



Standard & Generalized

# McDonald-Kreitman Test



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## Your MKT Results

Comparison Number:	Neutral Region:	Testing Region:	<a href="#">Counts correspond to SITES/CHANGES:</a>
<a href="#">Comparison 1</a>	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 were already aligned)

Input Sequences: [120597.1.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	1	2
Non-Neutral	1	1	2
TOTAL	2	2	4

### Estimates:

Neutrality Index (NI): 1.000

Proportion of adaptive substitutions ( $\alpha$ ): 0.000

$\chi^2$  value: 0.000

p-value: 1.000

