

Fig. S2

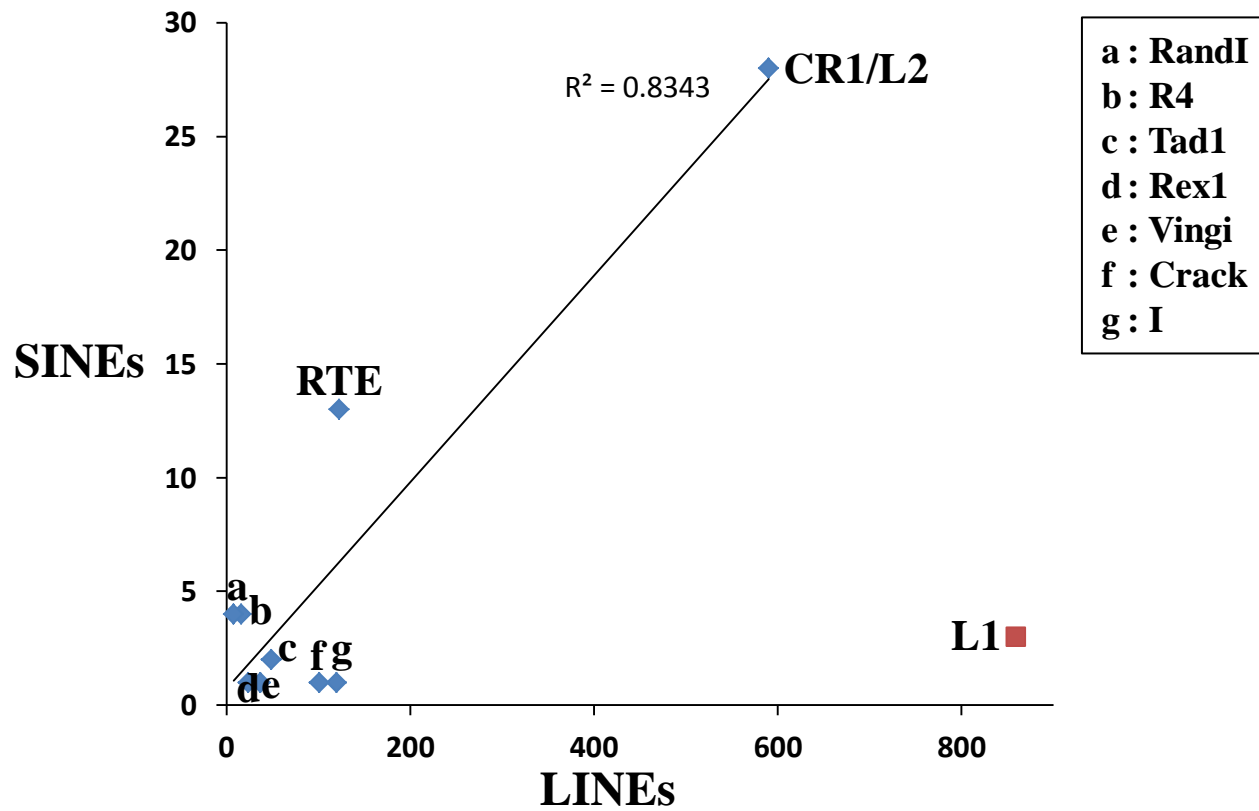


Fig. S3

	Box A	Box B	
TS	<u>GACAAGAGGGGT</u> TGCTCTGATGG TAAGCAACCTCCACTTCCAACCAAGAGGTTGTG AGTTCGAGTC ACCCCAAGAGCAAGGTGGGGAGTT		90
RTE-1_STu	tttcttgat·t·attg·ctcctt·gttg·tta·a····at·ttt·gtatt·gatgta·gttttat·ta·ttttct·tcct·ttacttgg		3961
TS	CTTGAGGGAAGGATGCCGAGGGTCTATTGAAACAGCCTCTCTACC-CCA--GGGTAGGGGTAAGGTCTGCGTACACACTACCCTCCCC		177
RTE-1_STu	a·t·t·t·t·cttga·t······tcc··········t··cga····t·c··········t········		4051
TS	AGACCCAC-TAGTGGGATTATACTGGGT-TG(TTG) ₀₋₁₄ -3'		207
RTE-1_STu	········c········tc······a·ttggttggttg-3'		4095

