Figure S1. Comparisons of the 3’end-sequences between SINEs and LINEs

MIR(SINE) : L2(LINE)

```
MIR                  CAAGTTACT-TAACCTCTCTGTGCCTCAGTTTCCTCATCTGTAAAATGGGGATAA
L2B                  CCTGCCACTCTGGGTTATMATTGTCT--GTKNGCANGTCTGTCTCCCCCACTGGA
                     *  *  *** *    * *   ** **  **   *   *****            *

MIR             TAATAGTACCTACCTCATAGGGTTGTTGTGAGGATTAAATGAGTTAATACATGTAAAGCG
L2B             CTGTGAGCTCCGCGAGGGCAGGG-ACTGTGTCTGTCTTGTTCACCACTGTATCCCCAGCG
                   *     *  *       **    ****    *    *     * *  **    ****

MIR             CTTAGAACAGTGCCTGGCACATAGTAAGCGCTCAATAAATGTTGGTT--ATTA-----
L2B             CCTAGCACAGTGCCTGGCACATAGCAGGCGCTCAGTAAATGTTTGTTGAATGAATGAA
                * *** ****************** * ******* ******** ***  ** *
```

MIR(SINE) : THER1/THER1_MD(SINE) : MON1(SINE)

```
MIR             -------ACAGTATAGCATAGTGGTTAAGAGCACGGACTCTGGAGCCAGACTG-CCTGGG
THER1           TGAGGCAGCTAGGTGGCGCAGTGGATA-GAGCGCTGGACCTGGAGTCAGGAAGACCTGAG
THER1_MD        -AGGTCAGCTAGGTGGCACAGTGGATA-GAGTACTGGGCCTGGAGTCAGGAAGACCTGAG
MON1            -AGAGAAGCAGCGTGGCCTAGTGGATA-GAGCACGGGCCTGGGAGTCAGAAGGACCTGGG
                        *    * **  ***** ** ***  * *     **** ***   * **** *

MIR             TTCGAATCCCGGCTCTGCCACTTACTAGCTGTGTGACCTTGGGCAAGTTACTTAACCTCT
THER1           TTCAAATCCGGCCTCAGACACTTACTAGCTGTGTGACCCTGGGCAAGTCACTTAACCTCT
THER1_MD        TTCAAATCTAGCCTCAGACACTTACTAGCTGTGTGACCCTGGGCAAGTCACTTAACCTCT
MON1            TTCTAATCCNGGCTCTGCCACTTGTCTGCTGTGTGACCTTGGGCAAGTCACTTAACTTCT
                *** ****  * *** * *****    *********** ********* ******* ***

MIR             CTGTGCCTCAGTTTCCTCATCTGTAAAATGGGGATAATAATAGTACCTACCTCATAGGGT
THER1           GTCTGCCTCAGTTTCCTCATCTGTAAAATGGGGATAATAATAGCACCTACCTCCCAGGGT
THER1_MD        GTTTGCCTCAGTTTCCTCATCTGTAAAATGGGGATAATAATAGCACCTACCTCCCAGGGT
MON1            CTGTGCCTCAGTTACCTCATCTGTAAAATGGGGATTAAGACTGTGAGCCCCATGTGGGAC
                 * ********** ********************* *  *  *      **     **

MIR             TGTTGTGAGGATTAAATGAGTTAA--TACATGTAA---AGCGCTTAGAACAGTGCCTGGC
THER1           TGTTGTGAGGATCAAATGAGATAA--TATTTGTAA---AGCGCTTTGCAAA---CCTTA-
THER1_MD        TGTTGTGAGGATCAAATGAGATAA--TAATTGTAA---AGTACTTAGCACAGTGCCTGGC
MON1            AGGGACTGTGTCCAACCTGATTAGCTTGTATCTACCCCAGCGCTTAGAACAGTGCTTGGC
                 *       *   **      **   *   * **    **  *** * * *   * *

MIR             ACATAGTAAGCGCTCAATAAATGT---TGGTTATTA------
THER1           -------AAGCGCTATATAAATGCTAGCTATTATTATTAT--
THER1_MD        ACATAGTAAGTACTATATAAATGTTAGCTATTATTATTATTA
MON1            ACATAGTAAGTGCTTAACAAATACCA-TAATTATTA------
                       ***  **  * ****        ******
```

MIR3/THER2(SINE) : L3(LINE)

```
MIR3            GTCAGGAGACCTGGGTTCTAGTCCTAGCTCTGCCACTAACTAGCT--GTGTGACCTTGGG
THER2           GTCAGARGACCTGGGTTCAAATYCCRNTTCTGACACTTNATAGCT--GTGTGACCTTGGG
L3b             AATACTGGAATGGGTTGCCGAGGGAGATTGTGGAATTTCCTTCTCTGGAGAGNCTTTAAA
                   *   **   ** * *          * **  * *   *      * * * * **

MIR3            CAAGTCACTT-----CACCTCTCTGGGCCTC-----AGTTTTCCTCATCT---GTAAAAT
THER2           CAAGTCACTTAACGTCACCTCTCTGNGCCTC-----AGTTT-CCTCATCT---GTAAAAT
L3b             AATAGAATGNATNCTCATCTGTCTGGGATGNTTTAAAGGTAATCCTGCCCAAAGNTNGGN
                 *    *        ** ** **** *         ** *   *    *    *

MIR3            GAGNGGGTTGGACTAGATGATCTCTAAGGTCCCTTCCAGCTCTAACATTCTATGATTCTA
THER2           GAAGGGGTTGGATTAGATAGCCTCTAAGGTCCCTTTCAGCTCTAGA--KCTATGAT----
L3b             GNANGGATTGGACTAGATGACCTCTGAGGTCCTTTCCAATTCTGAGATTCTATGGTTTTA
                *   ** ***** *****   **** ****** ** **  ***      ***** *

MIR3            TGATTCTAAAAAAA
THER2           --------------
L3b             AA------------
```

