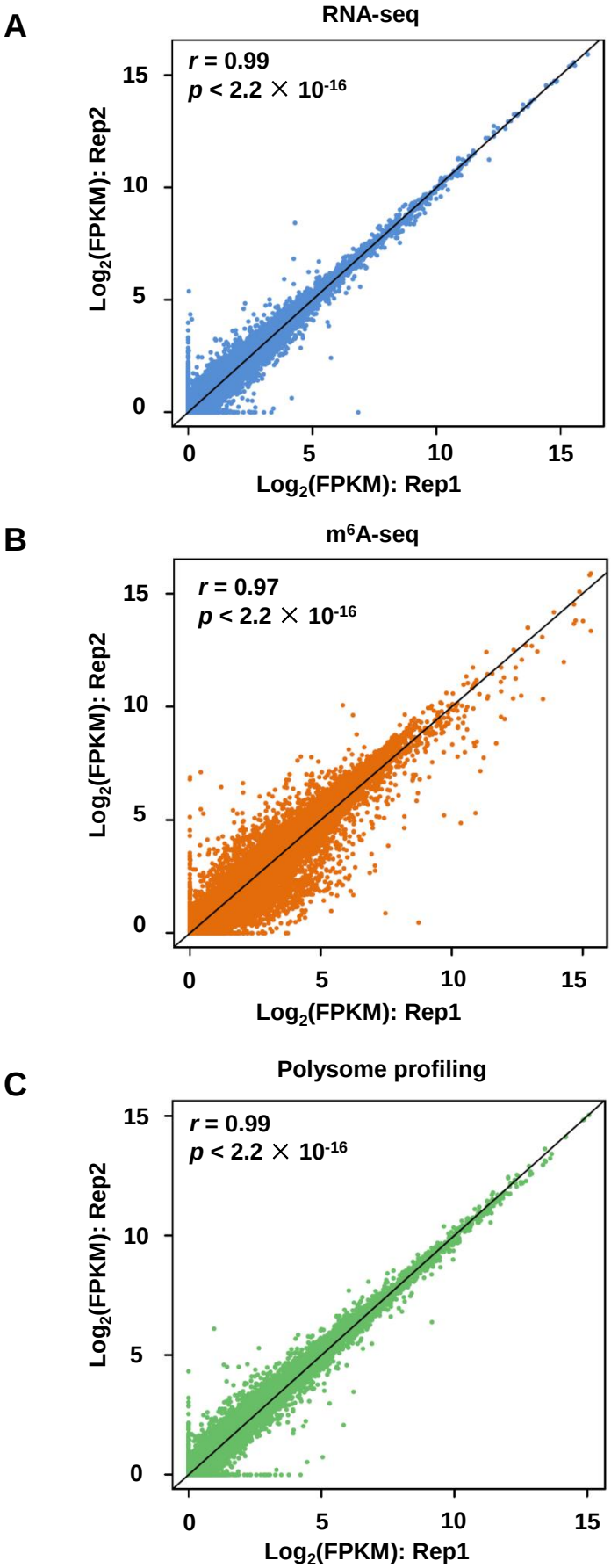
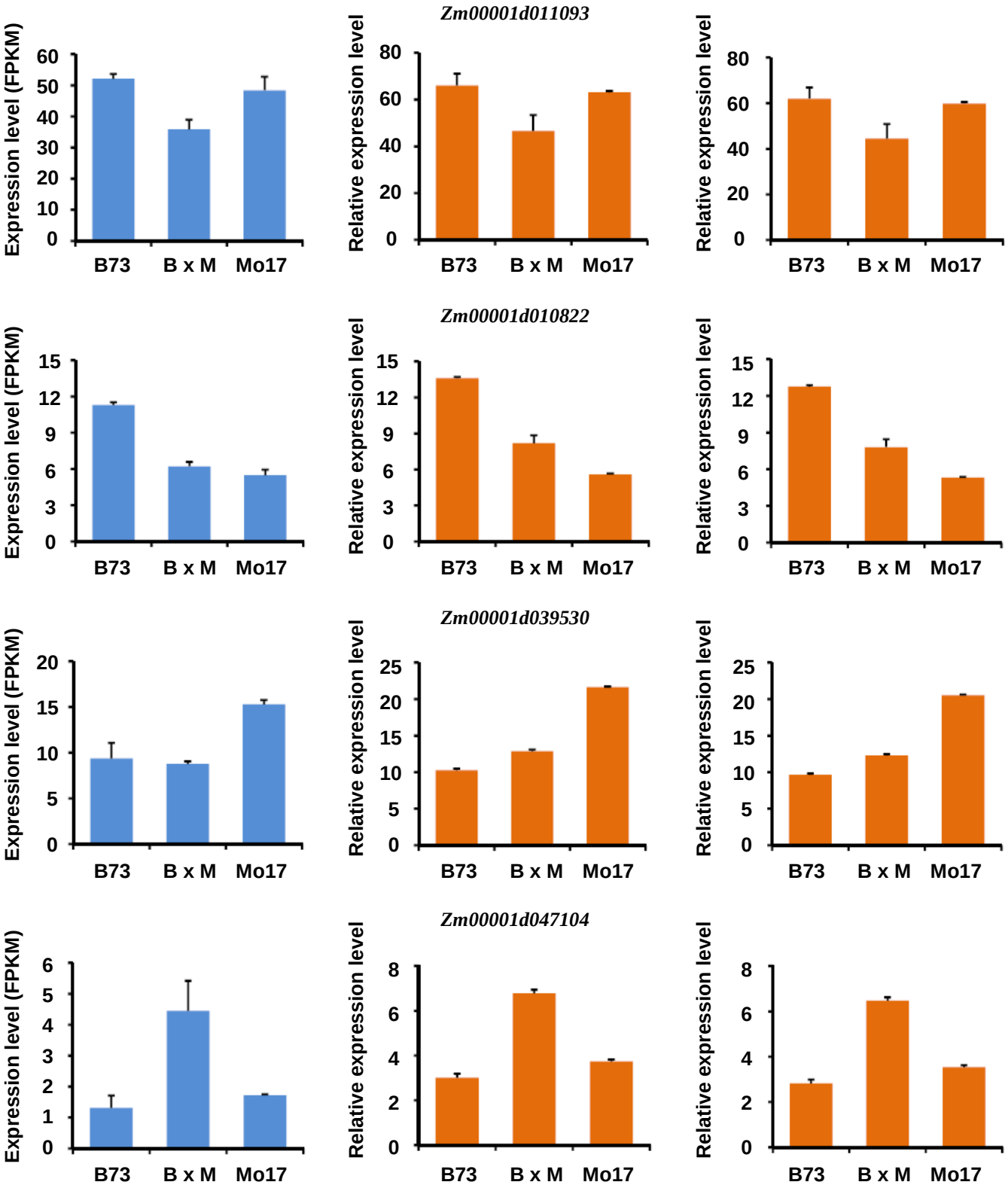