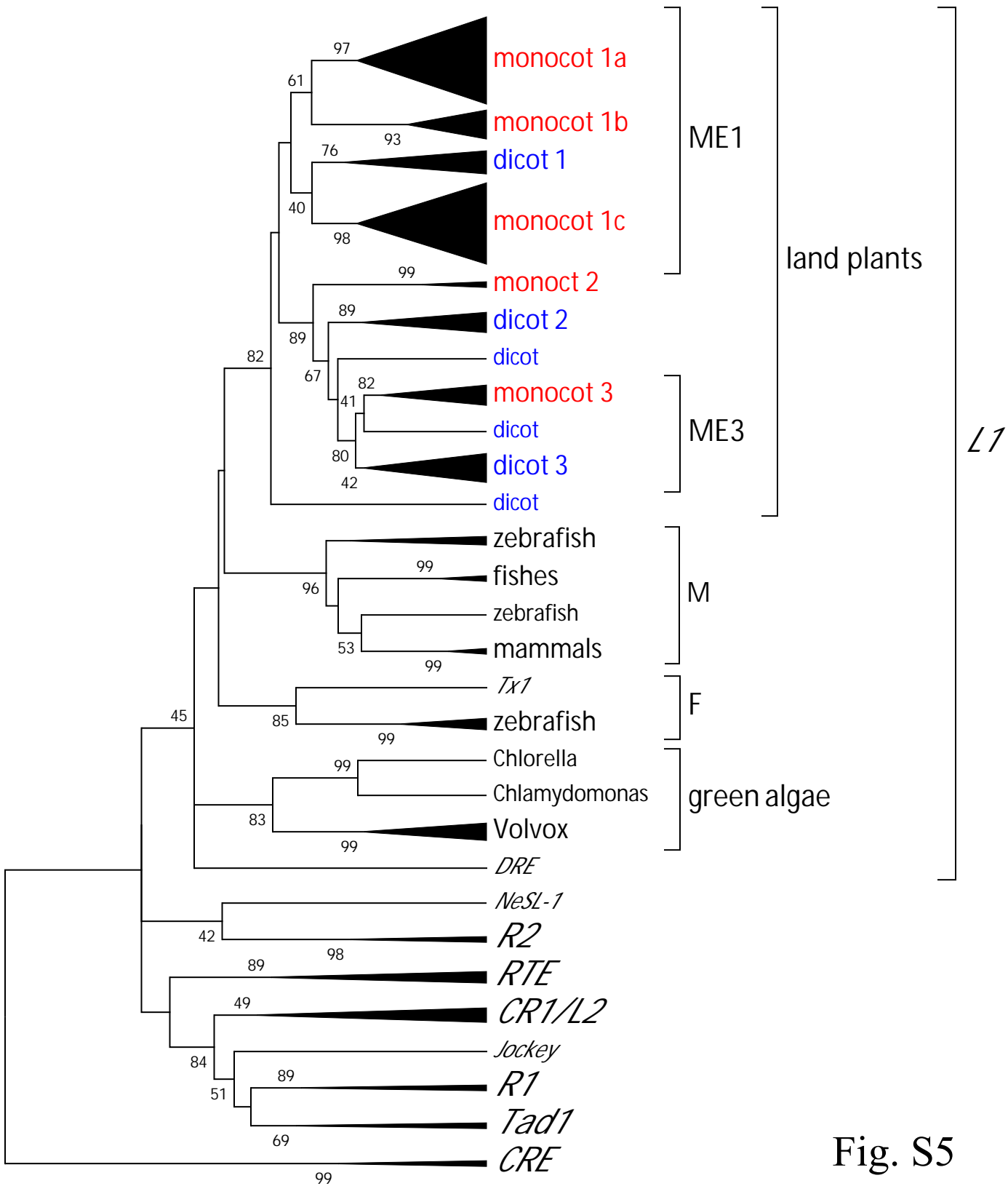
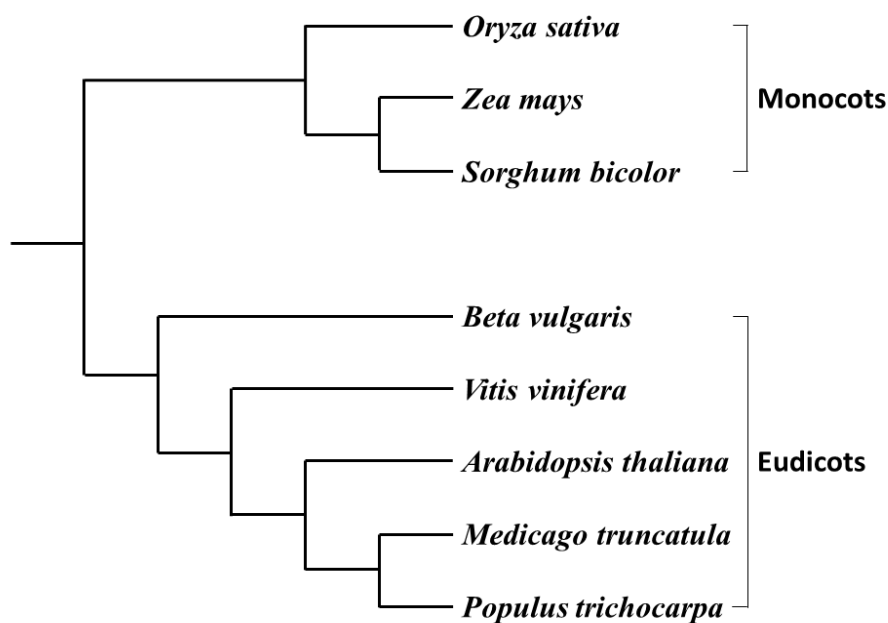


