

Figure S4a.

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TransibN1_AG : CACATTGGGCAAACGCCTGTATAAAAATCGAAAAxxxGAAATTGATTTTCATCCCGCGTTTGTATGGCCGTTGCCACTGTG
2L 5119823-5118806 : CCGGCCGAGACCGGC CAATC ..... G. .... G. .... G. .... G. .... G. .... G. .... G. .... CAATC
2L 8712511-8711509 : GGAAGTATTACCTAT CAGTG . . G . . A . . . . . xxxA . . . . . A . . . . . T . . . . . CAGTG
2L 20018136-20017277 : AGAACCAGTTGGAAC CAGTG ..... xxx ..... C. .... CAGTG
2L 20114414-20115455 : TTGACGTGGCAAGC CAATG ..... xxx ..... CAATG
2L 23799431-23798415 : GGTACGAAACACGC CAATG ..... A . . . . . xxx ..... CAATG
2L 26104831-26103068 : AATTACTCTTTCC CAATG ..... xxx ..... G. .... CAATG
2L 26230738-26229720 : GCTCATGAATCCAC CAGTG ..... xxx ..... CAGTG
2L 27942244-27943258 : ACACGAGACTGCG CAATG ..... xxx ..... G. .... CAATG
2L 29228399-29227384 : CACGCATCCTCTGC CATTG ..... xxx ..... G. .... CATTG
2L 46313828-46312914 : TGTGCGCTGAACG CAGTG ..... xxx ..... CAGTG
2R 8144738-8145756 : GAAGCGAAGCCAC CAGTG ..... xxx ..... CAGTG
2R 11369580-11368562 : GAGCAGCAGCACCC CATTG ..... xxx ..... CATTG
2R 22247416-22246400 : AAGCAGCGGCCTC CCGTG ..... xxx ..... CCGTG
2R 22299245-22300260 : TCAGGGATGAGAC CAGTG ..... xxx ..... CAGTG
2R 27175422-27174152 : TACGCCCGACCGT CACAG . . G . . . . . xxx----. . . . . A . . . . . G . . . . . CACAG
2R 30585530-30586513 : GAAACGCACCGGC CAGTG ..... xxx ..... G. .... CAGTG
2R 39256338-39255331 : CGGACGCTTTTCG CAGTG ..... xxx ..... CAGTG
2R 42675394-42674267 : TTTAACTATTGGA CTGTG ..... xxx ..... CTGTG
2R 43075924-43076941 : ATTTTTTCTTTCT CATTG ..... xxx ..... G. .... CATTG
2R 45171313-45172328 : ATTGCAATGGCAG CAATG ..... xxx C. .... G. .... CAATG
2R 52938105-52937140 : TGGAGTGTCTCTG CAATG ..... xxx ..... A. .... CAATG
2R 58350365-58349349 : GCTCACTCAGCTC CATTG ..... xxx ..... CATTG
2R 59515839-59516855 : ACATGACTAGCC CAGTG ..... xxx ..... G. .... CAGTG
2R 60219464-60220478 : CAGGGTACTCTTT CATATG . . . . . T . . . . . xxx . . . . . G . . . . . T . . . . . CATATG
2R 60905378-60904363 : CAACGCAGCAGC CACAG . . . . . xxx . . . . . T . . . . . T . . . . . CACAG
2R 62298466-62296973 : GAGCCATCTTTAT CAGTG . . . . . A . . . . . xxx . . . . . T . . . . . T . . . . . CAGTG
3L 6940556-6941406 : AACAGTTGTTGCG CAGTG ..... xxx ..... CAGTG
3L 13551031-13552046 : TGTCGATTTTAC CATTG ..... xxx ..... G. .... CATTG
3L 16304955-16305971 : TCCACTGTAACG CAGTG . . . . . G . . . . . xxx . . . . . G . . . . . CAGTG
3L 20046623-20047640 : CATAGCTTTTGCT CAATG ..... xxx ..... CAATG
3L 20346726-20347741 : AACATTTGTTGT CAGTG ..... xxx ..... G. .... CAGTG
3L 24406891-24405877 : TTGAGCTATTGCA CATTG ..... xxx ..... CATTG
3L 39688132-39689148 : GGGCTCTCGTCT CAATG ..... xxx ..... CAATG
3R 28454268-28453252 : TGGTAGTGTGTG CAGTG ..... xxx ..... G. .... CAGTG
3R 28657488-28658505 : AGGAGCAGTGCC CAGTG ..... xxx ..... CAGTG
3R 29529360-29528379 : GGCCGGATCTCC CAGTG ..... xxx ..... G. .... CAGTG
3R 37506679-37505664 : GGCAGCTTCCAC CAGTG ..... xxx ..... CAGTG
3R 41072498-41073486 : ATTAGCCGTTGA CAGTG ..... xxx ..... G. .... G. .... G. .... CAGTG
3R 51768770-51767266 : ATCTTTAGACGA CATTG . . . . . C . . . . . xxx . . . . . A . . . . . A . . . . . CATTG
U 7556694-7555780 : TGCACGCAGGCC CAATG . . . . . C . . . . . xxx . . . . . CAATG
U 11176774-1117791 : GACGCGAGCCG CATCG ..... xxx ..... CATCG
U 14010308-14011323 : ATCGGTTACTGCC CAACC . . . . . G . . . . . xxx . . . . . T . . . . . G . . . . . CAACC
U 14253260-14254261 : CCCCCTGCACGT CAGTG ..... xxx ..... CAGTG
U 23855743-23856761 : GGTAATGCGTCC CAGTG . . . . . xxx . . . . . C . . . . . CAGTG
U 28858008-28856995 : TTTAATTAGCTG CAGTG ..... xxx ..... G. .... CAGTG
U 30138472-30136500 : CTGAAAATCACCC CAGTG . . . . . C . . . . . xxx . . . . . -T . . . . . CAGTG
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Legend to Supplementary Figure S4a. Alignment of mosquito *TransibN1* AG elements to the *TransibN1* AG consensus sequence. The consensus sequence is shown in the top line. Dots indicate nucleotide identity with the consensus sequence; hyphens represent alignment gaps. The internal portion of *TransibN1* AG is not shown and is marked by xxx. Target site duplications are highlighted. Coordinates of the reported elements are shown in the first two columns (sequence name, beginning-end).