Figure S1. The repeatability between two biological replicates for RNA-seq data (A), m^{6}A-seq data (B) and polysome profiling data (C) in hybrid. The Pearson correlation coefficient (*r*) and *p*-values are shown in the top left corner.


Zm00001d011093
Expression level (FPKM)
Relative expression level
Relative expression level
0
10
20
30
40
50
60
0
20
40
60
80
0
20
40
60
80
B73
B x M
Mo17
B73
B x M
Mo17
B73
B x M
Mo17
Zm00001d010822
Expression level (FPKM)
Relative expression level
Relative expression level
0
3
6
9
12
15
0
3
6
9
12
15
0
3
6
9
12
15
B73
B x M
Mo17
B73
B x M
Mo17
B73
B x M
Mo17
Zm00001d039530
Expression level (FPKM)
Relative expression level
Relative expression level
0
5
10
15
20
0
5
10
15
20
25
0
5
10
15
20
25
B73
B x M
Mo17
B73
B x M
Mo17
B73
B x M
Mo17
Zm00001d047104
Expression level (FPKM)
Relative expression level
Relative expression level
0
1
2
3
4
5
6
0
2
4
6
8
0
2
4
6
8
B73
B x M
Mo17
B73
B x M
Mo17
B73
B x M
Mo17

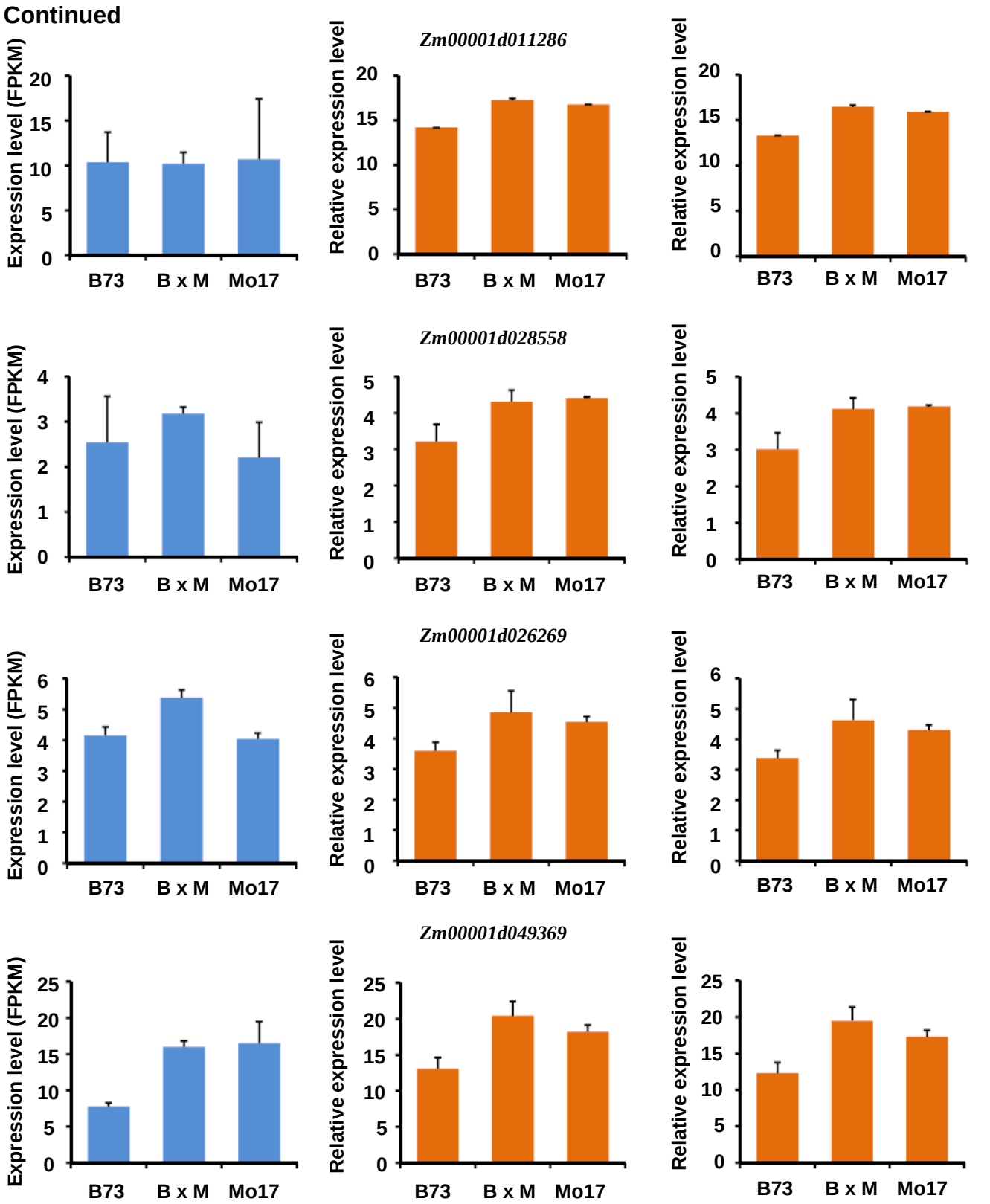
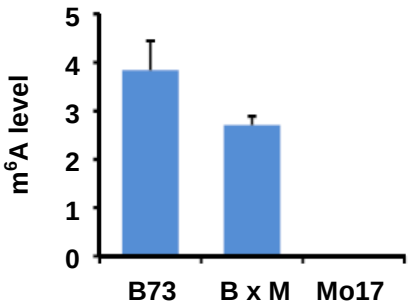
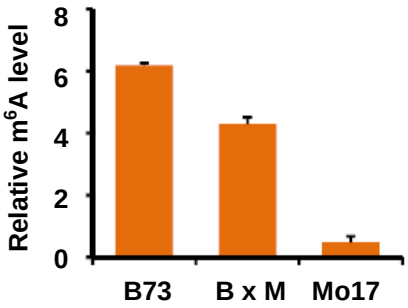
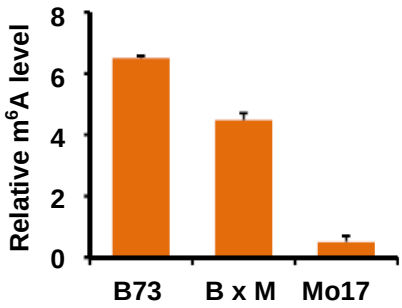


Figure S2. RT-qPCR validation of eight genes at the mRNA level in F_1 hybrid B73×Mo17 and its two parental lines B73 and Mo17. The mRNA levels were determined by RNA-seq (blue) or RT-qPCR (red), respectively. The relative mRNA level of each gene was compared to the internal control genes *Zm00001d034600* (middle) and *Zm00001d042939* (right). Data are represented as means + s.d of two independent biological replicates.

