

**Table S2. Pyrosequencing validation of RNA-seq results of parental homoeolog expression ratios (Nipponbare/9311) in the reciprocal hybrids (N9 and 9N) and tetraploids (NN99 and 99NN) for 20 genes representative of the range of gene expression levels in rice**

| Gene           | N9       |         | 9N       |         | NN99     |         | 99NN     |         |
|----------------|----------|---------|----------|---------|----------|---------|----------|---------|
|                | Pyro-seq | RNA-seq | Pyro-seq | RNA-seq | Pyro-seq | RNA-seq | Pyro-seq | RNA-seq |
| LOC_Os03g10800 | 0.50     | 0.82    | 0.52     | 0.88    | 0.93     | 0.89    | 0.26     | 0.46    |
| LOC_Os02g44870 | 1.17     | 1.06    | 1.16     | 1.09    | 0.89     | 0.86    | 0.54     | 0.55    |
| LOC_Os02g45070 | 0.90     | 0.83    | 0.96     | 0.81    | 0.77     | 0.70    | 0.49     | 0.36    |
| LOC_Os02g08120 | 1.15     | 1.12    | 1.42     | 1.11    | 1.29     | 1.06    | 0.78     | 0.62    |
| LOC_Os01g42260 | 1.15     | 1.24    | 1.17     | 1.22    | 2.07     | 2.78    | 1.56     | 2.19    |
| LOC_Os07g38730 | 1.16     | 1.21    | 1.19     | 1.14    | 1.51     | 1.46    | 2.80     | 3.06    |
| LOC_Os09g20350 | 1.07     | 1.16    | 1.07     | 1.16    | 0.89     | 0.87    | 1.69     | 1.34    |
| LOC_Os01g18670 | 0.89     | 0.80    | 1.01     | 0.90    | 4.26     | 4.75    | 1.27     | 1.39    |
| LOC_Os07g43870 | 0.90     | 0.99    | 0.90     | 0.96    | 2.53     | 3.05    | 1.22     | 1.40    |
| LOC_Os08g06010 | 1.08     | 1.24    | 1.12     | 1.14    | 0.48     | 0.52    | 2.86     | 2.87    |
| LOC_Os01g01700 | 1.02     | 1.24    | 1.04     | 1.24    | 1.44     | 1.53    | 0.44     | 0.46    |
| LOC_Os09g24440 | 1.37     | 1.50    | 1.29     | 1.62    | 0.80     | 0.92    | 0.52     | 0.59    |
| LOC_Os05g23860 | 1.32     | 1.45    | 1.28     | 1.32    | 0.47     | 0.45    | 1.30     | 1.17    |
| LOC_Os03g56270 | 1.01     | 1.04    | 0.99     | 1.06    | 1.15     | 1.19    | 1.95     | 2.01    |
| LOC_Os08g22354 | 1.00     | 1.08    | 0.95     | 0.92    | 0.56     | 0.55    | 1.10     | 1.01    |
| LOC_Os05g45930 | 0.95     | 0.96    | 0.76     | 1.00    | 0.28     | 0.28    | 1.81     | 2.09    |
| LOC_Os03g10340 | 1.08     | 0.99    | 0.91     | 0.96    | 0.98     | 0.95    | 0.53     | 0.55    |
| LOC_Os10g39760 | 0.83     | 0.99    | 0.82     | 0.82    | 0.26     | 0.26    | 0.83     | 0.70    |
| LOC_Os10g30100 | 0.98     | 1.04    | 0.97     | 1.11    | 0.51     | 0.56    | 0.68     | 0.64    |
| LOC_Os05g45050 | 0.86     | 1.62    | 0.86     | 1.57    | 0.36     | 0.43    | 1.43     | 2.41    |

**Table S4. Summary of biased homoeologs in the *in silico* hybrid, the reciprocal hybrids (N9 and 9N) and tetraploids (NN99 and 99NN)**

|       | <i>in silico</i><br>hybrid | N9    | 9N    | NN99  | 99NN  |
|-------|----------------------------|-------|-------|-------|-------|
| N > 9 | 2,765                      | 2,398 | 2,334 | 3,448 | 3,046 |
| N < 9 | 3,058                      | 1,579 | 1,564 | 3,268 | 3,614 |
| Total | 5,823                      | 3,977 | 3,898 | 6,716 | 6,660 |

**Table S5. Summary of RNA-seq clean data**

| Samples    | Total Reads | Total Nucleotides | Q20 Percentage |
|------------|-------------|-------------------|----------------|
| Nipponbare | 39,297,824  | 3,536,804,160     | 96.93%         |
| 9311       | 38,674,310  | 3,480,687,900     | 97.13%         |
| N9         | 68,450,232  | 6,160,520,880     | 96.99%         |
| 9N         | 68,354,908  | 6,151,941,720     | 96.88%         |
| NN99       | 67,917,614  | 6,112,585,260     | 96.83%         |
| 99NN       | 64,825,692  | 5,834,312,280     | 96.93%         |