Alignment score: 2.5 MFE ratio: 0.768

PggD5310_c30_g1_i1

||0|

3 '

200

sRNA abundance: 282

Abundance

Fragment

TTCCACAGGGGGA-CCCTTCAGTCCAATCCATC '3

CCTCGAGGGAAGTCAGGTT

٠5

p-value: 0.005