**Supporting Information**

**Tables**

**Table S1. Non-coding AT- and GC-rich sequences used in this study.** AT-rich sequences (AT01-08) were amplified from the genome of *Arabidopsis thaliana* (chromosome 4)*,* whereas GC-rich sequences (GC01-GC08) were amplified from *Chlamydomonas reinhardtii* (+chromosome 1, \*chromosome 2).

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Sequence name | Length (bp) | GC-content (%) | Sequence position within genome | Primer sequences (5’-3’) |
| AT01 | 1,054 | 17.7 | 4,145,887 | for: AATCTATGTTTGTCAAGTGTTAGrev: TGTGAGTTGTATATGTTTTGTTG |
| AT02 | 975 | 18.1 | 5,227,639 | for: TCTAGATTTTAACTCATTGAACTGrev: TGAAGTTTGGTCCATATTAAAAC |
| AT03 | 962 | 19.3 | 1,095,268 | for: TATACAAATTAAAGAAAGCCAGCrev: AATTCTCAAAACTGTACTAAGAG |
| AT04 | 1,010 | 21.9 | 1,956,554 | for: CAAAACCGAATGAATAACATAACrev: ACAATCTCTTGATTTTATCATGG |
| AT05 | 965 | 23.1 | 2,527,446 | for: ATTCTTTCTCTTGCTTATTCAACrev: ATTGATTACAATTCAACCTGTAG |
| AT06 | 960 | 24.5 | 313,339 | for: AATATACCAAGAGGTTTTGAAAGrev: ATTTATACAAATGTGAGTGAGTG |
| AT07 | 978 | 19.9 | 6,808,034 | for: TACTTTCCGTTTAATCTGATTTCrev: TTTCTTGTAATCTAGTGTTTAGC |
| AT08 | 1,021 | 20.7 | 8,729,507 | for: TAGATCCAATAAGCCCTATAATCrev: TGCTTGAGTTAAATTTCATTTTG |
| GC01 | 1,032 | 85.3  | 5,762,266+ | for: AGGAGACGGCGGAGCAAGCAATGrev: CCCAGCCCCGCAACTTCCAG |
| GC02 | 926 | 78.4 | 131,592+ | for: GGAGGTGGAGGTGGAGGCAGAGrev: CGGCGTCAGCAGGAGCGATTTC |
| GC03 | 935 | 78.0 | 4,848,100+ | for: CTGCGCAGCAGGCCCAAACAGrev: GACGTCTCAGCCCCCGTCTGTG |
| GC04 | 1,040 | 76.3 | 4,830,042+ | for: TCTGAACTCCGTAGGGCGTGACCrev: GGCGGAGATGGCTGCGATTATGG |
| GC05 | 1,053 | 79.9 | 2,471,777+ | for: CTGCTGGCTTGCCTCAAGGACACrev: CACGTGCACGAAGCCGTACATGG |
| GC06 | 954 | 77.6 | 851,088+ | for: GCACCGTCGGAGTCGGGCrev: CTTGCGGATCAGCGCCTCCAC |
| GC07 | 957 | 76.2 | 1,033,328+ | for: ACCACAGCGATGGCGGCTTGrev: GTCCGCTCAGCGCATCTGATACC |
| GC08 | 1,029 | 75.9 | 416,710\* | for: CTCACCTGTCAGCTCCACGATGCrev: GAGCTGAAGGCGGCTGTGAAGG |

Abbreviations: for = forward primer, rev = reverse primer.