

SUPPLEMENTARY MATERIALS

to the article K. Ustyantsev, M. Biryukov, I. Sukhikh, N.V. Shatskaya, V. Fet, A. Blinov, I. Konopatskaia
"Diversity of *mariner*-like elements in Orthoptera"

Supplementary 1

Mariner transposase sequences used as queries in the tBLASTN search

Transposase	Species	Subfamily	Accession number/Reference
Cbmar1	<i>Caenorhabditis briggsae</i>	<i>briggsae</i>	AC099767
Avamar	<i>Adineta vaga</i>	<i>elegans</i>	AAZ67106
Cemar1	<i>C. elegans</i>		T19555
Dtmar1	<i>Dugesia tigrina</i>	<i>cecropia</i>	CAA56763
Hsmar1	<i>Homo sapiens</i>		U52077
Fungia	<i>Fungia</i> sp. <i>Kusabiraishi</i>		BAB32436
Bytmar	<i>Bythogreaa thomydron</i>	<i>irritans</i>	CAD45367
Cpmar1	<i>Chrysoperla plorabunda</i>		AAA28265
Himar1	<i>Haematobia irritans</i>		U11642
Hsmar2	<i>H. sapiens</i>		AAC52011
Rfmar	<i>Rhinolophus ferrumequinum</i>		AC157888
Ammar	<i>Apis mellifera</i>	<i>mellifera</i>	AY155490
Ccmar2	<i>Ceratitis capitata</i>		AAO12864
Famar1	<i>Forficula auricularia</i>		AY155492
Desmar1	<i>Mayetiola destructor</i>	<i>mauritiana</i>	U24436
Mboumar	<i>Messor bouvieri</i>		AJ781769
Mos1	<i>Drosophila mauritiana</i>		X78906
Hvmar1	<i>Heliothis virescens</i>	<i>vertumnana</i>	DQ174779
Porpmar2	<i>Portunus pelagicus</i>	<i>marmoratus</i>	(Bui et al., 2008)

Supplementary 2

Partial consensus nucleotide sequences corresponding to the conserved region of MLE transposase catalytic domain of 26 out of 75 MLE Orthoptera lineages (Ortmar) for which no full-length representatives from either *L. migratoria* or *L. kohalensis* genomes were identified (see Supplementary 3). The lineage sequences were assembled from sequencing of PCR amplicons derived from 14 Orthoptera species (Table 1)

Ortmar4 *Consensus from 504 copies*

AGGTGGGTNCCNAGGATGNTAACCGATCAGAATAAAGAGGCAAGGAAAAACAATAGCCTCCCAACACTTGCAGCGCTTC
CGTTTGGAGGGAGATGAGTTTCTGAAAAAATTTGTGACCGGGGACGAAACATGGGTGCATTTTTTTGAACCCGAATCA
AAGAGGCAGTCAATGGAGTGGCGTCACACAAGCTCGCCGAGGAAGAAAAAATCAAACTGTGCGATCGGCAGGGAA
AGTTATGGCAACAGTTTTCTGGGATACAGAGGGTGTGATTCTGGTTGATTTTTTGGAGCAGGGATGCACAATAAATTCTG
TTCAATACGTCACAACCCTCAAAAACTTAAAGCACGTCTTCAGCGAGTTCGCCAACAAAATCAATGGCAGATGTTCT
TCTTTTGCATGACAATGCAAGACCACACACCAGTTGTCACACCTCTGACGAGATTGTCAAAAATTGGATGGGAAGTTTTG
CCTCATCCCCNTACTCNCNG

Ortmar7 *Consensus from 17 copies*

AGGTGGGTNCCNAGGATGCTCAGCGAACCGCAAAGGAACTGCGTATGGGGCTAGCACTGCAACACCTGTTCCGGTAT
CATGAAGACCCCTGCTTTTCCTGGAGCGGATTGTCACCGGTGACGAGAGCTGGTGCCATCACTTCGAGCCAGAGACAAAG
CGGGACAGCATGCAATGGAAGCATGCGTCTGCTACCTCCCTCAAAAAATCAAGGCTGTGCCCTCAGCAGGGCAAGGTG
ATGCTCACCCGTCTTTTTCGACGTCGGAGGTCGATACTCATCGAATTCCTCGAGCACGGAAAAACCATTAACAGTGACG
TGTACTGTGAGACACTCCGTAGCCTACGCAAGTCCATCAAGACAAACGGCCTGGGCTGCTCATGGAGGGAGTGATTCT
GCTCCATGATAACGCGCGTCCACACGTCTCCAGGGTACACAAAAGTGTACTGGCCAAGTTCAAGTGGGAGCAGCTTGA
GCATCCGCCCTACTCNCNGA

Ortmar10 *Consensus from 52 copies*

AGGTGGGTNCCNANGATGNTTACAGAGCACCATAAAGAACAGCGAATGGGGCAAGTTTGACATTTCTGGAGGCCTAC
CACAAACATGGTGATTCATTAAGTGGATCGAATCGTAACTGGTGACGAGACTTGGGTGAAACACGTCAATTGCGAGACAA
AATTACAGTCCATGGAGTGGGGGCACACAAGCTCCCCCAAAAACCAAGAAAATGTTTGAAACCTTGTGCAAGGA
AGATGATGGCGACAGTGTTTTGGGATAGGCAAGGTGTGCTTCTTATTGATTTTTCTCGAACGTGGAGCAACCATAAATTCT
GCCCGTACTGTCAAACCTTGCACAGCCTTAGAAGAGCAGTTCAAAAACAAACGCCGAGGAAAGCTGACGTCCAAAATT
TTGTTTTTGCACGACAATGCCCGACCTCACACGGCAAACCGCACTAAAGAACTCCTTAATTCATTCAAATGGGAAATTTT
CCCTATCCNCCCTACTCNCNG

Ortmar11 *Consensus from 40 copies*

AGGTGGGTGCCNAGGATGTTGACCGAAGACCACAAACGTCAACGCGTTGAAGCGGCCCAAGAACTTCTTCAAGATCAC
GGAACCTCATGGCGAGGAATACCTCGACTCCATCGTCACTGGAGACGAGACTTGGGTGCACTACCGCACACCCGAAACC
AAAGAACAGTCCAAACAATGGAAGCACCCAGAGTCCGCGAGATCGCGAAAATTCAAACAAACGCAAAGTGTGCGCAA
AGTGATGGCAACAGTGTTTTGGGACAGGAAGGGGTATTGTTGTGCGAGTTCTTGCCACCGGTACAACAATCAACGCT
GCCAGGTACTGCGAGACACTGCAAAAATTGCGCCGTGCAATTCAAAACAAGAGGAGGGGTATGCTGTCCAAGGGGGTG
CGTTTGCATCAGGATAACGCTCGACCGCACACCGCTAAAGCCACCAACGAGCTCATCGCAAAATTTGGATGGGGTATTG
TCAAACACCCNCCCTACTCNCNG

Ortmar14 *Consensus from 41 copies*

AGGTGGGTNCCNAGAAATGCTCATGATGTTACAAAAACCAAGCGACTTGGAAAGTGCCTTGACATTCCTCACACGGTAC
AGTGAAGAAGGAGAGGACTTCTTGAATCAAATTTGTGACAGGTGATGAGACTTGGGTACGTCATGTCACACCCGGAGTCA
AAACAGCAATCAATGGAGTGGAGACACACTCGATCTCCACAAAAACAGAAATTCAGACGACGATGCTGCACAGAA
AATCATGTGCACGGTGTTTTTGGGACCGAAAAGGTGACTGCTTGTGAAATTTCTCCCAAGAGGTGAAACCATCAATGCA
GCCAGATACTGTCAGACTTTGAAAAATCTTCGACGTGCGATAACAGAAAGGAGAGGGAAAGCTCAGCAGAGGAATT
GTTCTGCTTACGATAATGCTCGGCCACACGCTGCAGGTGACACAAAACTTATTTCAGCAGTTTGGATGGGAGCAGT
TNGACCACCCNCCCTACTCNCNG

Ortmar17 *Consensus from 23 copies*

AGNTGGGTNCCNAGNATGCTTACCGACGACCATAAGCTCACCCGTGTTAGGGTCTGTCAACGCCTACTCACTCGCTTCA
ACAACGAAGGTGATGCNTTTTTGAGCCGAATTGTCACCCGAGATGAAACATGGGTGCATCACTACGAGCCTGAGTCAA
AGCGCCAGAGTATGGAGTGGAAACACCCCTGGATCGCCGACGAGGAAGAAGTTCAAGATGGGGCCATCNGCAGGAAAG
GTCATGTTAACCGTGTTTTTGGGACTCACAGGGGGCCATACTGGCAGAGTTCATGGAAAAGGGAACGACTATCAACAGTG
CGAGGTATAGTGAAGTGTGGAAACGAAAGCTGAAGCCAGCAATCCGCACCAACGCCGAGGTTTGTCTGTCGAAGAAG
GTTTTGTTGTCATGACAATGCACGGCCACACACGGCCCATCACACTATTGAAACCATCAACANGNTGNNAATTTGAGG
TATTGGAACACCCNCCCTANTCNCNG

Ortmar18 *Consensus from 25 copies*

AGGTGGGTNCCNAGGATGCTACCGAAGACCACAAGCGGCAGCGCGTGGAAATGTGCGGAGGAAGTTTTGCGGCGTTT
TGGAGAGGAAGGAGAGGAATTTTATAGATGGTTTTCGTAACGGGGGATGAAACATGGGCTCATCACTATACACCTGAGACA
AAGCAGCAGTCCAACAATGGCCACAGCTCGTCTCCAAAACCGAAAAAGTTCAAGGCAACACTGTCAGCCGGAAA
GGTGATGGCAACTGTGTTTTGGGACCGTCGCGGCTTGTGTTAGTGGATTTTCATGCCTAAAGGAACCACTATCAATTCTG
AGAGATATTGTGAAACCCCTCCAAAAGCTTCGCCGAGCCATTAAGAACAACCGCCAGGAATGCTGACCAAAGGAGTCA
ATTTTCATCACGACAACGCGCGCCCGCATAACGGAATCGGACGACCGAGCTGATCAAGAAGTTTGGATGGAAAATCGT
GGAACACCCCTACTCNCNGA

Ortmar20 *Consensus from 24 copies*

AGGTGGGTNCCNAGGATGCTACCGGTCAGCACAAAGAGCAACGAATGCATAGTGCACGACAGTTTTTGGAGCGCTAT
AGACAAGATGGAGACAGTTTGTTCACATTGTTACGGGAGACGAGACGTGGATAGCGTACACCAANGCAGAATCA
AAACAACAGTCAATGCAGTGGCGCCATCCCGGTTACCCAAAACCAAAAAAGTGTAAGCAATCGCCGTACACGAATTGC
AAAATGATGGCTACCGTGTGTTTTGGGACGACAAGGGCGTCTTTTGTGATCGAATTCATGGACCGTGGGACAACCAATACAG
CTGACGTGTAAGTCAACGCTACCAAACCTGAGACGTGCGATCCAAAATCGACGCCGCGGAAACTGTGCTCTGGCA
TCATCCTCTGCACGACAACGCACGCCCGCATGCCGCTGCCAAAACCAAGAGANGATTCAAGAGTTTCGTTGGGAAC
TCCTTGACCACCCNCCNACTCNCNG

Ortmar23 *Consensus from 174 copies*

AGNTGGGTNCCANNATGNTGACGGACGGCCACAAAACCTCGACGAATGGCGTCAGCTTTGGAGTTCCTTGAGCGTTATC
ATGATGAAGGAGACAACCTTTTTGAAATCAATCGTGACTGGGGATGAAACCTGGATTCAATACGACACACCGGAAACAA
AACGACAATCACAACAATGGATGCATTCAAATTCACCAAACAACCAAGAAATTCAAACAACCTTCAACAACAGAA
AGACCATGGCTACTGTGTTTTGGGACCAACAAGGTGTGTTGCTTGTGGAGTTTATGGAGCCCGGAACCACAATCACTGC
AGCTGTTTATTGTGAAACTTTACAACGTTTGCCTAGAGCCATTCAGAACAAACGAAGAGGAAAGCTGACCGCTGGAGT
TGTCTGATCCATGACAATGCCCGTCCACACACTGCTGGAGCAACTCAACGGCTTCTCGAACAAATTCGATGGGACATT
TTCGATCATCCNCCNACTCNCNG

Ortmar24 *Consensus from 13 copies*

AGGTGGGTGCCGAGGATGTTGCTGATGACCACAAAAGTCGCCGATGGCAGCAGCGTTGACATTCCTACCCGTTATG
AGGCTGAAGGTGGCGATTTATGAAGAAAATTGTGACTGGCGATGAGACCTGGATTNNTATGTCACCCCGGAAACAAA
ACAACAGTCAAGTCAATGGATGCACACACTCACCAAACAACCGAAAAAGTTAAGCAAACCTTCAATGACAAGA
AGATGATGGCTACAGTCTTTTGGGACCAAAAAGGTGTTTTGCTTGTGAGTTTATGGAACGGGGGTCTACGATCAATGC
AGCTGTTTATTGCCAGACATTACGANGACTGCGGAGAGCCATACAGAACAAGAAAGAGGCATGCTGACGTCTGGGGT
CCTCTTGATTGATGACAACGCTCGCCCTCACAGTGCTCATGTCACCCAACAGCTTCTTGAGGAATTCGATGGGACGTTT
TTGACCACCCCTACTCNCNG

Ortmar25 *Consensus from 12 copies*

AGNTGNGTGCCNAGGATGTTGACNGAGGNGCACAAAANCAAACGTTTNGNCAGTGCCTTAACTTTCTGGAGCGTTAC
CACGAGGAAGGTGATGATTTTTGAGTCAAATTTGTAACGGGGGATGAAACCTGGGTGGCCTACATTACACCTGAATCAA
AACAGCAGTCTATGGAATGGCGACATTCAACTCACCAAAGAAAGTTAAGCAAACAATGTCAGCCCGGAAAA
TCATGTGATCCGTGTTTTGGGACAGAAAAGGGGTGTTACTGGTGGACTTTTTGCCCGTGGTGAGACAATCAATTCAGC
AACGTTATGTGAGACCTTACACAATTTGCGCCGCTCAATTCAGAACAAAAGGCGTGGCATGCTCAGTAAGGGCGTCCTT
TTGCTTCATGACAACGCTCGCCACATGCGGCTCATCGAACCAAGACCTCATCACATCATTTTTGCTGGGAACAACCTCG
ATCACCCNCCCTACTCNCNG

Ortmar31 *Consensus from 37 copies*

AGGTGGGTNCCNAGGATGCTCACAGAAAACCACAAACAGCAACGTGTGCGATGTTCCGAGCAGTTTTTGCACAATGT
GAAGACAACAAGGAAGAATTCCTGGATTCATGTTACAGGCGATGAAACTTGGGCGTTTTCACTTTACCCCGGAAACC
AAGCAGCAATCACGTGAATGGCGTCACTCAACTTCGCCCCAAGCCGAAGAAGTTCAAGCAAACGCAGTCTGCTGGGAA
AGTCATGGCAACCGTCTTTTGGGACAGAAAAGGCTGCTTTTGTGACTTTTTGCCTCATGGAACAACGGTGAATTCC
GACAGATACTGCGACACATTAAGAAAATTGAGACGTGCGATCCAGAACCGCCGAGAGGAAGATTGTCAAGTGGTGTG
AGGCTTCTCATGACAACGCTCGACCTCATGTCTCACATCAGACTCAAGAACTGCTGACAGATTTTGGCTGGACTGTTG
TCCCCANCCCCNACTCNCNG

Ortmar36 *Consensus from 13 copies*

AGNTGGGTGCCNANGATGCTACCGACCACCACAAAGAGCAAAAGAAATGCTAGTGGACGAAAGTTTTTGGCCCGTTAT
CAACAAGATGGAGATGATTTGTTTTCTCACATTGTTACTGGGGACGAGACGTGGGTATCCTACGCCAACCCAGAAACAA
AACTGCAATCGATGCAGTGGCGACACTCATCTTCACCAAACCGAAAAAGTTAAGCAAACCTCAGTACACAAGTCGAA
AATTGATGGCTACAGTTTTTGGGACAAAAGACGGTGTCTTTTGGTTGATTTTCATGGAACGTGGGACAACAATACAGCT
GACAAGTACTGCGAAACGCTCAAAAAATTGAGACGTGCGATCCAAAACAACGCCGCGGGAAACTGTCATCTGGCATC
GTACTCCTCCACGATAACGCGCGTCCCCACACTGCTGCCAAAACCAATGAGAAAATTCAGATTTTTCGTTGGGAACTTT
TTGACCACCCNCCCTACTCNCNG

Ortmar38 *Consensus from 331 copies*

TGGGTNCCGCATGAGTTGAAACCCGAGAGACATTGAAAGGCGTTTGTGTGTTTGTGAACAGTTGCTTCAGAGGGCAAAAAAC
GGAAGGGTTTTCTGCATCGCGTTGTGACCGGGGACGAAAAATGGGTTTCATTACGATAACCCCTAACGCAAAAAATCATGG
GGGTATCCCGGCCATGCTTCCACGTCGACGGCCAAACCGAACATTCATGGGTCCAAGATCATGCTCTGCATTTGGTGGGAC
CAGCTCGGCGTCTGTACCATGAGCTGTATAAAACCAAGTGAAACAATCACAGGTGATCGATATCGAACGCAATTAATGCGT
TTGAGCCGAGCATTAAAAGACAAACGCCCGCAATACAGCGAGAGGCACGATAAGGTGATTTTGTGCACGACAATGCTAG
GCCCCACGTTGCAAGAGTGGTCAAACGTACCTGGAAACGTTGAAATGGGAAGTCTACCCACCCNCCNTANTCNCNG

Ortmar40 *Consensus from 99 copies*

TGGGTNCCGCACGANCTGAATGAACGGCAAATGGAAAATCGCAAAGTCACTTGTGAAATGCTGCTTCAACGCCACGAA
AGAAAATNATTTNTGCACCGAATTGTGACNGGTGATGAAAAATGGATTATTTTGAACCCGAAGCGNAGAAAATCGT
GGCTGTACCTGGNNAAGCCGGTCTTCAACANCAAGGCCAAATCGCTTCGGCAAGAAGACCATGCTTTGTGTCTGGT
GGGACCAGAGNGGTATTGTGTATTATGAACNTGAAGCCNGGCGAAACNGTTAATNCACAACGCTATCGNCAACAAAT
GATTAATTTAAATCATGCATTGATCGAAAGACGACCAGAATGGGCCAGAAGACATGGCAAAGTGATTTTGTACANGAC
AATGCNCCNNTCACACAGCAAAACAGTGAAAGACACCTTNAANTCNCNTTGGATGGGACATCCTTCNCACCCGCC
TACNCCNGANNTNGCNC

Ortmar41 *Consensus from 24 copies*

TGGGTNCCNCATGAGCTAAGTGACANTAACAAAAATCAACGAGTAAACATCTGTTCGTCATTGCTTCCCCGGCACCCGGT
TGGCTTGTGATAGGCACGAAGCATTCTTTTCGAACATTGTACCCGGTGACGAGAAATGGTGCCTGTATGTCAACATGAA
GAAGAGGAAAGAGTGGCTCAGCCCATCAAAAAAGCAACTCCCCGTGCCAAGGATAGTGCCATCCACAGAAAATCAT
GTTGTGTGTTTGGTGAACAAAGATGGCATTCTTACCATGAACTGCTTCCGAAAAACGTAACGATTACCTCAGCTGTGT
ATAGTGACCAGCTAAGACGGCTTGCCGTTGCTATTGACAACAAAAGACAAAGACAACAACCAGTCTTATTGCTCCATGA
TAACGCTCGTCCGATACAGCGCAATTGACCAAAGGTGTGATTGCTGAACTTGGCTGGGAACCACTTCTCATCTCCGT
ACNCCNGACNTNGCNC

Ortmar42 *Consensus from 20 copies*

TGGGTNCCNCATGAGCTCAAAGAAATCCATCTCACAAATCGCATCAATATCTGCGATACTCACCTCAAACGCAACGAAA
TCGATCCGTTTTTGAAGCGCCTCGTGACCGGCGATGAAAAATGGATTGTTTACAACAATGTTAAGCGTAAACGATCGTG
GTGCAGTGAAATGAGCGATCCAAAACGACAGCCAAATCCGATCTTACCAAAAGAAAGTTATGCTCTCAATATGGTGG
GACTACAAGGGTGTGGTGTTTTTTGTAGCTCCTACCGCGAACCAGAGGATCAATTCTGATGTGTACTGTGCTCAACTGG
ATGATTTGAATACATCTTTCGCGAAAAGCGGCCAGAATCATCAATCGCAAAGGCGTAGTGTCCATCATGACAATGCG
AGACCACACAAAGTTTGGTGAATCGTCAAAGTTGCTGCAGCTTGGATGGGAAGTTTTGCCNCATCCTCCTTACACNC
CNGACCTNGCNC

Ortmar43 *Consensus from 27 copies*

TGGGTGCCGCATGAGTTGAAACGATAGGCAGATGGAGCGACGCCAAAACACATGCGAAATCTTGCTCGCCAGACAAAAA
AGAAAGTGCCTTCTGCATCGAATTGTGACTGGCGATGAAAAGTGGATTATTTTGAAGATCCTAAACGCAAGAAATCGT
GGGTTGATCCCGCCAACCATCAACATCTTCCCAAGACCAATCGCTTCGGACGGAAGACGATGCTGTGCGTTTGGTG
GGATCAGCAGGGTATCGTCTACTATGAGATGTTGAAACCTGGTGAACCTGTCAATGCCACCCTACCACCAACAACCTG
ATCAAATTGCACCGTGTCTCGGTGAAAAAAGCCGGATTATCAACAAAGACATGACAAGTATTTTCTCCACGACA
ACGACCATCGCACACGTCAA AAAATGGTCCGAAACTACTTGGAGACACTCAACTGGGAGGTGCTACCCCATCCCGCGT
ACACNCCNGACCTNGCNC

Ortmar44 *Consensus from 13 copies*

TGGGTGCCGCATGANTTGACGCAAAAAAACCTTCTGGACCGAATCAACGCCTGCGATATGCTGCTGAAACGGAACGA
ACTCGACCCATTTTTGAAGCGGATGGTACTGGCGACGAAAAATGGATCACATACGACAATATCAAGCGAAAACGGTCCG
TGGTCAAGGCCGGTGAATCGTCCAAAACAGTGGCCAAGCCAGGATTGACGGTCAGGAAGGTTTTGCTGTGTGTTGG
TGGGATTGGAAGGGAATCATCCACTATGAGCTGCTCCCATATGGCCAGACACTTAATTCTACCATGTAATGCGAACAACT
GGATCGCTTGAAGCAGGCGATCGACCAGAAGCGTCCAGAATTGGCCAACAGGAAGGGTGTAGTGTTCACCCAGGACA
ACGCCAGACCACACTTCGTTGATGACTCGTCAGAAGCTACGGGAGCTCGGATGGGAGGTTTTATCGCATCCACCATA
CAGNCCNGACCTNGC

Ortmar48 *Consensus from 27 copies*

AGGTGGGTNCCNAGGATGTTGACGCTGGATCAAAAACGCATGAGAATGGACATATCGGAACAATGTTTGGCCCCGTTTTA
GGAGAAACGAACAAGATTTTTTGCGCCGGTTTTGTGACCACAGATGAAACTTGGGTGCACTACTATAACCCAGAGACAA
AACAACAGTCAAAGCAGTGGAAACATGCTGATTCTCCGCCACCAAAGAAAGCAAAGACAATTTCTTTCGGCTGGAAAG
GTCATGGCATCAGTGTCTGGGATGTGAAGGGGATTCTGTTTGTAGATTATCTCCCACTGGGCAAAACAATTAATGAGAG
ATACTATGCTAACCTCCTGGACAAAATTGCAACAAAAGATACGCGAAAAAAGGCCAGGTTTAGCAAGGAAGAAAGTCAT
CTCCATCAAGACAATGCGCGCCCGCACACATGTGCCGTCGCCATGGCAAATTAACACGAACTAAGGTATGAATTGTTG
CCACACCCNCCNTACTCNCNGA

Ortmar49 *Consensus from 21 copies*

AGNTGGGTNCCNAGNATGCTTTCGATGGAACAAAAACAGCAACGAGTCGATGATTTCAGAAAGCTGTTTATCGCTATTTA
CTCGCAACAAAAAAGATTTCTTTCGCGTCTTACGTGACCATGGACGAAACATGGATACATCACTACACTCCAGAGTCGAA
GCGGCAGTCATCTGAGTGGCGCACAGCTGGCGAAAGCCGTCCGAAGCGTCCGAAAAACGCAGCAGTCAGCTAGCAAAG
TCATGGCGTCAGTTTTTTGGGATACGCATGGTGTGATTTTTATTGACTACCTCGAAAAAGGTAAATCGATCAACAGTGAT
TATTATATTGACTTGGCTGGTGGCTTTGAAGGAGGAAATCGCAAAAAACGACCGCACATGCAGAGAAAAAAATCCTTT
TTCACCAAGACAATGCACCCTGCCACAAGTCGATGAAAAAATGGCAAAATTCACGAATTGGGCTTTGATCTGCTTCC
CCACCCCCNTACTCNCNGA

