |
| Xinong 511 | YRVWZ | B | A | A | 3.44 | 7.02 |
| Xumai 30 | YRVWZ | B | A | B | 3.26 | 6.61 |
| Yangmai 15 | MLYVWZ | A | A | A | 3.61 | 6.59 |
| (Yangmai 15/Zhoumai 18) F ₆ -1 | YRVWZ | B | A | A | 3.38 | 6.89 |
| (Yangmai 15/Zhoumai 18) F ₆ -2 | YRVWZ | A | A | B | 3.28 | 6.99 |

| | | | | | | |
|--|--------|---|---|---|------|------|
| (Yangmai 15/Zhoumai 18) F ₆ -3 | YRVWZ | B | A | A | 3.6 | 6.83 |
| (Yangmai 15/Zhoumai 18) F ₆ -4 | YRVWZ | B | A | A | 3.4 | 7.11 |
| (Yangmai 15/Zhoumai 18) F ₆ -5 | YRVWZ | B | A | A | 3.45 | 6.81 |
| (Yangmai 15/Zhoumai 18) F ₆ -6 | YRVWZ | A | A | A | 3.54 | 6.79 |
| (Yangmai 15/Zhoumai 18) F ₆ -7 | YRVWZ | B | A | A | 3.41 | 7.31 |
| (Yangmai 15/Zhoumai 18) F ₆ -8 | YRVWZ | B | A | A | 3.42 | 6.74 |
| (Yangmai 15/Zhoumai 18) F ₆ -9 | YRVWZ | B | A | B | 3.49 | 6.92 |
| (Yangmai 15/Zhoumai 18) F ₆ -10 | YRVWZ | B | B | B | 3.31 | 6.83 |
| (Yangmai 15/Zhoumai 18) F ₆ -11 | YRVWZ | B | B | A | 3.52 | 6.51 |
| (Yangmai 15/Zhoumai 18) F ₆ -12 | YRVWZ | B | A | A | 3.47 | 7.16 |
| (Yangmai 15/Zhoumai 18) F ₆ -13 | YRVWZ | B | A | A | 3.53 | 7.27 |
| (Yangmai 15/Zhoumai 18) F ₆ -14 | YRVWZ | B | A | B | 3.46 | 6.71 |
| (Yangmai 15/Zhoumai 18) F ₆ -15 | YRVWZ | B | A | A | 3.32 | 6.91 |
| (Yangmai 15/Zhoumai 18) F ₆ -16 | YRVWZ | B | A | A | 3.45 | 6.77 |
| (Yangmai 15/Zhoumai 18) F ₆ -17 | YRVWZ | B | A | A | 3.55 | 7.37 |
| (Yangmai 15/Zhoumai 18) F ₆ -18 | YRVWZ | A | A | A | 3.43 | 6.65 |
| (Yangmai 15/Zhoumai 18) F ₆ -19 | YRVWZ | B | A | A | 3.43 | 7.08 |
| (Yangmai 15/Zhoumai 18) F ₆ -20 | YRVWZ | B | A | B | 3.48 | 6.79 |
| (Yangmai 15/Zhoumai 18) F ₆ -21 | YRVWZ | B | A | B | 3.38 | 7.07 |
| (Yangmai 15/Zhoumai 18) F ₆ -22 | YRVWZ | B | A | B | 3.37 | 7.11 |
| (Yangmai 15/Zhoumai 18) F ₆ -23 | YRVWZ | B | B | A | 3.25 | 7.02 |
| (Yangmai 15/Zhoumai 18) F ₆ -24 | YRVWZ | B | A | A | 3.53 | 6.77 |
| (Yangmai 15/Zhoumai 18) F ₆ -25 | YRVWZ | B | A | A | 3.35 | 6.82 |
| Yangmai 158 | MLYVWZ | A | A | A | 3.37 | 6.88 |
| Yangmai 16 | MLYVWZ | A | A | A | 3.34 | 6.84 |
| (Yangmai 16/Ningmai 22) F ₅ -1 | MLYVWZ | A | B | B | 3.42 | 6.34 |