MAR1_MD(SINE) : RTE-3_MD(LINE)

```
MAR1_MD         ACCCTGGGCAAGTCACTTAACCCTGTTTGCCTCAGTTTCCTCATCTGTAAAATGAGCTGG
RTE-3_MD        AGGAGAAGGGGATGGCAGAGGATGAGATGGATAGATAGTGTCATGGAAGCAATGAACATG
                *      *    *  *  *        **  *   *    ****      ***** *  *

MAR1_MD         AGAAGGAAATGGCAAACCACTCCAGTATCTTTGCCAAGAAAACCCCAAATGGGGTCACAA
RTE-3_MD        AGCTTGGACAG-------ACTTTAGGAGATAGTGGAGGATAGAAGGGCCTGGTATGCTAT
                **   * *  *       ***  ** *  *     * ** *        ***  *   *

MAR1_MD         AGAGTCAGACACAACTGAAAAATGACTGAACAACAACAA------
RTE-3_MD        GGTCCATGGGACAACTGAAGGAATAAAAGACAAGAACAATATATC
                 *     *  *********  *  *    **** *****
```

MAR4_MD/WALLSI3（SINE）：RTE-2（LINE）

```
MAR4_MD         ACTTTTG----TCTTGCCACTGGACTTTGAT---GACTCTGGAAGAGAGAG-TGAGGCTG
WALLSI3         ACTTTTG----TCYTGCCACTGGACTTCAAT---GACTCTGGAAGAGAGAG-TGAGGCTG
RTE-2_MD        ATTTAGAGACATCTCCATCCCAAATGTTCATATGGGCTATTTGTGCCTGACCTGTGGTAG
RTE-2_ME        ATTTGGA---ATATCCACCCCAAATATTCATATGGACTATCTGTGCCCAACCTGTGGTAG
                * **       *       *   *  *  **   * ** *    *    *  ** **  *

MAR4_MD         ATGACTTTGTGCAACTCTGCCTCACTTAAATCCAATTTATGTACAA-GTCAAAAGACATC
WALLSI3         ATGACTTTGTGCAACTCTGCCTCACTTAAATCCAATTCATGCACAA-GTCAA--GACATC
RTE-2_MD        AGCCTTCTGAGCTCATATTGGTCTGATCAGCCACAGTTAGACACACTGTACATTGACCCT
RTE-2_ME        AGCATTCTGAGCTCATATTGGTCTGATCAGCCACAGTCGGACACACTGAAATTTCACTTT
                *    * ** **   * *   **   * *  *  * *     ***  *       **

MAR4_MD         ACCA--GTGATGTCATTTTGGTCCTCTTTGAGTACAAAGGACAACAACCAACCAACCA-
WALLSI3         ACCT--GTGATGTCATT--GGTCCTCTTCAAAAATGAAGGACAAACAACAAT-------
RTE-2_MD        AACATAGTGATGTCATTTTGGTCCTCTTTGAGTATGAAGGACAAC--------------
RTE-2_ME        ATCATGGTGATGTCATTTTGGTCCTCTTTGAAGATGAAGGACAACAACCAACCTATTAT
                * *   ***********  *********  *  *  ********
```

RTESINE1 ： RTE-1_MD（LINE）

```
RTESINE1        ACTTTTCGTGC-CACTGGACCCAGGCTTCCAACGCCGAGAGAGTGG-GACTGTCTCTGTG
RTE-1_MD        GCTGCGCGTGAACGCCGACACCAGGCCACAACCGCACCTCCCGTAACAACTGGCGTCCCA
                 **   ****  * * *   ******  * * ***       **    **** *

RTESINE1        CATCGACTTTTCCACTTAA-ATCTCCTTCACGCACAAGTGTCTTTGTGCACACTCATCTA
RTE-1_MD        TGCCCCATGTGCCACAAACTGTGCGCCTCAGCCTTTGGACTCCAAAGCCACATGAGGGTA
                   *   * * ****  *   *   * ***  *    *  **      ****      **

RTESINE1        CATCATAGATGAAAACGCACAAAGACAATCGTCATCCTCGGTTACCGAGAGACTACTACT
RTE-1_MD        CACCGTAGATGAAACTGCACAAAGACAATAGTCATTCTCGATCACCGAGAGACTACCACT
                ** * *********  ************* ***** **** * ************* ***

RTESINE1        ACTAC
RTE-1_MD        -----
```

SINE2-1_EC ： RTE-1_EC（LINE）

```
SINE2-1_EC      CACCCACTTCCAAAAAAATTGGCCATGAAAACCCTATGAATAGCAGTGGAGCATTGTCTG
RTE-1_EC        AGCAGGAAAAGAGGAAGACCAAATATGAGA--TGGATTGACTCCATAAAGGAAGCCATAG
                  *        *  ** *      **** *     **  *   **     * *      *

SINE2-1_EC      ATACAGCGCCAGAAGGTGAGAGGATGGCGCAAAAAGACCGGGCAGGGTTCCGCTCTGCTG
RTE-1_EC        GCATGAGTCTACAGGAGCTGAGTAGGGCTGTTGAGGACAGGACATTGTGGACATCACTCA
                  *     * * * *    *** * ***     * *** ** **  **     **

SINE2-1_EC      TACACAGG-GTCGCTAGGAGTCAGAATCGACTCGATGGCAC-TAACAACAAA-
RTE-1_EC        TTCATAGGAGTCACCAGGAGTYGGAGCCGACTTGATGGCATGTAACAACAACA
                * ** *** *** * ******  **  ***** *******  *********
```

AFRO_LA/PSINE1 ： RTE1（LINE）

```
AFRO_LA           ------------------TGGAAACCCTGGTGGCATAGTGG-TTAAGAGCTACGGCTG
PSINE1            ------------------GGGAAACCCTGGTGGTGTAGTGGGTTAAGTGCTACCACTG
RTE1_LA           CAGGGTCAGCGGAAAAGAGGAAGACCCT--CAATGAGGTGGATTGA-CACAGTGGCTG
RTE1_Pca          GAGGGTCAGCGAAAAAGAGGAAGACCCT--CGACGAGACGGATCGA-CACAGTGGCCG
                                     * * *****           ** *  *   *     * *
```

```
AFRO_LA         CTAACCAAAAGGTTGGCAGTTCAAATCCACCAGGTGCTCCTTGGAAACTCTATGGGGCAG
PSINE1          CTAACCACAAGGTCGGCAGTTCAAATCCACCAGGCGCTCCTTGAATACTCTGGGGGTCAG
RTE1_LA         C-AACAATGAGCTCAAGCATAACAA-CGATTGTAAGGATGGCTCAGGACCGGGCAGTGTT
RTE1_Pca        C-AACAATGGGCTTAAGCATAAAAA-CGATTGTGGACATGGCGCAAGACCGGGCAGTGTT
                * *** *   * *      *   ** * *               *    *     *

AFRO_LA         TTCTACTCTGTCCTATAGGGTCGCTATGAGTCGGAATCAACTCGACGGCAATGGGTTTGG
PSINE1          TTCTACCCTGGCCCCTAGGGTCGCCATGAGTCGGATCCGACTCGACGGCACTTGGCTTGG
RTE1_LA         TCGTTCTGTTGTGCATAGGGTCGCTATGAGTCGGAACCAACTCAATGGCACCTAACAACA
RTE1_Pca        TCGTTCTGTTGTTCATAGGGTCGCTATGAGTCGGAACCGACTCGACGGCACCTAACAACA
                *  * *  *      ********* **********  * **** * ****

AFRO_LA         TTTTGGTTTTTT
PSINE1          CTTGGC------
RTE1_LA         ACAACAA-----
RTE1_Pca        ACAA--------
```

