**Table S5** Top five most frequent and significant NUE motifs detected in PACs located in different genomic regions.

|  |  |  |  |
| --- | --- | --- | --- |
| **Region** | **Top five frequent NUE motifs** |  | **Top five significant NUE motifs** |
|  | **Motif** | **Percentage (%)** | ***Z-scorea*** |  | **Motif** | **Percentage (%)** | ***Z-score*** |
| 3'-UTR | AAUAAA | 5.29 | 40.57 |  | AAUAAA | 5.29 | 40.57 |
|  | AUAUAU | 4.88 | 28.65 |  | UAUAUA | 4.58 | 34.7 |
|  | UAUAUA | 4.58 | 34.7 |  | AUAUAU | 4.88 | 28.65 |
|  | AAAUAA | 3.84 | 18.87 |  | UAAUAA | 3.35 | 27.96 |
|  | AUAAAA | 3.54 | 10.61 |  | UUAUUA | 2.06 | 20.96 |
| intron | AAUAAA | 5.33 | 18.76 |  | AAUAAA | 5.33 | 18.76 |
|  | AUAUAU | 4.95 | 9.49 |  | UAUAUA | 4.56 | 11.71 |
|  | UAUAUA | 4.56 | 11.71 |  | UAAUAA | 3.36 | 10.77 |
|  | AUAAAA | 3.79 | 6.63 |  | AUAUAU | 4.95 | 9.49 |
|  | AAAUAA | 3.75 | 7.73 |  | AAGAAA | 2.67 | 8.83 |
| CDS | AAGAAG | 4.05 | 5.59 |  | GAGGAG | 2.2 | 6.58 |
|  | AAAGAA | 4.01 | 4.14 |  | AAUAAA | 2.71 | 6 |
|  | GAAGAA | 3.89 | 4.19 |  | AAGAAG | 4.05 | 5.59 |
|  | UGAUGA | 3.62 | 5.45 |  | UGAUGA | 3.62 | 5.45 |
|  | UGAAGA | 3.54 | 3.83 |  | AGGAGG | 1.85 | 5.38 |
| Intergenic | AAUAAA | 5.74 | 25.28 |  | AAUAAA | 5.74 | 25.28 |
|  | AUAUAU | 5.48 | 15.16 |  | GUACAU | 2.55 | 27.64 |
|  | UAUAUA | 5.06 | 17.63 |  | ACAUGG | 2.4 | 25.83 |
|  | AAAUAA | 4.38 | 13.53 |  | UACAUG | 2.87 | 24.24 |
|  | AUAAAA | 4.24 | 8.84 |  | CAUGGG | 1.74 | 24.27 |
| 5'-UTR | UUUAGU | 2.86 | 5.17 |  | CGCGCG | 0.95 | 7.02 |
|  | CGCGCG | 0.95 | 7.02 |  | UUUAGU | 2.86 | 5.17 |

aAll Z-scores listed in the table were statistically significant *p-value (binomial)* < 0.05.