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|---|--------|---|---|---|------|------|
| (Yangmai 16/Ningmai 22) F ₅ -2 | MLYVWZ | A | B | B | 3.49 | 6.38 |
| (Yangmai 16/Ningmai 22) F ₅ -3 | MLYVWZ | A | B | B | 3.22 | 6.45 |
| (Yangmai 16/Ningmai 22) F ₅ -4 | MLYVWZ | A | B | A | 3.36 | 6.85 |
| (Yangmai 16/Ningmai 22) F ₅ -5 | MLYVWZ | B | B | A | 3.54 | 6.96 |
| (Yangmai 16/Ningmai 22) F ₅ -6 | MLYVWZ | A | A | B | 3.39 | 6.36 |
| (Yangmai 16/Ningmai 22) F ₅ -7 | MLYVWZ | A | A | B | 3.21 | 6.58 |
| (Yangmai 16/Ningmai 22) F ₅ -8 | MLYVWZ | B | B | B | 3.35 | 6.85 |
| (Yangmai 16/Ningmai 22) F ₅ -9 | MLYVWZ | A | B | A | 3.09 | 6.6 |
| (Yangmai 16/Ningmai 22) F ₅ -10 | MLYVWZ | A | A | B | 3.24 | 6.63 |
| (Yangmai 16/Ningmai 22) F ₅ -11 | MLYVWZ | A | A | B | 3.34 | 6.71 |
| (Yangmai 16/Ningmai 22) F ₅ -12 | MLYVWZ | A | A | B | 3.41 | 6.72 |
| (Yangmai 16/Ningmai 22) F ₅ -13 | MLYVWZ | B | A | A | 3.51 | 6.76 |
| (Yangmai 16/Ningmai 22) F ₅ -14 | MLYVWZ | A | B | B | 3.06 | 6.35 |
| (Yangmai 16/Ningmai 22) F ₅ -15 | MLYVWZ | B | B | B | 3.25 | 6.65 |
| (Yangmai 16/Ningmai 22) F ₅ -16 | MLYVWZ | B | B | A | 3.25 | 6.52 |
| Yangmai 18 | MLYVWZ | A | B | A | 3.31 | 6.62 |
| (Yangmai 18/Zhengmai 7698) F ₆ -1 | MLYVWZ | B | B | B | 3.42 | 6.55 |
| (Yangmai 18/Zhengmai 7698) F ₆ -2 | MLYVWZ | B | A | B | 3.49 | 7.07 |
| (Yangmai 18/Zhengmai 7698) F ₆ -3 | MLYVWZ | A | A | B | 3.47 | 6.56 |
| (Yangmai 18/Zhengmai 7698) F ₆ -4 | MLYVWZ | B | A | A | 3.52 | 6.79 |
| (Yangmai 18/Zhengmai 7698) F ₆ -5 | MLYVWZ | B | B | B | 3.49 | 6.72 |
| (Yangmai 18/Zhengmai 7698) F ₆ -6 | MLYVWZ | A | B | B | 3.44 | 6.47 |
| (Yangmai 18/Zhengmai 7698) F ₆ -7 | MLYVWZ | A | A | A | 3.41 | 6.59 |
| (Yangmai 18/Zhengmai 7698) F ₆ -8 | MLYVWZ | A | B | B | 3.26 | 6.39 |
| (Yangmai 18/Zhengmai 7698) F ₆ -9 | MLYVWZ | B | A | A | 3.49 | 6.81 |
| (Yangmai 18/Zhengmai 7698) F ₆ -10 | MLYVWZ | A | A | A | 3.36 | 6.49 |

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|---|--------|---|---|---|------|------|
| (Yangmai 18/Zhengmai 7698) F ₆ -11 | MLYVWZ | A | A | A | 3.48 | 6.59 |
| (Yangmai 18/Zhengmai 7698) F ₆ -12 | MLYVWZ | B | A | A | 3.63 | 6.83 |
| (Yangmai 18/Zhengmai 7698) F ₆ -13 | MLYVWZ | A | B | B | 3.25 | 6.38 |
| (Yangmai 18/Zhengmai 7698) F ₆ -14 | MLYVWZ | A | B | B | 3.41 | 6.81 |
| (Yangmai 18/Zhengmai 7698) F ₆ -15 | MLYVWZ | A | B | B | 3.18 | 6.41 |
| (Yangmai 18/Zhengmai 7698) F ₆ -16 | MLYVWZ | A | B | B | 3.21 | 6.63 |
| (Yangmai 18/Zhengmai 7698) F ₆ -17 | MLYVWZ | B | A | A | 3.46 | 6.99 |
| (Yangmai 18/Zhengmai 7698) F ₆ -18 | MLYVWZ | B | B | B | 3.42 | 6.68 |
| (Yangmai 18/Zhengmai 7698) F ₆ -19 | MLYVWZ | B | B | B | 3.44 | 6.67 |
| (Yangmai 18/Zhengmai 7698) F ₆ -20 | MLYVWZ | B | B | A | 3.53 | 6.48 |
| (Yangmai 18/Zhengmai 7698) F ₆ -21 | MLYVWZ | A | B | A | 3.45 | 6.35 |
| (Yangmai 18/Zhengmai 7698) F ₆ -22 | MLYVWZ | B | A | A | 3.51 | 7.03 |
| Yangmai 20 | MLYVWZ | A | A | A | 3.22 | 6.73 |
| Yangmai 21 | MLYVWZ | A | B | A | 3.3 | 7.02 |
| Yangmai 22 | MLYVWZ | A | A | B | 3.45 | 6.49 |
| Yangmai 23 | MLYVWZ | A | A | A | 3.12 | 6.83 |
| Yangmai 24 | MLYVWZ | A | A | A | 3.47 | 6.6 |
| Yangmai 3 | MLYVWZ | A | B | B | 3.12 | 6.59 |
| Yangmai 33 | MLYVWZ | A | A | A | 3.27 | 6.84 |
| Yangmai 38 | MLYVWZ | A | A | B | 3.47 | 6.94 |
| Yangmai 4 | MLYVWZ | A | A | A | 3.41 | 6.64 |
| Yangmai 6 | MLYVWZ | A | B | B | 3.29 | 6.65 |
| Yangmai 9 | MLYVWZ | A | A | A | 3.4 | 6.61 |
| Yannong 1212 | YRVWZ | B | A | A | 3.59 | 6.92 |
| Yanzhan 4110 | YRVWZ | B | B | B | 3.37 | 6.84 |
| Zhengmai 7698 | YRVWZ | B | A | A | 3.37 | 6.96 |