Ortmar50 *Consensus from 15 copies*

AGNTGNGTNCNNAGAATGNTCACAGTGGAAACAAAAACAACAACGAATTGATGATTTCGAAGTGCTGTTTGAAGCTGTTT
ACGCGTGATAAAAAGGATTTTTTTCGCTCGATACATAACGATAGATGAAACATGGATTTCATCACTATACGCCGGAGTCGAA
AAGAGCGTCAGCCGAGTGGAGAAGAGAGGGGCGAAAGCCGGCCAAAGCGTCCGAAGACACAACAGTCAGCAGGCAAG
GTCATGGCTTCTGTATTTTGGGACATGCATGGAATTTTGTCTATAGACTTTCTTCCGAAGGGCCAGACGATCAACAGCGA
CTACTACATTGCGTTATTGGATCGATTGGATGACGTAATCAAGCAGAAAAGGCCCTCACATGGCAAAGAAAAACCGCTG
TTTCACCAAGACAANGCACCAGTCACACAAGTCGATGAAAACGATGGTGAATTCACGAATTACGATTCCAATTGCTTC
CACACCCCNANTCNCNG

Ortmar51 *Consensus from 15 copies*

AGNTGNGTNCNNAGGATGCTGACTTTGGACCAAAAAACGGCGCCGAATGGATGTTTCTGAGGAGATGCTGACTCGATTTA
GACGCAATAAAAAGGAGTTCTTTCGCGCCGACTGGTACTGTGACGAAACTTGGGTCCACCACTACACGCCCGAGACAA
AAGAGCAATCCAAACAATGGACAATGAAGGGAAAACAGCTCCGAAGAAAGCCAAGGTGATTCCATCTGCCGGTAAG
GTATGGAACAGTTTTTTGGGATGCGCGTGGTATTATCCATATCGACTACCTGGAAAAGGGGAAAAACAATTACTGGGGT
ATATTATGCAAGTTTATTGGACAACTGAATGAGGAAATAAAGAAAAACGGCCGCATCTCGCAAGAAAAAAAGTTTTG
TTTCACCACGACAATGCGCCAGCTCACACCTCACTCGTTGCCATGGCCAAAATTCATCAACTGAAGTTTCGAGTTGCTTG
ACCATCCNCCNTACTCNCNG

Ortmar52 *Consensus from 13 copies*

TGGGTNCCGCACGAGCTCACAGACGAGCAGAAAGCAAAACGGATGAAACTTCTGGTGATTTTCATTTCCATGTGTGAC
CAGGATCCATTGCTTCTGAACACCATCGTCACGGGAGATGAGACCTGGTGTACCAGTTCGATCCGGAATCAAAACGGC
AATCGATGTCATGGTGTTCACCGTCTTCCCCGCGACCAAAAAAAGCCGTCTGCAAAAATCCAAGGTGAAAAACTGT
TGATCGCTTCTTCGACAACAACGGCATCCACAAGGAATTTGTTCTGCAGGTCAAACCATTAATGCTGCATTTTAC
CAGTCCGTTTTGAACCGATTGTTACAGCGTATCCGGCGGGTTCGGCCAGAGTTGCACAGGACTGGAAAATGGATGCTGC
TCCATGACAATGCCCTGCACACTGCGCGATCCGTGTGCGCCAATTCCTGGCGCAGAAGATGGTAACTGTTCTTGAACA
CCNCCNTACTCNCNGAT

Ortmar62 *Consensus from 10 copies*

AGGTGGGTGCCNAGGATGTTACGCGGGAACAAAAGGAGTTACGGATGGGAATCTGTTCTGACATTTTAAAAAACATTA
GGNAGGATCCTGAACCTGTTGGAAAGAGTTATTACGTGTGACGAATCATGGTTTTTTTACCTATGACCCAGAAACTAAGCG
ACAATCAATGCACTGGAAGAGTCCGAATTCACCACGAAAGAAGAAAGCTCGAATGTCCAAATCAAAATCAAGGCCAT
GATGATGTTTTTTTTTGACATCCATGGAATTCGTATGTAATTTGGGTTCTGAAAGGTCAAACCGTGAATAAAGAATACT
ACCTTGGGGTTTTTGCCACCCCTCCGTGAGCGAGTGCAGAAAGCGACCCAGAGTTGTGGAAGAACAAGTCGTGGATTC
TGCATCAGGACAACGCCCCAGCCACACTGCACTGGTGGTTAAGACATTTTTTGCCAAAGCATGGGATCCCTGTGTTGNA
TCATCCNCCNTACTCNCNG

Ortmar75 *Consensus from 24 copies*

AGGTGGGTNCCNAGGATGCTAAAACAGTTTGAAAATGGGACTTCGCGTAACGTCAATAGCATCGTTACAGGTGACGAA
ACTTGGCTTTATTATTACGATGTCCCAACAAAATCCCAGAACAAGGTGTGGCTGTTTGAAGATGAGAGTACTCCTGTGAC
TGTGCGAAAGTCAAGGTCAGTGAAGAAAAGGATGATTGCAGTATTCTTACTAAACGGGGCATCCTGACTCGGGTTGTG
CTAGAAACACAAAGGACAGTTACTGCGAAGTGGTACAGTGAGACTTGTCTGCCTCAGGTTCATCCAGGCTCTCAAGCAG
CTCCGTCCAAGGTCACGGCTCAACACTTGGCTCTTGCATCACGACAATGCTCCAGCACATCGTGCTAATGTAACAATGG
ATTTTCTTGCCAGATCAGGGTTGACTGTGCTTGATCACCCNCCNTACTCNCNGA

Supplementary 3

Consensus nucleotide sequences of 27 *L. migratoria* (Lmmar) and 24 *L. kohalensis* (Lkmar) MLE lineages.
The following characteristics are denoted in the headers of each lineage in italics: TIRs (if present), TSD (if present), number of genomic copies from which consensus was derived, the corresponding Orthoptera MLE lineage (Ortmar).
If TIRs are present, their sequence is in lowercase. If TSD is present, "ta" dinucleotides are included in the corresponding sequence

Lmmar1 *TIRs | TSD | Consensus from 438 copies | Ortmar45 lineage*

tacgagggtcattcaagtcttaagcctcagattttttTCTCCGACTGGAAAGAGATAGAAACATGCGCATTGTTTTAAATGAGGCCGCGTTCATT
GTCAATACGTCCCAGAGATGGCAGCACCGTACGGCAGATGGAATTTTACCGCCAGCGGCGAGAATGAGAACTGTTTTAGATA
CTTAAATGGCGACGTTTTCTTACTTGAACAGCGTGCAATCATTCTGTTTTCTGAATTTGCGTGGTGTGACACCAATTGAAAT
TCATCGACAGTTGAAGGAGACATGTGGTGTGAGTTATGGATGTGTCGAAAGTGCCTCGTGGGTGCGACAGTTAATGAA
GGCAGAACATCGTGTGACAACAAACCGAAACAACCTCGGGCTCGCACAAAGCCGGTCTGACGACATGATCGAGAAAGTGGAA
GAGAATTGTTTTGGGGGATCGCCGAATGACTGTTGAACAGATCGCCTCCAGAGTTGGCATTCTGTGGGTCTGTGCACACA
ATCCTGCATGACGACCTGAAAATGCGAAAAGTGTATCCAGGTGGGTGCCACGAATGCTGACGGACGACCACAAGGCTGCC
CGTGTGGCATGTTGCCAAGCAATGTTGACGCGCAACGACAGCATGAATGGGACTTTCTTTTCGTCGGTGTGACAATGGATG
AGACGTGGATGCCATTTTTCAATCCAGAAAACAAAGCGCCAGTCAGCTCAATGGAAGCACACAGATTACCCGCCACCAAAAA
AATTTTCGGTAACCGCCAGTGTGAAAAAATGATGGTGTCCATGTTCTGGGACAGCGAGGGCGTAATCCTTACCCATTGCGT
TCCAAAGGGTACTACGGTAACAGGTGTCATCTACGAAATGTTTTGAAGAACAATTCCTTGCATCGCAACAAAAACG
TCCGGGAAGGGCTGCGCGTGTGCTGTTTACCAAGACAACGACCCCGCACATCGAGCTAACGTTACGCAACAGTTCTTCTCG
TGATAACAACCTTTGAAGTGATTCCTCATGCTCCCTACTCACCTGACCTGGCTCCTAGTGACTTTTGGCTTTTTCCATCAATGAA
AGACTCTCCGTGGCCGCACATTCACCAGCCGTGCTGCTATTGCCTCAGCGATTTTCCAGTGGTCAAAAACAGACTCCTAAA
GAAGCCTTCGCCGCTGCCATGGAATCATGGCGTCAGCGTTGTGAAAAATGTGTACGTCTGCAGGGCGATTACGTGAGAAAGT
AACGCCAGTTTCATCGATTTTCGGGTGAGTAGTTAATTAgaaaaaatcgaggccttagaactgaaatgcacctcgta

Lmmar2 *TIRs | TSD | Consensus from 333 copies | Ortmar3 lineage*

tacagtttcatctcatgtttgaaagttttacagtgtagatacatcctCCCGCTTGTTTCAAACCTAGTTCAACCTGTTCCCGTGAGTGGCGCCGTCAC
AGCATGTCTCAAGATGGCTGCTACACTTGACGTTTCGTCAGAAAGCAACGTGCTGTGATTGAATTCCTGTGCTGTGAAAAACGA
GACAGTGGGAAACATCCACAAGAGGTTGAAAAAGGTGTATGGAGATGCTGCTGTCGATCGCAGTACAGTTAGTCCGTTGGGC
AAGCAGGTTACGTGATGAAAGCGGGCACGGCAATATTGAGGATTGCTCTCGCAGCGGCAGGCCTCGTACTGCACACACTCC
AGACAATGTGCAGAGAGTTAACGAATTTGGTACTGCTGACAGACGCATCACAGTGAACGAATTTGTCAGCTACGTTGGGAT
AGGGGAAGAACTGTTGACAGATACTGAAAGTGTGGCGTTAAAAAGGTTTGTGCCAGTGGGTTCCAGGATGTTGAC
AGTGGCTCACAAAGAAACACGAAAAACGGTATGCAGCGAACTTTTGAACACAGTACGGGAATGGTGGAGATGAATTTCTTGG
AAGAATTGTGACAGGTGATGAAACATGGCTCCATCATTTTTACCAGAGACGAAGAGGCAATCAATGGAGTGGCATCATGCA
AATTCACCCAAGNAAAAAAAAAATCAAAAACCACACCTTCTGCTGAAAAAGTTATGGCTACGGTGTTTTTTCGATTCCGAAGGA
CTCTTGCTTGTGGACATCATGCCACGTGGAACCACATAAATTTCTGATGCATATGTGACGACACTGAAGAAAATTCAGCTCG
ACTGAGTCGTGTTTCGACCACATCGGCAAAAGCAGGATGTTTTGCTGTTGCACGACAATGCACGGGCACATGTCAGTCAAAA
AACCATGGAAGCGATCACAAAACCTCGGATGGACAACACTGAAACACCCGCTTACAGTCTGACCTGGCTCCATGTGACTAT
CATCTTTTGGGAAACTGAAAGACTCTCTTCGTGGAACAAGGTTTGAAGATGATGACTCCCTTGTGCACGCTGCCAAACAGT
GGCTCCAACGTGTTGGTCCAGAATTTACCGTGCGGGTATACAGGCGCTGGTTCCAAGATGGCGTAAGGCAGTTGAGAGGG
ATGGGGATTATGTGGAGAAATGAAAATATTGTTCTAaagatgtatctacacactgtaaaacttcaaacatgtagaataaaaactgta

Lmmar3 *TIRs | Consensus from 76 copies | Ortmar61 lineage*

gagggggaccctcaaaagaaaccggaCTCCGAGGGCGCTGCCATTCGTAGACGTAGTACAGGGTTCTCACGCTAGATGGCGTTAGTAGAGA
CCTTCATGAAACAGCTGTGACAGCGGCTCAGTGTAGAGCTGAACGTGCAAGTGTGGTATTGTGTTTCTCTGACTGTTGGCG
GGTTACCCCTGCGAAGTCTGTTATGGCAACTTTAAAAAGAACAAAGAGTGTGTGAAATTTGTTTCTGCTTAAAAAACTG
CAACGGAGACACACCAATGCTTCAGGAAGCTTTCCAGGAGGACGCTATGAGCCGCACACAGGTTTTTCGAGTGGTTTTGGGC
GCTTTAAACGTGGTGTGAGATGAGTGTGAAGACCAAGCTCGTTCTGGACGCCCTTCAACATCGCGAAACGAGGAGAACATTG
AAAAGGTCCGCCAAAAGATCAACGAGGATCGTCGCCAAACGATCGACCAATTTTCAGCAGAGACAGGAATAAGTTGGAGC
TCGTGCCAGCGGATTTTGTGAGTGGATTTGCACATGAGACGTGTTTCTGCTAAATTTGTTCCGCGCCTTCTCACACAGGAGC
AAAAAACCATCCGCATGAATGTGTGTCAGGACTGAAAACAGAGATTGCACGTGATCCAAACTTCTGAAACAAAGTCATTAC
AGGGGATGAGAGTTGGTGTACGGGTATGACCCAGAAACCAAGCAAGCGTCAAGCCAGTGGAGGACTCCCAACTCTCCCA
GACCAAAAAAAGCAAGGCAAGTGAAGTCAATGTGAAGACGATGATCATTGTCTTTTTTGTGTTTCTGTTGGAATTTGTGCATCG
GGAATTCGTACCCCTGGCCAGACTGTTAACCAGCACTTTTACTTGGATGTTTTAAGGCGTCTGCGAGAGGATGTGAGGAGG
AAACGCCCGGAACCTTTGGCGATCAGGTGACTGGTTTTCTGCATCACGACAACGCTCCAGCACACACGGCCTTACGAGTGC
CCACTATTTGGCATCTCAGAGGTGTTCTGCTGCTCCCAACGCTCCGTTATTCGCCGACCTTACAGCCCGTGCCTTTTTCTCTA
TTTCCAGTAATGAAAAACGCTAAAAAGGGAGCGTTATGATGATGTGGAGGCGGTAATAAACAGCTTTCGCAAAAGGGCAAT
GGACAATATCAAACCTGAAAGAGTTCCAAACATGCTTCCAAACAGTGGGAAAAAGAGACTTGACAAGTGCATCGCATGTAATG
GAGAGTATTTGAAGGTGACTGAAGTAATTTTGTAAAAAGGTTTCATCAATAANTTTTTATGACAAAAAtccggttcttttgggtccccctc

Lmmar4 TIRs | Consensus from 138 copies | *Ortmar59 lineage*

aggtgcgacaataaagtaatgagactgatTTTCTTTGCAAGATGTGGCAACCCTGCAGGCTTGCCTAGGCACAATATCTTTGACCTTGGTC
TATAAGCTGCTTCTAGTCCAAGCGGCACATCGATGCAACTGCTCAGTCGTGAGTTGTGCTGTAATAAGTTAACACGTGTT
TGTGTCCTCGTCCAGGAAATGGAACCGCATAATATGCGCAACGGTATGCCATTTCTTTTTGCGTTAAATTGGGTGAAA
ACGCGACGACAACCTTACGGTAAGCTTACAGAAGGCTTTTGGAGAGGAGGTTATGTCAAGAGCTCAAGTTTTCGTTGGCA
TAAAATGTTTGTAGTGAAGGCAGAACGAATGTTGAAGATGAAGACCGCAGTGGACGACCATCAACCTCACGGACGGATGT
CAACTTGGCCAGGGTGCCTGAACTCGTACGATCTGATCGAAGATTATCCGTGAAAATGATTGCAGAAGAACTGAACATC
AATCGAGAAAACGGTTCGTCTAATAAATACTGAAGATCTTGGTATGAGAAAGATTTGTGCAAAAATGGTCCCCAAAAATC
TCACACCACAACAGCGAGAAAACCGGAAAAATGTGGCAGCCGATCTGTTAGAGCAAACGGAAATCAATCCAGAATTGT
TGAGCCGTGTTATCACTGGTGTATGAAAGTTNTTTTTTCAGTACGATCCAGAGACAAAACGCCAAAGTTCGCAATGGTG
CTCAAAGGGATCACCCAGACCAAAAAAAGCTCGCATGTCAAAGTCAAAGTGAAATGCATGCTTGTGTGCTTCTTTGA
TTCCAAGGGAATTGTTCAAAAAGAGTGGGTGCCTCCTGGACAAAACAGTTAACCAATATTAATAAAAAGAAATTTTAGAA
AGACTTCGTAAGAAGAGTTCTTCGTGTCCGTGCCAACATTGCTGATAATTGGATTCTGCATCACGATAATGCGCCATCCCAT
ACTGCTCTGTCACTACAGCAATTTTAACTCAAACAATTTTCACTACTACCACAGCCACCTTATTCACCAGATATCGC
TCCGTGCGACTTTTTCTATTTCCAAGAGTCAAACGGCGGTCAAGGGACACCATTTTCAAACAACACAAGATGTCCAA
AAAGCTGTGACGAGGGTCTGGAGGATATTACAGAAGATGAGTTCCAGAAATGTTACCATCAATGGCAGAAGCGCTGG
AAAAAGTGTGTCAATCAGAAGGGAACACTTTGAAGGAGACAACACTAAACTTGACTAAAACGGTAAGCAACANN
TTTTTCAcactgtctactatttattgtcgcacct

Lmmar5 TIRs | Consensus from 571 copies | *Ortmar46 lineage*

agggcgcttgaagaagtcctgcaaaGTCCGAGAGATGGCACCACCGGCGGTATCGAGGTCATGTTTAGTTAGTAGCATCTTTGGAAAG
AACGCACACCAAGTTTCAGCCATATTTGGTCTATTTCTTTGTGTTTGGCATTCTGTGTAATCAAGGAAGTTCGAGTATTGTC
AAAGAATGGACGAAAAAGAATTTCTGTGGTGTAAACATTACTTTATGAAAGGCAAAACGCCTCAGGAGACTAAAGA
GAAGCTTGATAAACATTATGGTACTCTGCACCTTCGATTAGAACAGTTTATAAGTGGTTTCAAAAATTTTCGGAGTGGCCA
TATGGGCACAAGTGACGCTGAACGTTCTGGACGCCCTGTGGAGGTTACGACTCCAGAAATCATTGATAAAATCCATGATAT
GGTGATGGATGACAGAAGAGTTAAGGTGCGTGAGATTGCTAGTGTGTTGGGCATCTCGAATGAACGGGTACATAATTTTT
GCATAAACATTTGGACATGAGAAAGCTATCCGCAAGATGGGTGCCGCGATTGCTCACGCTTGACCAAAAACGGAATCGTG
TGAAGTGTGCAAGGAAGGTTTTCAGCTGTTTCAGGAAGAATCCCGAGGACTTTAAGCGCTGTTTTCGCTCACTGTGGATGA
AACATGGATACATTACTATCTCTGAGACCAAAGAACAATCTAAACAATGGGTTACCAAGGGAGAATCTGCACCAAAAA
AGGCGAAGACCGGTCCTTCGGCCGAAAAGTTATGGCGACGGTCTTTTGGGATTTCGAAGGGATAATCCTCATCGACTAT
CTGGAACAGGGTAAAACCTATTACAGGTGCATATTATTCATCGTTATTGGACCGTTTGA AAAACCGAGCTGCAAGAAAAACG
CCGCGATTGGCCCAAAAAAGTCTTTTCCATCACGACAATGCACCAGCACACCTCAGCAGTTGTGGTTCGCAAAA
TTATTGAAATAGGATTCCAACCTCGTTTCACATCCCCCTATTCTCCAGACTTGGCTCCCTCGGACTACTATTTGTCCCA
ATTTGAAGAAATGGCTGGCGGGACGAAGATTTCAATCAAACGAGGAGGTGATTGCAGAACTAATAGCTATTTTGCAGGC
TTGGACAATTCCTATTATTCGGAAGGGATCAACAAATTAGAACAGCGTTGGACGAAGTGTATAAGTCTAAAAGGAGACTA
TGTCGAAAAATAAAAATGGTTTTCCCCAACACGTTAGTAGTTTTTATTTtttcacggacttttcaaacgcccct

Lmmar6 TIRs | TSD | Consensus from 582 copies | *Ortmar30 lineage*

tacgaggttaagtcaattattatccgcaatttagttataTTTTTGTATTATGTTGGTAGTACTGTCGTTTTACGTTGGTGACGCATGCTTTGTTTATTG
TTGTTATATCTTTGCAATTTTCAAGCTGCTACGTTAGTTTCGTTGCTGCTGCCGTGCTGTTAATCATGGCTGCTCCGCTGTCT
ATTTGCACAAAGAGGCAAGCTTACAGTGATACGTTTTTTTGGGCGGAAGGTGATCAGGGGCCGAAATTCATAGAAG
ACTTTCAGTACAGTACGGGAGCAGTGTTTTGCCACAACGAAGTGTGTACGAGTGGATTGAAAAATTCGAAATGGTCG
ACGAGTGTAAAGCACGATGAAGGAGCCGGACGACCGTTTACCGCCACAATGAAGAAACCATTGAGCGATCACGTGAA
ATGATTCTCTTAGACAGACGATTAACCTATTGATGAAGTGGCTCATCGTCTTCAAATAGTTCATGGTTCTGCCTACGAAATTA
TTCACAACAGACTTGGGTTTCGTAAGTTTGTGCAAGATGGTCCCAAAAACAACCTCACACAGTTGCATAAGCAAAACGCG
CCTCGACATCTGCAAAAAACATTTGGATCGCTATGGTAACGAAGGGGACAACCTTCTTAGACAGAATCACTACTGGTGACG
AAACATGGATCCATCATTACGAGCCGGAGAGTAAACGGCAGAGTATGGAATGGAACATCCAAATTCGCCGTGCAAGAA
AAAGTTCAGACCCAACCGTCCGAGGAAAACTGATGCTTACGGTTTTTTGGGATGCACGAGGTCCTGTACTGGAACATT
ATGGTGAAAGGGGCACAACAATAACAGTGTACGTTACAGTGAGATGCTTACTGACAGGCTAAAGCCTGCAATTCGAAG
CAAACGCCGAGGATTGCTGTGAGAAGGTGTTGTGTTGTTGCACGACAATGCCCGTCCGCATACTGCTGTCCACACTGCTG
AAACGCTCCAGAACTCAAATTCGAAGTACTGGATCATCTCCATATAGTCCCGATCTTGGCCCTTCTGACTATCACTTGT
TGGTCCACTCAAACAGGCATTAAGGGGCCGTCGATTTGACTCGGACGAAGCAGTGAAGGAAGCGGTGCATTCTCGGCTC
GCAGCTCAACCGAAAACCTTTTATGAGGGCATAAGGAAGCTTGTAGAGCGATGGACGAAGTGCATTGAAAAGCAAG
GAGACTATGTCGAAAAATGATGTTCTTGTAAAGTTTCGATTTTTATTACAATAAAAATTTtataactactttgcgataataatgacttaccctcgta

Lmmar7 TIRs | Consensus from 103 copies | *Ortmar2 lineage*

gggatgctgaaaagtaatgectccaattttTCGTCTGTTTCGACGATGGTTGAGGTTTTCGCATGTCCTGCATATTACTCGGTTGTCCTTGC
CGCGTAGCTGACGCAAAGTACAACCCTCTGCCGCTAGAGGGCTTCGAGTAGTACCGAGTAACATGGCGGTCTGTAAAGT
GACTATGTCGGTGCCTGAGAAACAGCGTGTGTAATCGAGTTTCTAACCGCAGAAAACACGCCTCCAATTGAGATCCAC
AGAAGAATGAAAACCTGTGTACGGTGACGAGTGCATCGACATCAGTAATGTGCGCCGGTGGGCTGCCCGTCTCGTAAA
CACGGTCTAACCTCAACGTCTGTGACAGAGCACGGAGTGGACGACCGCGTACGGCAACAGACGAGACTCATCGGAAT
CGGGTTGATCAACTCATCAGAGAGAATCGTCGGATAACACAGGCACAACCTCTCACTGCAGTGTGGCATATCACGGGAGC

