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

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 have the same order as input. Alignments generated by muscle)

FASTA format: 120610.1.fas

Alignment from species 1: 120610.1.1.txt
Alignment from species 2: 120610.1.2.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	**1**	**0**	1
Non-Neutral	**0**	**0**	0
TOTAL	1	0	1

Estimates:

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

   χ^2 value: NULL
   p-value: NULL