| | | | | | | |
|---------------|--------|---|---|---|------|------|
| Zhengmai 9188 | YRVWZ | B | A | A | 3.45 | 6.73 |
| Zhenmai 168 | MLYVWZ | A | A | A | 3.29 | 7.11 |
| Zhenmai 9 | MLYVWZ | A | A | A | 3.54 | 7.03 |
| Zhoumai 18 | YRVWZ | B | A | A | 3.46 | 6.95 |
| Zhoumai 30 | YRVWZ | B | A | A | 3.45 | 6.77 |
| Zhoumai 32 | YRVWZ | B | A | A | 3.42 | 6.81 |
| Zhoumai 36 | YRVWZ | B | A | A | 3.52 | 6.79 |

^aMLYVWZ represents the cultivars or the lines were released or most suitable for planting in the Middle and Lower Yangtze Valleys Wheat Zone; YRVWZ represents the cultivars or the lines were released or most suitable for planting in the Yellow-Huai River Valleys Wheat Zone

^bA, the YM12-like allele; B, the YZ1-like allele

^cGW, grain width; GL, grain length

Table S4. Prediction of candidate genes for the genomic regions of *QGW.yz.2D/QGL.yz.2D*, *QGW.yz.4B/QGL.yz.4B*, and *QGL.yz.5A*

| Gene ID (<i>Triticum aestivum</i>) ^a | Chr ^b | Physical location (Mb) ^c | Annotation ^d | Orthologs in rice ^e |
|---|------------------|-------------------------------------|--|--------------------------------|
| TraesCS2D03G0925700 | 2D | 526.15 | 14 kDa proline-rich protein DC2.15 | Os04g0554500 |
| TraesCS2D03G0926200 | | 526.18 | NA | Os04g0554300 |
| TraesCS2D03G0926300 | | 526.19 | Vesicle-associated protein 1-3 | Os04g0554200 |
| TraesCS2D03G0926400 | | 526.25 | Probable trehalose-phosphate phosphatase 1 | Os04g0554000 |
| TraesCS2D03G0926500 | | 526.29 | Putative glucuronosyltransferase PGSIP8 | Os04g0553800 |
| TraesCS2D03G0926600 | | 526.30 | Serine carboxypeptidase-like 19 | Os11g0432900 |
| TraesCS2D03G0927000 | | 526.47 | Serine carboxypeptidase-like 18 | Os11g0432900 |
| TraesCS2D03G0927100 | | 526.54 | Serine carboxypeptidase-like 19 | Os11g0432900 |
| TraesCS2D03G0927200 | | 526.59 | Serine carboxypeptidase-like 19 | Os11g0432900 |
| TraesCS2D03G0927700 | | 526.71 | Probable pectinesterase 68 | Os04g0553500 |
| TraesCS2D03G0927900 | | 526.72 | Acyl-acyl carrier protein thioesterase ATL3, chloroplastic | Os04g0553300 |