GTGTACAGGCCCTGATTGCAGAACTGCGGTACAGAAAAGTGTGTGCACGGTGGGTGCCCGTATGCTCACCCCTGACAT
GAAACAAAGGAGATTGGACATCTGTCAACAATTGCTGTTGCGTTTTGAGCAGGAGGGTGTGGGTTTCCTTAACAACATT
GTGACTGGTGATGAAAGCTGGGTGCCACATTTTGACCCCTAAGCAAGCAGCATCACAGGATACCGCCACCACCGGA
TCACCACCCCAAGAAGTGCAGACCATGCCGTCGGCAGGCAAGATCATGCTCACTGTTTTCTGGGATGTTCCGAGGTG
TCGTGCATATGGAGTTCATGCCTAAAGGCACCCACATAAACTCCGCACGGTACAGCGAGACTCTCCGCAAACCTGAAAGC
ACGCATTGCAAGAACTCGTCCCCACATGGAACACCCCTCCTTCAGCATGACAATGCCAGACCCGCACACGAGCGCTGC
GACATCTGCAACGATCCGCCGCCTTGGATTCACTGTCATCGATCATCCTCCATACAGTCCAGACTTGGCTCCATCCGATTT
TCACCTCTTTCAAAGCTTAAAGAACACCTTCGCGGTGTCCACTTTACAACCTGATGAAGCAGTGCAAGCGGAGGTGAG
GCGGTGGTTCAGACAACGAGGTCCAAACTTCTACAGTGACGGGATCCACAAACTGGTCTCTCGTTGGGAGAAATGTGT
GCGTCGCCAGGGTGACTATGTTGAGAAATAAATATGTAGAAATGGTGAATAAAGATGTGGTATTGTAATACAGTTTGGTTT
ATTTCAAAGCCGTAAGGTATTCCCGNAAAAAATcgagcattactttcagcatccc

Lmmar8 TIRs | TSD | Consensus from 61 copies | *Ortmar9* lineage

tacnagggtgagtcacaaatgaaaaccttaaatTTGTAATAACAAATCGAAATTTTCGCGCCNTTATCCTGTAAGTTGGTAAGCGTGCTACAAAC
AGCGTGCAGAATGGCCTGTAGGTGGCAGCATAGTGCAGATGCACACATAACCGTCGCAGTATCAGTATAAAGATGGCCCG
CCCATTGCGACTTGCACCAGGAAGAACAGCGTTCCTGTTATTTCGGTTTTTGCGTAGTGAAGGTGTGAAACCTATTGAA
ATTCATCGACGAATGAAGGTTTCAGTACGGTGTGCATGTTTGTCCAGCAGCAAGTCTACGAATGGAGTAGGAAGTTCG
CAAATGGTGTGACTTCAGTGAAGATGCTCCTCGTCCAGGTGACGCAACAGATTGTGACTCCACAGAACATTGCAG
CAGTTGAAGCCATAGTGAAGGAAAACCGCCGAGTGACACTGAATGACATTGCAGCATGTTTACAGATTAGTCATGGGTC
AGCACACCACATTGTGCATGATGTGCTCCAGTTTCACAAAGTGTCTGCAAGATGGGTGCCACGGCAGCTGACTCCTGAA
ATGAGAGAACGACGTGTTGATGCTTGTGAAGAAGTTCCTTCGGCGCTTTGAACGAGAAGGTGATGGCTTCCTTGAAGAA
TCGTTACTGGGGACGAAACCTGGGTTCACTTCCACCAACCGGAAACGAAGAGAGCGAGCAAGGAATGGCGCCATTCT
CATCACAAAACCAAAGAAGTTTCGAACAGAACCATCAGCAGGGAAGGTATGCTGACTCTCTTTGGGACGAAAAAG
GCGTCATTTTGGAGCATTACATGCCTAGAGGGACCCTGTCACCAGTGCATCATAACAGATCTCCTAAAAAATCATCTG
CGGCCTGCAATCAAATCAAAGCGACGTGGATTGCTGTGACGAGGTGTCCTTTTGAACATGACAATGCAAGGCCCCACA
CTGCCGTACAACAGTTGCAACAATCACAGACCTGCATTTTGAAGTGTCTCCTCATCCACCATACTCACCAGACCTTGCC
CCAAGTGATTTCCATATGTTTGGACCACTCAAAGAAGCAATGGGAGGAAAGAAGTTCCGTTCTGATGAAGAGGTACGCC
ACGCGGTGCATGAGTGGTTGCGCGGACTACCAAAGAATTTTTTCTAAAGGAATTTATGCATTTGTAAGCGCTGGAG
GACTTGCATTGAGCGTGGGGGAGATTATGTTGAAAAGTGATACAGCTTTGTACCCTTCTGCACAATAAATAATATTNN
AAAAATatttaaggtttcatttgactcacccctgta

Lmmar9 TIRs | Consensus from 333 copies | *Ortmar47* lineage

agggtggttgataagctgtgtaaaTTTGTATGAAAGAGCGGGAAATTTTCGGAACCTGCACTGTTGTTGGTAAGCCTGATATTTCCACG
GATATTACAGCAAGTTTCGAACGGCAGCTGTTATTAGTTGATTGTTGGCTGCCAGCTGAAGTGGTAAGTGCCTAGTTAGTT
CCTTAGGATGGAGAAAAACGAATTTTCGTGCGGTCATTAACATTTTCATTTGAAGGGTTGGACAGCTGCACAGATCAAAT
CCGAGTTGGATGAGGTCCATGTTGGTTCGACCAACATGAAAGACATTTACTTTTGGATCAATGAGTTTAAACGTGGTC
GGAGAAGCACGGAAGATGGAGCACGCTCCGGTTCGGCCCGTTGAAAGTCAACACAGGAAACCATCGATAAGGTGCATGA
TATGGTAATGGAAGATCGAAGATTAAGTTTCGCGAGATAGCTAACATTTGATGGCATCTCAACTGAACGAGTGCATTACAT
CCTCCATGAAAACTGGCCATGAAGAAGCTCTGTGCGCGATGGGTGCCGCGCCTGCTCACTTTGGACCAAAAAACGGAAA
CGAAAGAATTTCTGCTCAGAATCTCACACTGTTTCAGGCGCAATCCACAGGACTTTTTCGCGAGATTTCAACTGTGGAT
GAAACTTGGATCCACCATTACACTCCAGACAAACAACAGTCCAAACAATGGACGAAGAGTGGGAGAGTGCACCA
AGAAGGCGAAGACTGTTTGTGTCAGCTGGAAGGTGATGGCCACTGCTTTTTGGGATTTCCAGGGTATAATCTGATAGA
TTATTTGAAAAAAGGCAGATCCATAACTGGGCCCTATTATGCTGCTGCTGGATCGTTTGAACAGGAACTAATTGAAAA
ACGTCCAAGATTGGCACGGAAGAAAGTGTGTTTCATCAGGACAATGCTCCAGCCACACAGCAGCTATCGCAATGGCAA
AAGTGCACGACTTGGGATTGCAATTGGTTTCTCACCCACCCTATTACCAGACTTGGCTCCGAGTACTTCTTCTATTCC
CAAACCTGAAAATTTGGCTTGGTGGGAAGAAATTTTCATCGAATGAGGAAGTGTCCGCCGCTGTGACAGACTATTTTGCA
GAGTTTGACAAAGCCTACTTTGCCGATGGGTTGAAAAAATTGAAAACCTCGCTGGACCAAGTGTATAGCCTTGCAAGGAG
ACTATGTCGAGAAATAAAGTGAATTTTCGCCTTTAAAACAANTTTTTATTCTATTTaccagacttacaaccgctt

Lmmar10 TIRs | TSD | Consensus from 83 copies | *Ortmar29* lineage

tacgagggetatccacaagctacattacgttttCGTTTGTGTCCGTTAGGGGCGGGGCTAGCGCGGCCATCTTGGTGTGATGGCATTCCGCCC
CTCAGTCGGCATCTGCCGTGCTAGTGAGAGGTTTCGTGCTGTACTCCGTTGAGTTACTGTGACAGTTTGAATGTGACG
GTTAATTTGAAAATGCCCGGAAGTGTGAAGTGCCTGTAATAAAGTTTTCTGACTGCAAAAACTGTACACCGATAGAA
ATCATCGGACGCTTTTGTGAAGTGTATGGGACACATAACTGAAAGTGGAGTGCCTCAATGGGTCATAAAAAATTTAA
AAATGGCCGAACCTAACGTTACAGCAAGCAAGCAAGTGAAGACCCAGCATAGTACTGCCGAACCTGTGCAAAAAAG
TCGATGCCGCGGTCCGTGAAAACCGTAATTTACAATAACGGAACCTCTATGAGTTTTCCACAAATTTACGAAGTTTGT
TGCACGAAATCATTACCGAAAAGCTTGGTTACCACAAGTTTTGTGCAAGATGGATAACCAAAAACTTTGACAGAGATTAC
AAAAATCAGCGAATGGCTGCAGCGTTAACGTTTTTGGACGCTTACGAGAAAGATGGCGACTCATTACTCGATCGCATCGT
TACTGGTGACGAAACATGGGTTAAGCATGTGAAGTGCAGACAAAATTCAGTCAATGCAGTGGGGGCACACAAATTC
CCCCAAAACCCAAAGAAATGCATGCAGACAATGTCGGCAAGGAAGGTGATGGCGACTGTCTTTTGGGACAGAAAAGGT
GTGATTTTTGTGGATTTCTGGAAAGAGGCACTACAATAAACTCTCAAAGGTATTGCCAAACTCTGCACAACCTCAGAAG
AGCAATACAAAACAAGCGCAGGGGAAAGTTGGGCTCAAAGATCTTGTGATTACGACAACGCCCGGGCCACACGGC
AAATGCCACTCGTGAAGTTCTCGAATCTTTAAGTGGGAGTTGTTTCTCATCCGCCGTACAGTCCCAGCTGGCACC

GCGACTTCCACTTATTCCCAGCAATGAAGAAGTGGTTGGCTATGCAGCGTTTTGATGACGACGCACAGCTTCAAGAAGAG
GTAACCACGTGGTTGAAGGCGCAGGCCGCCGAATTTACGACGAAGGAATTTCCAAGCTCGTCCATCGCTACGATAAGTG
CCTTAATTTAAATGGCAACTATGTAGAAAAGTAGTATTTAAGTGTGGCTTTCATCTGTATATAATNAAAAAAANTTCCAATA
CTTTATTTATTTTAAATTCaaaacgtaatgacttttgatagccctcgta

Lmmar11 TIRs | TSD | Consensus from 117 copies | *Ortmar19* lineage

tangagggtgtttttaagtaagggccgtCGCGGTATAGTCCCAGTTCGCGCGGACGCCGCAACAAGCCACCGGCCACTTGCCGG
CATCCTTCCCCTTCACTGATGCCAGTTGCAGCTCTGTAGCTGACGTGTACGCATCGCTGTGCTACTTTATAATGTTTAC
GATTATTGAATCGCCCCGCCGTGTGAGATACGGTCAGTGATACGTTTTTTGACCGCGAGAAGCCTATCAGCTGCAGAAA
TTCATCGTCAAGTAAACAGAAGTTTATGGCTTGAATGCAATGAGTGAAGGTAAAGTGCCTAATGGGTTAGAGAGTTTAA
AAATGGCCGTCAAACCGTCCATGACGAAGAACGCTCAGGCCGCCCTCTGTGATCACTGATGATTTGGTGGCTGCAGTC
GAAACAAAGATTCTGTGAGGACAGAAGATTCACAATTTCCACTCTTTCTTTGGAATTTCCACAAGTTTCAAGATCGGTTTT
GTACAAAATTGTGTCTGAAAACCTAAACTTTAAGAACTGTGTTCTCGGTGGGTACCCAGACTCCTCACAGAGGACCAC
AAAGGGAAGAGATTTGCCACTTCAATGGACTTTTTGATTGCTTACGAGGAAGAAGGGGATGACATGTTGAGTCAAATTGT
CACTGGAGATGAAACATGGGTATCCCATCACTCCCGAAAGCAAGCGACAATCGATGGAATGGCGACACACAACCTCAC
CCGTCAAGGTCAAAGCCAAACAGACGCTGTCAAAGCGCAAGATTATGGCAACTGTGTTCTGCGGACCTGTTCTGGGCGCGGTTT
GCTAGTGGACTTTATGCCACGAGGAACGACAATCAACTCAGATGCCTACTGTGCAACTCTAAAGAAGCTCCGCAGAGCA
ATTCAAAAACAAAGGCGCGCATGCTGACAAAAGGAGTTTTGCTCCTGCACGATAACGCTAGGCCCTCACACCTCTCAAAA
AGACTCGGGATTGATTGATTCTTTTGGCTGGGAAGTTTTGGACCATGCACCATACAGCCCCGACCTTGCTCCTAGCGATT
TTCACCTTTTCCGGTACCTGAAACACCATCTTGGCGGGCAGCGCTTCAATGACGACGATGAAGTGAAGCGGCCGTGAA
CTCTTGGCTGTGCGAGCAGGCCGCCGAATTTTGAAGAGGGAATTA AAAACTTAGTTGTACGGTATGACAAGTGCTTAA
ATAAACAAGGCAACTATGTAGAAAATAGGTAAGTGTGTAGAAATCAGAAAATAAAAGTTTTNTTTACAAAAGTATTG
TATCTTTTTTTAAAAATAAAaaccgcttacttaaaaaaacacctcgta

Lmmar12 TIRs | TSD | Consensus from 8 copies | *Ortmar16* lineage

taatccnaaaagtaaggtctctattttttataagtaacaGAACTCTGTTTGTGTGGCAGTTGGTCCACACTNTTATGAAGAGTGCTTCCCNCNCTG
TGTGTAACATGCGCACNCCNCTGAGGGCCTCAGTCTTGNCTTGGCAGCCNNTGAGAATGGAGTCCCGTGGGATG
TTACCGCAAAGTGCGAATTGNGCGCAGTTATTCGGTTTTTGAACGCAAAAGGGCACTGCCCGATTGAAATCCATCGCCA
ATTGACCGAAAGTGTATGGTGAGTCTGTCATGGATGTCAAAAATGTTCTGTAAGTGGTGTAGAGAGTTTGCAGCTGGTCGG
ACTGAAATTCACGACGAACAAGGAGCGGGAGACCGTCAATTTCTGAGGAGACAGTGTGAAAGTTGAGCAAAGCAT
GCGTGAAGATCGGCGGATCACCTGGATGATCTCTGCACGTTGGTTTCTGAGGTTTCCCAGAACCCGCTCACAGAATT
TTAACGGAAACATTGAACTACCGGAAGGTGTGCGCAAGATGGGTGCCACGCATGCTGACTGAAGACCACATGCGGCAA
CGAGTTGATGCTTCCCAGCATTTCTTACCGCTTGCAGCCGAACAGGACAACCTTTCTGGACTCAATTGTCACGGGTG
ACGAAACCTGGGCATACCCTTTACACCTGAGACCAAGCAACAATCACGCCAGTGGCGGCATCCTTCTCGCCAAAGC
CGCGGAAATTCAAACAACACAGTCTGCCGTAAGTGCATGACAACCGTGTGTTTGGGATCGGAAAGGGTATTGTTGG
TCGACTTTATGCCACTGGGACCACAATTAACGCTGACAGGTACTGTGAGACTCTGAAAAAATCAAACGGGCAATTCA
GAACCGGAGAAGAGGAATGTTGAGCAAGGGCGTACACATTCTCCATGACAACGCTCGCCACACGCTCGCTCGGCAAAAC
CGTTGCTCTCCTGCAACAGTTTCAGTGGAAATCATCACCCACCCACCCTATAGTCCCAGCTTGGCGCCAGTNACTATC
ACCTGTTCCCTAAGTTGAAAGAACATTTGGCCGAAAGCGATTTCAGCTCCGACGACGAGGTGAAAGAAGAGGTTTATA
ACTTTCTGAACAGCATGGNGGNGAGCTGGTATGACATGGCCTNNAAAAACTGCCACAGCGTCTACAAAAATGCATCG
ACAGAAATGGTGATTATGTGAAAAATAGCTAAATGTTCAAGCTGTAAACTGATGTAAANCATTGTAGAAATAAACANG
TCTAtgtactataaaaaatangacaccttctttgggatta

Lmmar13 TIRs | TSD | Consensus from 426 copies | *Ortmar37* lineage

taacagggttggaaacttaaatagtgcaaacACTGCTGTGGAGACACTATGCAATGGAATCTACTATTGTGCTGATAGCACACGTTGTTGA
CATACTACCTTACCTCCGAGCAAATGGACTCGCCCGTCCCACGTCACCGCGTGCACACAATCGAGGGAAACACAGTC
ACTTGTGAGCGAGCGGTCTAACGTAACGGTGTCACTATGTTTTCGAAACAGGAACAACGGAGTTGGATCAAGATTGAAT
GTGCCAGAGGTCGTACAGCAGCAGAGTGTCAATGAGTCTTCAAGAGGCGTGCAGGGGAATCGGCATTGCCGTACAGAA
CAGTGGCACGTTGGGTAAAAGCCTTCAACGAAGGTCGGCAAACCTGTGGCAGACATGCATCGGGCAGGTCGTCCTAGCG
TCTCTGAAGAAGAAGTGCATACTGTTGCCCGTTAGTGGACAGTGATCGACGCCAGACGATTCGTGAGCTCGCCACG
AAACCGGATTAGCGCATACTGCTGCTTCGCATCCTGAAGGAACGCCTGGGCATGCGAAAAATTGCATCACGATGGGT
TCCGATGAATTGACGGAATGCAGAAATGGATGCGTTACGACGCTGCTCAGACGCATTTGGACGCTATGAGCGCGA
AGGAGAGGCTTTTACGCCGTATCGTAACACTGGATGAGACATGGGCCACATCGTACGACGCAAAAATGAAACGCAA
TCCAACGAATGGCGTCTATATGGGTCGCCGCGAAAGTGCAGAAAGTGCAGAGCCCCAGTATGGTGAAGTTATGGTGA
TTCTCGTGTACGACTGTGATGGTGTATCCTAACGCATTACGTTCTCCACGGCAGACCGTCAATGCACAGTATTACTGTT
CGTTTTTGGAGCATCACCTGCGACCAGCTTTGCGAAAGAAGCGGCAACACTTTCTGCGCAACCCACCCATCATTGCA
CGACAATGCGCGGGCGCATAACGCGCAAGCTGTGGCTGCTCTGTTGCGGTCGATGGGACTGGGAAGTACTGTACCATCCA
CCATACTCCCCGACTTAAAGTCTTGTGACTTTGATTTGATTCGGAAGATGAAGGAACCACTTCGTGGCATTGCTTCAG
AACTGTTCCAGAGATTGACAGGCAGTAGACCGCTCCATTTCGACCATCAACAGAACAGGCTCTGCTAACGGTATACTA
CGCCTTCCACATCGCTGGCAACGGGTTCTACACAACGCTGGTGACTACTTTGAAGGACAGTAACAGGTGCAACATGTA
ACGCTTTTGTATCGGTTGTGAATAAATAgttccactatttaagttccaacctcgta

Lmmar14 TIRs | Consensus from 47 copies | *Ortmar56* lineage

atccaaaattttngggactggtgctgccatctgGAAAGTAGGAGTANTAGATCTTTGCACCGCTAGGTGGCGAGAGCTGCATATCTGATGAG
TCAGTGTGCAGAGTGGCATTACAGTGGGAGGACGTGTTGCGTGTCCACAGTGATTTCCGTAATACTCTGTGTTTGGTGT
GTGGCGATTTTACGATGGATCCGCGAACAGAACAGCGCGTGTGTATCAAATTCTGTGCGAATCTCGGGAAAAGTGCTAC
GGAGACCTTTGCAATGATTCAACAAGTGTTTGGGGACAGAGCATGAGCCGTANGCNTGTGTTTGTGAGTGGCATGCTCG
GTTACAGGGCCGCGGTACAGACGTCGAAGATGATGCTCACACTGGAAGGCCGTTAGCCGCACAACGCCAGACATTGT
TGCCAAACTTCAACAATTGGTTCGTGCGGATCGACGTCNAACCATTAAGACCTTGC GGATGAAGTGGGTATTGGTTAT
GGGACATGTCAACGAATGTTGACTGATGAATTGGGCATGCATCGTGTGCGCGAAAATTTGTGCCAAGGATCTTGACTG
CCGATCAGAAGGCACAGCGTGTGAAGTGTGCACNGACCTTCGTGACACCGCATCTGATGATCCAACCTTCTTGTACAG
GGTTATCACNGGCGACGAGAGCTGGATTACGGTTATGACCCAGAGACAAAGCAACAATCGTCCCAGTGGGAAGAGCCC
GGGCTCTCCAAGACCCAAAAAGCGAGACAGGTGAAGAGCAAAGTGAAGAGCATGATCATCGTTTTCTTTGATAACCAA
GGGAATTGTGCACAAAAGAAATTCGTCCACCCAAACAAACAGTGAATCCGCGTACTACTGTGACNTTTTGGGANGGCTC
CGTGA AACCGTGC GGCGACGACGGCCCGAACTTTGGCNTCAAGGGAAGTGGCTGCTGCATCACGACAANGCGCCCTG
TCACACGTCCTTGTCCACAGGACCTTTTGGCAAAAAACAACATGGCGGTTGTACCCACCCACCGTACTCNCAGAT
TTGGCACCTTGCACCTTCGCGCTATTTCCAAAACTGAACTCAAGTTGAAAGGCCGTCGGTTCCGACTCTAGAGAGG
ATCAGAAGACATCGCTGGCNGTGCTAAACACCTCAAAGAACAGGACTTCAGAAAACGTTTGACCAGTGGCAGAA
GCGCTGGGACCGGTGTGTACGTGCGGATGGAACTACTTCGAGGGTGATGGTGACCATTAGTCCAAAGGTAAGGTTTT
CAAcagatggcagcaccagtcccgaattttgat

Lmmar15 TIRs | TSD | Consensus from 52 copies | *Ortmar8* lineage

tacgaggnnttttttaagtaagaccgtttgCCACACCGCGGCCGACGCGTGC GGTCGGCGTTCGTGCGCATGCGCACTGGGTACCTACA
TCTGTTGTCTACGCACTGACGCCATTACAGTCTGATCTTCTTCTTGTGTACTGAGTGTAAAGATGCCTCCGA
TAATCGTGAGTCCCGCCGACTGTGAAGTACGGGCTGTTATAAGATTTCTTAGTGCTAAAGGCCTAAAAGCGATCGATATT
CATCGTGAGATCTGTGCAGTTTACGGAGAAAACATTATGAGTGATGGAATGGTAAGAAAAGTGGGTGAGAGCATTAAAGA
TGGCCGCACAAATGTGCATGATGAACAACGGAGTGGGCGTCTTCGGTCGTTAATGAAAGTTTGGTGCAGGAAGTGGAC
AATAAGGTGAGAGAAAACAGACGCTTTACGATTTCTCCTTGC GGATGACTTTCTAATGTTTCTCGTAGTGTTTTGTAT
GGCATTGTGACCGAGCATTGAATTACCGAAAATGTGCGCACGTTGGGTACCGAAAATGTTGACGGATGTGCACAAAA
CCAAACGTTTAGCGAGTGCATTTACTTTCTTGGCGGTACCACAACGACGGTGTGATTTCTTAAGCCAAATTGTTACG
GGCGATGAAACATGGGTGGCCTACGTACACACAGAATCAAAGCAACAGTCCATGGAATGGCGGCATTACAGATCCACCA
GAAAAGTGAAGTTTAAAGCAAAACAATTTCTGCCCGAAAATCATGTGCACAGTTTTTTGGGACAGAAAAGGAGTATTGCT
TGTGGAATTTCTGCCTCGTAATGAGACAATCAATGCAGCAGCTTACTGTAAGACATTGCACAATCTGCGCCGTTCAATTCA
GAACAAAAGACGTGGCAAGTTGAGCAAGGGCATCGTTTTGCTGCAAGACAATGCCCGTCCGCATGTGGCTAATCAGACC
ACAGATCTCATCATCTTTTCGATGGGAACTCTAGATCATCTCCGTACAGCCCTGATCTGGCGCCAGTGACTACCAT
CTGTTCTGCACTTGAAGAAACACCTGGGCGGTCAGCGTCTTCAAGACGATGACGAAGTCAAACAGTTGTGATGCAGT
GGTTACAAGTACAGCGGCAGACTTCTATGAGGAGGGTATTCAAAAACCTGGTACAACGTTATGACAAGTGCCTCAATATT
GACGGAAATTATGTAGAAAAGTAGATTAAGGTACAGGCTTTCATGTA AAAATAAAATATTAGATATCTTAGCACGTCTT
TTTTTAATTTcaaaacggtactacttaaaaaancacgcctcgta