Figure S4b.

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TransibN2_AG : CACAATGGGCATTTCGCCGGATGAAATTCAAAAxxxAAAAATAATTTATCCCGCAATTTGTCTAAACTGCCCATTTGTG
2L 1229206-1230963 : AGTCAGTAACATCTTAATG.....xxx.....TAATG GGGAGCCCATGAAACA
2L 2089616-2091530 : ATATTTTTGCCGGTTCAATG.....xxx.....A.....A.....CATTG STATGGAGCGCTCTC
2L 2170283-2172340 : AAATTTTACCCTTCATTC.....xxx.....CATTG CTGATAGTATGGAAA
2L 2252107-2253892 : TGTAAGCCGGTATCAATG.....xxx.....CAATG ATGCGGTTCCGATTGG
2L 4182055-4184049 : ATGGAGGAGCCGCTAATG.....xxx.....T.....TAATC ACGAGCTATACGAGA
2L 4573850-4571975 : TCTCGACATCTGACTCAGTC.....xxx.....AT.....CAATG GGTTCGCTTACGTTT
2L 7014493-7012680 : TTCCACTTTTCATACAGTT.....xxx.....A.....CAGTT ATATACAAAAGAGCC
2L 10734918-10737530 : CATTTCACAGCACACATTC.....xxx.....CATTC ATCTCTCAGCAAAA
2L 17020534-17018712 : CAATAACATGCCCGCATGG.....A.....xxx.....T.....CATGG STTCAAGCGTCAAAC
2L 20182158-20183951 : TCGAGAATGACTTGCATTC.....xxx.....CATTC TGGCAACCAAAACCGC
2L 21232263-21234033 : CCCAGCCAAGCCCGCATTC.....xxx.....AT.....CATTC AAGGAAAACCAACAA
2L 23139669-23140800 : CCGTGAGATAGCCACCAATG.....xxx.....A.....CAATG AGCTGGTGGAGCCCA
2L 24782750-24784569 : TTCGTACAGAGTTGATCAATG.....C.....xxx.....CATTC TCGTAATTTTATAA
2L 32394929-32396712 : ATACATAATTTGCCAGCCTTC.....xxx.....CCTTC GTGTGATGGGTGGG
2L 42315451-42313664 : TAGAACGAAACCCGCCAGTC.....xxx.....G.....CAGTC GAGCGATTGAACAC
2R 2723033-2721042 : GCAGGAAGCCCAACCGTC.....xxx.....CGTC GGCAGCGTTGGCAGC
2R 5088053-5086059 : CCCCATATCCTTACACAG.....xxx.....CACAG ACACAGTCGTACTAC
2R 7767923-7766035 : ACCGGACGAGGACACAGTC.....xxx.....A.....CAGTG GCCAGCACC GGGTG
2R 9756593-9758384 : CTTTCGATGTGGCGGCACTG.....xxx.....CACTG GTGGCAGCAACAGT
2R 12786847-12788637 : TCGCATGTGCCCTGCAATG.....xxx.....GAATG GTGCAAAATTGTGTC
2R 18717091-18715307 : GCATACCACCACCAGTC.....xxx.....CAGTC GTGGCGTAGTGCTTC
2R 19142821-19140572 : CGTTGCCCTTCATCCGATTC.....xxx.....A.....GATTG GCAGCAATCCCCCA
2R 25221892-25220094 : CCTAAGCTCCCACCCGAATG.....xxx.....GAATG GTCTAAATATGGGAG
2R 29487916-29486129 : CACTAATACTCTCGTCATTC.....xxx.....G.....CATTC GCGTCATCGTTTGA
2R 29903707-29901922 : AGCAAACTCCCACATTC.....xxx.....CATTC GCATAATTTATCACA
2R 40734221-40732243 : GGCTACATTTGATCTCATTC.....xxx.....CATTC GCAAGGTCTCGCAAC
2R 41484089-41482326 : TTCTTTCACCCACACAGT.....xxx.....CACGT GTGAATGGAAGGAA
2R 44838408-44836585 : ACAACATAGCCGTGCCAATG.....xxx.....CAATG AAAAAAAAAACGCAAA
3L 27660824-27659035 : TGTGATTACTTCTAATCCATG.....xxx.....CCATG GTGAGCTCTAGTTTA