| | | | |
|---------------------|--------|---|--------------|
| TraesCS2D03G0928100 | 526.72 | WD repeat-containing protein 76 | Os08g0282500 |
| TraesCS2D03G0928200 | 526.73 | Protein TRIGALACTOSYLDIACYLGLYCEROL 1, chloroplastic | Os04g0553000 |
| TraesCS2D03G0928500 | 527.07 | Zinc finger protein ZAT1 | Os04g0552700 |
| TraesCS2D03G0928600 | 527.11 | NA | Os04g0552400 |
| TraesCS2D03G0928800 | 527.43 | NA | NA |
| TraesCS2D03G0928900 | 527.44 | O-fucosyltransferase 29 | Os04g0551300 |
| TraesCS2D03G0929000 | 527.65 | Squamosa promoter-binding-like protein 7 | Os04g0551500 |
| TraesCS2D03G0929100 | 527.84 | NA | Os04g0551600 |
| TraesCS2D03G0929300 | 528.07 | Probable plastid-lipid-associated protein 11, chloroplastic | Os04g0551700 |
| TraesCS2D03G0929400 | 528.25 | Expansin-B15 | Os04g0552000 |
| TraesCS2D03G0929500 | 528.25 | Expansin-B5 | Os04g0552200 |
| TraesCS2D03G0929600 | 528.26 | Expansin-B5 | Os04g0552200 |
| TraesCS2D03G0929800 | 528.30 | Cyclin-P2-1 | Os04g0552300 |
| TraesCS2D03G0930000 | 528.48 | Aquaporin TIP2-3 | Os02g0658100 |
| TraesCS2D03G0930100 | 528.48 | Probable aquaporin TIP5-1 | Os04g0550800 |
| TraesCS2D03G0930300 | 528.51 | Cysteine and histidine-rich domain-containing protein RAR1 | Os02g0535400 |
| TraesCS2D03G0930400 | 528.51 | NA | NA |
| TraesCS2D03G0930500 | 528.65 | NA | Os04g0550700 |
| TraesCS2D03G0930600 | 528.65 | Carotenoid cleavage dioxygenase 7, chloroplastic | Os04g0550600 |
| TraesCS2D03G0930700 | 528.66 | Acetylglutamate kinase, chloroplastic | Os04g0550500 |
| TraesCS2D03G0930800 | 528.94 | Protein argonaute 7 | Os04g0566500 |
| TraesCS2D03G0931100 | 529.14 | Ethylene-responsive transcription factor ERF034 | Os04g0550200 |
| TraesCS2D03G0931300 | 529.40 | Ethylene-responsive transcription factor ERF034 | Os04g0549800 |
| TraesCS2D03G0931400 | 529.42 | Ethylene-responsive transcription factor ERF038 | Os04g0549700 |
| TraesCS2D03G0931500 | 529.44 | Probable transcription factor MYB58 | NA |
| TraesCS2D03G0931800 | 529.52 | Probable isoaspartyl peptidase/L-asparaginase 3 | Os04g0549300 |

| | | | |
|---------------------|-----------|--|--------------|
| TraesCS2D03G0932000 | 529.52 | NA | NA |
| TraesCS2D03G0932100 | 529.62 | Probable low-specificity L-threonine aldolase 1 | Os04g0516600 |
| TraesCS2D03G0932300 | 529.68 | Homeobox-leucine zipper protein HOX17 | Os04g0548700 |
| TraesCS2D03G0932400 | 529.77 | NA | Os04g0548500 |
| TraesCS2D03G0932500 | 529.78 | Histone H4 variant TH091 | Os04g0583600 |
| TraesCS2D03G0932600 | 529.81 | Histone H4 | Os04g0583600 |
| TraesCS2D03G0932700 | 529.93 | Histone H4 | Os04g0583600 |
| TraesCS2D03G0932800 | 530.03 | Probable leucine-rich repeat receptor-like protein kinase IMK3 | Os04g0548400 |
| TraesCS2D03G0932900 | 530.04 | Uncharacterized protein At3g06530 | Os04g0548300 |
| TraesCS2D03G0933100 | 530.21 | Disease resistance protein RPM1 | Os04g0548100 |
| TraesCS2D03G0933200 | 530.21 | DeSI-like protein At4g17486 | Os04g0548000 |
| TraesCS2D03G0933300 | 530.22 | BTB/POZ and MATH domain-containing protein 4 | NA |
| TraesCS2D03G0933400 | 530.23 | Protein NRT1/ PTR FAMILY 8.2 | Os07g0100600 |
| TraesCS2D03G0933500 | 530.45 | Disease resistance protein Piks-2 | NA |
| TraesCS2D03G0933600 | 530.45 | Disease resistance protein PIK6-NP | Os11g0598300 |
| TraesCS2D03G0933800 | 530.46 | Nudix hydrolase 8 | Os04g0547900 |
| TraesCS2D03G0934600 | 530.60 | Ethylene-responsive transcription factor 5 | Os04g0547600 |
| TraesCS2D03G0935000 | 530.66 | NA | NA |
| TraesCS2D03G0935100 | 530.71 | Ethylene-responsive transcription factor 5 | Os04g0547600 |
| TraesCS2D03G0935500 | 530.76 | Ethylene-responsive transcription factor 2 | Os04g0546800 |
| TraesCS2D03G0935600 | 530.76 | NA | NA |
| TraesCS2D03G0935700 | 530.92 | Oleosin 16 kDa | Os04g0546500 |
| TraesCS4B03G0627300 | 4B 479.26 | bZIP transcription factor 16 | Os03g0239400 |
| TraesCS4B03G0627500 | 479.27 | Zinc finger protein 7 | Os03g0239300 |
| TraesCS4B03G0627600 | 479.27 | Protein TITANIA | Os03g0239200 |
| TraesCS4B03G0627700 | 479.28 | NA | NA |