Fig. S5

Fig. S6

ME1	monocot 1a	<i>Oryza sativa</i>	rice	monocot
ME1	monocot 1a	<i>Zea mays</i>	maize	monocot
ME1	monocot 1a	<i>Sorghum bicolor</i>	sorghum	monocot
ME1	monocot 1b	<i>Zea mays</i>	maize	monocot
ME1	monocot 1b	<i>Sorghum bicolor</i>	sorghum	monocot
ME1	dicot 1	<i>Beta vulgaris</i>	beet	eudicot
ME1	dicot 1	<i>Vitis vinifera</i>	grape	eudicot
ME1	dicot 1	<i>Populus trichocarpa</i>	cottonwood	eudicot
ME1	monocot 1c	<i>Oryza sativa</i>	rice	monocot
ME1	monocot 1c	<i>Zea mays</i>	maize	monocot
ME1	monocot 1c	<i>Sorghum bicolor</i>	sorghum	monocot
		<i>Medicago truncatula</i>	legume	eudicot
ME2	monocot 2	<i>Sorghum bicolor</i>	sorghum	monocot
ME2	dicot 2	<i>Medicago truncatula</i>	legume	eudicot
ME2	dicot 2	<i>Arabidopsis thaliana</i>	thale cress	eudicot
		<i>Beta vulgaris</i>	beet	eudicot
ME3	dicot 3	<i>Medicago truncatula</i>	legume	eudicot
ME3	dicot 3	<i>Arabidopsis thaliana</i>	thale cress	eudicot
ME3	monocot 3	<i>Oryza sativa</i>	rice	monocot
ME3	monocot 3	<i>Sorghum bicolor</i>	sorghum	monocot



