Translational regulation of duplicated gene expression evolution in allopolyploid cotton

**Supplementary Materials:**

**Figure S1.** Ribosome protected fragment (RPF) length histogram.

**Table S1.** Primers for the construction of Ribo-seq library

**Table S2.** Ribo-Seq data

**Table S3.** RNA-Seq data

**Table S4.** Expressed gene number on Ribo-seq

**Table S5.** Expressed gene number on RNA-seq



**Figure S1.** Ribosome protected fragment (RPF) length histogram.

**Table S1.** Primers for the construction of Ribo-seq library

|  |  |
| --- | --- |
| **Primers** | **Sequence** |
| PCR-R-A2 | CAAGCAGAAGACGGCATACGAGAttaggcGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT |
| PCR-R-D5 | CAAGCAGAAGACGGCATACGAGAatcacgGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT |
| PCR-R-AD1 | CAAGCAGAAGACGGCATACGAGAcgatgtGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT |
| RCR-F | AATGATACGGCGACCACCGAGATCTACACGTTCAGAGTTCTACAGTCCGACG |

\*Note: Lowercase letters - Barcode

**Table S2.** Ribo-Seq data

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Sample** | **Raw reads** | **Clean reads** | **Clean reads rate** | **The average clean reads rate**  | **Uniq\_map reads** | **Uniq\_map rate** | **The average uniq\_map rate**  |
| A2-1 | 57,010,760  | 15,388,017  | 27.0% | 27.0% (a) | 5,415,099  | 35.2% | 35.0% (a) |
| A2-2 | 60,761,532  | 17,557,413  | 28.9% | 6,115,329  | 34.8% |
| A2-3 | 65,558,930  | 16,537,991  | 25.2% | 5,769,612  | 34.9% |
| D5-1 | 44,021,847  | 16,547,907  | 37.6% | 37.0% (a) | 5,649,982  | 34.1% | 34.6% (a) |
| D5-2 | 40,251,467  | 10,636,569  | 26.4% | 4,209,469  | 39.6% |
| D5-3 | 46,092,333  | 21,652,671  | 47.0% | 6,508,408  | 30.1% |
| AD1-1 | 78,068,856  | 20,485,294  | 26.2% | 28.4%(a) | 2,299,885  | 11.2% | 17.3% (b) |
| AD1-2 | 72,600,499  | 19,656,057  | 27.1% | 3,899,578  | 19.8% |
| AD1-3 | 75,539,268  | 24,085,635  | 31.9% | 5,001,671  | 20.8% |

\*Note: Different letters in parentheses indicate student t-tests significantly different at the 0.05 level

**Table S3.** RNA-Seq data

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Sample** | **Raw Reads** | **Clean Reads** | **Raw Base(G)** | **Clean Base(G)** | **Effective(%)** | **Error(%)** | **Q20(%)** | **Q30(%)** | **GC(%)** | **Uniq map reads** | **Uniq map rate(%)** |
| A2-1 | 48,429,142 | 47,898,218 | 7.26 | 7.18 | 98.9 | 0.03 | 97.61 | 93.5 | 43.34 | 41,721,704 | 87.1 |
| A2-2 | 42,824,098 | 42,120,698 | 6.42 | 6.32 | 98.36 | 0.03 | 97.65 | 93.5 | 43.33 | 36,785,728 | 87.33 |
| A2-3 | 39,393,294 | 38,834,598 | 5.91 | 5.83 | 98.58 | 0.03 | 97.66 | 93.5 | 42.69 | 34,157,438 | 87.96 |
| D5-1 | 45,695,760 | 45,083,272 | 6.85 | 6.76 | 98.66 | 0.03 | 97.46 | 93.09 | 43.74 | 38,901,404 | 86.29 |
| D5-2 | 51,937,092 | 51,112,712 | 7.79 | 7.67 | 98.41 | 0.02 | 98.06 | 94.49 | 43.35 | 43,439,174 | 84.99 |
| D5-3 | 45,346,080 | 44,760,658 | 6.8 | 6.71 | 98.71 | 0.03 | 97.62 | 93.43 | 42.48 | 38,026,452 | 84.96 |
| AD1-1 | 57,242,368 | 56,484,000 | 8.59 | 8.47 | 98.68 | 0.03 | 97.88 | 94.12 | 43.98 | 50,461,998 | 89.34 |
| AD1-2 | 40,089,868 | 39,415,458 | 6.01 | 5.91 | 98.32 | 0.03 | 97.4 | 92.98 | 42.93 | 35,039,834 | 88.9 |
| AD1-3 | 57,676,392 | 56,908,806 | 8.65 | 8.54 | 98.67 | 0.02 | 98.06 | 94.55 | 43.94 | 51,192,482 | 89.96 |

**Table S4.** Expressed gene number on Ribo-seq

|  |  |  |  |
| --- | --- | --- | --- |
| **Ribo** | **expression（TPM>1）** | **non-expression** | **counts>0** |
| AD1 | 40,591 | 12,392 | 52,983 |
| AD2 | 29,491 | 12,791 | 42,282 |
| A2D5 | 40,791 | 14,329 | 55,120 |
| A2 | 23,465 | 6,292 | 29,757 |
| D5 | 21,922 | 7,082 | 29,004 |

**Table S5.** Expressed gene number on RNA-seq

|  |  |  |  |
| --- | --- | --- | --- |
| **RNA** | **expression（TPM>1）** | **non-expression** | **counts>0** |
| AD1 | 46,905 | 15,438 | 62,343 |
| AD2 | 43,291 | 17,920 | 61,211 |
| A2D5 | 47,879 | 17,122 | 65,001 |
| A2 | 25,006 | 5,860 | 30,866 |
| D5 | 26,356 | 6,654 | 33,010 |