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| TraesCS4B03G0627800 | 479.80 | Probable xyloglucan endotransglucosylase/hydrolase protein 28 | Os03g0239000 |
| TraesCS4B03G0627900 | 479.81 | RNA demethylase ALKBH10B | Os03g0238800 |
| TraesCS4B03G0628100 | 479.86 | Serine/threonine-protein kinase RIPK | Os03g0274800 |
| TraesCS4B03G0628300 | 480.05 | Serpin-ZX | NA |
| TraesCS4B03G0628600 | 480.13 | NA | Os03g0238700 |
| TraesCS4B03G0628700 | 480.13 | Purple acid phosphatase 3 | Os03g0238600 |
| TraesCS4B03G0629000 | 480.44 | Type IV inositol polyphosphate 5-phosphatase 9 | Os03g0238300 |
| TraesCS4B03G0629100 | 480.70 | NA | Os03g0237950 |
| TraesCS4B03G0629400 | 480.73 | Cyclin-J18-like | NA |
| TraesCS4B03G0630000 | 480.81 | 65-kDa microtubule-associated protein 7 | Os03g0237600 |
| TraesCS4B03G0630100 | 480.85 | NA | Os03g0237500 |
| TraesCS4B03G0630300 | 481.01 | Protein Barley B recombinant | Os03g0237401 |
| TraesCS4B03G0630500 | 481.34 | Protein indeterminate-domain 14 | Os03g0237250 |
| TraesCS4B03G0631000 | 481.86 | Anaphase-promoting complex subunit 6 | Os03g0236966 |
| TraesCS4B03G0631100 | 481.98 | NA | Os03g0236900 |
| TraesCS4B03G0631200 | 481.98 | NA | Os03g0236800 |
| TraesCS4B03G0631300 | 482.18 | Transcription factor MYB77 | Os03g0236300 |
| TraesCS4B03G0631600 | 482.19 | Transcription factor MYB77 | Os03g0236300 |
| TraesCS4B03G0632100 | 482.53 | Glutamate decarboxylase 1 | Os03g0236200 |
| TraesCS4B03G0632200 | 482.71 | Protein NRT1/ PTR FAMILY 8.3 | Os03g0235900 |
| TraesCS4B03G0632300 | 482.72 | NA | NA |
| TraesCS4B03G0632400 | 482.78 | Protein NRT1/ PTR FAMILY 8.3 | Os03g0235700 |
| TraesCS4B03G0632600 | 482.90 | Protein NRT1/ PTR FAMILY 8.3 | Os03g0235700 |
| TraesCS4B03G0633000 | 482.94 | Probable RNA-dependent RNA polymerase 2 | Os04g0465700 |
| TraesCS4B03G0633100 | 482.95 | Protein NRT1/ PTR FAMILY 8.3 | Os03g0235300 |
| TraesCS4B03G0633300 | 482.96 | Protein NRT1/ PTR FAMILY 8.3 | Os03g0235300 |