RTE1-N1_LA(SINE) : RTE1_LA(LINE)

```
RTE1-N1_LA      TTCCGAAAATTAGCCAATGAAAACC---CTATGGATCACAACAGAATATT--GTCCAATA
RTE1_LA         TTTGGACATGTTGTCAGGAGGGATCAGTCCCTGGAGAAGGACATCATGCTTGGCAGAGTA
                **  ** *  * * **      * *   *  ****  *  ***  **  *  *   * **

RTE1-N1_LA      TAGTGCTGGAAGATGAGCCCCCTAGGTTGGAAGGCACTCAAAATACACAGTGGCTGCAAC
RTE1_LA         CAGGGTCAGCGGAAAAGAGGAAGACCCTC-AATGAGGTGGATTGACACAGTGGCTGCAAC
                 ** *   *  **  **      *   *  ** *   *  *   ****************

RTE1-N1_LA      AATGGACTCAAGCATACCAACGATCATGAAGATGGCACAGGACCAGGCAACGTTTTGTTC
RTE1_LA         AATGAGCTCAAGCATAACAACGATTGTAAGGATGGCTCAGGACCGGGCAGTGTTTCGTTC
                ****  ********** *******  * * ****** ******* ****  **** ****

RTE1-N1_LA      TGTTGTACATGGGGTCGCCATGAGTCGGAGCCGACTCGATGGCAACTAACAACAACAACA
RTE1_LA         TGTTGTGCATAGGGTCGCTATGAGTCGGAACCAACTCAATGGCACCTAACAACAACAACAA
                ****** *** ******* ********** ** **** ****** ***************
```

SINE2-1_Pca : RTE1_Pca(LINE)

```
SINE2-1_Pca     AAAGGCCTGGCGATCTACTTCTGAAAATCAGCCAATGAAAACCCTGTGGATCACAGTGGT
RTE1_Pca        AGCGAAAAAGAGGAAGACCCTCGACGA--GACGGATCGACACAGTGGCCGCAACAATGGG
                *  *     * *    **    **  *    *  **  * **  **      *** ***

SINE2-1_Pca     CTGA--TCTGCAACTGATCATGGGGATGGCGCAGGACCGGGCAGCGTTTTGTTCTATTGT
RTE1_Pca        CTTAAGCATAAAAACGATTGTGGACATGGCGCAAGACCGGGCAGTGTTTCGTTCTGTTGT
                ** *    *  **  ***  ***  ******** ********** **** ***** ****

SINE2-1_Pca     GCATGGGGTCGCCATGAGTCGGG-CCGACTCGATGGCAGCTAACAACAA---
RTE1_Pca        TCATAGGGTCGCTATGAGTCGGAACCGACTCGACGGCACCTAACAACAACAA
                 *** ******* *********  ********* **** **********
```

TguSINE1 : CR1-X(LINE)

```
TguSINE1        ----------------------------------AGATTAGCTCAGTTGGTCAGAGCATG
CR1-X1_Pass     GGCTCCCCAGGGAAGTGGTCACAGCACCAAGCCTGACAGAGTTCAAGAAGCGTTTGGACA
CR1-X2_Pass     GGCTCCCCAGGGAAGTGGTCACGGCACCAAGCCTGTCAGAGTTCAAGGAGCGTCTGGACG
CR1-X3_Pass     --------------------------------------GTGTTTAAGAGGCATTTGGACA
CR1-X1_3end     GGCTGCCCAGGGCAGTGGGCACGGCCCCGAGC-TGCCGGAGTTCAAGGAGCGTTTGGACA
CR1-X2_3end     GGCTCCCCAGGGCAGTGGTCACGGCCCCGAGC-TGCCGGAGTTCAAGAAGCATTTGGACA
                                                        * * *    *     * *

TguSINE1        GTGCTAATAACACCAAGGTTATGGGTTTGATCCCCATATGGGCCATTCACTTAAGAGTTG
CR1-X1_Pass     ATGCTCTCAGGCACATGGTGTGACTCTTGGGGATGGTCCTG--TGCAGGGCCAGGAGTTG
CR1-X2_Pass     ATGCTCTTAGTCATATGGTTT-AGTTTTAGG--TAGTCCTG--CGAGGAGCAGGGAGTTG
CR1-X3_Pass     ATGCCCTTAATAACATGCTTTAACTTTTGGT--CAGCCCTG--AAGTGGTCAGGCAGTTG
CR1-X1_3end     GCGCTCTCAGACATAGGGTTTGAATTTTGGG--TGGTCCTG--TGTGGAGCCAGGAGTTG
CR1-X2_3end     ACGCTCTCAGACATAGGGTTTGAATTTTGGG--TGGTCCTG--TGTGGAGCCAGGAGTTG
                  **    *     * * *       **            *              *****

TguSINE1        GACTCAATGATCCTTGTGGGTCCCTTCCAACTCAGAATATTCTGTG--ATTCT-------
CR1-X1_Pass     GACTCGATGATCCTTGTGGGTCCCTTCCAACTCAGCATATTCTGTG--ATTCTGTG--AT
CR1-X2_Pass     GACTCGATGATCCTTATGGGTCCCTTCCAACTTGAGATATTCTATG--ATTCTATG--AT
CR1-X3_Pass     GACTAGATGATCGTTGTAGGTCCCTTCCAACT-GAAATATTCTATTCTATTCTATTCTAT
CR1-X1_3end     GACTCGGTGATCCTTGTGGGTCCCTTCCAACTCGGGATATTCTATG--ATTCTATG--AT
```

```
CR1-X2_3end     GACTCGATGATCCTTGTGGGTCCCTTCCAACTCGGGATATTCTATG--ATTCTATG--AT
                ****   ***** ** * **************    ******* *   *****

TguSINE1        -------------------------------------------
CR1-X1_Pass     TCTATG-------------------------------------
CR1-X2_Pass     TCTATG-------------------------------------
CR1-X3_Pass     TCTATTCTATTCTATTCTATTCTATTCTATTCTATTCTATTCT
CR1-X1_3end     TCTATG-------------------------------------
CR1-X2_3end     TCTATG-------------------------------------
```

