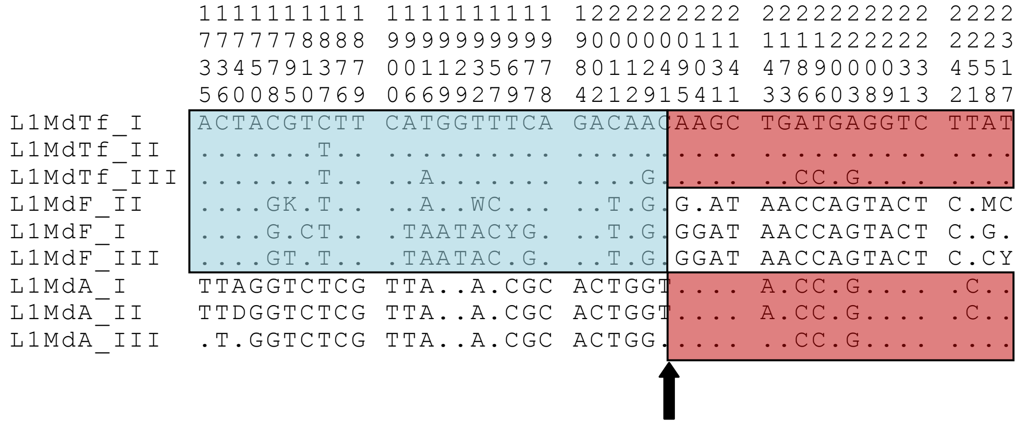
Alignment of parsimony informative sites showing the recombinant origin of the Tf families. The arrow indicates the position of the recombination breakpoint.



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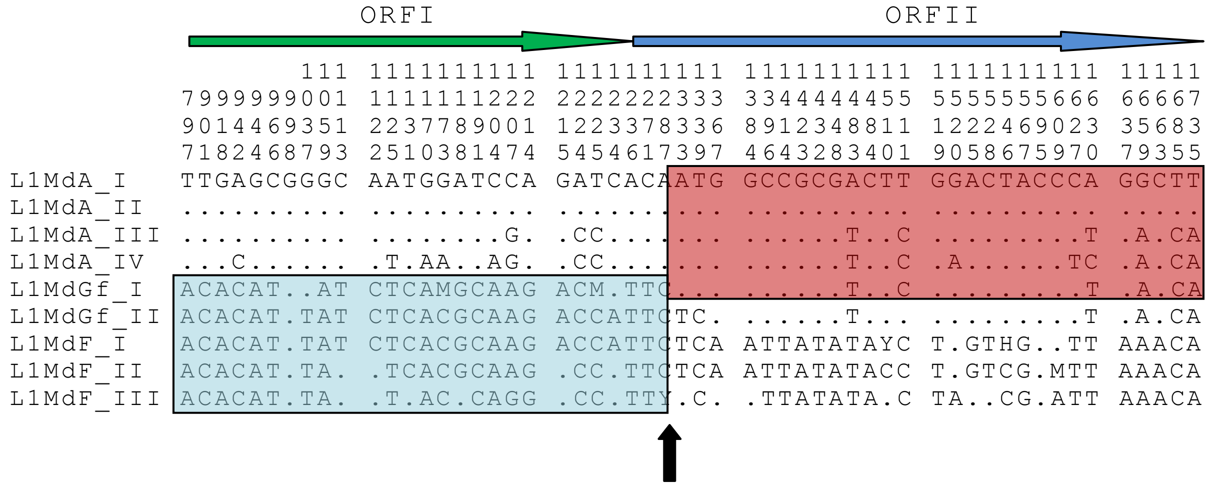
             7777778888 9999999999 9000000111 1111222222 2223
             3345791377 0011235677 8011249034 4789000033 4551
             5600850769 0669927978 4212915411 3366038913 2187
L1MdTf_I     ACTACGTCTT CATGGTTTCA GACAACAAGC TGATGAGGTC TTAT
L1MdTf_II    .......T.. .......... .......... .......... ....
L1MdTf_III   .......T.. ..A....... ....G..... ..CC.G.... ....
