**Additional file 1.** The nucleotide sequences of *Ppmar1* and *Ppmar2* transposases and their amino acid sequences.

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| --- | --- |
| **Name of the transposase** | **Nucleotide sequence of transposases (5’--3’)** |
| *Ppmar1* | TACTCCCTCCATACCCGAAATTCCTGACGTTTAGGACATGATTGTGGTAACCAAGGAGTGATTAATTAGGGGTTAGTTTTCCATCTTTGCCCCTAATAAATATGGTTACGGGTGCTCTTTGTACGAGAAAGTAAACCAGCTCGACTGGCTAGCGCGCGGAGGCCTCAGTCCTGTGGTGCGCGTTCGATACCTCGCGGACGCAGGTTTTTTTCTTGTTGCTGTTTATTCATTTTTGCATGGCACTGTTTAGGCAACGCACGTCGCGCGCGCTTAGCCGCTGCGGGCGTTAGTTTTCGAGTGGATTTGGGCCTGGCGCACGGAGGAGGTTGCATGGCTGCCCGAAAATTTCGTTGCATGCACTGGATTTTCAAAATTTTGTCCTCGCGCTGTGGAGGCTCGTTTGAGGCCGCGTTTTTTTTCATCTGGCGCGCTGGAAGGCCGACGTTTGGAGTGCTCGTTGCTTGTTCTATTTAAACGCCTGGAACCTTCCTTGTTGTCTTCCTATGCCGGACTCCTGTACTATGGCTGACCCAATAGATTCTGGCTTCGATCTGAACGTTCGGTTAGAAGAAGATGATGACGGCAATCTTCCCTTTGATCTCAACGAGCCAATATTGGAAGATCACAACAATGGTAAGCAAAAACGTCAAATTAGTTTCTCAGTTTCTCGTTTCCTTTTTTCTTTACTGAGCTTGTCGTTTCCTTTTTCGATAGGAATTGATTTGAACTTGCCATTAGATGAGTTTGGTGCTGTCGACTTCGACTATGTACAAAACCTCGCTGGTAAGCATGGCTAGTATTATGAATTCGCTTGTTTTTTTATTTCCTTTTGCTGGAACATGCCGTGAATAATAGTATTATGAACTCGCTTGTTTTTTATTTCCTTTTACTAGAACATGTGCTTGTTTTATTCCTATAGCTAGATCATGACGTCAATACTTTTTACGATGAATATGCTCGTTACAGTATAGCTAGAACATGCCGTGACTACATAGTAGTATGAATATGCTTGTTTTATTTCTATAACTATAACATGCCGTGAGTATATTTAGATCATGCCGTGAGTACTAAGTACTATTAAAATGCTTGTTTTTTATTTCCTTTTGCTAGAACAAGATGTTGAGGCTCCCGTTCAAGTACACCCTCCGAAGCATGACTATCCTGAACATGTTAGAAAACTAGTGTACCAAGCATTGTTGATGAGAAGCAAGAATGGGAAACTAGGCAATCATGATACAACAATTGTTTCCAGTCAATTTGGAGTAAAGATTCGATCAGTTCAGCGCATATGGAAGCAAGGTAAAAACCAACTTGCTCAAAACATTCCGGTCGTGGTTGCTAATCTAAAGAAAGGTAGAAGTGGCCGTAAAGCAACCCCTCTTGATTTGGAACAATTGCGCAACATTCCTCTCAAGCAAAGAATGACCATAGAAGATGTGTCTAGTAGACTTGGTATTAGCAAATCTAGGATACAAAGGTATTTGAAAAAGGGTTTGCTTAGGCGCCACTCTAGTAGCATAAAACCTTACCTCACCGATGCTAACAAGAAGACTAGGTTGAAGTGGTGCATTGACATGATTGAGCAAGGTTTGGTTGATGATCCAAAGTTCAGGGATTTGTTTGACTTTGTGTTTATTGATGAGAAGTGGTTCTACCTCTCTCAAAAATCCGAGAGATACTACTTGCTACCCGACGAAGATGAACCACATCGCACTTGCAAGAACAAGAATTACATCCCTAGGATCATGTTTTTGTGTGTTTGTGCTCGGCCAAGATTTAGAAATGGAGAATGTGTGTTTGATGGCAAAATAGGTTGTTTTCCACTAGTCACTTTTGAACAAGCTATTAGAGGAAGCCAAAACCGTCTTCGTGGAGAACAAGTAATCAAGCCAATTCAATCAATCAATAGGGAAGTGATAAGAGATTTCATGATAAATAGAGTGTTGCCTGCAATTAGAGCAAAGTGGCCAAGAGAAGATGTACACAAGCCAATTTTCATACAACAAGATAATGCTCCATCTCATTTAAAGGTGGATGATCCTCAGTTTTGTGAGGTTGCTAAGCAAGATGGGTTTGACATTAGGCTCATATGTCAACCACCCAATTCTCCAGATTTTAACATTCTAGATTTGGGTTTTTTTCGAGCTATTCAAGCAATTCAATACAAGAAAGATGCTAAGACATTGAAAGATCTAATTCCAGCAGTCCAACAGGTAAATGATCATCCATTACAGTGTTTAAATTGATCTTGAACAAATAATATAATCACTGATCTTGAACATGTTTTGTAGGCATTTTTGGAGTACTCTCCATGGAAAGCAAATAGGATATTTGTGACACTACAAACTGTTTTGAAGGAAGCAATGAAGATAAAAGGTTGCAACAAAATCAAAATTCCTCACATCCAGAAACAAAGACTTGAGAGAGAAGATAGGCTGCCATTGCAAATCCCTTGTGAAGCTTCCTTGCTAGCCGAAGCACTTGCAAGCCTTCCTGCGGCTAATTAGAAGATGCAAGCATGTTACTCTTTTGCAGCAGCAAGCATGTAAGAAGACGCGAGCATGTTAGTAGCAAACTATGAACAAACTAGTTTATGCATGTAGTAGTATGTTAGCTTGTGCACCTTAGTCATCTCGTCCCAACCGCTTGATAACATGCTCAGGAAGAAGTATTGTGTCACCATCCATTTCAAGTTTCTCCACATCAGGAATGTAGACCTCACAATCAAACTTTTCCATGTCATCGAGCCACTTCGCTGTCATGTCGTAGTCTTCATGTAAAAGGCCACAACGGGCACACATGCGAGCTTCGCGGCGAGCTTGGTAGCAGGCTTCTCCGAAGACGCCGCCGGCGTGGAACGTAACACAGCGAGGACACAGAGACTCGACGGAGTCGGGATCGACGGTGTCGGGCACCATCTCGAGGGAGTCTGCAACCATGTCGACGGAGTCCGGCAGCTCCTCGACGGAGTCCGGCACCATGTCGACGGTGTCCGGCAGCTCCTCGACGGAGTCTGGCACCTCCTGCGGCGCCATGTCCACGGTGTCCAGCGACGCTATGGAGCCCGACGAGATGTCCTGCACGGCGACGTCCAGCGCCGCAACGGACTCCGTCGTTTCCATCTGATCCGACGAGGCATCGACGTCCTGCGACGAGCGTGGCGGCGAGAGCACGGCGAGCGGGCAGGCGAGCGGGCAGGCGAGCGAGCCATTCGCGCGAGCGATGAATGCGAGCTGCTGTACCAGGCGCACACACGCGCAATCAATGCGGGCGAGTAACGATGCGAGCATGCGCGGCGGAAGCGCAACAGACGGGCAGCAGCGCATGGCCAGGGGCAAACGCGTGAAAAGAAGACCACGCGAGGCCACAACGTCAGCTTTTGCGCAAACGGGCACTTCGCCTAGAACGTCAGGAATTTCGGGTATGGAGGGAGTA |
| *Ppmar2* | TACTCCCTCCGTCCCAGTATAACGGGCGTATAACTTTTTTTACAGAGACCAAGGGACGGCGCGCGAGCGATGCATTCTTCTTCATCTACCCCTAATTAAACAGACGAGCGATGCATGCATGCAGTTTAATCACAAGCGATGCGTGCATGCAGATTTAAGAACGGCTTCTTTGCGCGCTCGCAGACCCACGTCTCACGCGCTCACACTCGTCGCCCACACTTGCTCGCACGCATGCATGACCAATCCTGTAGCAGTTAGAACGAGGATTATAGCGAAAATCACTTTGAACACAACATTTAGAAGATGGCGCCCAGAAATTGAGCTGGTGCGTATGGATTGAGAAGATTGCGCCCAGAAATCCAATTTCGTTTTCCTCCTATAAATAGGCATGAACACAACAGGTCTGTTGCCACTCTCTCCTCCTCTTCTCTCGTCCAGTTGCTTGCTCGAAATCAATGGTGAATTTGGACCTAAATCAACCTATCCATTGGGAAGAGATTGAGGACTATGATGGCCCTGTCATCGACCTTAATTTTGATCTTGTGTTTCATGATAGCAATGAAGGTATTACACAAATCCTTTATTCTGTTGTTTTGTTCCCCTAATGCTTACCGTTAGGATAGATCATGTATACTTGTTGTCTTGCTTGAAGAGGATGGCGGCCCGACCCATGGCGAAGAGGATGGTGGTGCACCTTCCCATGGAGAAGAGGACGGTGCCCCATCCCATGGCGAAGAGGATGGCACCCCTGCACCTAACGCCTATGAGACGAGTAAGACATGTCCTAGATTTTTGTATACTTGCTGCAGTAGGAGTGCGTATAACGAAGTAAATTGGGTTTGTTCGTATACAGTAGCTAGCTTGCTTGTTTGTTTGTATACATGTCCTAGAGTACATTAGCTTGCTTGCTGCACCAAAAAGTTTGAAACGGATTGGTTGTGCCTAGCAACAGAAAGAATTCTTGCACCTACCTTTGATTAATTTCTTTTTTTCCACACATTTGTAGATCAAGTTGGCAATGTTAGAAGGAGGAATCAATATACTGTGATCAACGCCGAGCCATATATAGCATGCTTCTAGGGCGAACTTCTGTCGGCATATTGAAGAAAGGAGCGACGAAGgCCGTTTCTGTTGAAACAGGCGTGCCTTTGAGAGTTGTGCAACGGATATGGCTAAACGGACAGTAGGGTGGTGGGGTAAACGCAGTCTCTAGCAAGAAGGCAAAGAATTGTGGCTGGAAACGAGTAGCCTTCGATCCGGAAGCCATCAAAGATGTGCCTTTGAGTAGCCGAACGACAATCCGGGATCTAGCAGGCGCTCTGAATATTTCAAAGAGCACATTGTTTAGGCAGATGAAAGAAGGGAAGTTTAGACGGCACACAAATGACATTAAGTTTACATTGACTGAAGATAACAAGAAAGCATGTGTTAAGTTTTGCCTCTCAATGCTAGAAAAATTAAGCATGCCGCAAGAACCAACTTTTGAGGGTATGTACAACATCGTGTACATAGACGAAAAGTGGTTCTATCGGATGAGGAAATTTCAAAACTACTACTTGGCGCCAGATGAGGACAAGCCAGAAAGAACCACAAAGAGTAAAAATTTCATAGAGAAGGTGATGTTGCTCGCAGAAATTGCGAGACCTAAATTTGATTGGGATGGAAATGTTACATTTTCTGGAAGGATAGGCATAATTCCTTTCACTTTCGTAGAGCTAGCAAAGCGAAGTAGTGCGAATAGGCCTGCTGGTACATTGGTGACCAAGGCAATGACATCGGTAACCAAGGAAACAAGCCGTGAGTACCTTGTAAATAAGGTATTGCCCGCGATCAAGCAAAAATGGCTAGCGGAGGAAGTTGGTACCCCCATATTCATCCAGCAGGATAATGCTAGGACGCATATTGCAATCAATGATGACGAGTTTTGTCGTGCGGCATCCGCAGATGGTTTTGACATAAGTTTGATGTGCCAGCCACCCAACTCTCCTGATCTCAATGTATTAGATCTTGGTTTTTTTGCGGCCATTCAATCCATGTTTCAAAAGTCGTCTCCAAGCAACATTGAAGACATTGTTGCCAAGGTAATCCAAGCTTTTGACGAGTATCCAGTTGATAGGAGTAACCGTATTTTCCTCACTCACCAATCATGCATGAGAGAAATTTTGCGTCAAAAAGGAGGGCAACACTATGCAATCCCACACTTGAAGAAGCAATCACTTGAGAGGAATGGTGTTCTTTCCATTAGATTACAATGTGACCTAGTAGTTGTGAATGAAGCAATTGTGTACATCAATTAGAATCTGTTATTGCAAATGTAATCAAACCTGTACTGTTTTTCCTTGCTTAAGCTAGATTTGTCAAACAAGTAAATTTGTTGTGTTCAAACCATAGTTAGATTTGTCAAACAAGTACGCCACATGTGTAGAAAATGAGTAGTACATCAAACGAGTAGCCAGAATTTTTTGTTACCATTCACACAGTTTATTCTTCATCGTTCTCGATAAAGGCGTCCTCCACAGTGCACTCGACATCTGCAAGGGACTCCGGGACATACGAGTTGCCGGCAAGAGAGTCTACATCCATGTAGCTTTGCTTATCGTCGCTGTCGTCAATCCCGGGTAGGAGTATATTGCAGTCGAACTCGTCGAGGCCGTAGATCCAAGCCGTGACCATGTAATCACAGTGGACGAGACCACAGCGAGAGCACGAACCCTTCAATACGCGCCTCTCATCAAGGAGCTTGTCACTCCTGGACGCGTCAGGGTCCTTCATGTTATCGTTTTCACGTGCGTCAATGTCGTCGGTGTCGTCGAGCCCGGCAAGGAGGGTGTCATCGGTGTCATGCACGCACTTCTGCTTGTGGTTGCCATCATCGAGATCGATGGGCACGGGCTTCTGCTTGTGGTCGCCGTCGTCGAGAATGCCTATGAGTGCGGGCTTCTGCTTGCGGTCGCCATCGTCGAGATCAGTGAGCGTGGGCTTCTGCTTGTGGTCGTCGTTGTCGAGATCGACGAGCGTGGGCTTCTGGTTGTCGTCTGCAAGGGACTTCAGGACATACGAGTTGCCAGTAAGAGAGTCTACATCCATGTAGCTTTGCTTATCGTCGCTGTCGTCAATCCCGGGTAGGAGTATATTGCAGTCAAACTTGTCGAGGCCGTAGATCCAAGCCATGACCATGTAATCGCAGTGGACGAGACCACAGCGAGAGCACGAACCCTTCAATACGCACCTCTCATCAAGGAGCTTGTCGCTGCTGGACGCGTCGGGGTCCTTCTTGTCATCGTTTTCACGTGCGTTAGTGTCGTCAGTGTCGTCGAGCCCGACAAGGAGGGTGTCATCGGCGTCGTGCACGCTCTTCTGCTTGTGGTTGCCGTCGTCGAGATCGATGGGCACGGGCTTCTGCTTGTGGTCGCCGTCGTCGAGATCGGCGAGCGCCGGCTTCTGCTTGTGGTCGCCGTCGTCGAGAATGCCTATGAGTGTGGGCTTCTGCTTGCGGTCGCCATCATCGAGATCAGTGAGCGCAGGCTTCTGCTTGTGGTCACCGTCATCGAGATGGCAAGCGCGGGCTTCTCCTTGTGGTCGCCCTCCTCACGACCACCCGGGGTCTCAGCGGCCATCACCGTGGAACTCACTCAATCGGGGTCTTCAATTGGGCCGATTAAAATGGATCAGTAACAGTGGCTCTAAGCGTCGCATGCATCACGCGTATTCCTCACACTTTTCTAAGTGGTCGCATGCATCACGCGTCAAGCAGTCATTACTGGCACTTCTCTGAGCAGTTGCATGCATCACGCGTTAAGCAGTACCACTTCTCTAAGCGTCACGCATGCATGCATGCATGCAGATTGCTGAGGGCAAAGATGGGAGAAAGCAGCGCAAAATGAAGGGACGCCTTGTATTGTGGGACAGCAGAAAAAAAGTTATATGCCCGTTATACTGGGACGGAGGGAGTA |
|  | **Amino acid sequences of transposase** |
| *Ppmar1* | MADPIDSGFDLNVRLEEDDDGNLPFDLNEPILEDHNNGIDLNLPLDEFGAVDFDYVQNLAEQDVEAPVQVHPPKHDYPEHVRKLVYQALLMRSKNGKLGNHDTTIVSSQFGVKIRSVQRIWKQGKNQLAQNIPVVVANLKKGRSGRKATPLDLEQLRNIPLKQRMTIEDVSSRLGISKSRIQRYLKKGLLRRHSSSIKPYLTDANKKTRLKWCIDMIEQGLVDDPKFRDLFDFVFIDEKWFYLSQKSERYYLLPDEDEPHRTCKNKNYIPRIMFLCVCARPRFRNGECVFDGKIGCFPLVTFEQAIRGSQNRLRGEQVIKPIQSINREVIRDFMINRVLPAIRAKWPREDVHKPIFIQQDNAPSHLKVDDPQFCEVAKQDGFDIRLICQPPNSPDFNILDLGFFRAIQAIQYKKDAKTLKDLIPAVQQAFLEYSPWKANRIFVTLQTVLKEAMKIKGCNKIKIPHIQKQRLEREDRLPLQIPCEASLLAEALASLPAAN |
| *Ppmar2* | MANLDLNQPIHWEEIEDYDGPVIDLNFDLVFHDSDEGDGGPTHGEEDGGAPSHGEEDGGPTHGEEDGGAPSHGEEDGAPSHGEEDGTPAPNAYETISTNKAKNCGWKRVAFDPEAIKDVPLSSRTTIRDLAGALNISKSTLFRQMKEGKFRRHTNDIKFTLTEDNKKACVKFCLSMLEKLSMPQEPTFEGMYNIVYIDEKWFYRMRKFQNYYLAPDEDKPERTTKSKNFIEKVMLLAEIARPKFDWDGNVTFSGKIGIIPFTFVELAKRSSANRPAGTLVTKAMTSVTKETSREYLVNKVLPAIKQKWLAEEVGTPIFIQQDNARTHIAINDDEFCRAASADGFDISLMCQPPNSPDLNVLDLGFFAAIQSMFQKSSPSNIEDIVAKVIQAFDEYPVDRSNRIFLTHQSCMREILRQKGGQHYAIPHLKKQSLERNGVLSIRLQCDLVVVNEAIVYIN |