**SUPPLEMENTAL TABLES**

**Table S1.** **Primers used in this study**

|  |  |  |  |
| --- | --- | --- | --- |
| **Primer ID** | **Forward primer (5’-3’)** | **Reverse primer (5’-3’)** | **R.E.1/Position/Probe** |
| **High resolution mapping (CAPS2 markers)** |
| SNP2788 | AGTGGAACCCTTCTGAAATCAA | ATTGCAATTTGACTGGTTGACA | *ApeK*I |
| SNP2830.7 | TCGTGCGTGTAGAGGATAAGAA | AAGCAAACCAAACACAATCCTT | *HypCH*4IV |
| SNP2830.9 | TTCTTTTTCTTGCTCTGTTCTCC | AAGAAACCAAGGGGGTCAAA | *Mnl*I |
| SNP2835 | GTCAAGGATACGATCATATCTTTCT | TCTAAAGTGGGTTCGTGGCTTA | *Hpy*188I |
| SNP2855 | AGGTGGACAATTCATCCAGAAG | AACGGCCCATAATCTCACATAG | *Taq*I |
| **High resolution mapping (Indel3 markers)** |
| Indel2823 | TATGCAAGCTAAGCCTGTGTTT | AGCCCTATATATGCACAACATTCA |  |
| Indel2829 | ATTTGATCAACCCCTGCACTT | CCGACTCCTACTCTCCATTCAG |  |
| **DNA sequencing** |
| Seq\_SBN1 | ATTTGATCAACCCCTGCACTT | CCGACTCCTACTCTCCATTCAG | 1730 ~ 919-bp of *FZP* |
| Seq\_SBN2 | TATATGCATGATCGCTCAGAGG | GGAGGTACGCTGCCGAGATA | 1020 ~ 200-bp of *FZP* |
| Seq\_SBN3 | GTGGGTGTAGACGAAGTTGGTG | AGCTAGCATGCATTGTCATCAT | 340 ~ -456-bp of *FZP* |
| Seq\_SBN4 | GAGGGGAATGTTGTGTGCTACT | TGCCCTTCTACACATTTCACAC | -355 ~ -1150-bp of *FZP* |
| Seq\_SBN5 | CACTTAAGAAGCTTTCAAATGGAG | TTGATACTTCATCCGTTTCAGG | -1071 ~ -1919-bp of *FZP* |
| Seq\_SBN6 | AGCATCTTGTAAAAGGCTTCAAA | GGGTGTGACCCTAAGGAATAGA | -1809 ~ -2588-bp of *FZP* |
| **Primer ID** | **Forward primer (5’-3’)** | **Reverse primer (5’-3’)** | **R.E.1/Position/Probe** |
| **DNA sequencing** |  |
| Seq\_SBN7 | ACAATGGCCTTGACAAGATGTA | GCACTCTCCTCTTGGTACTTGG | -2466 ~ -3261-bp of *FZP* |
| Seq\_SBN8 | GGTCAAACAGTTCGATCTCACA | ATGTCCCCTGAAAATCACTCAT | -3181 ~ -4004-bp of *FZP* |
| Seq\_SBN9 | GAAGAATGGAGATATGATGTGTGG | CTCTGTTCCATCTACCGCATC | -3906 ~ -4730-bp of *FZP* |
| Seq\_SBN10 | ACTGTAGTGTGGTGACCTCGAT | CGTAGTTGAGTACAAAGCGAGA | -4667 ~ -5495-bp of *FZP* |
| Seq\_SBN11 | CGGGCTATGTATGCACCAC | AGCTGAGCTAGCTATACCCATCA | -5414 ~ -6245-bp of *FZP* |
| Seq\_SBN12 | AAGCAGCTCGAGTCACTACTCA | AAACACAAAAATAGAGCTTGACCA | -6150 ~ -6934-bp of *FZP* |
| Seq\_SBN13 | TCAAAAATCGTCACTCATTTGG | GAGAGAGGCAAGACCTCAAGAC | -6801 ~ -7624-bp of *FZP* |
| Seq\_SBN14 | AGCACCCATAATTCAGTTTTGC | GGGGTCAAAAGAAAAAGGAAGA | -7547 ~ -8353-bp of *FZP* |
| **Genotyping of four grain number genes (CAPS2 markers)** |  |  |
| IPA1 | TCAGAAGCTTTACGTTGGATTTC | TGAGACTTCATGTGGTAGCTGGT | *BsiHKA I* |
| SPIKE | GGAGTACTTCTGAAGCGTTCGT | AGCCCTGACCAGCTAATTTGTA | *HpyCH*4III |
| **Genotyping of four grain number genes (Indel3 markers)** |  |  |
| GN1A | CTGCTTATTTATAGGCCACCTTG | GAAGCAGTTGAGCATGAGGAG |  |
| DEP1 | GACTGCTGCTCATGCTGTAAAC | CAACATAAGCAACCACTGAGACA |  |
| **Vector construction** |  |  |  |
| Vector\_p40 | CAGGTCGACTCTAGAGGATCCTTGAGGGAGTACGTATTTAACGA | GAGCTCGGTACCCGGGGATCCTACATCTTGTCAAGGCCATTGTG |  |
| Vector\_p66 | AATTCCCATTGAATTCTTGCCGATA | CCATGATTACGAATTCACAGTGAACAATACAAAACCTGTGA |  |
| **Primer ID** | **Forward primer (5’-3’)** | **Reverse primer (5’-3’)** | **R.E.1/Position/Probe** |
| **Vector construction** |  |  |  |
| Vector\_RNAi | TGACCATGGTAGATCTCAGCAGCAGCCACAGCA | ACCTGTAATTCACACGTGGCTGCTGATGCTGATG |  |
| **Real-time PCR** |  |  |  |
| QPCR\_Os07g47340 | TCGCGCCGCTTCCA | TTGCTAAAGCAGCAGCCTTGT | FAM-CAGCCCAGGATGGCT-NFQ |
| QPCR\_FZP | GTCGCTGCTGGACATGGA  | CGGCGCCGGAGAAGA | FAM-ACGGCCACGACTTCC-NFQ |
| QPCR\_UBQ5 | CCGCCTCCGCAAGGA  | AAGTGGTTGGCCATGAAGGT | FAM-CCAACGCCGAGTGCG-NFQ |
| **Development of NILs (CAPS2 markers)** |
| SNP2830.5 | TATGCCATGAGTGATTTTCAGG | GCTAGATCAACGGTCACGATTT | *Hpy*188I |
| **Development of NILs (KASP4 markers)** |
| TN13\_C2\_8 | GAGGCTTCTTGCCACGTGATGCTGAGGCTTCTTGCCACGTGATA | CACTACTATTTCAGCCAGCAAAGAAGATA |  |
| TN13\_C3\_6 | TTCTCGGAGACCACGGTAGAATCTCGGAGACCACGGTAGAG | CAACCCTCAAAAAAGTAGGGCAAAACTAA |  |
| TN13\_C6\_5 | GTTTTATTGCATTCAAATGCATACTGTCAGTTTTATTGCATTCAAATGCATACTGTCG | AGGCATGAGGAAGCACAGGGAATAT |  |
| TN13\_C7\_22 | CCCAAGTTACCCATCGTGAAGCTCCCAAGTTACCCATCGTGAAGT | AGCGGCGGCCTTTGATCGGTA |  |
| TN13\_C8\_20 | AACATCCACAACAGCTGGTTTGTCTAACATCCACAACAGCTGGTTTGTCA | GGTTGATGGCGATGATGGAAAGGAA |  |
| TN13\_C9\_16 | GTGTATCTGCATTTCATGTCTTTGCTAGTATCTGCATTTCATGTCTTTGCTG | TTTGCACTTGGGTGAGCACTTGCAA |  |

