Alignment score: 2.5 MFE ratio: 0.786

PggD5310_c30_g1_i1

|||0|

3 '

200

sRNA abundance: 1709

Abundance

Fragment

TTCCACAGGGGGA-CCCTTCAGTCCAATCCATC '3

CCCTCGAGGGAAGTCAGGTT

٠5

p-value: 0.004