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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: [120605.1.fas](#)

Alignment from species 1: [120605.1.1.txt](#)

Alignment from species 2: [120605.1.2.txt](#)

SEE RESULTS: ☐ Divergence corrected by Jukes&Cantor ☒ Without any correction for divergence

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