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| TraesCS4B03G0633400 | 482.96 | Pentatricopeptide repeat-containing protein At4g37170 | Os03g0235200 |
| TraesCS4B03G0633600 | 482.96 | Protein GID8 homolog | Os03g0235100 |
| TraesCS4B03G0634300 | 483.10 | F-box protein At3g07870 | NA |
| TraesCS4B03G0634600 | 483.13 | F-box/kelch-repeat protein At3g17530 | NA |
| TraesCS4B03G0634700 | 483.13 | NA | NA |
| TraesCS4B03G0634800 | 483.14 | Peroxidase N | Os03g0235000 |
| TraesCS4B03G0634900 | 483.15 | Peroxidase 15 | Os03g0234900 |
| TraesCS4B03G0635300 | 483.29 | NA | Os03g0234600 |
| TraesCS4B03G0635400 | 483.30 | Peroxidase 54 | Os03g0234500 |
| TraesCS4B03G0635500 | 483.77 | Ubiquitin-60S ribosomal protein L40-2 | Os03g0234200 |
| TraesCS4B03G0635800 | 483.95 | Metal tolerance protein 4 | Os03g0226400 |
| TraesCS4B03G0636500 | 484.73 | NA | Os03g0226600 |
| TraesCS4B03G0636800 | 485.26 | DNA (cytosine-5)-methyltransferase CMT1 [UniProtKB/Swiss-Prot:A0A0P0VUY4] | Os03g0226800 |
| TraesCS4B03G0637000 | 485.38 | Proline-rich receptor-like protein kinase PERK5 [UniProtKB/Swiss-Prot:Q8GX23] | Os03g0226901 |
| TraesCS4B03G0637300 | 485.44 | Coatomer subunit gamma-1 [UniProtKB/Swiss-Prot:Q8H852] | Os03g0227000 |
| TraesCS4B03G0637400 | 485.45 | DNA polymerase I [UniProtKB/Swiss-Prot:Q04957] | Os03g0227300 |
| TraesCS4B03G0637500 | 485.46 | Glucan endo-1,3-beta-glucosidase 7 [UniProtKB/Swiss-Prot:Q9M069] | Os03g0227400 |
| TraesCS4B03G0637700 | 486.44 | NA | Os03g0227500 |
| TraesCS4B03G0638000 | 486.94 | Cytochrome P450 90B2 [UniProtKB/Swiss-Prot:Q5CCK3] | Os03g0227700 |
| TraesCS4B03G0638700 | 487.42 | Probable receptor-like serine/threonine-protein kinase At4g34500 [UniProtKB/Swiss-Prot:Q6NKZ9] | Os03g0227900 |
| TraesCS4B03G0639000 | 487.83 | Uncharacterized protein At1g01500 [UniProtKB/Swiss-Prot:Q8GUH2] | Os03g0228200 |
| TraesCS4B03G0639100 | 487.85 | AP-3 complex subunit sigma [UniProtKB/Swiss-Prot:Q8VZ37] | Os03g0228400 |
| TraesCS4B03G0639300 | 488.04 | NA | Os03g0228500 |
| TraesCS4B03G0640200 | 488.24 | Leucine-rich repeat receptor-like serine/threonine-protein kinase BAM1 [UniProtKB/Swiss-Prot:O49545] | Os03g0228800 |

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| TraesCS4B03G0640400 | 488.44 | Transcription factor bHLH19 [UniProtKB/Swiss-Prot:Q1PF16] | Os03g0229100 |
| TraesCS4B03G0641100 | 488.80 | Protein DETOXIFICATION 48 [UniProtKB/Swiss-Prot:Q9SLV0] | Os03g0229500 |
| TraesCS4B03G0641300 | 488.82 | 7-methyl-GTP pyrophosphatase [UniProtKB/Swiss-Prot:Q54TC5] | Os03g0229600 |
| TraesCS4B03G0641600 | 489.81 | Inactive poly [ADP-ribose] polymerase RCD1 [UniProtKB/Swiss-Prot:Q8RY59] | Os03g0230300 |
| TraesCS4B03G0641900 | 490.16 | Inositol-tetrakisphosphate 1-kinase 2 [UniProtKB/Swiss-Prot:Q10PL5] | Os03g0230500 |
| TraesCS4B03G0642200 | 490.18 | 2-carboxy-1,4-naphthoquinone phytyltransferase, chloroplastic [UniProtKB/Swiss-Prot:Q0WUA3] | Os03g0190100 |
| TraesCS4B03G0642500 | 490.61 | Homeobox-leucine zipper protein HOX19 [UniProtKB/Swiss-Prot:Q8GRL4] | Os03g0231150 |
| TraesCS4B03G0643100 | 490.93 | Branched-chain-amino-acid aminotransferase 3, chloroplastic [UniProtKB/Swiss-Prot:Q9M401] | Os03g0231600 |
| TraesCS4B03G0643200 | 490.97 | Squalene monooxygenase SE1 [UniProtKB/Swiss-Prot:O48651] | Os03g0231800 |
| TraesCS4B03G0643400 | 491.35 | Protein SHORT HYPOCOTYL IN WHITE LIGHT 1 [UniProtKB/Swiss-Prot:F4I3V6] | Os03g0231900 |
| TraesCS4B03G0643600 | 491.36 | Transcription factor bHLH49 [UniProtKB/Swiss-Prot:Q9CAA9] | Os03g0231950 |
| TraesCS4B03G0643700 | 491.36 | F-box protein SKIP22 [UniProtKB/Swiss-Prot:Q9ZUB8] | Os03g0232000 |
| TraesCS5A03G0034700 | 5A 12.25 | Transcription factor bHLH25 [UniProtKB/Swiss-Prot:Q9T072] | Os12g0632600 |
| TraesCS5A03G0035400 | 12.53 | ADP-ribosylation factor-like protein 2 [UniProtKB/Swiss-Prot:Q9ZPX1] | Os12g0632100 |
| TraesCS5A03G0035500 | 12.53 | Glycine-rich RNA-binding protein 8 [UniProtKB/Swiss-Prot:Q03251] | Os12g0632000 |
| TraesCS5A03G0035600 | 12.59 | Pyridine nucleotide-disulfide oxidoreductase domain-containing protein 2 [UniProtKB/Swiss-Prot:Q3MHH6] | Os12g0631800 |
| TraesCS5A03G0036100 | 12.89 | Protein transport protein Sec61 subunit beta [UniProtKB/Swiss-Prot:P38389] | NA |
| TraesCS5A03G0036600 | 12.98 | Short integuments 2, mitochondrial [UniProtKB/Swiss-Prot:Q8L607] | Os11g0447300 |
| TraesCS5A03G0036700 | 13.07 | NA | Os12g0631600 |
| TraesCS5A03G0036800 | 13.08 | Deoxyuridine 5'-triphosphate nucleotidohydrolase [UniProtKB/Swiss-Prot:Q10FF9] | NA |
| TraesCS5A03G0037100 | 13.10 | Mechanosensitive ion channel protein 2, chloroplastic [UniProtKB/Swiss-Prot:Q56X46] | NA |
| TraesCS5A03G0037600 | 13.18 | WAT1-related protein At3g30340 [UniProtKB/Swiss-Prot:Q9LI65] | NA |
| TraesCS5A03G0037900 | 13.55 | ATP-dependent RNA helicase DEAH12, chloroplastic [UniProtKB/Swiss-Prot:F4KGU4] | Os12g0631200 |