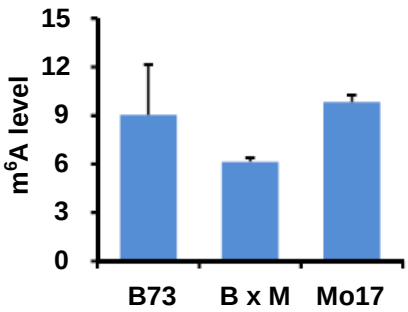
Zm00001d011093

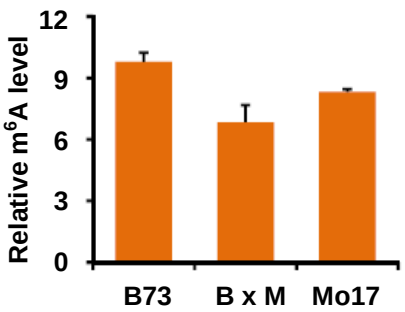


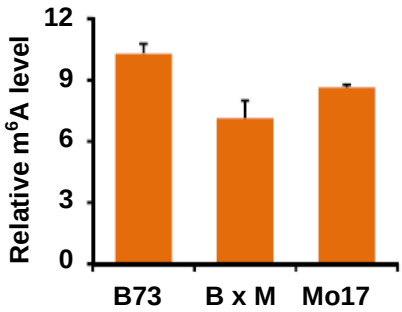




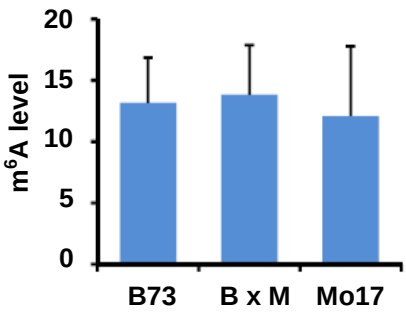
Zm00001d010822