3L 29505347-29507134 : ACGAAAAGGTGCACCATTC.....xxx.....G.....CATTC GACCACAATTCATT
3L 34962407-34964402 : AAGAAGGAACCAATCCAGTC.....xxx.....CAGTC GCCACTGCTATGAG
3L 40833349-40831590 : ACACACAGGGCCGATCAATG.....xxx.....A.....CAATG GCCAGTTGCATAG
3R 662089-660298 : TTTAACACTCTACACAGTC.....xxx.....CAGTG ATTTACCATACACA
3R 7439751-7441730 : AAAACTTACTCCTCCCATCG.....xxx.....CATCG CCGTGGTGTGATTTA
3R 21327992-21326192 : AGTGTGTTTGTGTGACTG.....xxx.....CACTG TTAGGCTGGCGGAT
3R 25880487-25882264 : GAGCGAATCGGGGCACTG.....xxx.....A.....CACTG TTTGGCTTCGGAGG
X 11068447-11070272 : CCAATACAATCATTACATTC.....xxx.....T.....A.....CATTC GTGAGTTCAACCGT
X 12420031-12422325 : TCCGTGGCCTCGCAATGC.....A.....xxx.....G.....A.....A.....C.....CAATG TGGCGTCTGTGCA
X 15942596-15940943 : TTATTGAAATCGCCAATAG.....G.....xxx.....A.....A.....CATTC GTGTACAGCGGTGA
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Legend to Supplementary Figure S4b. Alignment of mosquito *TransibN2_AG* elements to the *TransibN2_AG* consensus sequence. The consensus sequence is shown in the top line. Dots indicate nucleotide identity with the consensus sequence; hyphens represent alignment gaps. The internal portion of *TransibN2_AG* is not shown and is marked by xxx. Target site duplications are highlighted. Coordinates of the reported elements are shown in the first two columns (sequence ID, beginning-end).

Figure S4c.

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TransibN3_AG : CACAGTG-GGCAGCTGCCGGGATGAAAGTCCAAAAxxxACTTTTATCCCGC---TTTTTGTCTAC-GGTGCCCACTGTG
2L 6093702-6094171 : AGGTGATGCTCAAACACTTC.....-C...C.xxx.....G---.....T.....AGTTGGTGTGATCAATACGT
2L 38028097-38029120: ACGCTTGAACCCTTCTCTG.....TT.....TT.....xxx.....A---.....TTCTGCTGTGATTTTACATC
2R 40263414-40264380: ATTTTCTAACCCAGCAACC.....-.....A.....xxx.....T.....C.....TA.C.....A...CAACGGGGAAGGATCGCTCC
2R 45193683-45192640: CAATTAATTTCCAACCATTT.....-.....A.....C.....CT.....xxx.....A---.....CATTCAACAGAAGATAAGCA
2R 52261880-52260739: ACTACTCTCCCTCGCTTGT.....-.....A.....CT.....xxxG.....-.....G-.....CGTGTAATACATTAGCCATAT
X 11090120-11091791: TACTAGCCATCCTCTATTC.....-T...A.....A.....xxx.T..G.....T--...A..G...-A...CATTGTGCCCTTGAACCAGG
X 10428461-10430292: ACCACGGCCAGCCCAAGG.....-.....TG..G.....xxx.....GG...TTT..G...AAG.A-.A.....CCAGCAATGGGGTAGCCTGC
X 6203512-6205032 : CACGAAAGGGGCACTCGGTC..T.....-.....T.A.AT.C.....T...xxx.....G..T.TT--...A.C.A-.....CGGTCGTACACTTTGCACCC