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| TraesCS5A03G0038100 | 13.56 | Protein FERTILITY RESTORER RF2, mitochondrial [UniProtKB/Swiss-Prot:F1SZ41] | NA |
| TraesCS5A03G0038900 | 13.95 | NA | NA |
| TraesCS5A03G0039100 | 13.97 | ABC transporter G family member 48 [UniProtKB/Swiss-Prot:Q8GU84] | Os02g0318500 |
| TraesCS5A03G0039300 | 14.00 | CBBY-like protein [UniProtKB/Swiss-Prot:Q94K71] | Os12g0630700 |
| TraesCS5A03G0039700 | 14.17 | G-type lectin S-receptor-like serine/threonine-protein kinase At2g19130 [UniProtKB/Swiss-Prot:O64477] | Os12g0640700 |
| TraesCS5A03G0039800 | 14.17 | G-type lectin S-receptor-like serine/threonine-protein kinase At2g19130 [UniProtKB/Swiss-Prot:O64477] | NA |
| TraesCS5A03G0040100 | 14.39 | (E)-beta-caryophyllene synthase [UniProtKB/Swiss-Prot:B2C4D0] | NA |
| TraesCS5A03G0040500 | 14.53 | (E)-beta-caryophyllene synthase [UniProtKB/Swiss-Prot:B2C4D0] | Os08g0139700 |
| TraesCS5A03G0041100 | 14.65 | Probable E3 ubiquitin-protein ligase ARI2 [UniProtKB/Swiss-Prot:Q84RR2] | Os03g0233500 |
| TraesCS5A03G0041300 | 14.79 | ATP synthase subunit epsilon, mitochondrial [UniProtKB/Swiss-Prot:Q41898] | Os08g0250200 |
| TraesCS5A03G0042000 | 15.06 | NA | NA |
| TraesCS5A03G0042100 | 15.07 | NA | NA |
| TraesCS5A03G0042400 | 15.11 | NA | NA |
| TraesCS5A03G0042800 | 15.37 | NA | NA |
| TraesCS5A03G0042900 | 15.38 | NA | NA |
| TraesCS5A03G0043200 | 15.98 | NA | NA |
| TraesCS5A03G0043300 | 16.08 | NA | NA |
| TraesCS5A03G0043600 | 16.13 | NA | NA |
| TraesCS5A03G0043700 | 16.14 | Thaumatococcus-like protein [UniProtKB/Swiss-Prot:P81370] | Os12g0630500 |
| TraesCS5A03G0043900 | 16.17 | Zeamatin [UniProtKB/Swiss-Prot:P33679] | Os12g0630500 |
| TraesCS5A03G0044100 | 16.20 | Osmotin-like protein OSML13 [UniProtKB/Swiss-Prot:P50701] | Os12g0630500 |
| TraesCS5A03G0044200 | 16.21 | Thaumatococcus-like pathogenesis-related protein 3 [UniProtKB/Swiss-Prot:P50697] | Os12g0629600 |
| TraesCS5A03G0044400 | 16.25 | Thaumatococcus-like pathogenesis-related protein 3 [UniProtKB/Swiss-Prot:P50697] | Os12g0629600 |