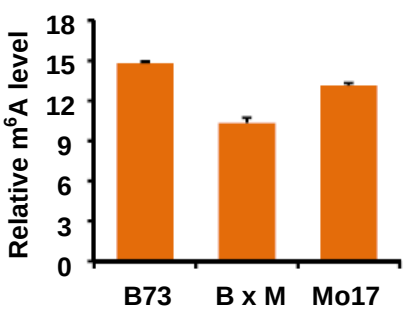


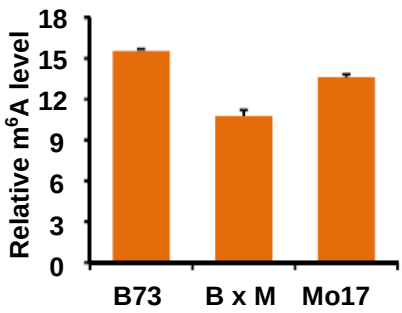




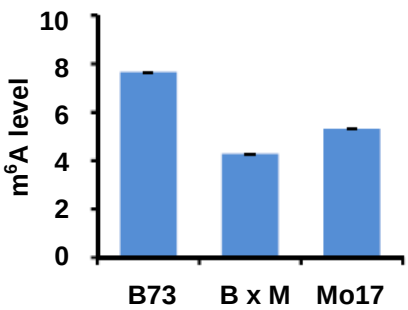
Zm00001d039530

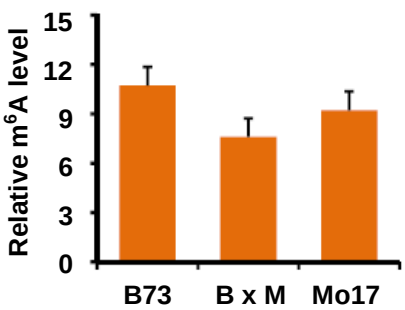


