**Table S2: The total percentage of TE homologous sequences in symmetric (allelic) and asymmetric (PA, PA$_d$ and AL) genes on chromosome 10.**

| TE% | Genes in Nipponbare | | | | Genes in 93-11 | | | |
|---|---|---|---|---|---|---|---|---|
| (length)[a] | Allelic | PA | PA$_d$ | AL | Allelic | PA | PA$_d$ | AL |
| 0 | 9(8%)[b] | 8(14%) | 5(10%) | 6(9%) | 4(3%) | 2(3%) | 4(6%) | 1(2%) |
| 0-5% | 44(37%) | 9(16%) | 15(31%) | 15(23%) | 57(45%) | 33(49%) | 29(40%) | 14(30%) |
| 5%-10% | 27(23%) | 22(39%) | 14(29%) | 22(34%) | 35(28%) | 17(25%) | 13(18%) | 13(28%) |
| 10%-20% | 28(23%) | 12(21%) | 7(14%) | 14(22%) | 22(17%) | 9(13%) | 21(29%) | 10(22%) |
| >20% | 12(10%) | 5(9%) | 8(16%) | 7(11%) | 8(6%) | 7(10%) | 5(7%) | 8(17%) |
| Total genes | 120 | 56 | 49 | 64 | 126 | 68 | 72 | 46 |

[a] The proportion of TE-related fragments (the total length of all small pieces of TE homologous sequences contained in a gene divided by the length of this gene).

[b] The first number is the amount of the genes within each range with its corresponding percentage in brackets.

**Table S3: The sequence sizes and numbers of non-alignable regions (insertions) in Nipponbare and 93-11 on chromosome 10.**

| Nip. insertion length | 93-11 insertion length | | | | | |
|---|---|---|---|---|---|---|
| | <0bp | 0-300bp | 300bp-1kb | 1kb-5kb | 5kb-10kb | >10kb |
| <0bp | / | 6 | 151 | **183** | **56** | **61** |
| 0-300bp | 11 | 4 | 34 | **81** | **19** | **25** |
| 300bp-1kb | 151 | 34 | 18 | **47** | **16** | **13** |
| 1kb-5kb | **171** | **31** | **16** | 52 | 22 | 25 |
| 5kb-10kb | **64** | **11** | **8** | 20 | 15 | 16 |
| >10kb | **59** | **5** | **9** | 23 | 18 | 60 |

Note. The bolded numbers represent the insertions and the others (>1 kb) stand for the non-alignable regions which were used in this study.

