

Table S6 Tandem repeats within the MoTeRs

Repeat	Consensus Sequence of Repeat Unit	Length	Location	Copies
MoTeR1 and MoTeR2				
A	CCCGAA	6	1-12	2
B	CCCAA	6	13-63	8
C	<u>GGGGCTATTTATGCGCTTTAATTTGTGC</u> ^A	28	477-553	2.8
D	<u>TATTT(ATGCGCTTTAATT)TGAGCGGGGC</u> TATTA(ATGCGCTTTAATT)TACAAATT ^B	55	510-636	2.3
E	ATTGCTATTATTATCGTTACTATTATTATT	30	668-724	1.9
F	TTTCGTAGGCTTTGC	15	794-852	3.9
MoTeR1-specific				
G	<u>TTTACCTGTTTTATT</u> AGCGGTTTACCTGCTTTTATTACCTGGTTCCCC	48	909-1174	2.6
H	GTTTTTACTAGCAGTTAAATTTACCTTTTTAAGGTTA <u>TTTACCTGCTTTTATT</u> CAC AGGGCACCCCT	67	1203-1389	3
I	ATAACCCAGGGTTA	15	1904-1953	3.3
J	TTTTTG	6	4690-4832	23.8
K	TTTTTTC	7	4916-4941	3.7
MoTeR2-specific				
L	CGCCAAAAGTCCAGTATATATATCGATTAAATTCGAATTTGAATTGGTTAAC CCCCTGTATATTAATTTGGCTGAAAAATCCTGGAATATACGTGCCTTTTTAAAA CAACTTTTTGCCGTCCCTATCCAGATAACATGGTTTTTTAGCAATGTTTCTATCC TCAGGGTTACCAATTTTATATTTGGTATTTATTCGATTTATTATTGGATTTTA ACCCCGATTTTCGACCGACTATTATCGATTTATTA	253	1072-1539	1.9
M	TATTTATTCGATT	13	1251-1277	2.1
N	ATTGGATTAATCCGCTAAATAA	22	1522-1578	2.6
O	TTTTTCTTTTC	13	1618-1642	1.9

^A Sequence motifs that are present in two different tandem repeats are underlined in the same style.

^B Sequences in parentheses are duplicated within a single repeat unit.