SINE2-1B_ACar/SINE2-1_ACar : Vingi-2_Acar(LINE)

```
SINE2-1_ACar        CTCTATCAGCTCCAGCTCCATGCGGGGACATGAGAGAAGCCTCCCACAAGGATGGT
SINE2-1B_ACar       CTCTATCAGCTCCAGCTCCATGCGGGGACATGAGAGAAGCCTCCCACAAGGATGGT
Vingi-2_Acar        TTCTAACAG---CAACACCA---GAGGCACTCCAAGTGGCCAGCTACTGGGCAAAA
                     **** ***   ** * ***   * **   *   **  ***  * **  **

SINE2-1_ACar    AAAA-CATCAAAACATCCGGGCGTCCCCTGGGCAACGTCCTTGCAGACGGCCA--ATTCT
SINE2-1B_ACar   AAAAACATCAAAACATCCGGGCGTCCCCTGGGCAACGTCCTTGCAGACGGCCA--ATTCT
Vingi-2_Acar    GACA--TTTAGTATTAATGCCAAGTTTTTGTTTTTTTTTCTTAAAAAAAATCTCTATGTT
                 * *   * *  *     *         **       * ***  * *    *   **  *

SINE2-1_ACar    CTCACTCCAGAAGCAACT----------CCGGTTGCTCCTGACACGAAAAAAAAAAAAA
SINE2-1B_ACar   CTCACACCAGAAGCGACTTGCAGTTTCTCAAGTCGCTCCTGACACGAAAAAAAAAA---
Vingi-2_Acar    TGCAAATCCATTACAACTTGTACCCTC-GGTTTCGCTTCTGACACGAGAAATAAATAA-
                  **    *     * ***              * *** ********* *** ***
```

SINE2-1_XT : L2-4_XT(L2-3, L2-6, L2-2)(LINE)

```
SINE2-1_XT      CTTAGATTGTAAGCTCCTCTGGGGCAGGGACTGATGTGAATGATGAATAATCTCTGTAAA
L2-4_XT         AATTGTTTATATGTACATGTTAACT---GTTCTGTCTTTTGTACCCCTCTATTCTGTAAA
L2-3_XT         CTTTATATGT-TA--CTCTGTATGT---CCAATGTATGTAACCCA----CTTATTGTACA
L2-6_XT         CCTTGTTTGT-TAAACTTTTTAAGA---TCCCTGTTTGTT-TAAA----TTTATTGTGAA
L2-2_XT         ATTTATCTAT-TA--TCTTATTAAC---CCCCTGTTTGTATTAATGTATTCTACTGTACA
                  *    * *                        * *                 ***  *

SINE2-1_XT      GCGCTGCGGAAATGTGTTGGYGCTATATAAATAACAGGAAATAAATATAAATAAAT-
L2-4_XT         GCGCTGCGTAAAT-TGATGGCGCTATATAAATAA-TAATAATAATAATAA-------
L2-3_XT         GCGCTGCGGAATA-TGTTGGCGCTTTATAAATAAATGTTAATGTAATGTAATGTAAT
L2-6_XT         GCGCTGCGTAATT-TGCTGGCGCTATATAAATAAATGATGATGA-------------
L2-2_XT         GCGCTGCGTACAT-AAGTAGCGCTTTATAAATAAAGATATACATACATACATACA--
                ******** *       * * *** *********      *
```

MIR_Xt(SINE) : L2-5_XT(LINE)

```
MIR_Xt          AC-CCTGGTTCGATTCCCTGTGGCAACTCCTTGTGACCCTGGACAAGTCACTTAATCTCC
L2-5_XT         ACGTTTAAATCAAAACTGAAAAGCCACCTGTT-TAGCCTGGCATTTATGTCCACATAACT
                **   *   ** *  *      ** **   ** *  **  * *    *  *   **  *

MIR_Xt          TGGTGTCCCAGCATACTTAGTGCGCCTATAATGGCTGCCTTGCTTGCTGTAAAGCGCTTT
L2-5_XT         T--TTCCTCTGCACACATAG---ATATGTACTG---ATCTGAGACAAGCTTATGCGCTTT
                *  *  * * *** ** ***      * ** **     **         * * *******

MIR_Xt          GAGTCCCACGGGAGAAAAGCGCTATATAAATGATWCCC-TTACCCTTA---
L2-5_XT         GGGTCCCACGGGAGAAAAGCGCTTTACAAATGTTTGTTGTTGTTGTTGTTG
                * ********************* ** ***** *     **    **
```

SINE3 : CR1_DR(LINE)

```
SINE3-1         CTGGCGCCGTTGTCCTGTGGCTGCCGTCGCATCATCCAAGTGGATGCTGCACACTGGTGG
SINE3-1a        CTGGCGCAAA------ATGGCTGCCGTCGCGTCATCCAGGTGGATGCTGCACACTGGTGG
CR1-4_DR        ATATTCGCTATTGCGTTTTAACCTGTTTGGTCAATGATTGTTTTTAGTAATGTTTAATTT
CR1-7_DR        ATTGCTTTTAAT----GATTTTATGGATTAACACTATGATTTATTACTCTTCTGTCTTGT
CR1-9_DR        ATGTCTCTTAGG----TTTCGTTTGTGTTATTCATGTTTGTTATATTTGACCTCATGTAT
CR1-13_DR       ATGGTTCATA------TTTTTATTGTTTTATT-GCATCTTTTATTGTTGTGCTGTTTT--
                 *                                      *      *         *

SINE3-1         TGGTGTGGAGAGACCCCCCCTCATGATTGTGAAGCG-CTTTGGGTGTATGGCCATACACA
SINE3-1a        TGG-ATGAGGAGATTCCCCCCAATG--TGTAAAGCG-CTTTGAGTGCCCAG---------
CR1-4_DR        GTTTTAGCATGTCTGT-TGATGCTTATTGTAAGGCGACCTTGGGTGTCTTG---------
```

```
CR1-7_DR        TTTTTATAATGTGCCTGTGACAT--ACTGTAARGTGTCCTTGAGTGCTCTG---------
CR1-9_DR        GTTTGTTTATCTTTTTGTTGCATTCCTTGTAAAGTGTCCTTGAGC-TCTGG---------
CR1-13_DR       GCTTGCCTTGTGTTCTAGTATTTTGCCTGTA--GCG-CTTTGAGT-ATAAG---------
                                           ***   * * * *** *      *

SINE3-1         ATAAATGCGC--TATATAAATACACATTAC-ATTAC-ATTA------------------
SINE3-1a        --AAAAGCGC--TATATAAATGTAAGGAATTATTATTATTATTATT----------
CR1-4_DR        --AAAGGCGCCATTTACAAATAAAATGAATTATTATTATTATTATTATTATTATTA
CR1-7_DR        --AAAGGCRCC---TATAAATAAAGGGTATTATTATTATA-------------------
CR1-9_DR        --AAAGGCGC--TATATAAATAAAAATTATTATTATTATTATTAT--------------
CR1-13_DR       --AAAAGCGC--ATTACAAATAAAATGTATTATTATTATTATTATTATTA------
                  *** ****    ** ****  *    *  ****  ****
```

