

(a) 3' junctions

AAAAAAAAA TAGCCAAATGCCT 99%

AAAAAAAAAAAAA GCCAAATGCCT 1%

(b) Full length R2s

a 28S 0 R2
GTA ACTATGACTCTCTTAA GGGGATCATGGG

b -4
GTA ACTAAGACTCTCTT GGGGATCATGGG

c -17
GTA A GGGGATCATGGG

d 0
GTA ACTATGACTCTCTTAAAGG GAGTTTG GGGGATCATGGG

e 0
GTA ACTATGACTCTCTTAAAGG ACTCTCTTAAAGGACTCTCTT GGGGATCATGGG

5' truncated R2s

f 28S 0 R2
GTA ACTATGACTCTCTT AAGGAAGATGCAT

g -3
GTA ACTATGACTCTCTT A GCTAAGACAGA

h -8
GTA ACTATGACT CCTTGGGAGT

i 0
GTA ACTATGACTCTCTTAAAGG CATTAAC TA GACAGACGGAC

28S target site

(c)

Top strand TGACTCTCTTAAAGGTAGCCAAATGCCT
Bottom strand ACTGAGAGAATTCATCGGTTTACGGA

TGACTCTCTTAAAGG → 2nd strand synthesis TAGCCAAAT
ACTGAGAGAA CCCCTA.....TTTT ATCGGTTTA
TTCC cDNA