Your MKT Results

Comparison Number:	Neutral Region:	Testing Region:	Counts correspond to SITES/CHANGES:
Comparison 1	1 (synonymous)	1 (non-synonymous)	Changes

Genetic code: Universal Code
Low frequency variants excluded if ≤ 20 %

INPUT SEQUENCES for Region 1:

Number of Sequences for Species 1: 10
Number of Sequences for Species 2: 1

Length of the Alignment: 60
Percentage of gaps within the alignment (excluding end gaps): 0.0%

View Alignment for Region 1
(Sequences were already aligned)

Input Sequences: 120598.1.txt

SEE RESULTS: ○ Divergence corrected by Jukes&Cantor   ● Without any correction for divergence

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Comparison 1:
   NEUTRAL REGION: 1 (synonymous)
   TESTING REGION: 1 (non-synonymous)
   CHANGES

Contingency table:

	Polymorphism	Divergence	TOTAL
Neutral	**0**	**1**	1
Non-Neutral	**1**	**1**	2
TOTAL	1	2	3

Estimates:

Neutrality Index (NI): NULL
Proportion of adaptive substitutions (α): NULL

χ^2 value: 0.750
p-value: 0.386