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Legend to Supplementary Figure S4c. Alignment of mosquito *TransibN3_AG* elements to the *TransibN3_AG* consensus sequence. The consensus sequence is shown in the top line. Dots indicate nucleotide identity with the consensus sequence; hyphens represent alignment gaps. The internal portion of *TransibN3_AG* is not shown and is marked by xxx. Target site duplications are highlighted. Coordinates of the reported elements are shown in the first two columns (sequence ID, beginning-end).

Figure S4d.

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TransibN1_DP : CACTATGGTCCGAACGACCACTTTTGTGGCCAAAA-CCTAxxxTTAATTTTGGCCAACAAAAGTGGTCGTTCCGACCATAGTG
Contig1006 3582196-3583547: CTCTTCTTTTGGGCCATTG.....-.....xxx.....CATTGTAGCATGACAATAAA
Contig1160 1464143-1462912: ACACTACCGTACATACACCC.....-.....xxx.....CACCCCATGGACACACTC
Contig138 431334-430521 : CATAAAAGATGCGTCAATG.....-.....xxx.....CAATGGTTAGAGAGCGAAA
Contig1421 431059-429882 : GGTGCTGAGGCGAGGCGAGG.....-.....xxx.....CGAGGGCTGGAGCACGTAGC
Contig1828 716750-717172 : AACGACGCCCGGTCGCCG.....C.....-..AA.....-..AA.xxx.....CATGGTGCGCCGGCAGCAGC
Contig2138 3719-4888 : ATATTTTGTGCGAAACATTG.....-.....C.....-.....xxx.....AC.....ACATTGTTTGTGGGATATTG
Contig2803 345220-344414 : AGGCAAAAATTCGCGCGCTG.....C.....-.....xxx.....G.....CGCTGTCGCCAAGCTGCGTT
Contig3323 1183750-1182915: GGCTATTTCTCTTTACAGTG.....A.....A.....xxx.....A.....T.....CAGTGACGTGACTCCCGCCG
Contig4055 469237-470472 : ACACATTCGGAGAGCAGTG.....-.....xxx.....G.....CAGTGTAGCCACCAGCAAGG
Contig410 329647-332793 : TGAACCTCCTCCCTCCCTCCG.....T.....-.....xxx.....A.....CTCCGTCTGACCGATGAAT
Contig4374 876591-877958 : TGGAGGCACTGAAGGCACTG.....-.....xxx.....CACTGCCACGGGACTCTGTG
Contig4922 2719081-2717796: GATCCGCAAGCGAGGGGTTG.....-.....xxx.....GGTTGGTGATTTGAAGGT
Contig5482 238752-239176 : GACTGCACAGCCACCACCC.....C.....-.....Txxx.A.T.....G.....CACCCCCTCGCGAGCACCGA
Contig6780 952419-953428 : CGAAAAGCCGGCCTGATG.....-.....xxx.....TGATGTTTCGCTAACTCTTC
Contig7446 1535599-1534365: CTCTCTCTTCTCACGGTC.....-.....xxx.....CGGTCGTTCTTGGGGTCCCT

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Legend to Supplementary Figure S4d. Alignment of fruit fly *TransibN1_DP* elements to the *TransibN1_DP* consensus sequence. The consensus sequence is shown in the top line. Dots indicate nucleotide identity with the consensus sequence; hyphens represent alignment gaps. The internal portion of *TransibN1_DP* is not shown and is marked by xxx. Target site duplications are highlighted. Coordinates of the reported elements are shown in the first two columns (sequence ID, beginning-end).