Lmmar16 TIRs | TSD | Consensus from 53 copies | *Ortmar21* lineage

tacgaggtgttcataaagtaagttcccaatGCGCTACAGTCCGAGGAATGCGGTTAAGTGCATCTGGCAACACTGTCATGCAGCTCG
GTTCCCTCTCTCCACTGCCACAAGTTGGAGCTGTCTGCGACGTTTCAAGTGTAGGCTTGGCAGCCATTAGCGATGGAGCT
TCCGCTTGTCTTCCCGCCAGGTGCGAGTTACGATCAGTAATTCGTTTTTTGTGCGCAAAAAACACTGCGCCGATGGATAT
TCATGCACAACACTGTGTGAAGTTTATGGTGACAAGTGCATGAGTGTACAACACGTTTCGTAAGTGGTGCAAGAATTTAAA
GAAGGACGTACAGATGTCCATGACGAACAGCGTTCTGGTAGGCCATCGGTTTCGGACGAAACGATCGCAAAAGTGGAA
GAGACAATGCTGAAGGATCGACGAATAACAGTTTCGGGAACCTTTGTGAGCTTATCCCTGATGTAAGCAAGTCCACCATAA
ACAACATTTTACAGAAAATTTAGGTTATTCCAAGTTTGTGCAAGTGGGTCCCGAGAATGCTTACGGAAGACCACAA
ACGGCAACGCGTTCAAGCGGCCCGCAATTTCTCCAGGCCTACGAAAGCCATGGAGAGGAATTTCTGGACTCCATTGT
CACTGGGGATGAGACCTGGGTCCACTATTGACACCGGAAACGAAGGAACAATCCCGTCAAGTGGAAACATCCATCGTC
ACCGAAGCCGCGTAAGTTAAGCAACAACCTGTCTGCCGGCAAAGTGTGCGGAGCGGTGTTTTGGGACAGGAAGGGGTT
ATTGTTGTGCGAATTTATGCCTACTGGGACAACAATAAATGCTGATCGTTATTGTGAAACATTAAGGAACCTTCGCCGAG
CGATTCAGAACAAGAGGAGGGGCATGCTGACGAAGGGAGTGTGATTTTTCATCAAGACAACGCTCGTCCGCATGTGCGCC
GTGTGACAACCTGACTGATGACAACCTTCAATGGGATTTGTACACATCCGCCCTACAGTCCAGATTTAGCCCCAAGT
GACTATCATCTTTCCCGAATTGAAGAAACACCTGGGCGGACGCAATTACGCAACCGGAGAGGAAGTGAAGAAGAA
GTTCTACGCTACCTTCGACGCGCGGGAGAATTTACGACGACGCGCATCAAGAAGATGGTACACCCGAATGCAAAAA
TGCAATTAATCTTAACGGCGATTATGTGCAAAAATAGGAAATATTCTAAGCTTTTTTTCAATATATAATGTTATTTAAATAAAT
TTGTTTTTCATTTTGAAAAAAAAttgggaaccttactttatgacaacctcgta

Lmmar17 TIRs | Consensus from 9 copies | *Ortmar55* lineage

tgttcaaaaagtaagtgactttTCAAANTGNNNNNNNNAANNNTACATTCNATTATCNATNTTTTTNNNNNNNNNTNGTACANATGTCCC
NAANATATGTTACAGTTTCAAGTGTACAGCACTTCNTTTNTTTTTGACAGATAGAAAGGTTAGANGTGTTTTAGTGTG
CTCGGCGATTTCTATTATATAAAAAANTGNAGCAAGAATTTGCATCAAATTTGTGTGAAAAATGGAATCAAGTGCTC
TAAAACACTTGAAATGTTGACAGTGGCATAACGGTGTGCTGCTCTAAGTAAAANAATGTTTACAAGTGGTACAAGCTCT
TCCAAGATGGCCGAGAAGATGCCAATGACGAACCTCGCTCTGGACGCCCCAGCACATCAACAACAGATGATAACGTCGA

AGCTGTGAAGAAAATTGTTTTGGAAAATCGTCTGAATTACCGTAAGAGAAGTTGCTGAGGATGTTGGCATATCGGTCGGCT
CGTGTCAATGCAATTTTTTCGGATGTTTTGGGCATGAGACGTGTGTCAGCGAAGTTTTGTTCCAAAACCTTCTCAATTTTGATCA
GAAGAACCGTCGCATGAGCATCGCTCAGGAGCTCTGAATGACGTCAATGATGATCTGATTTGCTCAAAAAGGGTGATAA
CTGGTGACGAAACATGGGTTTACGGTTATGACGTGAAACCAAAGCCCAATCGTCCCAATGGAAGCATCCCGGAGAGCCA
AGACCGAAAAAAGCACGCCAAGTTTCGATCAAATGTCAAAGTTTTGCTCACTNTTTTTTTCAATTACCGTGGCGTAGTGCAT
CATGAATTTTTGCCTCAAGGTCGTACGGTCAATAAGGAGTATTACCTTGACGTTATGCGCCGTTTTCGAGAAAGCAATACGC
AAAAAANGTCCGGAATTGTGGAAAAACAATTCATGGCTTTTGCATCACGACAATGCACCTGCTCATTATCGTTGCTTGTG
AGAGATTTTTTGGCCAAAAACAACACGACAATCATGCCTCAGCCACCATATTACCGGATTTGGCCCCCTGCGACTTTTTTC
CTGTTCCAAAACCTGAAGAGACCTATGAAAGGACGAAGATTTGCAACGATTGAGGAAATAAAAACTGCATCGCTGGAAG
TACTCAAGGCTGTACCAAAAAGTGCTTATGAGAAGTGCTTCGAGGATTGGAAGAAGCGTTGGCACAAGTGATTTGATCT
GAGGGGATTACTTTGAAGGGGACAACATGAATATTGATGAATAATAAATATTTTTTCATAAAAATATaaagtcaccttacttttgaaca

Lmmar18 *Consensus from 11 copies | Ortmar57 lineage*

TNNNANNTNTGTCAGGANAGTAATGAGACTGTTTCTCTATTTTTCAGGAACTACACACAGTAGNACAATGAAACCAGTGGA
GCTGATAGAGGCATCCTTTGGCTACAAGCAGTGAAAAATTTGAAGTACCTACGGTGAACACAAGTGAGTTATAACATATTT
TGTGAGGGTGTGTTAGTGTTCGCTCGGAGAGATGGCGAGTACAAAACCTGGAACAACGCTACGCCATCAAATTTTGTG
GAAACTCAAGGACAATGCAGCAGAAAACATTTAGAAAAATTAACACAGGCGTATGGGGACCACACAATGTCCCGTGCACAA
GTGTTTCGGTGGCATAAGGCATTTATGGACGGTAGAGAGGAAGTTGAAGATGAGGCACGTTACAGGAAGACCAAGCACG
ACACGAAACGATGAAAATGTTGCCAGAGTGAGGGACCTGGTAAGAACAGATCGGCGCTAACGGTTAGGATGATTGCT
GATGAANTGAACATTAATCGCCAAGCAGTGACGAAATTTCTACTCAAGATTTGGGAATGAGAAAAATTTGTGCGAAAA
TGGTGCCAAAGAACCTTGACAATTAACAACAAAGGAGCATCGCATGACTGTGTGTCGTGACCTCATCAACCGCACTGAAA
CTGAACCAGACATTTTCAAACATGTTGTGACAGGTGATGAGACATGGGTTTTTCGAGTATGACCCTGAAACCAAAAAGACA
AAGTGCTGAGTGGCACACAAGCAGCTACCACGACCGAAGAAGGCCAGGAAAAGCAAATCAAAAATCAAGGTCATGT
TGATTTGCTTCTTTGATCATCAAGGCGTGATCCATAAGGAATTTGTTCTCAAGGAAAAACATTTGAATCAACAATTTTACA
TCCAGGTCCTTGAAAGACTAAGGAATCGGGTCATTCGTGTCCGTCTGACATGTCCCAATCATGGATCCTCCATCACGAC
AATGCGCCGTGCCACACTGCTCTCTCTGTTAATGAGTATCTTGCATAAAGGGCATTCTGTTTTGCCACAACCCCCCTAT
TCCCCAGATCTCAGTCCCTGTGACTTCTTCTATTTCCCAAAAATNAAAAATGCTGTTTCGTGGCCATCATTTTGGGTCCGTA
GAAAACATGAAAGGNTCGTGACACAGGAACCTCGAAGGGTGTCACTTGAGGACTTCCAGCAATGCTTCCGTGAGTGG
GAGNACGCTGCGTCGGTGTGTAGCTTCCCAAGGNACTACTTCNAAGGTGATCATGTGGTTTTGTAATGCATTGTA
TAAANNTGNNNNNTTTNNTGNCANACNT

Lmmar19 *TIRs | TSD | Consensus from 91 copies | Ortmar54 lineage*

tacgaggtgttagaaaagtaagattgGCAACACTGCGGGAGATCTGGCAACGTTGTGTCTACCGGCCGATGCTAAATCTGATTGTTG
ATCCCTTCCACTTCCCTCAGTCCGAGTTACAACCTCCGTACAGTTAACACATTAGTTTTACAACGCCATTAGTAAAGTTGTG
TTTTCAATTGTGCGTCACAGAAATGGAGCATCGGAATTTAGAGCAACGTTGTGCAATAAAGTTTTGTGTTAAACTTGGTGAA
TCCGCGAGTGTGACTTTTGAAGGTTGAAACAGGCCTATGGGGAACAGTGCTTATCGAGAGCACAAAGTTTTCCGCTGGC
ACAAATCATTTTTGGAAGGCCGAGAACACGTTGAAGATGAACCTCGCTCAGGGAGACCTTCGACTTCAAAAACCTGACGA
AAACATTGATCGTGTGAGGGCTCTTGTGAGATCAGACCGTCTGTTTAAACAATAAGGATGATCAGTGAACAGCTAAATTTAA
ACACTTTCACCGTGCATCAAATTTGTGACAGATGATTTGAACATGCGAAAGGTTTTGTGCCAAATTTGGTGCCGAAAAATCTC
ACAACAGACAGAAAGGATCTCGAAAAACAGTGTGCGTTGATCTTCTTGAGAGGATTGCTAATGACCAAGAATTTCTCA
ATTGTGTGATCACTGGTATGAACTTGGATATTTGAGTACGATCTGAAACAACAGCGGCAAAAGTAAAGAATGGCACAC
TCCGTATCTCTCGGCCGAAGAAATGTGCAATGAGCAAGTCAAAGATCAAAGACCATGCTGATTGTTNTTTTTGACAG
GAAGGGTATCGTGACAAAGAATTCGTTCCACCAGGACAAAACGTCAACCAAGTGTTTTATAAAAAGTGTCTTGAAAAG
TTGAGGAAAAGAGTGATCCGTGTGAGACCAGAAATTTGCAGACAAGTGGATGCTTACCATGACAATGCTCCGTGTGAC
ACGGCCATTTGCATCCGTGAATTTTTGACCTCAAAACGCATTAATGTTGTTTCTCAACCCCCCTATTACCTGATTTGAGT
CCTTGTGACTTTTTCTCTTCCCGAAATTTGAAACATGCTCTAAAAGGACGTCATTTTGGAACTCTGGAGAACATTCAAAA
GACAGTGACCGACCAGTTAAAAGCCATAACCAATTTGAAGACTTCCAGCGCTGCTACCAAGAGTGGGAACGACGACTCCG
CCGATGTGTAGCTGCCAAGGGAACACTTTGAAGGGGATAACATTGTTGTTTGAATAATAAAAACCTTTGGTTAGTAT
GAAATcagtcctacttttctcacacctcgtgta

Lmmar20 *TIRs | Consensus from 12 copies | Ortmar5*

agggtgtaccaaaagtaagttcccaATGAGCTACAGCCTCGAGGGAAGGTGCTAGGCTACATCNNAACAGTGCCNTGCGCAGCG
NTTNCNCACCTCGAGCCNCCCGTCCNCAATTCGCTACGTCGCTCAGTGTGGCTTGGNAGCCGTCAGAGATGGAAG
TGTGATCGCCCTCCCGCAAGTGCGAGGTTTCGAGCAGTAATCCGGTTTCTCCACGCAAGGAAGTTACCGCCCGTGG
GATTCATCGGCAACTGACTGAGGTTTATGGTGAAGAGTGCATGTCCGTTACGACGTCGCAAAATGGTGCAGGGCTTTT
GCTGAGGGTTCGACGGAAGTTACGATGAAGAACGGAGTGAAGACCGCCGGTTTCGGATGCGATTGTCCAGAAGATC
AACAGTGAGCTGCTCAAAGATCGGAGGGTCACTGTCCGTGAACTTGTGAAACGCATTCCTGAAGCTTCCACGGCACAA
TTGAAAGAACCTTAAACAGAAACGTTGGGTTATCGCAAGGTGTGTGCTCGCTGGGTCCCCGGATGCTGACTGACGGACA
CGAGGAGCAACGCCTTGACTGTGCTCGCAAGTTTCTTCAACAATGTGAGGGGGGAGGCAACAAGAAGAGGTTGTTGGA
CTCTATCGTCACGGGTGATGAAACGTGGGTGTTTTCATTACCCCCAAAACAAGCAACAGTCTCGTCAGTGGCGTCACT
CCGGTTACCGCCACCAAGAAATTTCAAACAACGCAGTCGGCAGGAAAGGTTATGGCGTCTGTGTTTTGGGATCGTAA
GGGGTACTCCTCATCGATTTTCATGCAACCTGGGACGACAATAAACGCAGACAGATATTGTGAAACATTGACCAAACTGC
GGCGAGCAATCCAGAATCGCCGAGAGGACGACTGACGGAGGGAGTAGTGCTTCTTACGACAACGCTCGACCCACG

TCGCTCGTCAAACACAGGAGCTTTTGAAGAAATTTGGGTGGACTGTTATGCCCATCCCCGTACAGCCCGGACTTAGCC
CCCAGCGATTATCACCTCTTCCCCAAGCTAAAGGAACACTTAGGTGGCAAACGCTTCAAGAGCGACGATGAAGTCCGAG
CAGAGGTCACACNCTTCTCAATGGGTGGCGGGAGACTTCTTNGACTTAGGAATACAAAAGCTGGAGCACCGTCTTCA
AAAGTGTGTCGAAAAAATGGAGACTATGTTGAAAAATAGACAAACGTGAGCTTTTCAACNATGTATAAATTAATAACAAT
AAAAATGTTTTCTATTTGTAAAAAATAtgggaacctacttttggtaacaacct

Lmmar21 *Consensus from 98 copies | Ortmar53*

TTNAATAAANAATNANNATANNNNNNNNNNNNNNNNAANTNNNNNNNNNNNAAATTTAATCTTANGATATTNTGTTAGCT
TAATNTGAAACAATNANNCNNTAGTAGTTTCATNTTTGGGACTCCNGNTTNCNGCCTGTGAGAGGCAGGCAAGTTCAGA
CATGTTACAGTATCGCCTACCGCTGCAATGGAGGTAACACGCGAGGAACAATACGCGGCTTTGAAATTCTGCTTTCGTCTCA
AGAAATCTTACAGCTGAGGCCTATACAATGTTACAGGAGGCATATGGAGAGTCTGTTCTTCCCTACAGCACAGCTCGAAGG
TGGTTAAAAATGTTTAAAGAGGGGAGACAATCAATTTCAAAGGAAGGTGGACCCCGGTGCTCCAGTTACTGCTCTTACGGA
AGAAAACATCAACACTGCTGCTGCTATTGTGAAAGAGGATCGACGAATTACCCTAAGATCACTTTCTGAAATACTGAACA
TTTCATTGGGTGCCACCCACACGTTGGTGACAGAAACATTACACATGAGACGTGTTTGTGCGCGATGGGTTCCAAGACTG
TTGATTCCCGAACAAAAGGACATTCGCGTGCAGGTCTGCATGCAGTTAAAGTTGATGTTAGAGGAAGATCCGGAGTTTCT
TTCAAATGTAATCACTGCTGATGAAACTTGGCTACATCATTTTGTCTGAGAGCAAAACAGCAAAGCTCAGTGTGGAAT
CTCCTTATCACCAACCCCAAAAAAGCAAAAGTGGTTGCTTCTGCTGGAAAGTTATGGTCATCTCATCTTTGATATTC
ATGGAATGGTTTATCAGCATGTCGTACCTGCACACACATCAGTAAGTGGACAATACTACAGGGATGTCCTGAAAACATTGC
AAGTCCATATCAGGCGCAAAGACCACATTTCCGTGAAGCAGGCTGGATGCTGCACCACGATAATGCGCGGCCGCATATT
GCCAATGTTGTTGCTGAATATCTTGCAAAAATCAACGTGAAGTGCATCCCTCACCTCCCTATAGTCCGGATTTAGCCCAT
GTGACTTTTTTCTATTCCTAACTTGAAGAAACGCCTTCGTGGGAGGCATTATCCATCATCAGAAGCAGTGGTGAAGGCTG
CGGAGGCGATTTTGAAGGACCTCTCAAAAATGGTTTCCAGCATGATTTGAAAGACTGGCAGAAACGCTGGGACAAGTG
CATCGCATTCATGGGAGACTATTTTGAAGAAGACCATCAAATATGAGGATGAGTAAAGGTATGTTGNAAAAANNTAT
GATNATCTTTATTGAACAGCNCTCNTA

Lmmar22 *TIRs | TSD | Consensus from 39 copies | Ortmar12 lineage*

tacgagggtatttcggaagtaagatacaCCGTACGCCAGAGGAACAGAAGAGTTTGGCGAGCAAGTTGGCAACACTGGTGTAAAC
TTGAACCGTTAGCTTTCTCCTCGCGGTCGTTCCGACAGTTGAACGTTGCTTCTGGTTGGAGTAGGTCGTGTTAAAAATGGC
TGCGCCGATTACAATCCCGCAATCGAAGTCGAGTCCGCTCAGTACGTTTCTTTCATGCAAAAGGTCAGCGACCAGCG
GATATTCACAAAGAAATGTTTCTGTTTATGGGAACATTGATGATCGACAAAATGTAACGAAATGGTGTGTCGTCATTTCTCT
GAAGGTAGGACCGATGTTTATGACGAACAAAGAACAGGTCGGCCATCTGTGATCTCTGATGCCCTTCTTCGGAGAACGG
AGGAAGCAATTCGTGCAATAGACGTCTCAAATGAAAGAATTGCATCAGATCATAACCGACGTGTCAATGACAACCTCT
TTATGACGTTGTGACTGTCAAGTTAGGGTACAGGAAATGTGTGCGCGCTGGGTTCCAAAAATGTTAACGGAAGAACAC
AAAAAGAAAAGGATGGGCTTTGCACTCGACTTCTCACACGCTATGCTGAAGCAGGTGATGAGTTCCTTGATCACATTGT
GACAGGTGACGAGACGTGGGTTTATCACCATACACCTGAATCCAAGCAACAATCAATGCAATGGCGCCATTGCAATTCAC
CAAAAGCCAAGAAATGCAAAACGTGATTTACGCGAAGAAAATCATGGCTTCTGTTTTTGGGACAGACAAGGCATTCT
TCTGTTGGAATTTATGCCTCTGGAACGACAATTAATGCTGCTGCATATTGCCAGACTTTGAAACGCTTTCGAAGGGCAAT
TCAAAACAAACGCAGGGGAATGCTGACAAATGGAGTCCGCTTGCTTTCATGACAACGCTCGGCCCTCACACAGCGCTCGTA
ACCAAAGCACTACTCAAACAATTCAAATGGGACGTATTGGACCATCCGCCATACAGCCCGGACCTTTCGCCCCACCGACTT
CCATGCTTCCGTTACCTGAAGTCAATCTTGGTGGAAAATCATTCCACGACGATGAAGAGATCAAAGATGAAGTTGAAA
TGTGGTTCCGACAACAGGCGGCAACCTTCTATGACTGTGGGATACAAAAGCTTGTGCACCGACTTAACAAATGTTTGGAT
AACGGGGGTGATTATGTCGAAAAATAACAATAATCCAGTTAATAAGATGTAAGTACTGACGTTTTCTAAATAAATGTTCTATTT
AAGGAATGCGAGCCATgtatcttacttttgcgaatgcacctgta

Lmmar23 *TIRs | TSD | Consensus from 61 copies | Ortmar66 lineage*

tacaaggtgcnttcataagtaatngaccaattTTTTCTGACNCAANGGTACACCACAGCGTGTGTAACCNGCTGGGCTAAGTGGAGGG
GGGTGTTAGCTTCAAANGCTCTTTGTCTCATTGCGCTGCGAGCTGCCGGAGAGTCAGGACGTGCNTTTCGTCAACCC
CGTTTTGAGTTTATGTAACACGGCACAATGGATCGTTCTGTAGAGCAACGGTACGCCATCAAATTTGCGTTAAACTTGG
GAAGTCCGCCACCGAAACGTTTCCATTACTTACGCGTGCCTTTGGGACTGATTGCTTGTCCAAATCACAAGTTTTCCGAT
GGCACAAGTCATTATGGAGGGCCGAGAGGAGATCACCGACGAACCTCGCAGTGGACGGCCATTAACCTCACGAGTCCG
ACGAAAATGTGACGCGTGTGCGGATTTGAACTCTGACAGACGGCTGAGCCTTCAATTGATAGCACAAAACCTCTAAA
CATGGCAAAAACAACCGTTTTCCGCATTGTGACCGAAGATTTGAACATGAGAAAAGGTGTGTGCCAAAACCTCGTCCAAA
AGTGTGACCGACGAACACAAGCAGATGCGAGTCTTCGGTGCCGAGAAATGTTGAAATGTGTGAAAATGATCCCTCA
TTTTTAAACTCAGTTATCACTGGTATGAGTCTGGATTTTTGAGTACGACCCTGAGACAAAAGGACAGATTCAGAG
TGGCACACCCCATCGTCGCCCGTCCCAAGAAGGCACGCATGAGCAAGTCCAGGATGAAAACCATGCTCATTGTCTTCT
TTGACGTCAGAGGCATTGTCCACCACGAATTCGTACCTACCGGGACTACTGTGAACTCGGCTTTCTACTTGGAAAGTGCT
CAAAAGACTGAAAAGGAGGGTCTCGCGCTGCCGAAAGCGACATCAAGGACACATGGAAAACCTTACCACGACAATGCGC
CGAGTCACAGCGCCTTCAATTGTCAACGAGTTCTGGCCAGGACCAACACCCCATTTGGTTCCCGAGCCTCCCTACAGTCC
TGACCTGGCTCCCNCTGACTTTTTTTTTGTTTCTCGGTTAAAAGGAGTCATGAAAGGAAAACATTGGGACACGATTGAA
AGCATCCAGGCGCATGTTACATCAGCTCTAAAGGACATTCGGAAAAGGCNNNNNNNCTTCCAGGCATGGAAAACACCG
CCTCCAGAAGTGTATCGANGCAAGAGGGTGCTATTTTGAATAATTTTGATTATTTGTACGAATATATCAATAAATGATTTT
TTATGaatttgctencattacttatggaacgcacctgta

Lmmar24 *TIRs* | *TSD* | *Consensus from 20 copies* | *Ortmar1 lineage*

tacgagggttattccaaaagtaaggctccgattCGCNGTAAATATTTGAAAGCGGGCCCAAGGACAAAACACGCATGCGCGCCGACTCCTGG
CATACTTTGNGCGTTAAACAGCCGCCAGTATCGTTGTTACTGTTGCTGTGTGCTGTTGATAGTGTGAGTTCACAATGTTTAA
GACAATCAATCAGCCCGCCGATGTGAAGTAAAGGGCAGTGATACGGTTTTTTGTCTGCAAGAAACATTTTCAGCGGCAGAA
ATCCATCGGCAGATTAAGTGAAGTGTACGGTCCTAACATAATGAGTGACAGTAAAGTGCAGCAAGTGGGTGCGAGCCTTAA
ATGAAGGACGGGAAATGTGCACGATGACCACGCTCCGGCCGACCATCCGTGATTTTCAGACGAGTTGGTTCATGCGGT
TGACGACAAAATTCGTGACGATCGACGATTTACTATTTTCAGTTTGAAGTGCATTTCCCGAATGTGAGTAGAACAACG
TTGTACAGAAATGTGTCTGAACATTTGAAGTTTCGAAAATTTGTCGCCCCGTTGGGTTCCAGGCTGCTTACCGAGACCCA
TAAAATGAAAAGAATGGCTTCTGCTCTTGCATTTTGGAGCGATATCATGAGGAAGGTGACAGTCTTTTAGACCATATTG
TCACAGGGGACGAGACATGGGTTTCTCACATCACCCCGAGTCTAAACGTCAGTCAATGGAATGGCGTCACACGTCATC
GCCAGGCAAGGTCAAGGCAAAGCAGACAATCTCCACACGCAAGGTTATGGCGACCGTGTTTTGGGATAGACATGGAGTA
TTGTTAGTCTGACTTTATGGAAAGAGGGACAACGGTCAATAAAGCCGCCTACTGCGCTACCCTGACTAAACTTCGACGTGC
AATCCAGAATAAGCGACGTGGTCTTTTGTGCTCTGGAGTGTGTTGTTGTCATGACAATGCCAGACCCCATACTGCGAAGG
ACACGCAAACCTAATCAAGAACTTTGGATGGGAACAGATGGACCACCCACCGTACAGTCCGGACTTGGCGCCAAGTGA
TTTCCACCTGTTCCGCTACCTAAAGGAGTTTCTTGGCGCAAGCGCTTCGACACAGATGATGAAGTGAAGAAGCTGTTA
AAGACTGGTTATCTTCGACGGCGCCGATTTCTACGACTTAGGCATTCAAAAGCTTGTGAACGATATGACAAATGTCTAA
ATAAGTATGGAGATTGTAGAAAAATAGAGAAAGACGGAAGGATGTCAATAAAAACAATTGCGTTGGAACAAGTTTGA
TTTTGGATGTTTTTGTTTTaaaccgacctacttttgaataatccctgta