L1MdF_II     ....GK.T.. ..A..WC... ..T.G.G.AT AACCAGTACT C.MC
L1MdF_I      ....G.CT.. .TAATACYG. ..T.G.GGAT AACCAGTACT C.G.
L1MdF_III    ....GT.T.. .TAATAC.G. ..T.G.GGAT AACCAGTACT C.CY
L1MdA_I      TTAGGTCTCG TTA..A.CGC ACTGGT.... A.CC.G.... .C..
L1MdA_II     TTDGGTCTCG TTA..A.CGC ACTGGT.... A.CC.G.... .C..
L1MdA_III    .T.GGTCTCG TTA..A.CGC ACTGG..... ..CC.G.... ....
```

Alignment of parsimony informative sites showing the recombinant origin of the Gf_I family. The arrow indicates the position of the recombination breakpoint.



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                    111 1111111111 1111111111 1111111111 1111111111 11111
             7999999001 1111111222 2222222333 3344444455 5555555666 66667
             9014469351 2237789001 1223378336 8912348811 1222469023 35683
             7182468793 2510381474 5454617397 4643283401 9058675970 79355
L1MdA_I      TTGAGCGGGC AATGGATCCA GATCACAATG GCCGCGACTT GGACTACCCA GGCTT
L1MdA_II     .......... .......... .......... .......... .......... .....
L1MdA_III    .......... ........G. .CC....... ......T..C .........T .A.CA
L1MdA_IV     ...C...... .T.AA..AG. .CC....... ......T..C .A......TC .A.CA
L1MdGf_I     ACACAT..AT CTCAMGCAAG ACM.TTC... ......T..C .........T .A.CA
L1MdGf_II    ACACAT.TAT CTCACGCAAG ACCATTCTC. ......T... .........T .A.CA
L1MdF_I      ACACAT.TAT CTCACGCAAG ACCATTCTCA ATTATATAYC T.GTHG..TT AAACA
L1MdF_II     ACACAT.TA. .TCACGCAAG .CC.TTCTCA ATTATATACC T.GTCG.MTT AAACA
L1MdF_III    ACACAT.TA. .T.AC.CAGG .CC.TTY.C. .TTATATA.C TA..CG.ATT AAACA
```
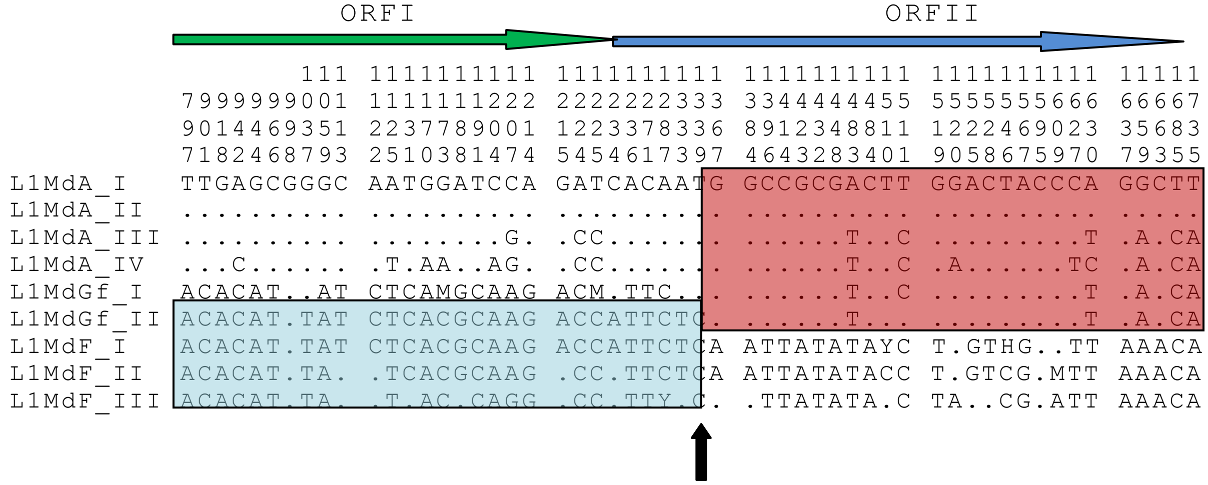

Alignment of parsimony informative sites showing the recombinant origin of the Gf_II family. The arrow indicates the position of the recombination breakpoint.