Figure S4e.

```

Hopper
arm_X      3321783-3320398 : TAAGCCAAATTTACAATGCG.....CACTATGGGGCATTGGCCGTGTTTTTTTT---ACAAAAATTAxxxCACATTATTGT--AAAAAAACAGGCCAAATGCCCATAGTG
arm_X      7692469-7690997 : TTTTAAATTTTATACCGCTA.....T.....T.....-A.....TAATGCTCCACATGTGCAGT
arm_X      11113816-1111529 : GTTGACGGGCGGTGCATTG.....T.....T.....-A.....CGCTAGGCTGCAGCTAGCTG
arm_X      21065414-21065981 : AAAATATGGACCTAATAATG.....T.....T.....-A.....CATTGCTGGCGACCTTAATGG
arm_3R     14159016-14157541 : GATCGAAAATAAAGACATTG.....T.....T.....-A.....GCAATGCTATGAACAATAGT
arm_3R     23683981-23682517 : GGTGCGGTATTGGACCAATG.....T.....T.....-A.....CATTGCTGAGGTGTTGAAAT
arm_2R     2651771-2653244 : ATTTTCGTGTGGCGCGCTG.....T.....T.....-A.....CAATGCTAATCTGACGGCGG
arm_2R     818021-816534 : AGAGCCTGGAGCCACTCTA.....T.....T.....-A.....CGCTCTCTGCGTGGGCTCA
arm_X      21643270-21644741 : TGCATAGTGCCAAACCAATG.....T.....T.....-A.....CTCTAGAGCCACATCGAATG
arm_2L     11615564-11614088 : ACCAAAGCCACGCCCAATG.....T.....T.....-A.....CAATGATGCGCGTTACGCA
arm_2L     14466034-14467508 : CTGGATGCGTTGCCACACAG.....T.....T.....-A.....CAATGCCCCAGCCATCCA
arm_3L     23114503-23113036 : CAAAAATTCGAGAGAGCCTG.....T.....T.....-A.....CACAGCTCGGAGCCATAAGT
3h         101990-100832 : CCCAGCAACTCCGCACAATG.....T.....T.....-A.....GCCTGGAGCCACCTTAGAG
3h         537419-538842 : AAGAGGCGGATGGGGCAGTG.....T.....T.....-A.....CAATCTGTCTAATCTCCGC
AABU01002545 8291-9763 : TGTAAACCAATCACACATTG.....T.....T.....-A.....CAGTGGTCTGATCAGGGGA
AABU01002746 156961-15550 : CTGTCTCTTCGGCACTATG.....T.....T.....-A.....CATTGCTGAAATTCCTTTAA
AABU01002753 12062-12884 : GTATTGTCAATGGAACACC.....T.....T.....-A.....CATTGCTGTAGATTCACC
AABU01002753 12062-12884 : GTATTGTCAATGGAACACC.....T.....T.....-A.....CAACCTACCACCAAGACA

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Legend to Supplementary Figure S4e. Alignment of fruit fly *Hopper* elements to the *Hopper* consensus sequence. The consensus sequence is shown in the top line. Dots indicate nucleotide identity with the consensus sequence; hyphens represent alignment gaps. The internal portion of *Hopper* is not shown and is marked by xxx. Target site duplications are highlighted. Coordinates of the reported elements are shown in the first two columns (sequence ID, beginning-end).

Figure S4f.

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TransibNI_DM
arm_2L     21096809-21096313 : TGCTCCATGTTATCACACTG.....A.....Axxxx.....T.....GACTGGGACAAGAAATATG
arm_2L     21318542-21317319 : -GGCAGGGGACCCCAAGGG.....T.....A.....G....xxx.G.C....A....G.....T.....CAAGGTCTAAGTGAGAGGC
arm_3L     21700662-21700244 : CTATGCACACGCAACCAACA.....T.....T.....xxx.....T.....A.....A.....CACCCTACCAGCAACACACA
arm_3L     21812579-21813116 : TTCGCTCACTCTCCTCTTG.....T.....C.....T.....G....xxx.....A.....A.....CATTGGAACGAGCCATCGGA
arm_X      1939342-1938788 : CACACACACATGGACCGCG.....C.GC.C.T.....C.....xxx.G....A....A.....AA.....C.....CGCTGGTGTGCACGCGATTA