Lmmar25 *Consensus from 5 copies* | *Ortmar15 lineage*

ANNANTNAAAANNGTNTNTAAATNNNNNCNNNNNCNNNNNNNTNNNNNTNTNTNTNTTTTAAACNTTTTNNNNANNTN
ANNTNCCCTCCGATCGTCCATCTAANCANGTANGNNNNAGGGAGGGGTTCGNACCTNCGCGCATGCNATTGCGCNGCTC
CCCCACNACAACCTCTGCCGTTTNCAGTCCAGTGTGTGACGTGAGCCGAGCTACGTCCGTGTAAACNTGGNCGCTACG
CTCGATGCTCCCGCAAATGTGAGTTACGAAGTGAATCCGTTTTCTGCAAGCAGAAGGATGTAAGTGTGCGGAAATCCA
TCGCAGAAATGAGCAACGTGTATGGTAAACAACGTTATGAGTGTAGTGTTCGGGAATGGTGTGCAAAAATTTAAAGAAG
GACGAACAGACGTCCATGATGAAGGTGGACAAGGTCGCAAGTCTGTGCGCACTGTAGGCCTCGTTGAGCGTGTGATCA
GGCGGTGAGATGCAAAACGAAGGTTTACAATTAGCGAAGTGTCTGATGAATTTCCAGACATTTCAAGGCTGCTTTGTACA
CAATGTGACTCAAGACTAGGCTATCGGAAATGTTGTGACGTTGGATCCCAAAAATGCTGAGTACCAGCCACAAAACG
CAAAGGTAGGGCTGAGCATNATCGTTTCTCACACGTTATGCCAATGAGGGAAACGTTTTTTTTAAGTTCGATTGTTACTGGC
GATGAAANGTGGGTCTCTATGACAATCCTGAAAACAAAGGAACAATCAAAGCAGTGGATGCACACAGCTTCCCCAAGCA
AGCCAAAAAAGTTTAAACATTCCTGACGAAAAGAAAAACAATGGCCACTGTGTTTTGGGACCATAAAGGAGTGTGCT
GGTGGACTTTATGGAGCAAGGTACGACGATAACCAAGGAAGTTTATTTGAAACTTTACGTCGCTCTCCGANAGCCATTC
AANACAAACGCAGAGGAATGCTTTCGTCTGGNGTTGTTTTGATCCATGACAACGCCCGACCACACAGTGCCAACATGAC
AAAAGACCTCTCAAAAAGTTTAAATGGGAAGTTTTTGAACATCCACCGTACAGCCCGGACCTAGCACCAAGTGATTATC
ACCTGTTCCGAAAACCTGAAGTCATGGTTAGGTGGGACGCGCTTCGCTACTAACGAAGAATTCAGGACGCCGTCAAGAC
TTACCTGTCTCACTGGCGGCAACATTTCTCGAGGAAGGCATCGAAAAGCTTGTGTACCGGTATGACAAGTGCCCTCAATC
GTTTTGGCGATTATGTAGAAAAATAAGTTAAGACTTTACTGTACTTTTTGGTAATAAAAATTATTTTCTGTANATTTTTCTTG
TNGNNNNNNNNANNNNNANTNCTNTNNNNANNNNTNCNCNCTNCNNTATNNNNANANNCTCNNNNNANGNNTTNNN
GNNATGNCNCCCCNNNNNNNTCNAATCNNNNNNATCTACANCTCATCGNANNTTGAANA

Lmmar26 *TIRs* | *Consensus from 32 copies* | *Ortmar60 lineage*

ggggacncaaaaantaaccggaatCGTAATGCTGCACATNGTGTACTTGTAGTAGCAGGTTGNGCCGCCAGAGGGTTGTAGTAGGAGC
TCTGCTGAGTCAATTCTGCCACGNGGCGTACCACACAGTGAGAAGTGTGGTTCTTTTGGCAGTTCTTTGAGTGTGCGTA
CAGTGCAGACGTGACACGAGGAAATGGCTAGTTCTTACGAACAACGTGCGGCAGTGAAGTTTTGTTTCTTGTGCGCA
AGAACGCAGCAGAAACTGTTGCGATGATTACAGACGCTACAAAGACCATGCTCTTAGTAAAACGCAAGTGTACGAAT
GGTTTTCTCGGTTTAAAAAGGGAGAAATGGTGGTTGAAGATCAGCCCCGTTCCGGTCGACCTTCAACTGCTCGAAGCG
AAGACAACATCGACAAAATCCGTGATCTCATAGTGAAGATCGACGCAGGACAATCGACCAACTCGAGAATTTGTCGG
GGTTGTCTGGAGCTCAATTCAGCGCATCTGACCATCGATTTGGGGATGCGAAGAGTGGCAGCAAAATTCGTGCCGAA
GCTTCTTACCGGAGATCAAAGGATCGTCGCTTCAAGCCTGTCACGAAATGAAGGACGCGTTCAAAGATGATCCACAT
TTTTTCAACAAAATCAATACAGGTGATGAGTCAATGGTGTATGGGTACGATCCAGAAAGTAAACAACAGTCAACACAATG
GAAGTCACTGGCTCACCTCGACCAAAAAAGCTCGACAAGTGAATCGAATGTGAAAACGATGTTGATCTGTNTTTT
TTGACATCAAAGGATCGTACACTCTGAATTTGTCCCTGAAAACGACAGTAAACCAACAATTTATTTGGAGGTTATG
AAACGGCTTCGAGAAGTTTGTGCGGAAAACGTCGGCTTTGTGGGATCTGGCGTGTGGTTCTGATCAGCAGACAACG
CTCCCGCGCACGCGCTTCAGCGTTTCGCGAGTTTTTGGCCTCAACGAAGACGACTACTTTGACCCACGCGCCTATTTCG
CCGGATTTAGCACCTCGACTTCTTCTTATTTCCCGAGGATGAAAAGAGACTTGAAGAGGGAAGCGTTTTGCGGATGTGGA
AGACGTAACGCAATGTATGAAAGTGTAGCAGGTATCAAAGAGGACGAATTTAAAAGGTGCTTCGAAACACTGGAAT
GAACGTTTGGACAAGTGTATTAATGCTAATGGAGAGTACTTCGAAGGAGATTAAGGTTGTATTTGAAAACAATAAAGTATA
TGCTTTCTAGAAAGAAattccggttattttgggtcccc

Lmmar27 *TIRs* | *TSD* | *Consensus from 483 copies* | *Ortmar6 lineage*

tacgagcgctccagaaagtaagtccggttCAATTTATCTCCGCTGCAGCGCTGCGATTGCAGTTCCGCACATGCGCTGTAGACGATGTG
TATCAAGGAGAAGAAGCTGCGCCATTTGGAGATCGCTGTGAGTTACGTACGCTTTGTTGTGCTTGTGTTGAAATGTGCGCG
TTGATTGAAAATCCCGCCGCTGTGAAATCAGGTCGGTGTATTCGGTTTTCTGAATGCGAGGAAAGTGAACCAAGTGA

TTTATCGGCAAATTTGCGATGTTTACGGACCAAATGCGATGAGTGATTTCGATGGTGAGAAGATGGGTCCGACAGTTCAAT
GGCGGGCGTAGTGTGACGATGAAGAACGAAGTGGGCGTCCACCTTTGGTTACAGAAGAAGTGGTTCACGCGATT
GATGACAAGATCCAGGAAAACCGTAGGTTTACAATTAGTGCTCTCGCTATGGACTTCCCCCAAATTTACGATCACTGAT
GCATGAAATTTGTACCAAACAACACTGAAATTCGGTAAACTTTGCTCACGTTGGGTACCAAAGATTCTCACTGAGCAACAC
AAAACACAACGGATGGGTAGTGCACCTTGAGTTTTTGACCCGTTATGCTGAAAGCGGCGAAGAATTTCTGAGACGGATAG
TCACAGGAGATGAAACGTGGGTTTCTTACGACACCCCTGAGAGTAAGCGGCAATCAATGGAATGGAGGCACACTTCAT
CCCCACCAAAGGTAAAGCCGAAGCAAATCATGACACCTCGGAAAATGATGTGCACAGTGTCTGGGACTGGAAAGGCA
TCCTACTCATTGACTTCTTACCGCGTGGTCAAACAATCAAAGCAGATGCTTATTGCGAGACACTTCGGAAAATTGCGCCGT
GCAATTCAGAATAAGCGCCGGGGACTGCTGTCAAAGGTGTTGTTTTGCTTACGACAACGCACGACCACACACTGCA
AATGTGACGAAAAACCTCCTACAGGGATTTGGCTGGGACGTGTTGACCATCTCCGTACAGCCCTGACCTCGCTCCTA
GCGACTTTCATCTGTTCTTACATCTCAAGTCTTTCCTTGGCGGTTCATCACTTACCAATGACGACGAGCTGAAAGAAAC
TGTTTCCAACCTGGTTGAAGACACAGGCGGCAGATTTCTATGAAGAAGGTATACAAAACCTGGTGCCACGCTATGACAAA
TGCCTGCAAAATTTGCGCAGTTATGTGAAAAGTAGTTTAAAGAGTTGTAGAATTTTGTGCAATAAAAAATTTCTTCTGTATC
TGTGTACAATTTCAATTTATTACCaacgggaacttcttgacgcgcctcgta

Lkmar1 TIRs | TSD | Consensus from 97 copies | *Ortmar32* lineage

tacgaggtaggctgaaaactaatgcacacatccttagagcgcgaacgaaaTGACCTNANAAGCGCGCCAGGTGGCATGTGGAAGTAACATTCCC
CCTCAATACGCATACGCAGGTTTGAAGTCGTTGCGTTCATCCTGTGAATTTGAGAAGCGGAAAGTATGGAGGCGTGTCT
AGTGCTATGTCAACGCGAGTTAAACAGCGTGTGTTATCGAATTTTAACTGCTGAAAAAGTGACTCCTACTGAGATTCA
TCGTCGTTTAAAGGCTGTTTATGGTGACGATGNTGTTGATAGGTCTACTGTAATCGATGGGTAATAAAAATTTGTTGGTTG
CGATCCTGGAAAAACCCATAATTTGTTGATGAAACNCGCAGCGGACGTGTGACCAATGCCTTAGACGATAAACATCGCAA
ACTCGTCGACGATTTGATTCAAAATGACCGNCGAATCACTCAAAGCGTATCGNAAACCATATTGGAATATCCAAGGAA
CGTGTNAGTTTCATTATTGAACAATGGGATACCGTAAAATCTGTGCACGATGGGTACCACGCCGTCTCACAGACGAGA
ACAAACAGCGTCGATTGGAATGCTGNGAGCAACTTTTGACGCGTACCCTGACGAAGGAGACGACTTTNTTTTGAATAT
TGTGACGNNGGACGAGTCATGGGTCCATATTACGACCCAGAAGAGAAAAGACAGATCGCTGAATATCGACATCCGTCT
TCTCCTCAGGCGAAAAAGTTCAAAACACAACCATCCGCAAAAAAACTTCTTTTACTGTTGTTTGGGATGCTCACCNAG
TTTATGTGACNGATTTTCTGGAACGAGGGGCAACGGTAAATCTTCTCAGTACATACAGACTTAAAAANACCTNCGACGT
CGAGTTTGTGCTGTAGAGCGACTGGCGCCAATAATCTTGAACACATGACAACGCTCGTCCACACCTCGCGCGCAAC
TGGAGAGGCTCTGCGAACTGAAGTTTGAACCGATTCCACACCTCCTTATTTCCCGGATCTTGCCTTGGCAGTTTTTA
TTTTTCCCTCTACTCAAGAGAGACCTCAAGGGTAATCTTACACCTCGGACGATGAGGTGAAGGCAGNTGTCAAGNCCT
GGATTGAGAAAAGTCGGAAGAATNTTTCAGTGACGGAATGAAAAAATTTGTTACANGTTGGGAGAAATGTGTTAGNCT
TAACNGTACTATGTTGAAAAATAAATATNTGATTTTGAACCTAAGAATTGTACTTTAATGTACTTTTTGCCCGATCTTGC
TATNTGTTTTgtgcgctctacaagcatgtgtcacttctcagcctaccctcgta

Lkmar2 TIRs | Consensus from 11 copies | *Ortmar26* lineage

acgagcgtgtccgaaagttaagaccgtttCGTTTACCGCCAACGCAGTGCTAGTGTGCGAGTTCGCGTATGCGCACTCGTCTCTCTGG
TTCATTGTCTTACTACTGACCTCATTACAGCCGGATTGTGTTGTGTTTACATTTGTTAGTGATCGTTCAAAAATGTTGAAGAC
AATTTCTGAGCCCCGCGACTGTGAAGTGCCTTCTGTAATACGGTTTTTGAACGCAAAGAATATTAACCAGCTGAAATTC
TCGTCAACTTGTAGAGATTTATGGTGAAAATGTAATGAGTGATGGAATGGTGAGAAAGTGGGTTAGACAATTCATGATG
ACGAACCAATGTTTCATGACGAAGCAGGAGTGGGCGCCTCTGTTGTCAATGATGTTTGGTTGAAAAAGTGAATGAG
AAAATTCGTGAAAACAGACGGTTTCAATAAAGATGCTTGTGATGAGATTCCACAATTTCAAAAACCTGTTTGCACGA
GATTGTCAAAAATCGCTTAAATTATCGAAATTTGTTTCCCGTTGGGTTCCGAAAATTTGACGGATGTCCAAAAACGAA
GCGACTTGGCAGTGCTTTGACATTCTTACCCGATACAGTGATGAGGGAGATGAATTTTAAACAGTATTGTGACCCGGTGA
TGAAACTTGGGTTTGTGATGCTACTCCAGAGTCAAACAACAGTTCGATGGAGTGGAGGCACTCACGATCCCCCENNAA
AAAAAANTCAAAAACAANGTTGTCAGCACAAAAATCATGTGCACTGTGTTCTGGGACAGACAGGGCATTCTGCTTGT
TGAGTTCCTTCCAGAGGTGAAACCATCAATGCGGTACGATACTGTGAAACGTTGAGAAAATTCGTCGCGCAATTC
AACAAAAGGCGTGAATGCTCAGTCAAGGCATTGTGTTGCTTCATGACAACGCACGTCCCCATTATGCTGGTGTCACTC
AAAACCTTATTCAACAATTCGGTTGGGAGCAGTTCAATCACCCCGCTACAGCCCCGATCTCGCACCTTCTGACTACCAC
TTGTTCTTGAACCTTGAAGCGTATTTTGGAGGAAGGCGCTTTGACAGCGATGACGACGCAAAAACCGGTGTTTACGACG
TGGCTGTCTCACTGGCGGCATCTTCTATGAAGAGGGCATAGAAAATTTGGTTTCCCGCTATGACAAAATGTCTGAACAA
TGGTGGCAACTATGTAGAAAATAGTTTAGGAAATGCTCTTTCATGTAATAAATTTTGTAAAAAATGTGTTTCTGA
GTTNTTTTaaacgtacttctcagcgcgcctcgta

Lkmar3 TIRs | TSD | Consensus from 25 copies | *Ortmar71* lineage

tangagtagggtcaaaaagtccggaaatGGTCGCTACAGTCAAGNATTTGTTTGGTGGAAAGGAAATTTTGTGTTGGGAGGTTGGCA
TCACTACTAGGGAAGGTGCTGTGCCGTTACGACGGCAGTTGGAGTTGGTTTCCCGCTGCGGTGATGATATTTAGACG
TAGTTTTTTTCTTTCGTCGGATTGTGAAATGTCGTCTTACAGACGAGCGTGCCTAATATCAAATNTGCGTGTGCTGGAGA
AATCACCTCGGAGACTCTTGAAGATGCTGAAGAAAGCATAACGAAACGATGCAACGAAGAAAACGGCAGTTTACGAGT
GGCACAAGCGTTTTCTGTGACGGTGCACAACAATGAAGATGACGTTCCGACTGGGCGGCCTTCCACTTCCACCACAG
ATGAGAATGTTGAGCGGTTGACAACTTGTGCGTGCAGGACAGGCGAACAACCATGACACTATTGCTCCGAACTTGG
TATTTACATGGGAGTGTTCACAGCATTTTATAATGATTTGAACATGCATCGTGTGTTGCTTGCACATGTTCCGAAAAT
GTTATCCCTGAGCAAAAAGAAATGAGAGTGACCATGTCCAGGGACTTGATTGAAATGGCTGATGCAGACGACAGCTT

CTGCGCAAAATTGTAACAGGTGATGAGACGTGGTGCTTTCTTTACGACCCTCAGACGAAACGGCAGTCTGCTGAATGGA
AGTCAAAAACATCACCAAGAAAAACAAAATTCGCTTGGACAGAAGCCGGGGTAAAGTAATGTTGGAGGTGTTCTTTG
ATTACCAGGGCTTGATTCATTATGAATTTATTCCTGAAGGGAAAACAGTCAACAAGAATTGTACACAGAGATCTTAAAA
CGGTACGAGATGCAATTCGACGAAAACGACCTGAAAAATGGACAGGGAATGATTGGTTTTTGTAGCATGACAATGCC
CGTCACATCGATCCCTAATGGTGAACAATACCTTGCCAAGAACAATGTTACCACTCTGGAACACCCTCCATATTCTCCCG
ATCTTGACCACCGGATTTTTACCTGTTTCCACGGCTGAAAATGACATTGAAGGGACATCATTTTGTGATTTCGTAGAGG
TGATGGAATAATGCGACGAAGAGGCTGATAGAATTTGAAAAACGGCTTTTCAGGAGTGTTCACAACAATTGTANGAACG
GTGGAATAAGTGTGTAGATGCAGAAGGAGAGTATTTTGAAGGAAAATAAGGAAAANATGTTANACATACTTTCAATAAAT
TTTTATTAACCAattccgggaactttttgacctacctcgtgta

Lkmar4 TIRs | TSD | Consensus from 4 copies | *Ortmar1* lineage

tacgagggttattccgaaagtaaggtccgaATCGCCGTAGCTAATCGAATGTGCGCGAACATTGAAACGCGCATGCGCACCGACTCCCGG
CATGCCTTGCGCGTTAAACGACGCCATTTGCATTGGTATTGTTGCAGTGTNCTGTTTACAGTGNACAGTTCAAAAATGTTTAA
ACAATTGATCAGCCC GCCGACTGTGAAATACNTTCAAGTATTCCGTTTTTGACAGCAAGGAACGTTTCAGCAGCGGAAA
TTCATCGACAGATAAGTGAAGTGTACGCCCCAATGCGATGAGTGACAGCAAAGTGCCTAAGTGGGTGAGAGCTTTCAA
GGACGGACGGGAAAATGTCCATGNTGAACCCGATCAGGCCGACCATGATGATCAGTAAGATTGGTCAATGCCGTG
GACGAAAAGATTTCGTGAAGACCGGCGATTACAATTTCAACTTTAGCATTGGAATTTCCGAATGTGAGTAGAACAACTTT
GCACAAAATTGTCTCTGAAAATTTGCAATTTCAAAAATTTGTGCTCACGTTGGGTTCCAGGCTGCTTACTGAGGAACACC
AAATGAAAAGAATGGCTTGTGCTCTTGATTTTTTGGACCGATATCATAAGGAAGGTGATCAACTTTTAGAGAACATTGTCA
CAGGCGACGAGACGTGGGTTTTCTCATGACCCAGANTCTAAACGTCAATGGAATGGCGTACACGACATCACC
AGTCAAAGTCAAGGCCAAGCAGACAATCTCAACACGCAAGGTTATGGCAACCTTGTTTTGGGATAGACATGGAGTCTTG
TTAGTCGAGTTTATGCAGCAAGGGACAACAATAAATGCAGCCGCTTACTGCGCTACCCTGACTAAACTTCGACGTGCAAT
ACAGAATAAGCGACGTGGCCTTCTGACGTCTGGAGTTTTGTTGCTGCATGACAATGCCAGACCCCATCTGCCATTCAAA
CCCAAAATCTGATCAGATCTTTTGGATGGGAACAGATTGACCACCCACCGTACAGTCCAGACTTGGCGCCGAGCGATT
TCACTTGTTCGNTACCTAAAGGAGTTTTCTCGGCGCAAGCGCTTCGCCACAGATGACGAGGTGAAAGAAGCAGTTGA
AGACTGGTTATCCTCACAGGCGGCAGACTTCTATGACTTCGGCATACAAAAGCTTGTAGAACGTTATGACAAATGTTTAA
ACAAAATGGAAACTATGTAGAAAAATAGAGAAAGATGTAAGGAATTAATAAAAANNNTTTTTTAAAAATCTGTGATGG
TTTTATTTTTATAAGAAAtcggacctactttccgaataaccctcgtgta

Lkmar5 TIRs | TSD | Consensus from 35 copies | *Ortmar35* lineage

tacgaggcactccagaagtaagagtactGTTACCCTATCGGACTGTGAGATTTTTTTTTCAAGTTTGGCAACACTGAGTGGTATGGAGGT
TCTTCTGAACATAAATAGTACCGTTGGACTTCGGCAGTACGAATGCTCGCCTTGTAAACGTGCGTTTTGAGTAAAATATGCC
GATAACAAATCCCGCCAAGTGCAGGTTGCGCGCTGTTATTCGGTTTTCTTCTGCGGAAGGAAAAACTCCGACTGAAATT
TTTTACGGATCAAAAATGTTTACGGCGAAGGTGTTATGAATCGTACAAACGTGTTAAGTGGTGTGAGAGTTAATGA
AGGCAGAACGAATGTTTCATGACGATCAAAGGAGTGAAGACCTTCCATTTTACCAGTATGAGTTGGTGCAAAAAATGAG
GAAACTGTTTCGTGAAGACCGTGCATTGACAGTGGATGAAATTTCCGCGATGTTCCACAACCTCTCCAGATCTCTTTGCA
CGAGACAATTACAAAAACGCTGGGATTCGAAAATTTGTGCGCAAGATGGGTCCCAAAAACAACTGACAGAACAGCACAA
AGTGAATCGGGTTCGTAGTGTCTGCGGAGTTCCCTTGAGCGATTGAAATGGAAGGTGAGGACTTTCTTAGCTCAATTGTGA
CTGGAGATGAAACCTGGGTAGCTCATTACACACCTGAGACAAAAAGACAGTCATCGCAATGGCGTACACAGGTTCCCC
ATCTGCCAAAATTCAAAACCAATTTTCGACAAAAAATCATGGCAACCATTTTTTGGGACCGTAAAGGAATCATT
TGATGCAATTTCTCCTCAAGGGGAGACGATTAACGCAGCAGTATCTGTGAGACCTTAAAAAACTCAAGCAGGACCAAT
TCAAAAACAAACGAGGGGAATGTTGACGAAAGGAGTGTGCTTGTGTCATGACAACGCTCGCCCGCACACGGCCAAACGC
CACCAGGCGCTTTTGGACTCATTGGTTGGGACATTTTGAACCACCTGCATACTCCCTGACTTGGCGCCTTCAGACTT
TCATCTTTTACCTCCCTGAAGACTCACATGGGTGAAAAAANTTTCAACCGACGAGGAAGTGAACAAGAAAGTCTTG
AACTGGAAGACGGAGATGGCGGGAGAATCTTTGAGGAGGGCATCAAAAAGCTTGTGCCACGGCTCACTAACTGTATAG
AACGAGAAGGCGACTACGTAGAAAAATAGCCAACAACCTGAAACAACAAAACCTGTAANTTTTTNAAAATAAATTTTTN
AANNAANNANAAAAATCGactactttttctggacgtgcctcgtgta