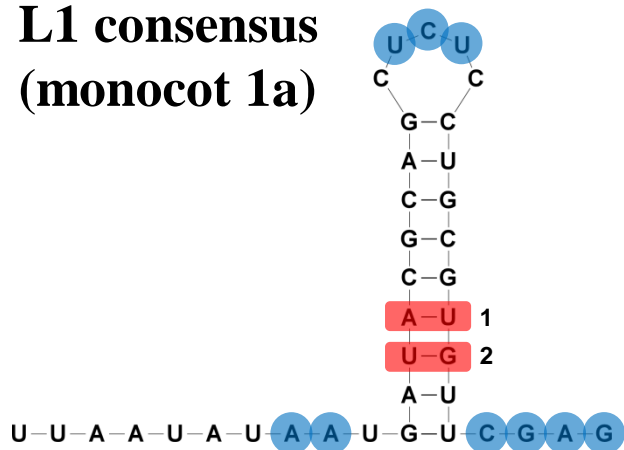
Species phylogeny (APG III system)

Fig. S8

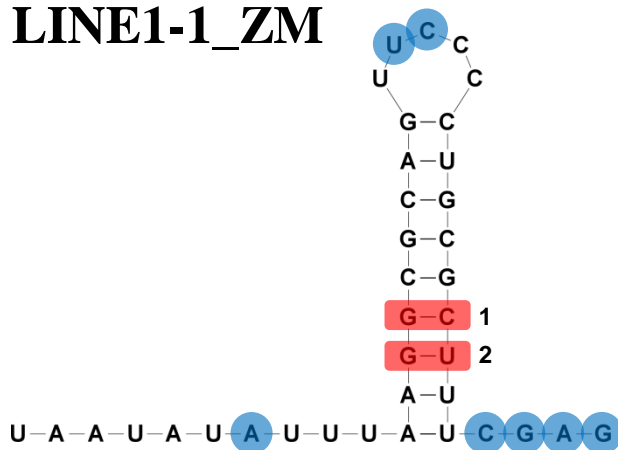
```
SINE2_consensus TCGGCCTGGGTGAGAAGGTCACCTTCTTCTTAATAYAATRCC--CGGGGGCNGTCTTWCCCCTCCSC--GGTCGAGTTT
ZmSINE2.1      ...a...t.....-----C...G...---...t...A.....G.a.....
SINE2-1a_SBi   ...a...c.....-----gC...G...---...t...A.....G.a.....ttttt
SINE2-1c_SBi   .g...t.....-----g.tC.aG...---...gc.g.g.....G.a...c...tt
SINE2-1_SBi    .....-----t.....tTg.aAg.tg...c...a.....aa.g.C.....ttttt
ZmSINE2.2      ...t.g...ctcog.tt-g.g.....T...A.-gt...g...T...a.....c.....
ZmSINE2.3      .....g...acc.ttgtt.ggtc.....T...A.-gg.a...g...T.....C...c.....
ZmSINE3        c.c.gg.tc.a.togc.....aa.....gtg.aAagtca...ac...cT...t-----aaaaa
```

Fig. S9

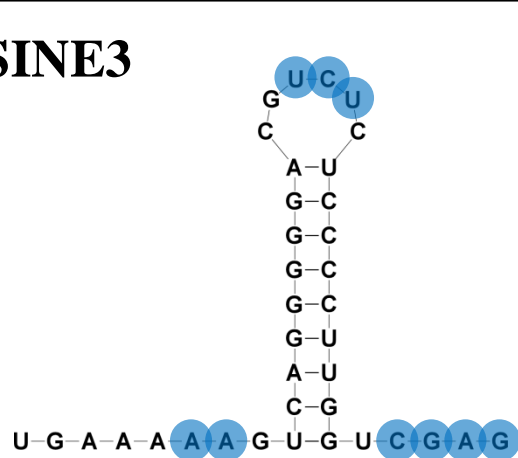
```
Monocot 1a      CTATTTTAGACCTTT|TTTCT-CTTCTYTTAATAAATG---ATAGGCAG---CTCTCCTGCGTGTTCGAGAAAAAAAA-3'
                ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
LINE1-1_ZM     CTATTTTAGACCTTAT|TATCTCCTTCT--TAATATATTT--AAGGCAG---TTCCCTGCGCTTTCGAGAAAAAAAA-3'
                | || || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
SINE2_consensus GGCCTGGTGAGAAGG|TACCTTCTTCT--TAATAYAATRCCGGGGCNGTCTTWCCCTCCSCGGTCGAGTTT-3'
```