SINEX-1_CM/SINE2-1_CM : CR1-2_CM(LINE)

```
SINEX-1_CM      ATAATCCCTCCAAAACCAAAAACAATAATAAATTGGTCATTTTCAATCYAHGACTGTTTG
SINE2-1_CM      ATAATCCCTCCAAAACCAAAAACAATAATAAATTGGTCATTTTCAATCYAHGACTGTTTG
CR1-2_CM        ATTTCCCCCCT----CCTCGCTCCCTCCC---TTCCCTCCCCTCA--CCCTGACCATTTC
                **   *** *     **     *  *      **        ***  *   ***  ***

SINEX-1_CM      TGGGACATTGCTGTGCGCAATTGGCTGCCGCGTTCGCCCACAAATATACAGTCAATTCAC
SINE2-1_CM      TGGGACATTGCTGTGCGCAATTGGCTGCCGCGTTCGCCCACAAATATACAGTCAATTCAC
CR1-2_CM        CC--CCCTCCTCGCTCCCTCCCTTCCCTCCCCTCACCCTGACCATTTCCCCCCTGCTCGG
                     * *    *  * *      *   * * *   **     ** * *   *   **

SINEX-1_CM      TTTACAGTRTRTTCTGTGAAGCGCTTTGGGACGTCCTCCCGACGTGAAAAGCGCTATATC
SINE2-1_CM      TTTACAGTRTRTTCTGTGAAGCGCTTTGGGACGTCCTCCCGACGTGAAAAGCGCTATATC
CR1-2_CM        GTCATGACCCAA-CTGTGCAGCGCCTTGGGACGTCCTCCTGACGTGAAAGGCGCTYTAT-
                 * *         ***** ***** ************** ********* ***** ***

SINEX-1_CM      AAATGCAAGG--ATTATTATTATT--
SINE2-1_CM      AAATGCAAGG--ATTATTATTATT--
CR1-2_CM        AAATGGAATCTTGTTGTTGTTGTTGT
                ***** **     ** ** ** **
```

BflSINE1 : Crack-16_BF(LINE)

```
BflSINE1        ACC-CCAGGCACGTTAAAGAACCCACCACACGTGCGATGGTGCGGTGTGAGATGGTGCAA
Crack-16_BF     ACTGTTTTTCAGTTTACCATATGTTTGCTTTCTGTTATTTCAAAGTTATAATTTGTATAA
                **       **  ***    *           **  **      **   *  * **  **

BflSINE1        ATCCTTC-CGTCTAGAATTGGTGATTCTCTACAAATC--ACCCGGACTCCAGGAAGAATA
Crack-16_BF     TTTGTACATTTCTGTTGCAATTATTTCTGTATTGTTTTAATGTGGACTCCAGGAAGACTA
                 *  * *   ***        *  **** **    *   *   ************** **

BflSINE1        GTGACATATCAGTCACTAATGGAGATCTGTATAA-CCAAACCAAACCAAACCTAA
Crack-16_BF     GTG---TATT--TCACTAATGGAGATCTAAATAAACCAAACCAAACCAAACCAAA
                ***   ***   ****************  **** ***************** **
```

SINE2-4c_SP : CR1-4_SP(LINE)

```
SINE2-4c_SP          TCCACCCAGGTGTAGTAAA--TGGGT-ACCTGGTAGGAATTTATTCCTTGAATGC
CR1-4_SP             TGTACCATGGCACCATGAAGTTGTGTGATCTAATGCAAGTTAA--CATTTAATAT
                     *  ***  **     * **  ** ** * **  *   * ** *  * ** ***

SINE2-4c_SP     TTTTAGCGCCTTAGGGCAGCTGGGCTAAAGCCAGGGTAATAATACTACTTTGTAGGCGCC
CR1-4_SP        TTCTTTAATCTTAAGTATGTTG----AATATTAATTTAA----ATTA-TTTGTATGCGCC
                ** *     **** *   * **    **    *   ***    * ** ****** *****

SINE2-4c_SP     TTGAGCATCCCCTGGGATGGATACGT-GCGCAATATAAATGTAGCTATTATTATTATTA-
CR1-4_SP        TTGAGCATCTCTAGAGATGGATATGTTGCGCTTTATAAATATTGTTATTATTATTATTAT
                ********* *  * ******** ** ****  ******* * * **************
```

SINE2-3_SP : CR1Y_SP(CR1X_SP)(LINE)

```
SINE2-3_SP      GAGAAGAGTCACTACCTT-TGCACGTTAAGAACCCACTGCACTATTCGTATAAGAGTAGG
CR1Y_SP         GCCTTCCGTCAAYRMCTGACGGGAGGCAGCAACTAAGTCCGGGAACTTTTTACTGGCACT
CR1X_SP         GCCTTCCGTCAATGCCTGACGGGAGACAGCAACTAAGTCCAGGAAATTTTTACTTGCACC
                *      ****    **   *   *  *  ***  * * *   *    * **   * *
```

```
SINE2-3_SP      G-GGAAACCCCGGTGTAGTGGTCCACCTGCACACCCCAACCAGGCCGAGTATAATACGGC
CR1Y_SP         ATGTAAATAGCATTGCACCATGCACCTTGCTC-TCGTA---AGCACACACACACTCATCA
CR1X_SP         ATGTAAATAGCATTGCACCATGCACCTTGCTC-TCGTATTAAGCACACACACACTCATCA
                  * ***   *  ** *     *  * *** *  *  *   **  *    * * *

SINE2-3_SP      ATCTGCAAGGATCTTCAGTATTGAAGGAGGCAGA-TTATCTTGAAGAAGAAGAAGAA---
CR1Y_SP         GTCTGCAAGAATCTTCAGCAGTGAAGGAGGCAGACTTAACCTAAAGAAGAAGAAGAA---
CR1X_SP         GTCTGCAAGAATCTTCAACTGTGAAGGAGGTAGACTTAACCCAAAGAAGAAGAAGAACAA
                 ******** *******    ********* *** *** *   **************
```