Lkmar6 TIRs | TSD | Consensus from 89 copies | *Ortmar72* lineage

tacgaagggtactaggaagttttgcaataTGATGTAACAATGAGCCGACGGTGGCTGCATGCTGCTGTGTGCTGAGACATGTTTACTACTT
GCACAGTAGCCGTAGCGCCATGCTATGCGCTCAGTTGTTTATTAGCAGTGATAGTTTTAAGTGTCTGCTATGGCATCGTG
GTCACGAAGTGTAGATACGGGACGTTTTACGGTATAACTTCGCGCTGGTTTTAAACGTAGACCAGTGTGTTAGAAATAATG
ACGGTCGCACTAGGTGATGTTTGTCCACATCGTACAACATATTCAGTGGTACAGAGAATTCCAAGGGGAAATTTTAC
TCTGAAGGACGCTAAAAGGACGGGAAGACCAGCAATGCTAGTTACGGAAGAAAACATTAATGCTGTGAGGAAAAATGCT
TGACAAAGATAGGCGAGTGACCTATCAGCAGATAGAGGATACCTTAGGCCTAAATGCACCAGCAATTCATTTGATTCTGC
ATGAGCATTTACAAGTGAAGAACTTTGTTGTCTGTGGGTGCCGCATAGACTGACTGAAGAGCAGATGTGGCGACGTGT
GACTTGGTGCCGGGAGATGCTGAAAATGTTTAATAAGGGACAATCTCGGTATGTAACAGCATCGTGACAGGTGACGAG
ACGTGGCTGTACTATTATGATGTGCCGACCAAGACTCAAAAACAAAGTTTGGGTCTTTGAAGATGAGGACACACCCGTAG
CTGTCAGAAAATCCCGATCTGTAAAGAAGAAAATGATAGCTGTATTTTCAAATCGAGTGGAAATGTGGAGCGTGTGTT
TTGGACACACAGAAGACAGTACAGCTAAGTGGTACTGAACAGTGCCTACCCAAAGTCATTGAATCTCTGAAGAAC
CTGCGGCCAAAGTCAAGAATGGACACCTGGTTTCTCCATCATGACAACGCTCCAGCTCACCGAGCCAAAGCCTGCACA
GAATATTTGACAACCTACAGGACTGAAACTTCTTGTGACCCCTCCTTACAGTCCAGACCTTGCTCCCTGCGACTTTGCAC

TGTTCCCGCATGTGAAAATGAAGCTGAAAGGGATGCGGTTTTCAAGTGATGAGGACCTTCTAAGGGCTTGGGACAACG
AGTGTGCCTTACTCCCCTAGCGAAACTTGGCAGAGCTGGTTAAGGATTGGTTTCAGAGGATGGAGAAGTGTATTGAATG
TGGCGGAAATTACTTTGAAAAAATTAATAAATAATGCTGtattgcaaaactttcctagtagtaccctttgta

Lkmar7 TIRs | TSD | Consensus from 229 copies | *Ortmar65* lineage

tacnaggtcaggcagaaaagtaatgagactgGCAACACTACAAGCGATCTGGCAACGCTGCGCTGTTGTCCTTGATAGGGCACGTGTATC
AGTACCCTCCCATAGCTCAGTGCGAGTTTCAACTCCTCCGTTAACTACGTGATTTTTGTGACTGCTATTAGTGAAGTTGT
GTTTTGGTTGTGCGTCAAGCAAATGGAACAGCGGAATTTGGAGCAACGTTGTGCCATTAATTTTTGTGTTAAGCTTGG
AGAATCGGCAAGTGTGACGTTTAAAAAGTTAAAACAGGCCTATGGGGAACATTCTTTATCCCGAGCTCAAGTTTTTCGC
TGGCACAATCATTTTTGGAAGGCAGAGAACACGTTGAAGATGAACACCGTTCAGGGAGGCCTTCAACTTCGAAAAC
GATGAAAACATCGAACGTGTGAACACTCTTGTGAGATCAGACCGTCGTTAACATTAAGAATGTTGAGTGAACAATTA
ATTTGAACAGATTTACCGTTCATCAAATTTTGTGAGTGAACATTTGCACATGCGAAAAGGTCTGTGCCAAAATGGTGCCGAA
AAACCTCACAATTCAGCAGAAGGACAATCGAAAAACAAGTGTCTTGATCTTGTGACAGAATCGCTAATGAGCAAGA
TTTCTTTAGTCGTGTGATCACAGGTGATGAATCATGGATTTTTGAATACGATCCTGAGACCAAGAGGCAAAGTGAGGAG
TGGCACACTGCAAACCTCTCCTCGACCAAAAGAAAGCTCGAATGATCAAATCGAAGATCAAAAACAATGCTGATTTGTTTT
TGGACAGAAGGGAATCGTCCACAAAGAAATTTGTCTCCAGGACAAACTGTCAACCAAGTTTTTATAAAGACCTCT
TGAAAGGCTTAGAAAAAGGGTCATTCGCGTGAGACCAGACATTGCAGACAAATGGATGCTCCATCATGACAACGCCCC
ATGTCACACTGCCCTCTCCATAACAGAATTTTTGACCTCAAAGGCATTCTGTGGTTCCCCAGCCCCCTATTACCTG
ACCTCAGTCCCTGTGACTTTTTCTTTTTCTAAACTGAAAAATATCCTCAAAGGTGCTCATTTCCGGACTGTAGAAAAAC
ATTCAAAGAGTGTAAACGGACATACTGAAGACCATAACCGTTGAAGACTTCCAGCGCTGCTACCAACAATGGGAACAA
CGTCTCCATCGGTGTGTAGCTGCCCAAGGGAACACTTTGAAGGGGATAACATTGATGTTGAAAAAATAAAAACTTT
GGTAAATAAAAAATcagttctcattctttctgctgacctcgtgta

Lkmar8 TIRs | TSD | Consensus from 53 copies | *Ortmar28* lineage

tacgaggggagtgcaactgaaaacctaaAGTGTAAATATAAAATCGAAAAGTGGGCGCCAGTGGCCTGTAAGTTGGTACGCGTGTTTTAA
ATAATGTGCCGGATGTCCTAGTTTGCAGCACAGTGCAGATGCGCAAACACCGGCGCAGGAACAGTATAAAGATGGCT
GCCCCACTAGCAACGTGCACCAGACGAACACGCTTCGGTGATGATTTTGCAAAAGTGAAGGTGTGAAACCTATA
GACATTTATCGCAGAATGAAGGTCCAGTATGGGATGCCTGTTGTCCACAGCAAGTGTATGAATGGTGTAGGAAGT
TCGCANATGGTGTGACGTCCGTAGCCGATGCTCAGCGCCCGGCCAGGCACATCGTGTGTGACTCCCGAGACTCAG
CAGCAGTTGAAGCCATCGTAATGGA AAAACCGCCGAGTGACATTGGATGACATTGCGACAGCTGTACACATTAGTCAATGG
TTCAGCACATCATTATGCATGATGTGCTCAGGTTTCATAAGGTGTCTGCACGATGGGTGCCCGGCAGCTGACTCCGG
AGTTGAAGCAGCGGCGTGTGATGCGTGTGAAGAACTTCTGCGGCGCCTTGAACGCGACGGTGATGCCTTCCTTGCAC
GAATCGTACCCGAGACGAAAACCTGGGTCCATTACCATCAGCCAGAAAACGAAGAGAGTGAGCAAAGAATGGCGCCATT
CGACATCACCCAAACCAAAGAAGTTTCGAACACAGCCATCAGCAGGGAAGGTTATGCTGACCCTCTTTTGGGACGAGA
AAGGCGTCTCTTGGAGCACTACACGCCGCGAGGGACCCTGTTACCAGTAACACATACACAGACCTCTCAAAAATCA
TCTTCGGCCTGCCATTAGAACAAAACGACGTGGATTGCTATCGACAGGTGTTCTTCTGCAACATGACAATGCACGGCCCC
ATACGGCTCGTGCAACGGTTGCGACAATCGCAGAAAATGCGGTTTGAATGTCTGCCTCATCCACCATACTCGCCCCGACCTT
GCCCCGAGTGATTTCCATATGTTTGGACCCCTAAAAGAAGCACTTTCTGGGACGAAATTCATTCCGATGAAGAGGTGCG
CCAGGCGGTGCACGAGTGGTTGCGCCGTCTCCAAAANAATTTTTTCTACGGGAATTCAGGCACCTTCGGAAGCGTTGG
CAGACATGCATTGAGCGTGGAGGAGACTATGTCGAAAATGATACAGGTTTCATTGATGTGTGCACAATAAATAAATTTG
AAAAATAAAtaaggttttcatttgactctccctcgtgta

Lkmar9 TIRs | TSD | Consensus from 17 copies | *Ortmar2* lineage

tacgaaggtgctgaaaagtaatgctcctcgaattttatTCAGTTCTCAATATCGGTTGAGGTATTACATGTCATGATATTACTCGGTGCACTTT
CCCGCTTCGCTGACGCAAGTTGCAACCCTCTGCCGCTAGAGGGCTCCGAATTGTAGCGTGTAAACATGGCGGTGTGTAAC
GTAACATATGTCGGTGCATGAGAAACAGCGTGTGTAATCGAGTTTCTAACCGCAGAAAACGTGCCTCCAATTGAAATCCA
TAGAAGAATGAAAGCTGTGTACGGTGATGATTGTATCGACATCAGAAAATGTGCGACGTTGGGTTGTTCTGTGCTCGTAAGG
AAGGAAACGGAGGTGCTAACCTCAATGTGTGCGACAGAGCTCGGAGTGGACACCNGTACGGCTACTGACGAGGCTC
ATCGGAATCGGGTTGGTGAACCTCATCAGAGAAAATCGTCCGATAACACAGACACAGCTCTCAGGTAAGTGTGGCATATTA
CGAGAGCGTGTGCAGGCCATCATTGCAGAACTGCGGTACAAAAAATGTTGTGCACGGTGGGTGCCTCGAATGCTTACTC
CTGACATGAAACAGAGGAGATTGGACATCTGTGCAATTTCTTTTGGCTTTTGGAGCGTGAGGGTGTGAGGTTCTTAAAC
AACATTTGTACAGGTGATGAAAGCTGGGTTCAACATTTTACCCCGAAAACAAGAGAGCATCAATGGAGTTCCGCCACA
AAGGATCACCCGCCACAAAAGTTCAAGACCATTGCCATCAGCAGGCAAAGTCAAGTGTCTCAGAGTGTCTGGGATGTTCA
AGGTGTGGTGCATTTGGAAATTCATGCTTAAAGCCACCCATCAAAACTCTGCAAGGTACTGCGAGACCTCAGAAAACTGA
AAGCACGAATTCGAAGAGTTCGTCCACACATGGAGCACCCCTCTCCTTACGATGACAATGCCAGACCACACAGAGCGC
TGCGACATCTGCAACAATCCGACGCTTTGGGTTCACTGTATCGATCATCTCCATACAGTCCCGACTTGGCCCCATCCGA
TTTTCATCTGTTTCCAAAACCTTAAAGAACACCTTCGAGGACTTCACTTTGATAGTGTGAAGCGGTGCAAGCAGAGGTGA
GGTTGTGGCTCCGTCAACAAAGTCAAACATTCTACAGTGACGGTATCAACAAACTGGTCTATCGTTGGCAGAAATGTGTT
CGTATCCAGGGTACTATGTTGAGAAAATAAATATGTAGACATGAAGAATAAAGATGTAGAGTGTAAATGAAGTTTGTTTTA
TTGAAAAGCTTTAAGAGTTTTTACataaaaactcgaggtcattcttcagcagcctcgtgta

Lkmar10 TIRs | TSD | Consensus from 17 copies | *Ortmar67 lineage*

tacgaggtgtggcaattaataacgagactgCGACCTCTATCGCGCAGCCGCATGTTGGAAGTTGGTATTGGGATGCAGTTAACCTTG AACCTTCAAGAGCAGCCACCGTTTCGTTTCGTTCTATCGGCAATAGTTTGGTTTTGAGCGTCGGTTGTAATGGACGTT GTTCTGTAGAAGTCCCGCATGTGTAACCTTAAATATCGAGCAGCGCATTAACTCAAATTCCTTGTGAAATTAAGA AGTCGCCAACGGAATGTTTTATATGTTAACGGAGGTGTTTGGCGATAGTGTATGTCACGTGCGCGAGTGTGTAATGG CACAAACGGTTTTTCAGAAGGTCCGGAAAGAGGTTGAAGATAATGAACGTCCCGTTCGCAGTGTGAGTTCAAGAACTGAA GAAAACGTTTCAGAAAATTAATGAAATTTGTGCGGAAAGACCGACGTCTGAGCATTTCGGATGATCGCAGAAAATGGTGAAC ATTAACAAAGAGACAGTAAGACAAAATTTTGCATGATGAATTAACATGACAAAAATTTGTGCAAAAATGGTTCCGAAAA ACCTCTCTCAAGAACAAAAGACAATCGGAAGGACATTTGCTCTGATGTCATGGAACGACTCAAGGAAGAACCGGACT TGCTCACACGTGTCATCAGATGTGATGAAACATGGATCTTTCAGTACGACCCAGAAAACGAAGCGTCAATCGATGCACTGG AAGACTCCCACATCGCCAAGAATGAAAAAAGCGCGAATGAGCAAGTCAAACCTGAAGGCAATGCTGATCGTTTTTTTCG ATATCAGGGGTGTTATCATGACCGAATGGGTGCCTGAGGGTCAAACCGTTAATCAGAAATACTATAAAGAAGTCTAATCA AGCTGAGGGAAGAGTAAGGAAGAAAAGACCGGATTTGTGGAAGAACGACGCTTGGATTCTCCATCAGGACAACCGCGC CAGCCCACAAAGCCCTATCTGTGAAACAGTTTCTAGCGGACAAGCGCATTCTGTGCTCGAACATCTCCGTATTCACCA GATCTGGCTCCCTGTGACTTTTATCTATTTCCAAAAATTAAGAGTGCATTGAAGGGAACACATTTTCAGTCTGTTGAAGAG GTAAAAACAAAACGGCAGAAATGTTGAAGAACGTGACAATGGATGACCTACAGCATTGCTTTGAACAATGGAAGACAC GAATGCGAGNGGTGTATAGATAGGGGAGGGGATGTTGAAGGGGATAAAAAGTTAGTTGTAACCTTTGTTTGAATAAATC CCATTTCTGCCACcagctcgtatttaattncacacctcgta

Lkmar11 TIRs | TSD | Consensus from 10 copies | *Ortmar63 lineage*

tacgaggtgtgtcaaaaagatcgcgaatttgaattttCGCGGGTTACGTATATTCGAATTTTCGATTTTTTTGTAGCGTTATGTTGGTACTCATGT CTCTCACTTATGCCGACAAGCTCGGCCATTTGAATGTTCACTTAATTGTTGACAGCTGCTTTGCTTGCACGTGTTTTGGA TCGTCTTCGATTTTTACCTATCAAAAAATGGATCAAAGAACCTGTATCAAATTTTGTGTGAAAAACGAAATTAAGTGC GCGGATGCATTCGGAATGTTGATTGTGGCATAACGGAGAAGCTACCTTGGACCGAAGCAACGTTTATCGGTGGTACAAAA TGTCTCAGAAGGCCGAGAAGATGTGAACGACGAAGAGCGTGCCTGACGCCCCGAGCACTTCAACAACAGACGAAAAA ATTAATGAAGTGGAGAAAATGGTATTGGCCAATCGTCGAATCACCGTTAGAGAAGTTGTGAGGACCTAGACATATCGA TTGGCTCATGCCATTCGATTTTTATCAATGATTTGGGCATGAGACGGGTCCCGCGAAATTCGTACCAAAAATTTGCTCAATT GCGACCAAAAACAGCATCGCATGAACATTGCTAATGAGATGTTGGACTGTCCGCGACGACCAAAAATTTGCTCCAGAG GGTCAATACTGGTGCAGCAATCGTGGGTTTTATGTTTACGACGTGGAAACCAAAAGCTCAATCAATGGAAGCTGGCGC CACGAACCAAGACCGAAAAAAGCGCGCAAGTTTCGGTTCGAATGTGAAAAGTTTTGCTGACAGTTTTCTTCGATTGCAGG GGCGTGGTGCATCATGAGTTCTTGCCACAGGGTAGAACGGTCAATAAGGAATATTACCTGCAAGTTATGCGCAATTTGCG CGAAGCAATCCGCCAGAAAACGCCCCGATTTGTGGAAGAACAATAAATTTGGCTTTTGCACCACGATAACGCCCCCTGCTCA CACATCGTTGCTTGTGCGGACTTTTTGGCCAAAAACAACACGCTAATGATGCCGACGCCACCGTATCCCCAGATCTG GCCCCTGTGACTTTTTCTTGTTCCTAACTGAAGAGGCCATGAAAGGACGACGTTACGCTACGCTTGCAGAGATAA AGACGGGATCGAAGGAGGAGCTGAACAAGATAAAAAAAGATTTTTTGAAGTGCTTCGAAGATTGGAAAAACCGT TGGCACAAGTGTATAATATCTCATGGGGATTACTTTGAAGGGGACAAAATAGATATTCATGAATAAATAAATAATTTTTGA Aaaaacacaaaattcgcgatacttttgaacacacctcgta

Lkmar12 TIRs | TSD | Consensus from 34 copies | *Ortmar22*

tatgagggcgactcaaatgaaaaccgaacaccgccataacACACAGTCCGCGGAAAGGTGGCAACANTGTTGTTATGTATCGGTACTGCCAT CGTGTGGTAGGAGAACTGCATAGTGACAACCTCACAGGTGCNCGCAGTTGTTGGGTTATGTCCTTGTGGTGCAGCGGAC TGGTCTAGTGTGTTTCGTCACAGTGTAGAAATGGAGGCAAGCAAAGAAGAGCAGAGAGGTGTGGTTTCGTTTTCTGGTGG CTGAGAGTGTGGAGTACGCGAAAATTCATCGTCGCATGTCTGCTGTGTATGGTGAACACTGCATGTCCCTGACGAGTGT GTACGAGTGGCATAGGAGATTCGAGAAAGGGCGCACATCACTGCAAGACGATGCGCGTCCAGGACAGGCCCGTGCAGC CATTACCCCTGACGTGATAGGGCAGATTGATGTCCTTATCCGGGAAAACCGACGAATCACGGAGGAAGAAATTCGTGTT CAGGTCGGCATTAGCCATGGCTCCGTGCATGCCATTATCAAAGATCACTTGCATTTCCACAAAATTTGCGCGCAGTGGGT TCCGCATCAACTGACGGAGGGACAAAAGATTGACAGAATGGCGTCATGTCTGAGTCACTGCAGCGGTACCACGAGGA AGAGTATGCGTTTTCTGTCCCGTATCGTACAGGGGACGAAACGTGGTGCACCATTTCGAGCCCAGAGTAAACGGCA AAGCCAGCAATGGAACATCTCAATTTCCCCCGCCAAAGAAATCCAAAGCTGTTACACAAGTTCCGGTAAAAGTCAATG ATGACCTTCTTTTACAGCAGGGGGCCCTCTGCTTGTGACTTCCCTTGAGCGTGGAAACCACAATCAATGCGCAACGCT ATGACAGACACTTTGCAGAAACTGCGACGCGCCATAAAGTCAAACGCCCAGGAATGCTGTGCGACGGAATCATCCTGT TGCATGATAATGCTCGCCCCATACTGCCAATCTGACGAAGGCTACGCTTACGCGAATTTGGTTGGAAAACACTTCAACAT CCTCCGTACAGCCCGGATCTTTCACCTTGTGATTTTACATCTTTGGCGACTAAAGAAAGACATTCGTGGACGTCGATTC ATTCGGACGAGGAAGTGAAGAGTGGGTGGTGGATCCGTCAGCGACCTACCTTTCTACAAAACCTGGAATTT GATCGTCTCGTCTCCAGTGGGATAAATGTATCAACGCTTTTTGGTAATTACTTTTGAATAAAAACCTTTCCACGGTGAAGttgtagcgggtgttcggtttcatttgactcccctcata

Lkmar13 TIRs | TSD | Consensus from 24 copies | *Ortmar64 lineage*

tacgaggtgtgtcaaaaagtaacgggaattTTGTTATTTTCGCGGGTTGTATTAGTCNGATTCGCGCANTTTTTTCGTAGTTATGTTGGTAAAC ATGTCTTAAACGCATCTGTACACTGGTAGCCATATTGNATGATTAGTCTGTGTCAGTTGTGAANAAGGTTACGTGTGTTT GCTTGCANTGGCGATTTTTNATTTGTTGGAAAATGGATCAGAGAATTTGCATTAATTTTGTATAAAAACGGAATAA AATGTAACAAAGTTTTAGAAATGTTGAATATTGCTTTTGGTGTGAGTCCGCTATGAGTAAACAAGGGTTTACGAGTGGTAC AAGCGTTTTCAAAGATGGCCGTGAAGACGTTGAAGACGACGAGCGTTCTGGACGCCCCAGCACCTCAACAACCGATGA

AAACCGGAAAAAGTGAAAGAAATGATTATGAACGATCGCCGAATCACAATCAGAGAAGTTGCTGATGATGTTGGCATA
TCAATTGGCTCATGCCATGAAATTTTTTCGGATGTTTTGGGTATGAAACGTGTGACAGCAAAAATTTGTCCAAAGGTGTT
GAATTCGANCAAAAACACTGCGGCGAATGGAAGTTGCTCAGGAGTCGCTAAATGAAGTCAACAACGATGCAGAACTACT
GAAACGTGTCATAACAGGTGACGAAACATGGGNTACGGGTATGACGTCGAAACTAAGGTTCAATCGTCCCAGTGGAG
GCATTCTGGATCGCCAAGACCGAAAAAGCTCGNCAAGTGCGGTCAAATGTGAAGTTATGCTCACTGTTTTCTTCGAT
TTAAACGGCATAAGTGCACCATGAGTCTTGCCTAAAGGTCAAACAATCAATAAGGAGTACTACCTACAAGTTCAACGCC
GTTTGGGGAAAGCAATCCGAAAAAACGCCCGATTTGTGGCGAAACAATTCATGGCTTTTGCACCACGATAATGCACC
TGCACACACTTCATTGCTTGTTCGTGAATTTTTGGCGAAAAACAACACTGTAATGATGCCCCAGCCTCCATATTCGCCTG
ATATGGCCCCGTGTGACTTTTTCTNTTTCCAAAAATAAAAAGAACCTTAAAGGGNCGTCGTTTTACAAGCATAGATGAG
ATTAAANCGCATCGCTGAGAGAGCTAAATGCTATCCCAAAGATCGAGTCCAGAAGTGTTCGGGGACTGGAAGAAGC
GCTGGCATAAGTGTATAATATCTAATGGGGACTACTTTGAAGGTGATAACATTGTTGTAGATGAATAAATAAATNTTTCC
AAAAATNACaattcccgtacttttgaacacacctgta

Lkmar14 TIRs | Consensus from 14 copies | *Ortmar73* lineage

cgaagtcgttacgaaagtttgagacagacTGTGTTATGGTCCATTTTTGCCTTTCCAAGAAAGCTGGCCGACAGCGGCGTCCTTTCCGA
GTAACCTCGTCTAGTAGCAACTTNTCTNNGCTTAGCGCTGTGCTAGGAGGGCTTTCTNTGTTTCTGTTTACGCGGCATT
AGTTCCTGTGTCAGAATGGAGCCGGAAGAGAGCACTTTCNCGCAATGATTCTCTATGACTTTAAAAGTGGTTTAAACGAA
TCTGAAAGTCTTGATCGTTTGAACGGGCCCTTCGGGGACCTTGCTCCTTCCCGTGCACAATATTTCCGGTGGTTTCAAGA
ATTTAGAAGAGGTGCAACTTCGTTGAAAGATGAGGAGAGGAGCGGGCGTCCGGCGACTGCAATGACTGAGGAAAAACA
TCGCCGCTGTGGA AAAACTGGTGC GCGAAAACAATCGTGTGACATTTAAGGACATTGAAGCGACACTACAGATTGGAT
CGCCGGCAGTTTCCAAAATCCTGCACGAATATCTTCGAGTCAGGAAAGTTTCATCTCGATGGGTGCCTCACACTTTGAC
AGAGGCACAAAAGCGCATCCNTGTTGAATGGTGCGAAGAAATGTTGAACAGATTTCGACAGAGGCAACTCTAGGCGCGT
TCTGACATAGTTACTGGTGCAGAAACCTGGATTTATCAGTTCGATCCTGAAAATAAGCGCCAGTTCGACAGTATGGATTT
TTCCCGACGAACATCCACCAACAAAAGTGAAGCGGCCCTCGAAGTGTGCGAAAAGAAAATGGTGCAGCTTTCTTCTCCA
AAAGCGGACATGTTGCAACTGTTACCCTGGAAGAACAAAGAACTGTTACTGCTCTGTGGTACACAACAGTATGTCTACC
AAAAGTTTTTCAGAAAGCTTCAAGACCCGGCGCCAAAGACAGGACTGCGGGGAATCGTCTGCACCATGACAATGCGTC
TGCTCACACACTTACACTTACAGTTTCACTTGGAGTCCACAGAGGTTAAACTGATGACTACCCACTTACAGTCCG
GATCTGCGCCCTGTGATTTATTTCTGTTCCTCAGTCAAAAATCGCATGCGTGAAGAAGGTTCTCCAGCCCTGAAGA
AGCTGTTGAAGCCTACAAAAGTGAACCTGACGACTCGAGGAAAATGAGTGAATAACTGTTTTTCAGAAATGGTTTAA
GAGAATGCAAAAATGTATAGAGTGTGCTGGCGAGTATTTTGAGAAAATATAGTGATCAAATTTATTTCAAGTTTCTTAGTT
TTTgtgtatctcaaaacttctgtagccacctg