L1 consensus
(monocot 1a)

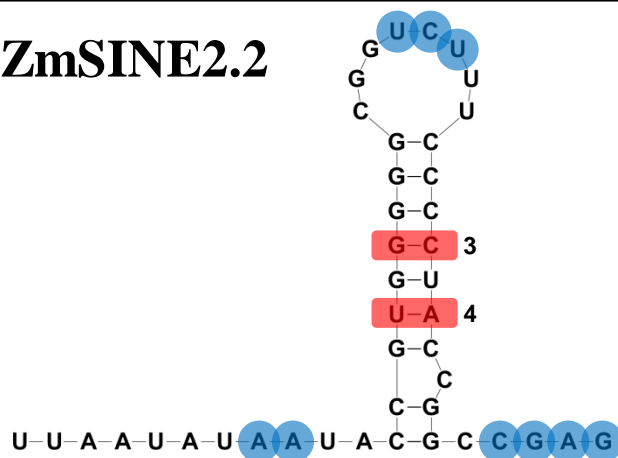
LINE1-1_ZM



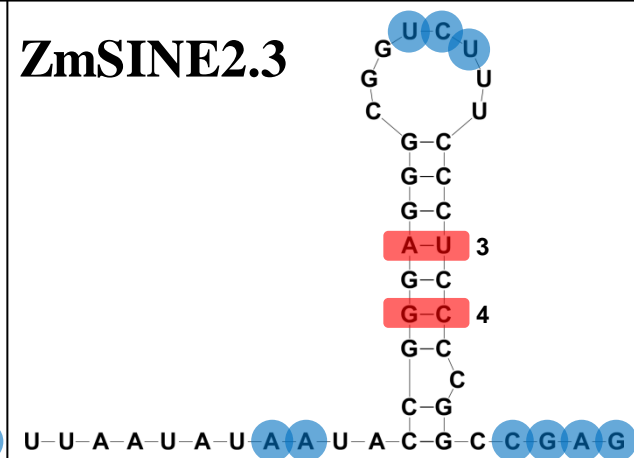
ZmSINE3



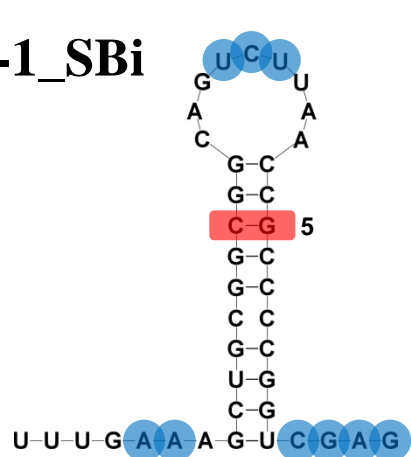
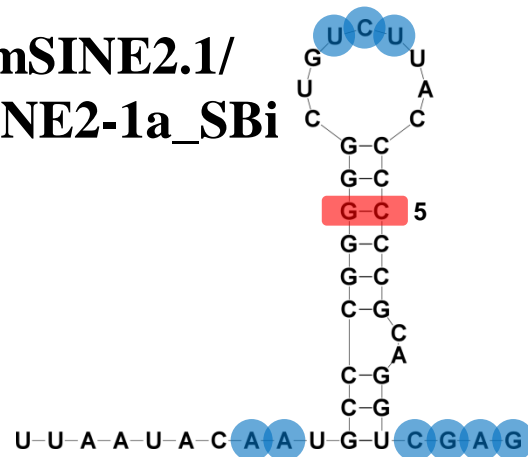
ZmSINE2.2