SINE2-8_SP(SINE2-6, SINE2-4b) : L2-1_SP/CR1-3_SP(LINE)

```
L2-1_SP         AATTTTTTACA-GTGTATGCACTTGGAGAGCAAAATAATTA---TTCTGTTTTATTTACT
SINE2-8_SP      TGCACACAGTGTGTGCGGGCAAGCACTGAATCCAATGACCGGGGTAATAGTATATT--T-
SINE2-6_SP      TGCATACATTGTGTGCGGGTAAGC-CTGAATCCAATGACCGGGGTAATAATATACT--TA
SINE2-4b_SP     GGTACCTGATATGCTTGAGCGC-TAGTTACTTTGGCAGCTCGGCTACGACCAGGGTAATA
                            *     *         *               *          *

L2-1_SP         AATGTAAAGCGCTTTGAGC------ATGTTTATGTAAA-GGCGCTATATAAATATCAA-T
SINE2-8_SP      --TGTAAAGCGCTTAGAGA-------CATTTGTATTA--AGCGCTATATAAAAGCTAAAT
SINE2-6_SP      TCTGTAAAGCGCTTTGAGAGGGCCTCCGGTCCTGAAA--AGCGCTATATAAGAACGAGCT
SINE2-4b_SP     TGTGTAAAGCGCCATGAGCGTCAGAACCTGGCGGATACCGGCGCTATATAAATAACCA-T
                  **********   ***                  *   ***********        *

L2-1_SP         ATGTATGTATGTATGT-----
SINE2-8_SP      ATTATTATTATTATTATTA--
SINE2-6_SP      ATTATTATTATTATTATTATT
SINE2-4b_SP     ATTATTATTATTATTATTATT
                **   * *   ***
```

Gecko(SINE) : I_AAe(LINE)

```
Gecko           AAAAAGTTATAGTGACGACTTCCTTCGGAAGGGAA---GTAAAGCCGTTGGTC----CCG
I-74_AAe        G---TAACAGACTAGAGAATACCCTTAAGGTACCTC-TAGCGTGCAATATTCGTCAACCG
I_Ele35         C----TATAAACTCTGTAAATTCCTGGAGTGCCCTTATGGTACCCCACCTTTTTCC-TCG
I_Ele37         CACATTATTCGCGAGGTTGAATCCTTCAGGTTCCTCCTCCTTTTTTATATTTTTG--TCG
I-62_AAe        AGCAAAATGTACAGGGGGGCCTCTCACTACGAAGCCCTCT----CCATATTCTCTACCGG
I-59_AAe        ATTACTCTGTATAAGTATTACTGCCCAGGAGGGCCAATGTAACGCCCTCTTTTTTCACGG
I_Ele14         TCAGTCTTCTGCTGACCGTATTTCTCCAGGGTCTCAGCCTTCTGCTGAGCCTTCTC-CCG
I-58_AAe        TCAGTCTTCTGCTGACCGTATTTCTCCCGGGTCTCAGCCTTCTGCTGAACCTTCTC-CCG
I_Ele10         TTGAAAGCCTGTAAAACTCCTTATTGAAAGCAGCCTTTCTGGCGCTTTTCTGACAAATGG
I-64_AAe        TATGGTTCGCCTTACTTTCCCCCGTTACACGAGTGCCCTTCAGGCACCTCATGTGG-CAG
                                                                           *

Gecko           AGATGAACTAGCCCAGGGC--TAAAAATCTCGTTAATAAAGATAGAAAAAAAAAA-----
I-74_AAe        AGATGAACCAGCCTCAGGC--TGAAAGTCTCGTTAATAAAGATAATAATAATAATAAT--
I_Ele35         AGACGAACCAGCCAAGGGC--TGAAAGTCTCGTTAATAAAGACAATAATAATAATAATAA
I_Ele37         AGGTGAACCAGCCACGGGC--TGAAAGCCTCGTTAATAAAGACAATAATAATAATAATAAT
I-62_AAe        AGACGAACCAGCCAACGGC--TGAAAGTCTCGATAATAAAGATAATAATAA---------
I-59_AAe        AGACGAACCAGCCACTGGC--TGAAAGTCTCCTTAATAAAGATAAAAAAAAAAA------
I_Ele14         TGTTGAACTAGCATAATGT--TAAAAAACACGTTAATAAAGATGAAAAAAAAAA------
I-58_AAe        TGTTGAACTAGCATAATGT--TAAAAAACACGTTAATAAAGATGAAAAAAAAAAAAAAA-
I_Ele10         TGATGAACTAGCCGTATGCGCTAAAAATCACCTTAATAAAGAACAAAAAAAAA-------
I-64_AAe        TGATGAACTAGCCAAACGAGTTAAAAATCACTTTAATAAAGAAAAAAAAAAAAA------
                 *  **** ***     *   * ***  * *  *********    ** **
```

SINE2-1_NV : CR1-16_NV(LINE)

```
SINE2-1_NV      TTGACTTGTTGAACGTATGTGAGCTTACTAGAAGCTTGTGTTCCTCAGTTCCAAGATGGG
CR1-16_NV       GTAACATTTCCTATTAGACACAATGTATTGTCAG--GGTGATTTTTAATTTTTAATTGTG
                 * ** * *   *        *   ** *   **   *** *  * * **   *  ** *

SINE2-1_NV      ACATTCTTAATACATTAGGATTTTAAATGTGAAGCGCTTAGAACA-TGGTTGGTATAAGC
CR1-16_NV       TAATGTTTATTTAATTGATATAT-AATTGTAAAGTGCCTAGGGCAATTATTGATG-AGGC
                  **  *** *  ***   ** * ** *** *** ** ***  ** *  *** *  * **

SINE2-1_NV      GCTATATAAATGCT-ATATTATTATTATT-------------------------------
CR1-16_NV       GCTATATAAATGCTGATATTATTATTATTATTATTATTATTATTATTATTATTATTATTA
                ************** **************
```