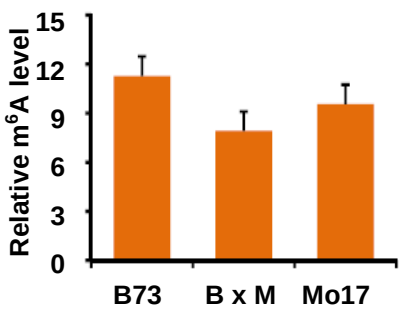




Zm00001d047104







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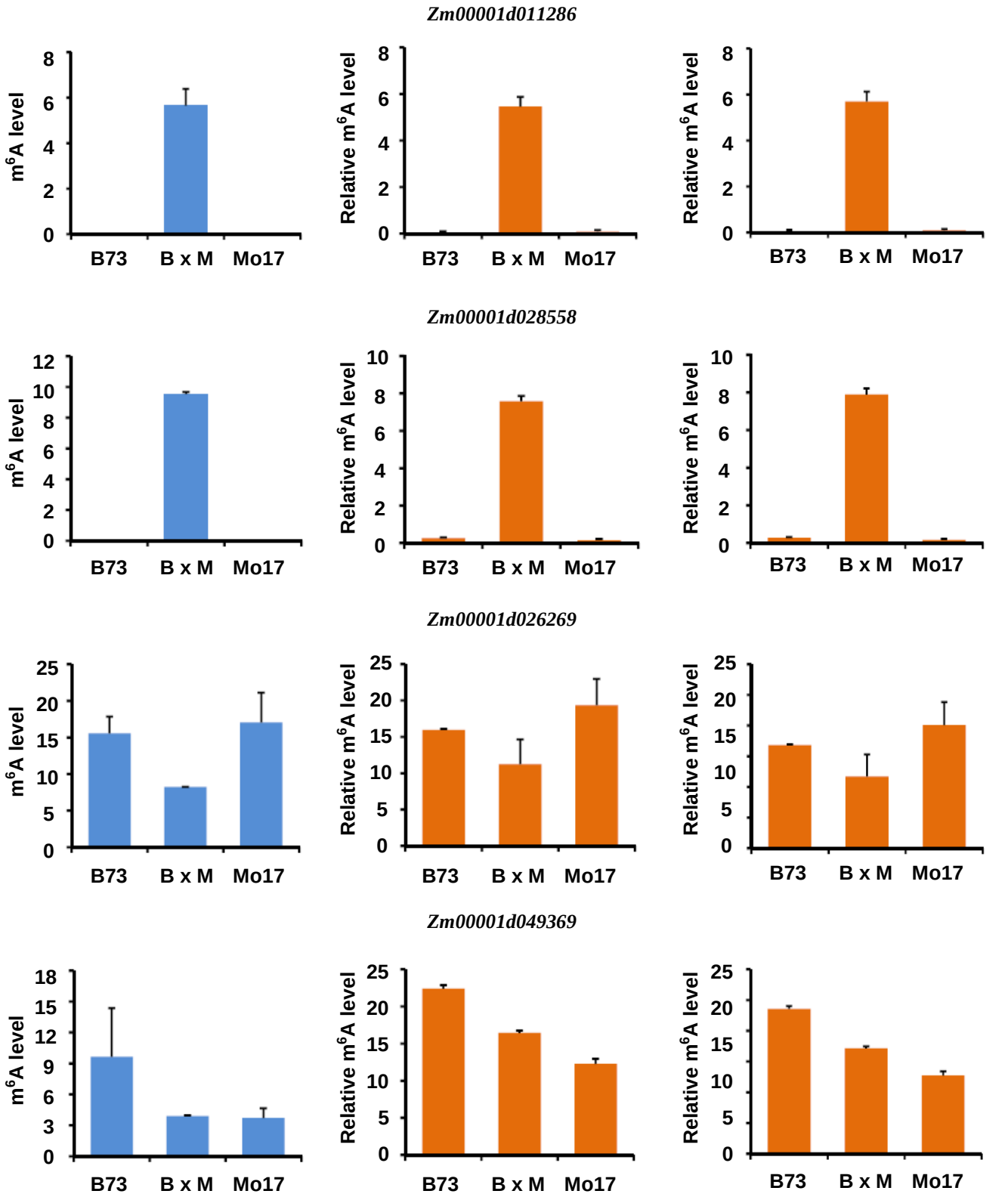
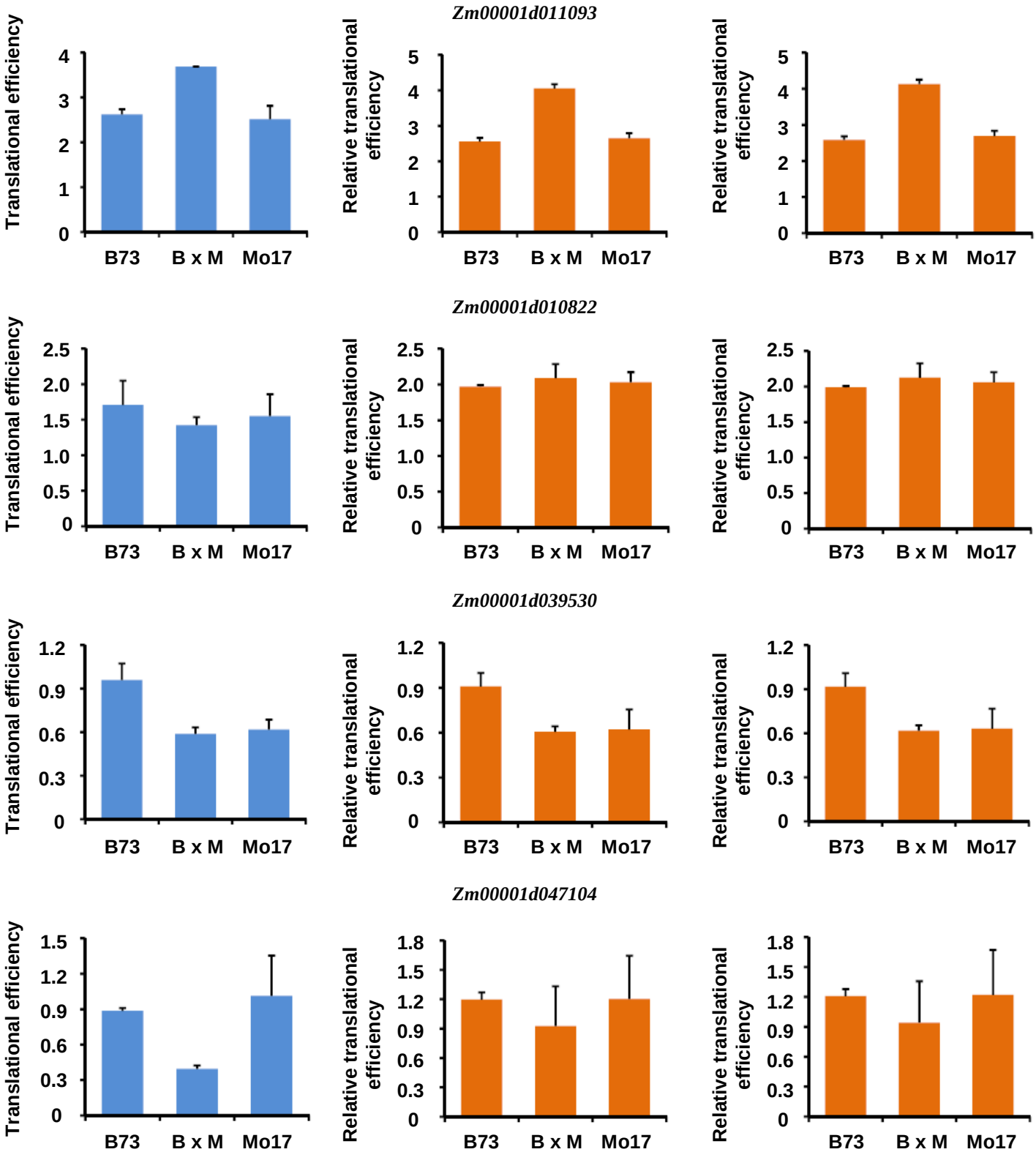