Lkmar15 TIRs | TSD | Consensus from 48 copies | *Ortmar68* lineage

tacacctgtattcaaaaagttccaggactgCCGCCCTGACAACANTACAGGTGGCGCCATCACTGCGGAATAAATTTGTATTACGTAGGAA
CGACCTTAGGCGATACCGAGACTTAGTTTCATTCAATTCGGACAGGTTCTATCCTGTAGGCGGCCATTCTGTAAAGTGT
TTCAGTGTGCTCTTGTATCGTAACAGTATGGAGCAACGAACAAACATCAAATTTTGTTTTAAATTGGGCAATCGCCCA
CAGAAACGTATGAAATGATTAAGGCTGTGTATGGTGAAGATGCAATGAGTCGTTCCGCGAGTGTTTGAGTGGTTCTCGAG
GTTTTCAGAGATGGGAGAGAATCAATGGAAGATGATGAGAGATCAGGTGCTCCGCGTTCAAGTCGCAATGATGAAAATGT
GGAAAAGGTGCAAGNTTATGTAGGTTAGACCCCGAATGACGATAGAAATGATAGCAGATTCACTAAACTTGAGCGT
GGGATCAGTTTACGATTATGGCAGAAGATTTCAA AAAAGAAAACACTGTGTGCGCGCTTCGTGCCGATTTCGCTCACTG
AGGAGCAAAAAGAGCATCGGGTGTTCCTGCGAAGAGTTGGTTTTTCATGGCCGATCAAAAATCCAAAATTTCTGCAAAA
ACATTGTCACCGGAGACGAGACTTGGTGTCTAGAGTACTATCCGGAGACAAAACGCCAAAAGTGTGATGAAATGGACGAGCC
CGGAAAAGAAGCAGCCGATGAAAGTTCGTGCTTCAAATCAAAGACGAAAACAATGCTGATCACCTTTTTTCGACAGTC
GGGGTATCATTACAGAGAGTTCCTTCGTCAAGGTTCCACTGTTACTGGGACATTCTACAGAGACGTTTTGGATCGACTT
TTGAAACGAATGCGGCGTGTGAGGCCAAAATGTTGGACAGTAACGAGTGGTGGTTGTTGCACGACAATGCACCGGCT
CACAAGTCCATTATTTAAGGGAGTTTTTTCGACGAAACGACAAGTTTTTCAGCATCAACCACCCTGCGTACTCACCTGATCT
GTCCCCCAGACTATTTTTGTTTCTAAACTCAAATGAAAGTTGAAGGGGTAGCGATTCACTTCAGTAGAGGCGATTGA
AGCGGCGGTGACAACGCAACTGAACAGTATCCAGTACAGGCGTTCCAGAAGGCGATGATGGAGCTGAAGATTTCGTGC
TAGGCGCTGTATCGAATTTGGGGGAGACTATGTAGAAGCCTGATAATAAATAGAAGTAATTTTCATTGTGTTGTTGATCTG
TGCGTGTCCagtcctggaacttttgaatacactgtgta

Lkmar16 TIRs | TSD | Consensus from 13 copies | *Ortmar58* lineage

tacgaggggggaccacaaaagtaacgggaattGGGCTGCCGCGGGGAGGGAGAGTGGGGAAAACCTCATTGTTGGACCAGGTGTCCGTTAG
TGACGCGTCTCCTGAGTTAGTGTGCGAAGTTCTGTGCTGTGAGTGCATCGGTTTCGTCCTGGGAATTTTTTTAGTGAAA
CAACTTTTTCCATTTTCGGCGAAAACGTGATGGCCGATTGTGCGAGAGCAACGCGCGTCTGTGAAAATTTTGTTCCTGTTGG
GGAAATCGGCCGCGGAAAACCTATTGTAATGCTTAAAGACTGCTTATGGGGATGCTGCCCTAAGTAAAACCAGAGTCTACGA
GTGGTTTTTACGTTTTTAAAATGGAGAAATGTCAATGAAAGACGAACCCCGTTTCAGGACGCNCTCAACGTCAAGAAG
TGACGAAAACGTGACAAAATCAATGCTCTCGTTCGTGAAGACCGTTCGCCGAACCATGATCAACTCTGTGAGATGTCT
GGAATATCATGGAGTTCAATTCAGAGGATTTATCCGAAGATTTGCACATGAGAAGAGTTGCAGCCAAATTTGTCCCTCG
CCTTCTCACAGGCGAGCAAAAAGGAGCGTGCAGTTTTCAGGCATGTTTTGAGCTTCAAATCAGCTCAAAGAGGACCCTGA
ATTTTTTTCCAAGGTGATTAAGTGTGATGAATCGTGGTGTATGGATACGACCCCGAAAACAAAGCAGCAATCAAGCCAGT
GGAAGACACCTGGCTCTCCTCGTCCNAAAAAGCTCGCCAAGTGAAGTCAAACATCAAGACAATGCTNATTTGTTTCTT
CGATTGCAGAGGTGTTGTGCACGCGGAGTTCGTTCTCCCGGTCAAACGGTTAACAGAAAGTTCTACTTGGAGGTTTTG

AAAAGATTGAGGGAGAGTATCCGGAAGAAAAGGGCAGATCTTTGGCGCACAAGCGACTGGTTCTTCCATCATGACAAC
GCGCCGGCCACACCGCTCTCTCCGTAAAGCAGTTTTTGACCAAAAACGGCATGACACCAATTGTCCACCCNCNCCCT
ACTCACCGGATCTGGCCCCCTGTGATTTCTTTTTGTCCCCAGACTCAAAGGGACACGAAAGGAAAGCGTTTTGCCAC
NGTGGAGGAGGTA AAAACA AAAATCGTGGAAAGGCCTAAAGAACATCCCAGATAAGTGAATTTNAAAAAATGTTTTGAAC
AATGGAAGGATCGTTTTGCAGAGGTGCGTTGTGGTCAAGGGAGAATACTTTGAAGGTGATCAAAAATTTGGTGTAAAAATA
TTAAGAAATAAAGAAGTTATGACGAaattcccgtntttttgggtccccctcgta

Lkmar17 TIRs | TSD | Consensus from 16 copies | Ortmar69 lineage

tacgaggtgtgctataaaataacgggactgaCGCTGCAGTGGAACGAGTGCGCATGCGCCATCCAACATTGACCAACAGCTGTTTAGT
GAGACTTCCTCTTCCAGAAATGCAGTTAGTCTCGTTTCTGTAAACAACATCGTTGAGTCATAACCTTCATTTAAGTTAGTGT
GTATTTTTGTTTTGCCGAAAAAATGGTTAGCGTGATAATAGAGCAACGAATTGTTATTAATTTCACTTTAAACTTGGAAA
AACCGCTACCGAAACCTATAATTTACTAAAAAGAGTGTATGGCAGTGAATGTTTATCGCGGACTCGTGTTCGAATGGT
TTAAGCGTTTTCAAGATGGTCGACAAGACGTTGAAGATGATTCGCGGCAAGGTCGTCCTCAACATCAAAAACGGATGA
GAATGTCAAAAAGTTGCTAATTTGATTCGGTCTGACCGTCGATTAAGTATTCGTGCAGTTGCTGAATCTGTAGGCATTG
ATAAGAATGCATACGGCAAATTTACGTGACAATTTGAACATGCGAAAAGTGTGTGCAAAAATGGTACCAAAAATCT
CACGTTGAACAACAATCAGCTCGCACAAATTTGTACTGACACTTTGAATGCCATTGAAAATGACTCAAATTTATTGG
AAAGGATAATAACATGTGATGAATCGTGGTTTTTACTTATGATCCGGAACGAAGCGCCAATCCATGCATTGGAAGACC
CCAACCTCACCGAGAGCCAAAAAAGCAAGAATGAGCAAGTCAAAAATTTAAAGCAATGATGATTGTTTTTTTCGATATTC
ATGGGATTGTGTACCTTCACTGGGTTCTGAAAGTCAACAATTAATCAACATTACTACCTTGAGGTACTTGGTAAACTA
CGTGAAAGAGTAAGAAAAAACGACCAGAAATGTGGAAGGACAAATCATGGGTTTTACACCAAGACAATGCGCCAGC
TCATTCGCGTTATCTGTTAAGCGTTCCCTGACCAAGTACAGCATCCCAGTGTAGAACATCCACCTTACTCACCAGACC
TAGCACCATGTGACTTTTATCTTTCCCTAAGGTGAAATCTGCTTTGAAAGGTACGAGATTTGAATCCGTAGAAGCTGTT
CAAGAGAAAGCGGCAAGAGTCTAAACGAGTTGACAAAAGATGACTTCCAGCACTGTTTCCAACAATGAAAAATTCG
ATGGAGCGTTGCAGGGATAGAGAAGGGGTGTATATTGAAGGTGATAATAAGTAATTATGTATAAAATGAAAAATAAATTT
TTTACAATAtcagtccttattttatagccacacctgta

Lkmar18 TIRs | TSD | Consensus from 12 copies | Ortmar70 lineage

tacgaggtgtaaaatgaatgactgattttCTAGTGTTCGATCTGGCAACACTGGGACGCGACACGTAGAGGGTAGGCAGGTAAC
ATCTGATACGCGTCCAGTACAAGTTTGAACACGCTAGAGTTGTTGCGCTGCCGTAGTGAATTTTTTTGTGAGAAAGGTT
TTTTTAGTGCGTTCTAAAAATGAGTGTCAATTTTGAACAACGTTGTGCTATCAGGTTCTGCTTCAGACTTGGACACA
GTGCAACGGAAACATTTGAAAAACTGCGTCAGGCCTATGGAGACAGTGTTTTGTGAGAGCCAGGTTTTTAGGTGGTT
TAAGGCATTTTCCAGAAAGGAGAATCAATTGAAGACGAGCCTCGCAGCGGAAGGCCTTCATCTTCAAGAACCAATGA
AAATGTTGGCAGAATCCGCGATCTCGTGCCTCAGATCGTCTTTGACAGTCCGAATGATCGGTGAAGAGTTGAATTTG
ACTCACACAACCGTTCATCAAATTTGACCAATGAATGGGGATGAGAAAAATCTGTGCAAAAATGGTCCGAAAAATC
TTTCAAGAGCAAAAAGACATCAGAAAGGAAAGGTGCCTTGACTTTTTGGGAGCAATGAAAACGATCCCCATTTTC
TGGAGCGTGTATTACAGGTGACGAGTCTGGGTGTTGAATATGACCCGAAACCAAGCGCCAGAGCATGGAGTGGC
ACACTTCAACCTCTCCAAGGCCAANA AAAAGGAAGAATGAGCAAGTCAAAAATCAAATGCATGCTGATTTGCTTTTTTGA
TAGCCAAGGAATCATTCAAAAAGAGTTTGTGCCTCAAGGCCAAATGGTTAATCAACATTTTTTACCGAGAAGTTCTCGATA
GACTTCGAAAAAGGGTCATGCGTGTGAGACCAACCATCAAAAACATGTGGGTGTTGCATCACGACAATGCTCCTTGTCA
CACCGGATTTCTATCATGATGTTTTGGCCAGTAAAAACATTCCTGTGGCTCCTCAGCTCCTTATTCAACCCGACTTGA
GTCCATGTGACTTTTTCTGTTCAAAAGATTGAAAAACACTCAAGGGACGTCATTTGGGACATTGCAGAATATTCAA
ACAGCCGTAACCGACCAACTGAAGGATTCCAGTATCCGAGTTCCAGCACTGTTATGAGGAATGGAAGAATCGTCTCCA
GCGCTGTGGCTTCCCAAGGTAGTTACTTTGAAGGAGACAATGTGAATTTGTAATTTTATTTCAATAAAAAAATTAGAAA
aaatcagtccttacttaatttacacctgta

Lkmar19 TIRs | Consensus from 25 copies | Ortmar33 lineage

cgttcaataagtaatgcaacacntttttNNNNNGCCAATTTTNNNTNAANA AAAATTTGGAATTTTGTGTTGGGACATCCTTAAACATCCCCG
GTCACTCATNTATTTCCATCAACTCCCAGTACGCGCAGTGTATAACCAGCCTTCAAATGGCGTCTGCAACTGAAAT
GCGTTC AAGCAAAGAGCAGTTATTGAATTTCTTTTGGCGGAAAACAGACCATCACAAATATTCACAGGCGTTTACAG
AATGTCTACGGACACCTGGCACTGGATAAAAAGCACGGTGAGTCTGTTGGGCGAAGCGTCTGTCTGCAACAGAACAAGGA
GAAGGAAATCTGTCTGATCTCCACGCGCAGGCCGGCCGCACACAGCTGTGACGCTGCAATGTTGGAACGTGCGGAC
ACTCTTATTCGAGGTGATCGACGAATAACAATAACAACACTCAGTGTCTCATCTTGACATCTGTGTTGGTAGTGTGACAC
ACTTGTCCACCAGTTAGCCGTATTCAAAGTTTTGCGCCCGTGGTTCCTCGAAGCCTAAGAGCATAAAGAGCAA
AGAAGGAACATCTGACGAATTTGCTGCTGTTATGAGGCTGATGGTGACGATTTCTTGTCAAACATAATGTCACAGGCG
ATGAAACATGGATTCACCACTTCGAGCCTGAAACAAAACGGCAATCCATGGAGTGGCACCACACAACGTCTCCTTCNN
NGAAGAAGTTCAAAAACAGTACCTCAGCTGGTAAAAGTCAATGGCTACAGTCTTCTGGGACTCTGAAGGGGTTATTCTGTT
CGATGTCTCCTCATGGTCAAACGATCAACTCCGAAGTCTATTGCGTGACTCTTAGGAAATGAAGAAACGATTCCAG
CGTGTTCGTGGCCACAAAATGCGAACGCACTTNTNCTTCTCCACGACAACGCAAGGCCACACACAAGTCTGCGCACC
CGAGAGGAGATCACA AAACTTCGGTGGACTGTTCTTCTCATCCACCCTATAGCCCGGATCTCGCACCTTCTGACTCCA
TCTCTTTGGCCACTGAAGGATGGACTCCGCGGGAAGCACTACAGCAATGATGGGGAAGTTATTGATGCAGCAAGAAC
GTGGCTCAGACACAGACCAGTAGAGTGGTACCATGACGGCATAACAGGCTCTCACATTAAGGTGGCGTAAGGCCATAGAA
TTGAACGGAGATTACGTTGAAAAATAGGNTTTTATAGCCAAAAGAATTTGGGAAACAATNTGNTNTATTTAAATNCTGAATA
AAACCATCNTGNTTTGAGAAAAanantgttcacttattgaacg

Lkmar20 TIRs | Consensus from 76 copies | *Ortmar34 lineage*

ggtgatcaaatattacagacattTGCTTTTGGAGCGCAATTTGAACGGAACGGGCTGCCGCTTGTACAGTGCATTGTTGCAGATGT
CAGGAGTTGGGGAAGCAGCTGGTATGCAAGTCTGGGCTGTTTGGCAGTAGCGCTCACGATGACGGAGCAACAAGTGCA
TCCTTCTGTTGCGCAACGCATTGTTATCAAATTTCTTGGTAACGAAGGTGTAACCAGCTGAAATTTGCAAAAGACTAAG
TGCACAGTTCGGCAATGAAACCCTGTCAAGGGCACGCGTGTATGCGTGGCATAAAGAGTTCGGGGAAAGGTCGTGAACGG
GTTGAAAATGAAACACATGATCGTCGTCCTCGGACCAGCATTACGGAAGAGAACAATTTCCAGTGTTCGTGACCTTATTGA
AGGTGATAGACGTCTGACGGTTTCTGCAGTTGCATCACAAGTTGGAATAAGCTATGGGAGCTGTCAAACAATCATCTACTA
AGGATCTAGGGTTCATAAAGTTTGTGCCAGATGGGTCCCTCGTCTTTTGGACAGCAGAGCAGAAGATGAGACGTTTGGAG
ATTTGTGAGAAGCTTACCGCACAAATTTGCAGAGGAAGGGGATCCTTTTTTGGACAAAATTGTCACCTGTGATGAAACTTG
GGTCCATCATTACACACCCGAATCCAACAGGCCAGTATGGAGTGGCGGAGGCAGGGAGAGGCAGCCCCGTTAAAGCC
AAGACCAGTTGTGACCCGGCAAGGTGCTTGCACAGTTTTCTTCGACCGGGCAGGGATCTTACACATTGATTTCTTGCA
TGAGCATCGCACAAATAAATGCTGCTTACTGTGACCTTCTGGACCGGTAAGAACTTCCCTACCGTTCCAAAAGACGTGA
CCGACCAATTCGAGACGTATCTCCTTCATGACAACGCTCGGCCCCACACTGCAGCCCTAATTGCACCAAATTACAGC
AAATGAGATGGACTGTACTTGAACATCCTCCTTATAGTCTGTATCACCCTGTGATTTTCATTTGTTTGGGCCACTTAA
AGAAGCACTAGGAGGACAACGATTCCAGGACAATGCGGGGGTTCAGGCCTTTGTGCACAATTGGCTTGTGACACAACCC
TCTTCTTCTATGATGCTGGGATTAATAATCTACCAATCCGGTGGGAAAAATGCATTACTAAAGGAGGAGATTATGTAGAA
AATAATTTGTACTGTGCTATGTTATCTGCTCAATACATTTGCAAAAAAAAAANaaagtctcgtcatattgatctacc

Lkmar21 TIRs | Consensus from 36 copies | *Ortmar13 lineage*

ggcaagtcaatatataagtcgcaaaCGTCAGTTTCCCTTATACCGTTTTAAATTACGAGCGCATTTTTTGCCAGCAGATGGCAGCATATGT
ATGCTTGTGCTATAGGCTGCGTGACATCTCGTAGGCACGCAGTCAGTCAGAGGCAGCCAGTGCACGATGGCGGTTGTGTT
GCATGAGTGTACACGAGAAGAACAGCGTGCAGTTGTGCGTTTTTGTGGGCCAAAGGACTGTCCACAGAAGAAGTGCAT
CGCGAAATGCATCCCGTGTATGGTGACAACCTGTTTCTCACGGAAAGCTGTGTTCAATTGGATCCAGAAGTTAACAAGGG
AAGGCAAAGCATCAGAGATGGGGAGCGTCTGGTCTGCTGCGGAGGTGTCAACTGCAGTCACAGTGCAGCGTGTGGA
ACAAATCATTTCGTAATGACCGGCGTGTGACGATCGATGACGTAGCGCGTGTCTGAGGCTGTTTACATGGAACCCGCATGGA
ACATCGTGCATGAGCAGTTGCATTTTCGTAAGATTTGTGCACGATGGGTGCCCGCCAGTTGTCTGAGGAACACAAAAAG
AACAGAATGGGTCTGCTTTCAGCAGCCTCACTCGGTACACTGAGGAAAGGAGGACTTTCATGGCACGAATTTGTACGG
GGGACGAGTCTGGGTTCCACTTTCAACCCGAATCCAAACAGTATCCATGGAATGGAACATCCACCTCCCCAANN
AAAAAAGTTCAAGACGATTCCATCAGCCCCGAAGGTTATGCTCACCGTGTTTTGGGACATGCAAGGGGTCATACCTGCAG
AAATTCAGCCTCACGGTGAGACTGTGAATGCCGCGTCTGACTGCACCACTCTGCGGGAACCTCCGACAGGCCATTCGCCC
CAAGCGACCTGGACTCCTGACAAAAGGAGTGATTTCTTCTGGATGACAATGCCCGCCCTCACACAGCAAGACCAACGCA
GGAGCTGTTACGAACATTTTCGTTGGGAACGCTTGGAAACATCCACCGTACAGTCCCGACTTAGCCCCAGTGATTTTCATC
TGTTTGGGCCCTAAAAATCATTGGGTGGCCGTCATTTGAAACTGATGATGCCGTAATCCAAGAGGTTACTCGTTGGC
TGCGACAGCAACCAAAAGACTTCTTTGCCACCGGCTTTCAAGGACTGTAAAGAGATGGGATAAGTGTCTGAATGTACA
GGGTGATTATGTGCAAAAGTAAATAAATGTCAGGAAGTACTTTGATTATTATGCCTCTATCCAGTtttgactattattgactacc

Lkmar22 TIRs | TSD | Consensus from 32 copies | *Ortmar74 lineage*

tacgaaggtgctactattgatccggaatTGGCAACAATGTTATTGTTTTGCGCAATTTAACGTAACAATCGTAAAGTTTCGACATTTTTAAC
CTTATAGAACTCAGAACGTTTTGTCGTTGAACGCTATTTGTGTTGTTTACATTGACAAGAAAGTTTCATCTCAGTCAAA
AAATGGAATTAAGTCGTGAACATTTTCGTGCGATGATTTACTACGATTTTCGACGTGGATTATCTCAACAACAGTGCATCG
ATCAACTTACTTCGACTTTTGGCGATGAAGCACCTTCCACAACTGATATCATTGGTTTTGTGAATTCATTCGTTGGCC
GTTGTTGCTCACGGATGAATTTAAAGAAGGTCGTCGAAATCGGTTGTTGTGCCAGAAAACATAGATGCTGTGCGCGA
ACTGATAATGCAAGATCGGCATGTGACGATCGTGAGATTGAGGCATCCTTGGGCATTAGTATGACAAGCATAACAAGA
TTTTACATGAACATTTAGCCGTGAAAAAGATTTGTTGCGGTTGGATTCCGCATAACTGACAATCGCTCAAAAAAAGGGT
CGTGTGATTGGTGCAAGAAATGATCAAAAAATAAATCGTGGTGCTTCAAAAAGCCGTGATAACATCTACACAGGTG
ACGAATCGTGGATATATGCGTATGAACCCGAAAGTAAACAACAGTGCAGTGTATGGGTCTTCCAAAATGAACCAACCCA
ACAAAAGTTGTTGCGCAAGAAGCACTTCAAAGCAAATGGTTCGCTGTTTTTTNGGAATAAGTGGACATGTGGCTACAG
TGCCCCAGAGAATCGTAGAACGGTCAATTTCTGAATGGTACACAACCAATTTGTTTGCACAAGTATTTGAAGATATAAGAA
AAAACAACCAGCGCCGAGAATCATTCTTACCACGATAACGCGAGCTCACACAAATCGAGCCAAACAACCTCAATATTTG
ACCGCTCAAAACATCGAGTTGATGGGTATCCGCCATACAGCCCTGACTTGGCACCGAATGATTTCTTTTTGTTCCCTAC
GTCAAGAATAAACTACGTGGTCAACGATTTTCGACGCCAGAACAAGCGGTTGATGCGTTCAAAATGCATGTTTTAGAAAT
ACCTCAATCGAATGGAAGAATTGCTATAAAAATTTGGTTCAAGCGTATGCAAACTGTATCGATCATCGCGGAGAATATTT
TGAAAAACAATAAAATCATTTCATGATAAATATTTTTATTATTTattccgatacataagtagcaacctcgta

Lkmar23 TIRs | TSD | Consensus from 34 copies | *Ortmar27 lineage*

tacgaggtggaatcaaaagtaaggttcccAAAGCGGTAGATCCGCAAGGAGAGGTGTTAGGCAAAATCTGGCAACACTGGCGTGTGCA
GCAGCTCCCCCTCTCTCGATCCCAATATTCCCCGCTTATCTCTGCCGTTTGTGTTGGCCTAGCAGTGTCCGCGATGGAA
GTGCCGATAGCCGCTACCGCCAAGTGTGAAATCCGTGCAGTTATACGCTTTTTTAAACGCGAAAGGGGTTCCACCTATAG
ACATTCATGGTCAGTTGTGCGAAGTTTATGGTGACAAGTGCATGTCTGTGCAACACGTCCGCAAATGGTGTAGGGAGTT
CACTGCTGGTTCGACGACATTCACGATGAAGACCGGAGCGGAAGACCGTCCATTTACAGACGAGACTGTCAACAAGGT
CGAGAGACTACTGCTCGAAGATCGAAGGATAACCATCAGTGAACCTGGCTCTTCGGGTTCTGAGATTTCCGCTAGCTCA
GTTTACAGAGAATTTTGTCTGAAAAATTTGGGTATCACAAGGTGTGCGCGCGGTGGGTCCCGCAATGCTTACAGAAGACC
ACAAGCGGCAACGTGTGCTGATTTGCCCCCAATTTCTGCAACAATGTCAAGACAAGAGAGAAGAATTTGTTGGACTCAA