ZmSINE2.3



SINE2-1_SBi

ZmSINE2.1/
SINE2-1a_SBi

SINE2-1c_SBi

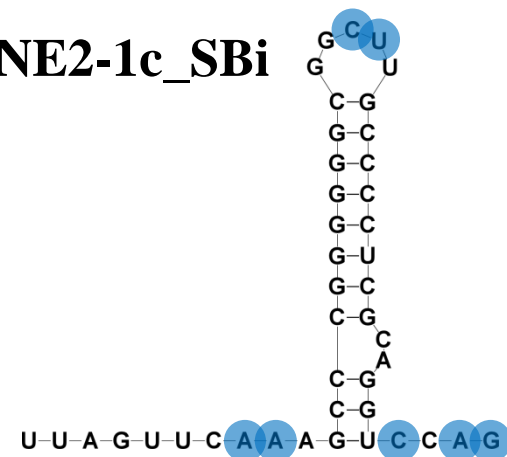


Fig. S11

```

                                Box A
SINEX-3_CR  --GGGGGGGTCGTCTAAATGGTTAAGACACTCA-AGCCGATTTGTTAAGGCTTCGAGAG
L1-1_CR     CACAGCGCGTCTTGCAGCGGGCTGGAGCCCGTTAGTCAGCGCCACATCTGGCCCGTTTA
                * * *** * * ** * * * * * * * *
                                Box B
SINEX-3_CR  ATCCTGGGTTCGAATCCCGGTCACCCACCAGGAAGGGCCCTGGTTTACAAAACCCATC
L1-1_CR     GTTTCTGCTTGTGTCTCCTCTGCCGTTCTCCTGGGGTGTGCTTAAGCAACCGACTTG
                * * * * * ** * * * * * * * * * * *
SINEX-3_CR  CACACCTTGGTGGTGTGTAGAC----CCCCCTGTGGTGCAGGGAGTCTCTGGGGTACAA
L1-1_CR     TGGGGTGGGGTGGGTTTGGCGGGGCGAGTGCGTAGCGCTGGTGTTCCTTTCTTTCTGGCG
                * * * * * * * * * * * * * * * * *
SINEX-3_CR  GGCTGGAGCTCTGGGCCT-GCAACTGGAGAGCTTTCAAGTTCAAGATCCAAGATTCAAGT
L1-1_CR     CGCGGTGGTGGTGGTTCTTGCGGTTAG---GCTGTGGTGT---AGGTTGGTGTGGGTT
                ** * * *** ** * * * * * * * * * * *
SINEX-3_CR  GGAGCTCTGGGCCTGTCAACTGGAGAGCTCTAGATGATCTGTGTGGTGCATGGCAGTGGCT
L1-1_CR     AGGTCCTGGCGGTGTTTTTGTGCAACCCCTCCCGGGGGCGGGGGGGCCA-GCCTCCTGCT
                * ** * * * * * * * * * * * * * * * *
SINEX-3_CR  GTAGTTGTCACCTAGCTGTTGAGAACTCCAGTAGGTGTGTGGTGCACCTGGCTGTTGAG
L1-1_CR     CTGTCTGCCGGTCCGGGTGGGGTGGGGTGG---GATGGATGGGGGTGGTGGTGGC---G
                * ** * * * * * * * * * * * * * * * *
SINEX-3_CR  GTTCCAGTAGGTGTGTGGTGAACAAAACCTTCTTCTTCTTCTGATCTCTGGCCCT
L1-1_CR     GTTTTCG---AGGTGTTTGTCTTC-TGTTTTCTTCTTTTCTTCTCT---TCTTGCCT
                *** * * * * * * * * * * * * * * * *
SINEX-3_CR  ATCGAGTTCTG-TGATATGATCCAGGCTGCCTT---GGCAGTAGGGTGGTAGTGCCTTA
L1-1_CR     GTCAGGTTCTGGTCTCGGGGACCAGGCTGCTTTCAGGCAGCAGGGGGCAGCGCTCTG
                ** * * * * * * * * * * * * * * * *
SINEX-3_CR  CCACCG--CAACCTTGTAAGGATGACT--TTAAAAAAAAAAA
L1-1_CR     CCCCTGTTCAACCTTGTAAGGATGATTCTCAAAAAAAAAAAA
                ** * * * * * * * * * * * * * * * *

```