Figure S3. RT-qPCR validation of eight genes at the m^{6}A level in F_1 hybrid B73×Mo17 and its two parental lines B73 and Mo17. The m^{6}A levels determined by m^{6}A-seq (blue) or RT-qPCR (red), respectively The relative m^{6}A level of each gene was compared to the internal control genes *Zm00001d034600* (middle) and *Zm00001d042939* (right). Data are represented as means + s.d of two independent biological replicates.


Zm00001d011093
Translational efficiency
Relative translational efficiency
Relative translational efficiency
0
1
2
3
4
5
B73
B x M
Mo17
Zm00001d010822
Translational efficiency
Relative translational efficiency
Relative translational efficiency
0
0.5
1.0
1.5
2.0
2.5
B73
B x M
Mo17
Zm00001d039530
Translational efficiency
Relative translational efficiency
Relative translational efficiency
0
0.3
0.6
0.9
1.2
B73
B x M
Mo17
Zm00001d047104
Translational efficiency
Relative translational efficiency
Relative translational efficiency
0
0.3
0.6
0.9
1.2
1.5
1.8
B73
B x M
Mo17

Continued

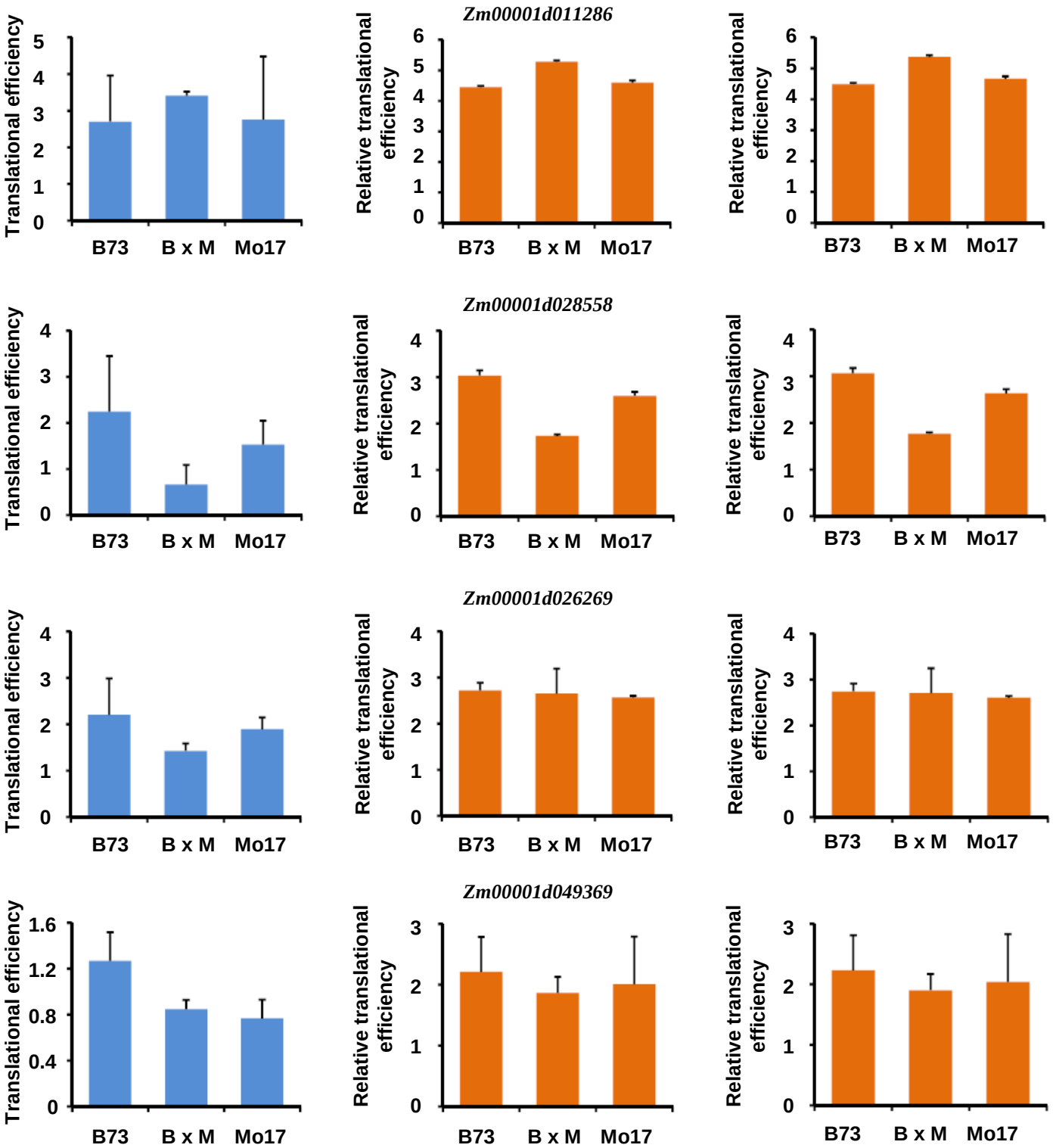


Figure S4. RT-qPCR validation of selected eight genes at the level of translational efficiency in F_1 hybrid B73×Mo17 and its two parental lines B73 and Mo17. The translational efficiency was determined by polysome profiling sequencing (blue) or RT-qPCR (red), respectively. The relative translational efficiency of each gene was compared to the internal control genes *Zm00001d034600* (middle) and *Zm00001d042939* (right). Data are represented as means + s.d of two independent biological replicates.

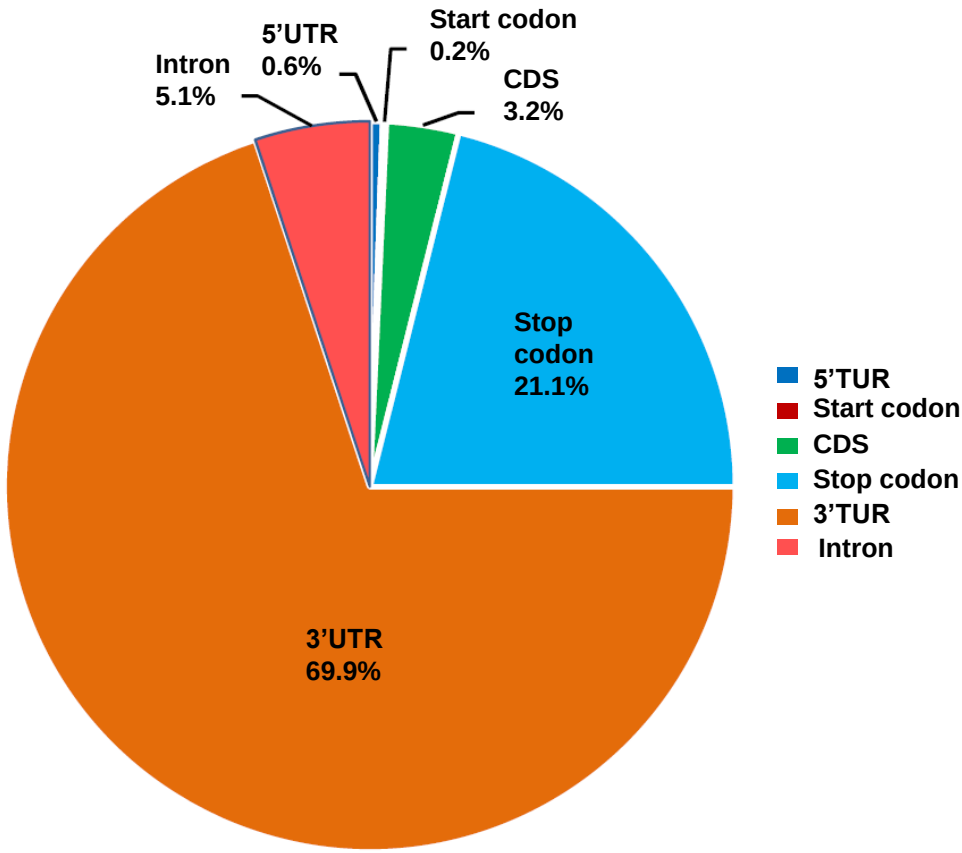


Figure S5. Pie-chart depicting the percentage of m^6A peaks within six transcript segments in hybrid.