arm_X      15386725-15387583 : CGATGTTCCCTTCGCCGGCG.....A.....T.....xxx.TT.....T.....A.....CGGCGGTTCGGTCAAAGAAG
arm_X      21998594-21999112 : ACATTTGCGCCTGAGCACCG.....C.ACGT.....T.....xxx.T.A.....T.....T.....T.....-A.....CACCGACGAGCCGCTATA
arm_X      22141281-22140789 : ACACACGCATAGAGACGTTG.....G.....A.....xxx.G.T.....-GGCCAACA.T.....-CGTTGATGTGCTCCCTCGT

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Legend to Supplementary Figure S4f. Alignment of fruit fly *TransibNI_DM* elements to the *TransibNI_DM* consensus sequence. The consensus sequence is shown in the top line. Dots indicate nucleotide identity with the consensus sequence; hyphens represent alignment gaps. The internal portion of *TransibNI_DM* is not shown and is marked by xxx. Target site duplications are highlighted. Coordinates of the reported elements are shown in the first two columns (sequence ID, beginning-end).

Figure S4g

Transib-N1_SP CACAGTGGGCCAGGGAGGAACCAAAGTGCGCCAAAxxxTTTGGCGCACTTTGGTTCTCCTGGCCCACTGTG

Contig12895 5655-6545:ATGGACCGGGTGGACCGCGGCACAGTGGGCCAAGGAGGAACCAAAGTGCGCCAAAxxxTTTGGCGCACTTTGGTTCTCCTGGCCCACTGTGCGCGGTGCGAATAGTTAAAA

Contig23311 409-1274:TAAGCTCTACGCAGGCGCGGCACAGTGGGCCAGAGAGGAACCAAAGTGCGCCAAAxxxTTTGGCGCACTTTGG-TCCACCTGGCCCACTGTGCGCGGCTTTCAGTCTCTT

Contig29183 3334-3891:CAATTAACCAGGGACCGACGCACAGTGGGCCAGGGAGGAACCAAAGTGCGCCAAAxxxTTTGGCGCACTTTGGTTCTCCTGGCCCACTGTGCGACGGCCCCCGACGGCCA

Contig30324 6923-6008:AAGAAAGTCAGCGAGCGCGGCACAGTGGGCCAGGGAGGAACCAAAGTGCGCCAAAxxxTTTGGCGCACTTTGGTTCTCCTGGCCCACTGTGCGACGTAGCGAGCGAGCTTT

Contig36576 2448-3366:TCGGGAGCGCACTGCGCGGCACAGTGGGCCAAGGAGGAACCAAAGTGCGCCAAAxxxTTTGGCGCACTTTGGTTCTCCTGGCCCACTGTGCGCGCCGCGCCGTGGCAA

Contig51741 1417-2323:GGAAGTACGTTCTGCGAGGCACAGTGGGCCAGGGAGGAACCAAAGTGCGCCAAAxxxTTTGGCGCACTTTGGTTCTCCTGGCCCACTGTGCGAGGTTTACGATTACGAA

Contig58992 635-1554:TTCGCGTAACCATGGCGACGCACAGTGGGCCAGGGAGGAACCAAAGTGCGCCAAAxxxTTTGGCACACTTTGGTTCTCCTGGCCCACTGTGCGCGGGGCGTACTGATGGG

Contig59342 3343-2426:CCAACCTCATGTTTCACGCGGCACAGTGGGCCAGGGAGGAACCAAAGTGCGCCAAAxxxTTTGGCGCACTTTGGTTCTCCTGGCCCACTGTGCGCGGGGCACCGAGCGTAT

Contig6151 1755-853 :ACCCGGGCCAGGGCGCGGCACAGTGGGCCAGGGAGGAACCAAAGTGCGCCAAAxxxTTTGGCGCACTTTGGTTCTCCTGGCCCACTGTGCGCGGGAGCGTATCCAAAA

Contig61636 561-1552:GTCTGTATCGGGGCGCGGCACAGTGGGCCAGGGAGGAACCAAAGTGCGCCAAAxxxTTTGGCGCACTTTGGTTCTCCTGGCCCACTGTGCGCGGTCTCATGGGCTTTC

Contig68912 65-978 :ATTGGCATCAAGCACCGACGCACAGTGGGCCAGGGAGGAACCAAAGTGCGCCAAAxxxTTTGGCGCACTTTGGTTCTCCTGGCCCACTGTGCGACGATCAGTCGATCAAAAT

Legend to Supplementary Figure S4g. Alignment of sea urchin *TransibN1_SP* elements to the *TransibN1_SP* consensus sequence. The consensus sequence is shown in the top line. The internal portion of *TransibN1_SP* is not shown and is marked by xxx. Target site duplications are highlighted. Coordinates of the reported elements are shown in the first two columns (sequence ID, beginning-end).