SINE2-5_NV : Rex1-24_NV(LINE)

```
SINE2-5_NV      TCTCTCATCCATGTAAACTGCGTGGCAGCACAGTGCGCCTTATATAGCAGTCCGAATAAG
Rex1-24_NV      TATTTTATCATAATAATATTTATAAC----TATTGTCGTATTTAAATTTTTCATATTATT
                * * * ***    ***  *   *  *     * **     * ** *    **  * **

SINE2-5_NV      ACCCCGTGTAATGTAAATCCAGAGTAATTCAGCCTAT-GGCTGCAATTCTGGATAAAGTC
Rex1-24_NV      TTTATTTTTTTTGTACATAATGCGTAATTCAGCCTTTTGGCTGCAATGCATATTTTTAAT
                      * *  **** **   * ************ * ********* *    *

SINE2-5_NV      GGCCCAGCTTCCTTTCCTTTCCTTTCCT--
Rex1-24_NV      AAACTATCTATCTATCTATCTATCTATCTA
                   * * **  ** **  *   * *
```

MgSINE : MGR583(LINE)

```
MgSINE          ----------------------------GGGGGGAATGGCGCAGTGGTTAAGCGCCA--T
MGR583          CGGTGCACTGCCGCTTTTCGCGGGCGGTGTGGAGAAACTGGCCGTGGCCTGACAACGACC
                                            * ** ***    ** ****     *  *

MgSINE          GGCTGTTACTTGAGTAACGTAGGTTCGAATCCTGC---TCCCTCCACCTCCTCCCCGCTT
MGR583          GGCCGGTCGGGCCGCCAGACCGCGCCCAACGCCGCAAATTCTTCCAGACAAGCCTCGGGC
                *** * *      *  *    *   * **  * **   * * ****      ** **

MgSINE          ACCGTGGCAAGGATAACCCG-----GCTGGCTATCGACAACAAC--CACCCGCCTGTG--
MGR583          AACCGAAAAGCTTTGAGGCGTTTTCGATAGCCACCAACTACTTCAGCGCCCGCCCCAGAG
                * *     *    * *  **     * * ** * * ** **  *  * ******   *

MgSINE          ----CCATCGAGCCCACACTTGTTGGGAAC----TTCGTCTCCATGGCTACAAACGACCG
MGR583          CGGCCCGCCAGCGCCCCGCGCGCCACGAACGCACTTTACGCCTAGGGACACCGATCGTAA
                    **  *    ** * *  *    ****    **     * * **  **  *

MgSINE          ACAGCTC---CGCTGTTTGGACACAGGCC-----CCTCTCGATGAAGAGC---CGTCAAC
MGR583          ACGACTCGAACTCTGACGAGGAATAGACTTACTGCCTTTTCACCCACACTTCACGGCACA
                **  ***   * ***    *  * ** *      *** *  *   * *     ** **

MgSINE          TGCCGTCAGACGAATCCTCCGTGCGCCTGAAGGCACGGGGTCGCGTCAGTGAACAAACCT
MGR583          AGCCGCTAGACGAACCCTCCGTGCACCTTA-GGCACGGGGTCGCGTCAGTGAACTAACCC
                 ****  ******* ********* *** * *********************** ****

MgSINE          G-TAAGCAGGACCGGGCACGAACCCGGTCAGGCTCGATTCGCTTCTATGC-CCTTGTTTT
MGR583          CCTAAGCAGGACCGGGCCCGAACCCGGTCAGGCACGATCCGCCTCTGCCCTCCTTGTTTT
                  *************** *************** **** *** ***   * *********

MgSINE          CCGC-TGTGTAAATAGAGAAAATAGAAAGCGCGCCGAGATACCCCTCGG-AGGTTGCTAA
MGR583          CCCCCTGTGTAAATAAAGAAGATAGAACGCGCGCCGAGATACCCCTCGGGAGGTTGCTAA
                ** * ********** **** ****** ********************* **********

MgSINE          CGGTCGGCTAATGAGCCGGGCCGAGCCCGGCGTTAAATAATACTACTACTACTACTA-
MGR583          CGGCCGGCTAACAAGCCGGGCCGAGCCCGGCGTTAACTAATACTACTACTACTACTAC
                *** *******  *********************** ********************
```

SINE2-1_BG : Tad1-24_BG(HaTad1-3_BG, HaTad1-5_BG)(LINE)

```
SINE2-1_BG      AAAAGCCGCCTTGTCACAG----CCGTAGTGAGACTTGCAAATGATATCTGAGGCATGA-
Tad1-24_BG      AAATATGTGAGGACTATAGA---CAACAAATAGAAAGGTGTGGGAGGTTTTCACCATAAA
HaTad1-3_BG     GGTTAACGAAGTACTACAG----TAATAAATTGA-AGGAGAAGGGGGTTTTTATCGGAA-
HaTad1-5_BG     AGGTAACGAAGGACTACAGATGATAAAAACTTGATAGGGGGAGGGGGTTTTTATCGTAAT
                               * **        *    **   *     *   * *    *   *

SINE2-1_BG      TGTTCATCACAACTATATCATCATTGTATCTGACTGAAGTCAACACCTGCATGGGCCAAA
Tad1-24_BG      GGTTTCCTCC-CGGGTAAA-----TAT---TATAGACTGTAGACACCTGCATGGGCCCAT
HaTad1-3_BG     GGTTTCCCCCTCATGTAAAATATCTATAAGTAGAGTTTATAGCCACCTGCATGGGCCCAT
HaTad1-5_BG     GGTTTCCCCCTCATGTAAA---TACATAGATAG-GTTCATAGCCACCTGCATGGGCCCAT
                 ***     *     **         *   *        *   ************** *

SINE2-1_BG      AAGGCGCCAAATCAGGACAATTGAATAATTTATTTATTTA--------------------
Tad1-24_BG      AGGGCGCCAAATCAGGATAA-TGAA-ATCAAATTCAAATTCAATAATAATAATAATAATA
HaTad1-3_BG     AGGGCGCCAAATCAGGTTAA-TGAA-ATCAAATTCAAAAATAATAA--------------
HaTad1-5_BG     AGGGCGCCAAATCGGGATAAATGAA-ATCAAATTCAA-----------------------
                * *********** **  ** **** *    *** *
```