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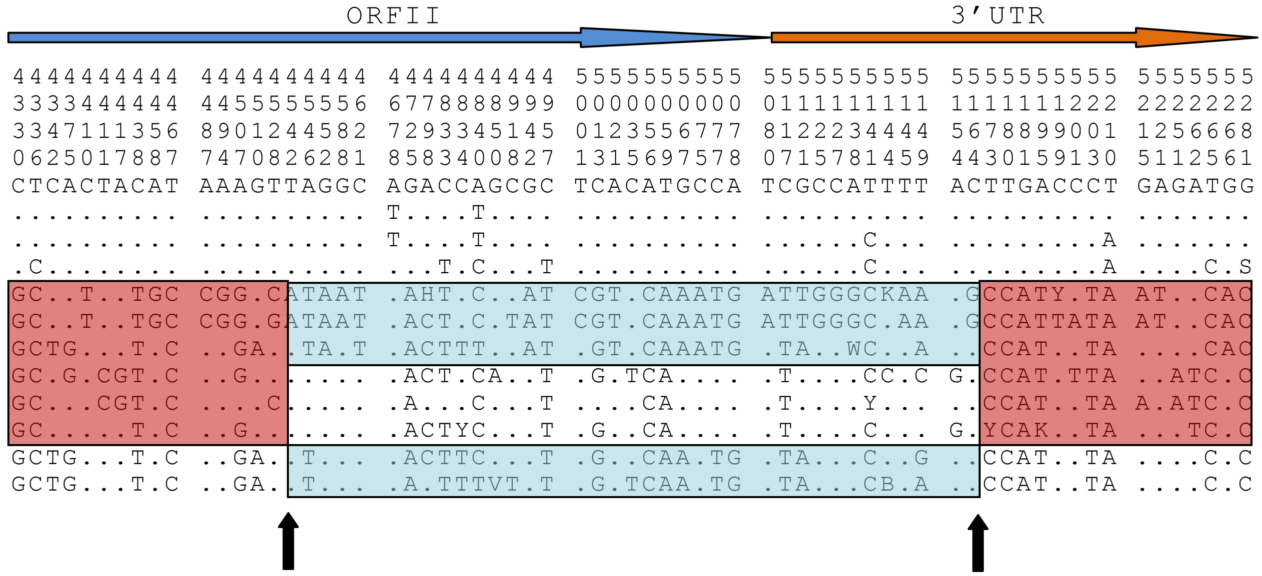
             7999999001 1111111222 2222222333 3344444455 5555555666 66667
             9014469351 2237789001 1223378336 8912348811 1222469023 35683
             7182468793 2510381474 5454617397 4643283401 9058675970 79355
L1MdA_I      TTGAGCGGGC AATGGATCCA GATCACAATG GCCGCGACTT GGACTACCCA GGCTT
L1MdA_II     .......... .......... .......... .......... .......... .....
L1MdA_III    .......... ........G. .CC....... ......T..C .........T .A.CA
L1MdA_IV     ...C...... .T.AA..AG. .CC....... ......T..C .A......TC .A.CA
L1MdGf_I     ACACAT..AT CTCAMGCAAG ACM.TTC... ......T..C .........T .A.CA
L1MdGf_II    ACACAT.TAT CTCACGCAAG ACCATTCTC. ......T... .........T .A.CA
L1MdF_I      ACACAT.TAT CTCACGCAAG ACCATTCTCA ATTATATAYC T.GTHG..TT AAACA
L1MdF_II     ACACAT.TA. .TCACGCAAG .CC.TTCTCA ATTATATACC T.GTCG.MTT AAACA
L1MdF_III    ACACAT.TA. .T.AC.CAGG .CC.TTY.C. .TTATATA.C TA..CG.ATT AAACA
```

Alignment of parsimony informative sites showing recombination between recent L1 families at the 3'end of ORF2 and in the 3'UTR. The arrows indicate the position of the recombination breakpoints.