**Table S4: Primer information for the amplification of gene fragments in Table 3.**

| NO. | Gene | Length | Reverse primer (5’ to 3’) |
|---|---|---|---|
| 1 | OsIFCC009208 | 832bp | GACAATTCAGGGAGGTTACGG<br>GAGCGAGCAGAAGCAGTGG |
| 2 | OsIFCC035754 | 828bp | AAGGTGAAAGTGTGGAGGAGAT<br>CAGAGGTTGGGGATTCGTAG |
| 3 | OsIFSC047991 | 1078bp | CATGCGACGAAGGTTGACTA<br>GAGGGAGTGCTTTGGTGTCA |
| 4 | OsIFCC019895 | 859bp | GAACAAGAAGGGGCGGTGAA<br>GCAGGTGTCGCAATGGTGAA |
| 5 | OsIFCC035751 | 831bp | TTACGAGATTCCAAGAGACCAA<br>TCCACCAGAGTTTCCATCAAG |
| 6 | OsIFCC035229 | 1013bp | GTTTTGCGAGTATTGGATGTTG<br>ATTGGATTGTTGGGATTATTGA |
| 7 | OsIFCC043050 | 1001bp | ACAACAAGAGCCCCCATAGC<br>CGTCTCCAACATCGGCATAG |
| 8 | OsIFCC045542 | 986bp | CCATTCTCTGCCTTCCTCTACC<br>TGCTTTTCAGTGTCAACCTCTC |
| 9 | OsIFCC023444 | 917bp | GGATGCTTGGGGTCAGATTT<br>CAGTGCTCATTTCGTCATTGT |
| 10 | OsIFCC026523 | 1062bp | CCCTTCTTTGGTGGCATTCA<br>GGGTGGTTGGGATGAGTGCT |
| 11 | OsIFSC046156 | 782bp | AGGGAGGAGCCATCTTCTATT<br>TTCCGCCTTCACCTAATGTC |
| 12 | Os12g31620 | 708bp | CCTCCGCCACCTGTCTGTAA<br>CGTGCCAAGCCCCTAATGAA |
| 13 | Os11g45330 | 1089bp | GTTGATTTGTGCCGAAGAGA<br>ATGCCACGGAGGTTTATTAGA |
| 14 | Os06g16790 | 928bp | GAGCTTAGGCGGGAGAAATCAC<br>CACCTTTCCAGCCATCCTCTAC |
| 15 | Os12g09730 | 1099bp | ACGAGCAGCGACGAATCAAG<br>GCGAGGAGGGCACACAGAA |
| 16 | Os10g04670 | 1014bp | GTGAGTTGGCGATTGACCTG<br>GATTAGGCAAGTCCCGCAGT |
| 17 | Os11g11550 | 844bp | TTGTTTCCTCGCCTGATGGT<br>AAACGCCAGAGCAGCATCTTA |
| 18 | Os12g28250 | 1004bp | GGCACCTACGCTCCTTGAT<br>TGGCTGTCACTTCAACCTCT |
| 19 | Os11g15670 | 1029bp | TACATTGCCGCTACTGGGAG<br>AAAGGCATTCTTGGGCAGAG |
| 20 | Os01g20720 | 1077bp | GCGGTGTTCCTCTGACGATA<br>GTTCTGCCACTCCTGCTGTC |
| 21 | Os12g18360 | 992bp | AATGCACATGATACAACACCACT |

|  |  |  |  |
|---|---|---|---|
|  |  |  | AGCCACGGCAGAGAAAGAAAG |
| 22 | Os04g41370 | 942bp | AATCACAGACATCCCAGAAGAA<br>GTGCCATCATCCCCATAGAA |
| 23 | Os07g29820 | 1061bp | ACAGATAGGTAGAGCCGAGAA<br>ACAAGTGGGCAGCAACAAA |
| 24 | Os02g25900 | 970bp | AAAGCAGCAGATGAGCCTAAG<br>AGTGGCCGATGATGATGAAG |
| 25 | OsIFCC040819 | 561bp | GGGTGGAGTGGGCAAGACAAC<br>TTGAACGACAGCAGGCGACC |
| 26 | Os12g37270 | 921bp | AGCAACTGGAAGGGAGATAAG<br>AACATCGTGCTCCAATAGCCT |
| 27 | Os12g03750 | 1068bp | GGGAGGCAGTTATTTGATGAG<br>CTGGAAGAATTTGATGGTGAGT |
| 28 | Os01g57270 | 899bp | CAAACAACCTGGAAACACAACT<br>AACTCTGGAACAACGAAACCT |
| 29 | Os05g16180 | 904bp | GCAGATGGTGAGTGGTGTAGTT<br>GCAGGTATCTTGGGAGTTGTT |
| 30 | Os08g10430 | 1060bp | AGCAAGTGCAAGGAGGATAA<br>TGGAGCTTGGGCATTACAC |
| 31 | Os01g05490 | 579bp | TCAGCCCACCTTATGT<br>CACCACCGACGAGAAA |
| 32 | Os03g61120 | 207bp | AGGCTCGTGGTTGTATT<br>CAACATCATTCCGTCCA |
| 33 | Os05g49760 | 192bp | TCGTCAGAAAGGTGGTG<br>CCGTGAACAAGCAGAGC |