TTGTTACGGGTGACGAAACGTGGGTGTTTCATTTACACCCGAAAGAAAACAACAATCACGTGAATGGCGCCACTCATC
TTCGCCTAAGCCAAAGAAGTTTAAACAACACGAGTCTGCTGGCAAAGTGATGGCTACTGTGTTTTGGGACCGTAAAGG
GATTTTGTGATCGACTTTCTGCCTCCGGGAACGACGATAAACTCAGACAGGTATTGTGACACACTAAGGAAACTCAGA
CGGGCGATCCAGAACCGTCCGAGAGGGAAACTGAGCAAAGGAGTCATGCTTCTTACGATAACGCTCGACCCACGTC
TCTCGACAAACCCAGGACCTACTGAAAGGATTTGGTTGGACTGTCATTCACGATAACGCTCGACCCACGTC
AGTGATTACCACTTGCTCCCGAAATTGAAGGAACACTTGGGTGGACTACGCTTCCGGACCGACGATGAAGTCAAAGAA
GAGGTTACTCGCTTCTCAACGGGTTGGCGGGGAGTTCTGCGACATGGGGATACAAAGTTGGAGCACCGTCTCCAA
AAATGCTTGGATAGAAATGGAGACTATGTTGAAAAATAGCTCAATGTTTAAAGCTTTACAACCATGTAAATTGCTATGAAA
ATAAATANTTTTTTCTATTTCTAAAAAATAgggaacctactttgagttcacctcgta

Lkmar24 TIRs | TSD | Consensus from 19 copies | Ortmar39 lineage

taccaggtgtgtaaatatgaaaccngaatttNCCCATGGATGGCCNTAGCTGTCAATGTANTTACCTTCAAACCGCATCATNGNCGCCATTTT
ATTTCTTTGANANCTGACANCAATNCNCACAANTNAACAANACAAGTTTCATATAANAGCATAGTTTTNAATNGCGTTGA
ACATGTCGANTTTTGTGCCTACAACTACGATTTGCGGACAGCATTGATTTTCTGTTACCATTTAAAGAAAAGTCTGCTGCAG
AATCGCATCGAATGCTTGTGCAAGCTTACGGTGAGCATGCTCTTGGTAAATCACAGTGCCTTTGAGTGGTTTAAAGAAATCA
AAAGTGGCGATTTTGACGTGAGAAACGAAGAAGACTGGAAGACCGCCGAAAAAGTTTGAAGACAGTGAATTGCAAGCAT
TGTTGGATGAGGATGACGCTCAAACCCAACAAGAAGACTCGCGGATCAATTAATGTAACACGAGAAGCCGCTCCATACGT
TTGAAAGCCATGGGAAAGATCCAGAAGGTGGGAAAATGGGTCCACATGAATTGAATGAAAGACAGCAAGAAAACCGA
AAAACCACTTGCGAAATGCTGCTCGCCAGGTACAAAAGAAAGTCATTTCTCCATCGAATTGTGACAGGTGATGAAAAGTG
GATATATTTTGAATCCTAAGCGTAAAAGATCATGGGTAACTCTAGGCAAACCATCAACATCGATTGCAAGGCCAAATCG
CTATGGAAAGAAGACAATGCTCTGTGTTTGGTGGGATCAGAAGGGTGTGATCTATTATGAGCTGCTAAAACCTGGNGAAA
CCGTTAATACTGAACGCTACCGACAACAATGATCGATTTGAATCAAGCATTGCNTGAAAAACGACCAGAAATATCAAGAA
AGGCAACACAAACCGATTTTGCTTCATGATAATGCACCATCACACACAGCAAACCGGTCAAGGAAACGATTGAGGCGT
TTAGTTGGGAAATACTTGCATGCGGCTTACTCACCAGACTTGGCTCCGCTCCGACTACTAATTTATTTGCATCGATGGGACA
CGCATTGGCTCAGCAGCGCTTCACTTCTTATGAAAATGTANGAAAATGGCTCGATGACTGGTTTTGCCTCAAAGAGCAAC
ANTTTTTTGGCGTGGCATTATAAATGCCAGAGAGATGGAAAAAATGTATAGCTAGCGATGGACAATATTTGGAATAAA
ATATTTTATCATTTTCATACAATAAACGTGATTTTCTATACAAaattccngttcatatttacacactgta

Supplementary 4

Diversity and distribution of Orthoptera MLE lineages (Ortmar) among the studied Orthoptera species. For each studied genome the number of copies of the corresponding Ortmar lineage is indicated. Taxonomy is according to NCBI Taxonomy and corresponds to that in Table 1 (Suborder, Family, Subfamily, Species). Species names are shown as acronyms of those indicated in Table 1: the first capital letter – the first letter of a genus, the second lowercase letter – the first letter of a species. Clusters (Roman numerals) correspond to those on Figure. Names of Ortmar lineages which may have been horizontally transferred between Orthoptera and species of other insect orders are highlighted in dark green boxes (see Table 2 and Supplementary 5 for more details)

Cluster	Lineage	Caellifera												Ensifera					<- Suborder	<- Family	<- Subfamily	<- Species	
		Acrididae						Pyrgomorphidae		Pamohagidae		Tettigonidae		Gryllidae		Eneopterinae							
		Acridinae		Eyprepocnemidinae		Gomphocerinae		Melanoplineae		Oedipodinae		Oxyinae	Pezotettiginae	Pyrgomorphinae	Pamphaginae		Tettigoninae	Gryllinae					Trogoniinae
		As	Ep	Na	Sp	Bt	Ln*	Oj	Pa	Cs	Pk	Gs	Tv	Cn	Gc		Lk*						
I	Ortmar1	16	0	0	4	11	0	20	28	14	2	0	0	8	270	286	22	1	4	4			
I	Ortmar2	4	13	0	0	1	1	103	16	1	13	0	0	55	5	2	0	0	0	17			
I	Ortmar3	78	36	8	8	15	16	333	17	1	88	0	0	31	0	0	0	7	1	1			
I	Ortmar4	458	322	5	273	7	0	40	0	0	217	0	0	2	11	1	0	1	13	0			
I	Ortmar5	1	21	31	65	46	12	37	56	0	0	0	23	21	0	0	0	0	4	0			
I	Ortmar6	6	0	1	0	0	0	483	6	6	0	0	0	6	2	5	8	2	0	0			
I	Ortmar7	0	1	17	0	6	1	21	30	0	0	0	0	6	8	1	5	0	0	0			
I	Ortmar8	58	20	0	3	8	52	18	0	12	5	2	0	0	0	19	0	0	0	0			
I	Ortmar9	32	15	4	4	3	61	10	3	13	6	0	0	0	0	0	0	0	0	0			
I	Ortmar10	15	7	14	29	12	10	58	31	0	10	0	0	0	0	0	0	0	0	0			
I	Ortmar11	113	19	26	79	31	2	16	43	0	0	0	4	0	0	0	0	0	0	0			
I	Ortmar12	48	29	1	11	1	39	10	0	0	18	0	0	0	0	0	0	6	0	0			
I	Ortmar13	2	0	13	5	2	0	3	1	0	0	0	0	0	2	0	0	2	36	0			
I	Ortmar14	10	32	9	32	73	4	45	0	0	0	0	24	0	0	0	0	0	0	0			
I	Ortmar15	19	5	0	9	8	5	1	0	0	0	3	1	0	0	0	0	0	0	0			
I	Ortmar16	1	0	0	1	0	8	2	0	0	0	0	8	421	317	0	0	7	0	0			
I	Ortmar17	0	1	0	0	5	1	7	2	0	2	39	0	0	0	0	0	0	0	0			
I	Ortmar18	10	9	0	4	1	0	8	15	0	0	0	1	0	0	0	0	0	0	0			
I	Ortmar19	1	2	0	1	0	117	0	0	0	0	0	0	0	1	0	0	4	0	0			
I	Ortmar20	1	14	6	0	11	0	23	0	0	0	0	48	0	0	0	0	0	0	0			
I	Ortmar21	0	0	0	0	21	53	14	0	0	13	12	0	0	0	0	0	0	2	0			
I	Ortmar22	0	0	0	0	0	0	0	0	0	0	0	2	0	14	1	0	34	0	0			
I	Ortmar23	0	0	0	0	3	0	1	0	0	0	0	0	1	276	0	0	0	0	0			
I	Ortmar24	0	0	0	0	0	0	0	0	0	0	3	17	6	0	17	0	0	0	0			
I	Ortmar25	0	0	0	0	0	0	0	0	0	0	2	13	6	0	5	0	0	0	0			
I	Ortmar26	0	0	0	0	0	0	0	4	0	0	36	0	0	0	0	0	0	11	0			
I	Ortmar27	0	0	0	0	0	0	0	0	0	0	0	0	0	2	4	34	0	0	0			
I	Ortmar28	0	0	0	0	0	0	0	0	0	0	0	0	0	6	1	53	0	0	0			
I	Ortmar29	1	0	0	2	0	83	0	0	0	0	0	0	0	0	0	0	0	0	0			
I	Ortmar30	0	0	1	10	0	582	0	0	0	0	0	0	0	0	0	0	0	0	0			
I	Ortmar31	15	0	0	0	0	0	0	0	0	0	0	0	0	46	0	0	0	0	0			
I	Ortmar32	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97	0	0			
I	Ortmar33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	25	0	0			
I	Ortmar34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	76	0	0			
I	Ortmar35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	35	0	0			
I	Ortmar36	0	0	0	0	0	0	0	0	0	0	0	0	0	13	0	0	0	0	0			
II	Ortmar37	286	118	110	166	42	426	105	383	0	11	66	29	4	0	24	0	0	0	0			
III	Ortmar38	10	3	4	336	3	2	12	1	80	22	11	0	7	5	1	0	0	0	0			
III	Ortmar39	0	8	3	45	4	2	1	1	0	25	25	0	17	0	19	0	0	0	0			
III	Ortmar40	0	0	0	1	0	0	0	9	0	42	40	0	53	1	0	0	0	0	0			
III	Ortmar41	0	0	0	0	0	0	0	0	0	0	25	12	0	3	0	0	0	0	0			
III	Ortmar42	0	0	0	0	0	0	0	0	0	0	0	0	24	0	0	0	0	0	0			
III	Ortmar43	0	0	0	0	0	0	0	0	0	0	0	0	62	0	0	0	0	0	0			
III	Ortmar44	0	0	0	0	0	0	0	0	0	0	0	0	13	0	0	0	0	0	0			
IV	Ortmar45	16	14	12	24	12	438	3	0	4	10	8	12	13	6	0	0	0	0	0			
V	Ortmar46	236	117	0	21	9	571	39	35	0	24	12	0	0	4	30	0	0	0	0			
V	Ortmar47	41	0	9	0	21	333	29	14	0	25	0	23	2	0	12	0	0	0	0			
V	Ortmar48	3	0	0	0	13	9	34	13	0	2	0	4	0	0	2	0	2	0	0			
V	Ortmar49	0	0	0	0	0	0	0	0	0	0	0	0	0	25	0	0	0	0	0			
V	Ortmar50	0	0	0	0	0	0	0	0	0	0	0	0	0	25	0	0	0	0	0			
V	Ortmar51	0	0	0	0	0	0	0	0	0	0	0	0	0	18	0	0	0	0	0			
VI	Ortmar52	5	5	13	6	36	2	21	35	0	0	2	1	0	0	4	0	0	0	0			
VI	Ortmar53	4	3	8	2	11	98	31	0	23	3	0	0	0	0	0	0	0	0	0			
VI	Ortmar54	4	8	5	3	2	91	8	0	1	6	3	0	0	0	0	0	0	0	0			
VI	Ortmar55	2	1	0	0	0	9	3	3	27	4	0	0	0	0	0	0	6	0	0			
VI	Ortmar56	2	1	3	15	2	47	16	0	0	0	0	0	0	0	0	0	0	0	0			
VI	Ortmar57	0	0	0	2	4	11	9	1	0	0	0	0	0	0	0	0	0	0	0			
VI	Ortmar58	0	2	0	0	1	0	0	0	0	0	1	0	0	0	0	0	13	0	0			
VI	Ortmar59	0	0	0	2	0	138	0	0	0	1	0	0	0	0	0	0	4	0	0			
VI	Ortmar60	0	0	0	1	0	32	0	1	0	0	0	0	0	0	0	0	0	0	0			
VI	Ortmar61	0	0	0	1	76	0	0	0	0	0	0	0	0	0	0	0	6	0	0			
VI	Ortmar62	0	0	0	8	0	0	0	0	0	0	2	1	0	0	0	0	0	0	0			
VI	Ortmar63	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	10	0	0			
VI	Ortmar64	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	24	0	0			
VI	Ortmar65	0	0	0	0	0	67	0	0	0	0	0	0	0	0	0	0	229	0	0			
VI	Ortmar66	0	0	0	0	0	61	1	0	0	0	0	0	0	0	0	0	0	0	0			
VI	Ortmar67	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	17	0			
VI	Ortmar68	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	48	0			
VI	Ortmar69	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	16	0	0			
VI	Ortmar70	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	12	0	0			
VI	Ortmar71	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	25	0	0			
VII	Ortmar72	0	0	0	0	0	0	0	0	0	0	0	0	36	7	89	0	0	0	0			
VII	Ortmar73	0	0	0	0	0	0	0	0	0	0	0	0	3	0	14	0	0	0	0			
VII	Ortmar74	0	0	0	0	0	0	0	0	0	0	0	0	2	0	32	0	0	0	0			
VII	Ortmar75	0	0	0	0	0	0	0	0	0	0	0	20	4	0	0	0	0	0	0			
Total number of MLEs per genome		1498	826	307	1187	415	4381	683	714	351	515	427	927	662	718	168	992						

* species with available genomic scaffolds.

Supplementary 5 (Sheet 1)

Potential horizontal transfers of MLE lineages identified in Orthoptera between Orthoptera and other insect genomes detected by MEGABLAST search

Orthoptera lineage	Cluster (subfamily)*	Full-length representative used as MEGABLAST query**	Order	Family	Species	GenBank assembly accession	N copies [§]	Max identity (%)
Ortmar1	I	Lkmar4	Phasmatodea	Phasmatidae	<i>Clitarchus hookeri</i>	GCA_002778355.1	320	94.82
Ortmar6	I	Lmmar26	Blattodea	Ectobiidae	<i>Blattella germanica</i>	GCA_003018175.1	2	92.389
			Coleoptera	Cerambycidae	<i>Anoplophora glabripennis</i>	GCA_000390285.2	10	93.981
Ortmar8	I	Lmmar15	Coleoptera	Curculionidae	<i>Sitophilus oryzae</i>	GCA_002938485.1	43	92.026
Ortmar9	I	Lmmar8	Blattodea	Kalotermitidae	<i>Cryptotermes secundus</i>	GCA_002891405.2	80	92.935
Ortmar13	I	Lkmar21	Odonata	Libellulidae	<i>Ladona fulva</i>	GCA_000376725.2	1	90.208
Ortmar29	I	Lmmar10	Blattodea	Ectobiidae	<i>Blattella germanica</i>	GCA_003018175.1	12	91.379
Ortmar32	I	Lkmar1	Blattodea	Kalotermitidae	<i>Cryptotermes secundus</i>	GCA_002891405.2	78	95.306
			Hymenoptera	Formicidae	<i>Lasius niger</i>	GCA_001045655.1	1	90.557
Ortmar37	II	Lmmar13	Odonata	Libellulidae	<i>Ladona fulva</i>	GCA_000376725.2	10	97.749
Ortmar39	III (<i>mauritiana</i>)	Lkmar24	Hymenoptera	Apidae	<i>Bombus impatiens</i>	GCA_000188095.3	3	91.473
					<i>Habropoda laboriosa</i>	GCA_001263275.1	1	90.293
				Formicidae	<i>Acromyrmex echinator</i>	GCA_000204515.1	4	91.144
					<i>Atta cephalotes</i>	GCA_000143395.2	2	91.76
					<i>Atta colombica</i>	GCA_001594045.1	32	92.261
					<i>Harpegnathos saltator</i>	GCA_003227715.1	257	93.207
					<i>Trachymyrmex cornetzi</i>	GCA_001594075.1	43	92.433
				Halictidae	<i>Dufourea novaeangliae</i>	GCA_001272555.1	1	91.409
					<i>Lasioglossum albipes</i>	GCA_000346575.1	8	91.182
Ortmar45	IV	Lmmar1	Blattodea	Ectobiidae	<i>Blattella germanica</i>	GCA_003018175.1	1	90.516
Ortmar46	V (<i>irritans</i>)	Lmmar5	Hemiptera	Reduviidae	<i>Rhodnius prolixus</i>	GCA_000181055.3	5784	95.412
Ortmar47	V (<i>irritans</i>)	Lmmar9	Hemiptera	Cicadellidae	<i>Homalodisca vitripennis</i>	GCA_000696855.2	1	90.572
Ortmar54	VI (<i>drosophila</i>)	Lmmar19	Hemiptera	Cicadellidae	<i>Homalodisca vitripennis</i>	GCA_000696855.2	15	97.035
				Delphacidae	<i>Nilaparvata lugens</i>	GCA_000757685.1	4	95.754
Ortmar58	VI (<i>drosophila</i>)	Lkmar16	Hymenoptera	Formicidae	<i>Atta colombica</i>	GCA_001594045.1	3	92.551
					<i>Trachymyrmex cornetzi</i>	GCA_001594075.1	4	92.626
					<i>Vollenhovia emeryi</i>	GCA_000949405.1	1	96.466
			Phasmatodea	Phasmatidae	<i>Clitarchus hookeri</i>	GCA_002778355.1	51	96.767
Ortmar63	VI (<i>drosophila</i>)	Lkmar11	Diptera	Drosophilidae	<i>Drosophila ficusphila</i>	GCA_000220665.2	7	96.393
					<i>Drosophila grimshawi</i>	GCA_000005155.1	35	99.246
				Tephritidae	<i>Ceratitis capitata</i>	GCA_000347755.4	7	93.646
			Hemiptera	Cicadellidae	<i>Homalodisca vitripennis</i>	GCA_000696855.2	56	95.875
			Hymenoptera	Encyrtidae	<i>Copidosoma floridanum</i>	GCA_000347755.4	1	92.615
				Formicidae	<i>Acromyrmex echinator</i>	GCA_000204515.1	10	94.202
					<i>Dinoponera quadriceps</i>	GCA_001313825.1	21	94.419
					<i>Pseudomyrmex gracilis</i>	GCA_002006095.1	1	92.25
					<i>Trachymyrmex cornetzi</i>	GCA_001594075.1	89	95.852
					<i>Vollenhovia emeryi</i>	GCA_000949405.1	11	93.967
			Halictidae		<i>Dufourea novaeangliae</i>	GCA_001272555.1	1	98.416
			Megachilidae		<i>Megachile rotundata</i>	GCA_000220905.1	1	91.648
			Lepidoptera	Hesperiidae	<i>Achalarus lyciades</i>	GCA_002930495.1	1	91.77
				Lycaenidae	<i>Calycopis cecrops</i>	GCA_001625245.1	3	97.438
				Pyralidae	<i>Amyelois transitella</i>	GCA_001186105.1	1	96.833
				Riodinidae	<i>Calephelis nemesis</i>	GCA_002245505.1	1	96.863
Ortmar69	VI	Lkmar17	Hemiptera	Cicadellidae	<i>Homalodisca vitripennis</i>	GCA_000696855.2	50	95.852

* Clusters and subfamilies are according to Figure.

** Corresponding sequences can be found in Supplementary 3.

§ Number of MEGABLAST hits with more than 90 % coverage and 90 % identity to the query sequence.

Supplementary 5 (Sheet 2)

Insect species for which potential horizontal transfer of Orthoptera MLEs was detected by MEGABLAST search

Insect Order	Family	Species	GenBank assembly number	Orthoptera lineages Num*	Sum number of copies**
Blattodea	Ectobiidae	<i>Blattella germanica</i>	GCA_003018175.1	3	15
	Kalotermitidae	<i>Cryptotermes secundus</i>	GCA_002891405.2	2	158
Coleoptera	Cerambycidae	<i>Anoplophora glabripennis</i>	GCA_000390285.2	1	10
	Curculionidae	<i>Sitophilus oryzae</i>	GCA_002938485.1	1	43
Diptera	Drosophilidae	<i>Drosophila ficusphila</i>	GCA_000220665.2	1	7
		<i>Drosophila grimshawi</i>	GCA_000005155.1	1	35
	Tephritidae	<i>Ceratitis capitata</i>	GCA_000347755.4	1	7
Hemiptera	Cicadellidae	<i>Homalodisca vitripennis</i>	GCA_000696855.2	4	122
	Delphacidae	<i>Nilaparvata lugens</i>	GCA_000757685.1	1	4
	Reduviidae	<i>Rhodnius prolixus</i>	GCA_000181055.3	1	5784
Hymenoptera	Apidae	<i>Bombus impatiens</i>	GCA_000188095.3	1	3
		<i>Habropoda laboriosa</i>	GCA_001263275.1	1	1
	Encyrtidae	<i>Copidosoma floridanum</i>	GCA_000347755.4	1	1
	Formicidae	<i>Acromyrmex echinator</i>	GCA_000204515.1	2	14
		<i>Atta cephalotes</i>	GCA_000143395.2	1	2
		<i>Atta colombica</i>	GCA_001594045.1	2	35
		<i>Dinoponera quadriceps</i>	GCA_001313825.1	1	21
		<i>Harpegnathos saltator</i>	GCA_003227715.1	1	257
		<i>Lasius niger</i>	GCA_001045655.1	1	1
		<i>Pseudomyrmex gracilis</i>	GCA_002006095.1	1	1
		<i>Trachymyrmex cornetzi</i>	GCA_001594075.1	2	136
		<i>Vollenhovia emeryi</i>	GCA_000949405.1	2	12
	Halictidae	<i>Dufourea novaeangliae</i>	GCA_001272555.1	2	2
		<i>Lasioglossum albipes</i>	GCA_000346575.1	1	8
		Megachilidae	<i>Megachile rotundata</i>	GCA_000220905.1	1
Lepidoptera	Hesperiidae	<i>Achalarus lyciades</i>	GCA_002930495.1	1	1
	Lycaenidae	<i>Calycopis cecrops</i>	GCA_001625245.1	1	3
	Pyrilidae	<i>Amyelois transitella</i>	GCA_001186105.1	1	1
	Riodinidae	<i>Calephelis nemesis</i>	GCA_002245505.1	1	1
Odonata	Libellulidae	<i>Ladona fulva</i>	GCA_000376725.2	2	11
Phasmatodea	Phasmatidae	<i>Clitarchus hookeri</i>	GCA_002778355.1	2	371

* Number of Orthoptera lineages which gave positive MEGABLAST hit(s) to the corresponding genome which had more than 90 % coverage and 90 % identity to the query.

** Total number of copies detected by MEGABLAST for all the Orthoptera lineages in the corresponding genome.

Supplementary 6

Transposase sequences used to root the MLE phylogenetic tree (Figure)

Transposase	Species	Family (conserved triad)	Accession number/Reference
Crmar2	<i>Ceratitis rosa</i>	<i>rosa</i>	AAK61417
Apismar4.1	<i>Acirtosiphon pisum</i>	(DD41D)	(Bouallègue et al., 2017)
Apismar4.2	<i>Acirtosiphon pisum</i>		(Bouallègue et al., 2017)
Apismar4.3	<i>Acirtosiphon pisum</i>		(Bouallègue et al., 2017)
Agrosa	<i>Anoplophora glabripennis</i>		XP_023311192
Aerosa	<i>Acromyrmex echinator</i>		XP_011049237
Apismar5.1	<i>Acirtosiphon pisum</i>	<i>LTIR*</i>	(Bouallègue et al., 2017)
Apismar5.2	<i>Acirtosiphon pisum</i>	(DD41D)	(Bouallègue et al., 2017)
HvLTIR	<i>Homalodisca vitripennis</i>		JJNS01075089
RpLTIR	<i>Rhodnius prolixus</i>		ACPB03001736
BtLTIR	<i>Bombus terrestris</i>		AELG01000709
Morosa	<i>Metaseiulus occidentalis</i>		XP_003748606

* The *LTIR* (DD40D) family of *Tc1/mariner* was recently established by (Bouallègue et al., 2017).