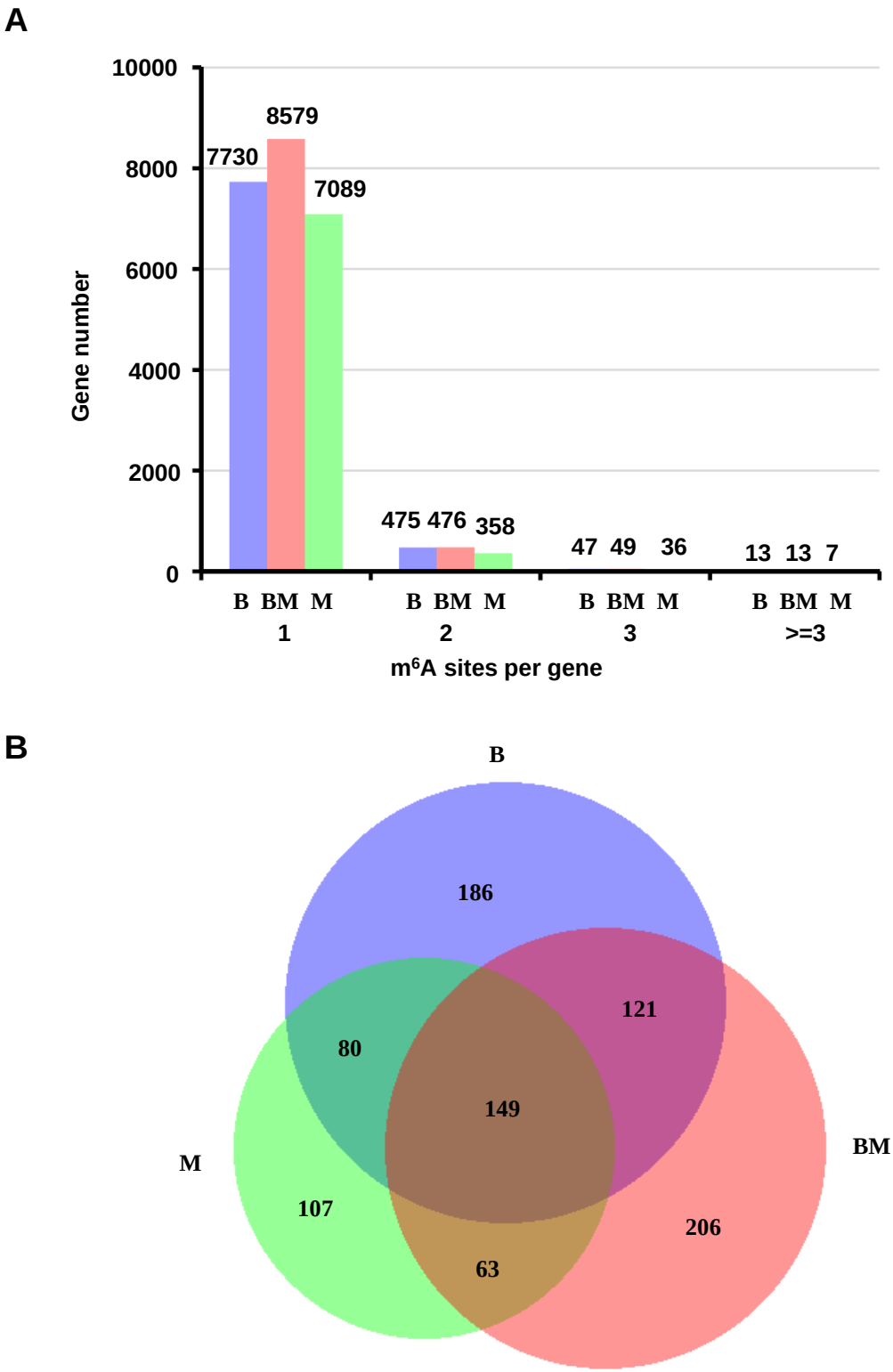


Figure S6. Comparison of gene numbers containing multiple m^{6}A peaks between hybrid and parents.
(A) No. of genes containing different number of m^{6}A peak between hybrid and parents.
(B) Venn diagram showing the overlap of genes containing multiple m^{6}A peak per gene between hybrid and parents. B, B73; M, Mo17; BM, B73 x Mo17.