EdSINE1 : R4-1_ED(LINE)

```
EdSINE1          ATCAAAAATG----AGAAAAGAAAATTCTCACAGTTCAACAACTAAAAGCAAAGAATAA
R4-1_ED          ATTAAAAACCTTGTAATTAAAAACATGATGGACGTCATGGAGCACTGTGGAGATCACAA
                 ** *****      *   ** ** **  *    **     * *     * * *  * **

EdSINE1         GCTAATAGTTGAAGAACAAATACAT--TTAAAGCGAAGGGATGGGATTAGTCTCCCCTGA
R4-1_ED         CCAAACATATGTAGTTGAACTACAAGACGAAGACGAAGGGACGGGATTAGTCTCCCCTGA
                 * ** *  ** **   ** ****     **  ******** ******************

EdSINE1         GCAAGGAACAATAGAAAATATTTCTATTAATACTTAATTAACTACTTTTTATTT
R4-1_ED         GCCAGGAACAATAGACACAAGTTCTATTAATACTTAATTAACTTCTTTTT----
                ** ************ *  * ********************** ******
```

R4-N1_ED(SINE) : R4-1_ED(LINE)

```
R4-N1_ED        GGAAGAAATGAAACAAAGAAATGCCTTCCTCATATTCCAAGAAAAACCTAAAATATATGT
R4-1_ED         ATTAAAAACCTTGTAATTAAAAACATGATGGACGTCATGGAGCACTGTGGAGATCACAAC
                   * ***      **  ***  * *     *  *        *      * **

R4-N1_ED        TAAACAAAAAGA-TTACTCTTTTTTAAACAG-CTCAGTGATGGAATTAGTCTCCCCTAAA
R4-1_ED         CAAACATATGTAGTTGAACTACAAGACGAAGACGAAGGGACGGGATTAGTCTCCCCTGAG
                 ***** *   * **   **     *   ** *  ** ** ** ************* *

R4-N1_ED        CTAGGAAGAATAGATGAAAAATCTATTAACACTTAATTAAATAATTTTTAT
R4-1_ED         CCAGGAACAATAGACACAAGTTCTATTAATACTTAATTAACTTCTTTTT--
                * ***** ******   **  ******** ********** *  *****
```

SINEX-1_CR : RandI-2(LINE)

```
SINEX-1_CR      TGGACTTTGAAGAGCGGCCTAGGACTTGGAGGTTGTAGTTTCGGAGGTTGTGACTCT---
RandI-2         CCGAGCAGGAACTCAAACCGAGAGGTGGGTGAGCCACGGCTCCCCCACACCTCCTCGGAG
                  **    ***      ** **   * ** *      *  **           ***

SINEX-1_CR      TTCGTGGTGAGGCGTCAGCGTGAGGGGGGCGGGCCCTCTCGCCCTAGTCACCTTGCCCCG
RandI-2         TGCGTGGTGAGGTGGCAGCGCGAGGGGGATGGGCCTCCTCGCCCTAGCCACCTTACCCCG
                * ********** * ***** *******  *****  ********** ****** *****

SINEX-1_CR      TTAATCCATGCCAGGCCCTATGGGCCGGCGTTGTAATTATTATTATTATT
RandI-2         ATAATCCACGCCAGGCCCCATGGGCCGGCGTTTGAATTATTATTATTATT
                 ******* ********* *************  ****************
```

SINEX-4_CR : RandI-2(RandI-3)(LINE)

```
SINEX-4_CR      CCCGCTCCCACCGGTGGGCAGGACCGGCAAATGATAAGGTGGTCGTGGTGACTTCCCGCC
RandI-2         GAGGTGGGTGAGCCACGGCTCCCCCACACCTCCTCGGAGTG--CGTGGTGAGGTGGCAGC
RandI-3         CCCCAGGGTGA----TGTCCCCAACCGGCCCCCCT----TG--CGTGGTGAGGCGGCAGG
                                * *     *              **  ********     *

SINEX-4_CR      TTCTCTCGAACTGGGTTGAGAGATGATCAGCGAAGGCGTTGCCCCGTTAATACATGCTAG
RandI-2         GCGAGGGGGATGGGCCTCCTCGCCCT--AGCCA---CCTTACCCCGATAATCCACGCCAG
RandI-3         GTA--GGGGATGGGCCCCTACACTG---ACCCG---CCTTGCCCCGATAATCCACGCCAG
                       * *  **              * *     * ** ***** **** ** ** **

SINEX-4_CR      GCCCTATGGGCCAGCGTTGGGATTATTATTATTATTATT
RandI-2         GCCCCATGGGCCGGCGTTTGAATTATTATTATTATT---
RandI-3         GCCCTACGGGCCGGCGTTTCGATTATTATTATT------
                **** * ***** *****   ************
```

SINEX-5_CR/SINEX-6_CR : RandI-5(LINE)

```
SINEX-5_CR      TGGTAGGCCGATAAGCTCAGATCTT-CGGATCCTATGAGCTGAGTAGAGGGTGATGCGTG
SINEX-6_CR      TGGTAGGCCGATAGGTCCAGAACTT-CGGTTCCTATGGACTGAGTGAAGGTGGATGCGTG
RandI-5         AATGGGGATTGTGAACTCACGCCAAGTCGGCCCCACTGGCGGCGCCACGGCTGCTGGCCC
                     **    *     **   *     *  ** *    * * *    **  * **

SINEX-5_CR      GGGTGCCTCTAGTCAGGG------TCCCACAG---GGTACGGTAGGGTT---CTAAGAAG
SINEX-6_CR      GGGTGCCTCTTGCCAAGG------TCCCACAGA--GATACGGTAGGGTTAGCCTCGATGG
RandI-5         CAGCCCTCGCGATCCAGGCTAACTTTCCACCTTTTGACACGGTGGGGTGAG--CAAAACT
                  *  *       *  **      * ****     *  ***** ****
```

```
SINEX-5_CR      GACTCTTCCTTAAGACACGCGGGGCCGTTGGCCCGT-GCGTAGCTATTATTATTATTATTA
SINEX-6_CR      GACTCTTCCTTAAGGCACGCGGGACC-TTGGTCCGT-GCGTAGGTATTATTATTATTA--
RandI-5         CACTCCTCCTTAAGAAACGCGGCCTCCTTCGTGAACCGCGTACATATTATTATTATTATT
                 **** ********  ******   * ** *      *****  **************
```