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| --- | --- | --- | --- |
| **Primer ID** | **Forward primer (5’-3’)** | **Reverse primer (5’-3’)** | **R.E.1/Position/Probe** |
| **Development of NILs (KASP4 markers)** |  |  |
| TN13\_C11\_21 | AATTGAATTACTCTTGTTGTTGAGTTGCTAGAATTACTCTTGTTGTTGAGTTGCTG | TCAAGAAAGCAGACCAGATTGAAACACTT |  |
| TCS10\_C2\_15 | TTCTAGCCTTAATATGGACCATTGCTTTCTAGCCTTAATATGGACCATC | GGCCATAATATGATTGAGGTGTCAAACTA |  |
| TCS10\_C2\_25 | GTAAATTTCTTCGGATTTAGGAATACTAGTGTAAATTTCTTCGGATTTAGGAATACTAGA | AGCGGCCTGTGATACGTGGCTA |  |
| TCS10\_C4\_14 | ATTCGCATCATTCTCACTTCCCGTACGCATCATTCTCACTTCCCGTG | GAGGTGTAGACAAGATTGGTGGTGAT |  |
| TCS10\_C7\_20 | GTACCTGATCTCGTTGTCTGTTTCTACCTGATCTCGTTGTCTGTTTCC | AATTAACTAACCATCGTGGGCTACTACTT |  |
| SNP2831 | CGGCATGATCTACTATGTCTAAATCGCGGCATGATCTACTATGTCTAAATCT | GGTAGTACGGCAAGCATGATCAGAA |  |
| **Transgenic plant identification** |
| hptII | CAAGCTGCATCATCGAAATTG | AGGTCGCCAACATCTTCTTCT |  |

1 R.E.,Restriction Enzyme

2 CAPS, Cleaved Amplified Polymorphic Sequences.

3 Indel, Insertion/deletion.

4 KASP, Kompetitive Allele Specific PCR.