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| TraesCS5A03G0044500 | 16.36 | Pathogenesis-related thaumatin-like protein 3.2 [UniProtKB/Swiss-Prot:Q8H995] | Os12g0630500 |
| TraesCS5A03G0044600 | 16.43 | Thaumatococcus-like protein [UniProtKB/Swiss-Prot:P31110] | Os12g0629600 |
| TraesCS5A03G0044700 | 16.44 | Thaumatococcus-like protein [UniProtKB/Swiss-Prot:P31110] | Os12g0629600 |
| TraesCS5A03G0044800 | 16.44 | Thaumatococcus-like protein [UniProtKB/Swiss-Prot:P31110] | Os12g0629600 |
| TraesCS5A03G0044900 | 16.45 | Thaumatococcus-like protein [UniProtKB/Swiss-Prot:P31110] | Os12g0629600 |
| TraesCS5A03G0045000 | 16.45 | Thaumatococcus-like protein [UniProtKB/Swiss-Prot:P31110] | Os12g0629600 |
| TraesCS5A03G0045100 | 16.46 | Thaumatococcus-like protein [UniProtKB/Swiss-Prot:P31110] | Os12g0629600 |
| TraesCS5A03G0045200 | 16.47 | Thaumatococcus-like protein [UniProtKB/Swiss-Prot:P31110] | Os12g0629600 |
| TraesCS5A03G0045500 | 16.79 | Dihydroceramide fatty acyl 2-hydroxylase FAH1 [UniProtKB/Swiss-Prot:O48916] | Os12g0628400 |
| TraesCS5A03G0045900 | 16.87 | NA | Os12g0628300 |
| TraesCS5A03G0046100 | 16.97 | Acyl transferase 15 [UniProtKB/Swiss-Prot:Q7XHC4] | NA |
| TraesCS5A03G0046200 | 16.98 | Thaumatococcus-like protein [UniProtKB/Swiss-Prot:P31110] | Os12g0629600 |
| TraesCS5A03G0046800 | 17.79 | Nucleolar complex protein 2 homolog [UniProtKB/Swiss-Prot:Q9ZPV5] | Os12g0163200 |
| TraesCS5A03G0046900 | 17.81 | PI-PLC X domain-containing protein At5g67130 [UniProtKB/Swiss-Prot:Q93XX5] | Os03g0415200 |
| TraesCS5A03G0047100 | 18.35 | NA | Os12g0607800 |
| TraesCS5A03G0048000 | 18.48 | ATP synthase subunit alpha, mitochondrial [UniProtKB/Swiss-Prot:P12862] | BAC19899 |
| TraesCS5A03G0048200 | 18.48 | ATP synthase subunit 9, mitochondrial [UniProtKB/Swiss-Prot:Q37550] | BAC19885 |
| TraesCS5A03G0048400 | 18.51 | Putative ATP synthase protein YMF19 [UniProtKB/Swiss-Prot:P43650] | BAC19860 |
| TraesCS5A03G0048700 | 18.51 | Ribosomal protein S12, mitochondrial [UniProtKB/Swiss-Prot:P28520] | BAC19872 |
| TraesCS5A03G0048800 | 18.52 | NADH-ubiquinone oxidoreductase chain 3 [UniProtKB/Swiss-Prot:P27062] | BAC19871 |
| TraesCS5A03G0049100 | 18.54 | Putative cytochrome c biosynthesis ccmC-like mitochondrial protein [UniProtKB/Swiss-Prot:P92527] | BAC19863 |
| TraesCS5A03G0049200 | 18.54 | NA | NA |
| TraesCS5A03G0050000 | 18.56 | NADH-ubiquinone oxidoreductase chain 4 [UniProtKB/Swiss-Prot:Q04050] | BAC19875 |
| TraesCS5A03G0050500 | 18.91 | Basic leucine zipper 19 [UniProtKB/Swiss-Prot:Q8VY76] | Os06g0716800 |

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| <u>TraesCS5A03G0050700</u> | 18.92 | <u>Anaphase-promoting complex subunit 5 [UniProtKB/Swiss-Prot:Q8H1U4]</u> | <u>Os12g0626300</u> |
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^aGene ID (*Triticum aestivum*), *T. aestivum* gene transcripts and their domains that were available in Ensembl (using the transcript table link).

^bChr, chromosome

^cPhysical location (Mb), the physical location is based on the Chinese Spring 2.1 reference genome (RefSeq v2.1)

^dAnnotation, the description of the corresponding gene, NA represents the unknown function

^eOrthologs in rice, the orthologs gene ID in *Oryza sativa*