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           3333444444 4455555556 6778888999 0000000000 0111111111 1111111222 2222222
           3347111356 8901244582 7293345145 0123556777 8122234444 5678899001 1256668
           0625017887 7470826281 8583400827 1315697578 0715781459 4430159130 5112561
L1MdA_I    CTCACTACAT AAAGTTAGGC AGACCAGCGC TCACATGCCA TCGCCATTTT ACTTGACCCT GAGATGG
L1MdA_II   .......... .......... T....T.... .......... .......... .......... .......
L1MdA_III  .......... .......... T....T.... .......... ......C... .........A .......
L1MdA_IV   .C........ .......... ...T.C...T .......... ......C... .........A ....C.S
L1MdA_V    GC..T..TGC CGG.CATAAT .AHT.C..AT CGT.CAAATG ATTGGGCKAA .GCCATY.TA AT..CAC
L1MdN_I    GC..T..TGC CGG.GATAAT .ACT.C.TAT CGT.CAAATG ATTGGGC.AA .GCCATTATA AT..CAC
L1MdA_VI   GCTG...T.C ..GA..TA.T .ACTTT..AT .GT.CAAATG .TA..WC..A ..CCAT..TA ....CAC
L1MdF_I    GC.G.CGT.C ..G....... .ACT.CA..T .G.TCA.... .T....CC.C G.CCAT.TTA ..ATC.C
L1MdF_II   GC...CGT.C ....C..... .A...C...T ....CA.... .T....Y... ..CCAT..TA A.ATC.C
L1MdF_III  GC.....T.C ..G....... .ACTYC...T .G..CA.... .T....C... G.YCAK..TA ...TC.C
L1MdF_IV   GCTG...T.C ..GA..T... .ACTTC...T .G..CAA.TG .TA...C..G ..CCAT..TA ....C.C
L1MdV_I    GCTG...T.C ..GA..T... .A.TTTVT.T .G.TCAA.TG .TA...CB.A ..CCAT..TA ....C.C
```
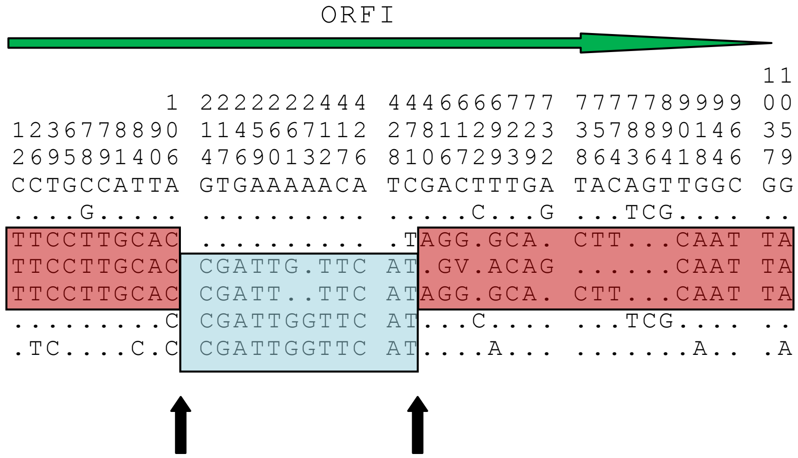

Alignment of parsimony informative sites showing the transfer of an ancestral coiled-coil domain (framed in blue) to the L1MdA_VI, L1MdA_VII, L1MdGf_II and L1MdF_III families. The arrows indicate the position of the recombination breakpoints.



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                                                       11
                    1 2222222444 4446666777 7777789999 00
           1236778890 1145667112 2781129223 3578890146 35
           2695891406 4769013276 8106729392 8643641846 79
L1MdA_IV   CCTGCCATTA GTGAAAAACA TCGACTTTGA TACAGTTGGC GG
L1MdA_V    ....G..... .......... .....C...G ...TCG.... ..
L1MdF_II   TTCCTTGCAC .......... .TAGG.GCA. CTT...CAAT TA
L1MdF_III  TTCCTTGCAC CGATTG.TTC AT.GV.ACAG ......CAAT TA
L1MdGf_II  TTCCTTGCAC CGATT..TTC ATAGG.GCA. CTT...CAAT TA
L1MdA_VII  .........C CGATTGGTTC AT...C.... ...TCG.... ..
L1MdA_VI   .TC....C.C CGATTGGTTC AT....A... .......A.. .A
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