ToxGenie Multi-Group Comparison Report

Report Date: 2026-06-29 13:40:53

Study Title:	In Vitro Mammalian Chromosomal Aberration Test
Analysis Method:	Dunnett's Multiple Comparison Test (via Log transformation) for % Tail DNA

Study No.:	Test-135	**Test Material:**	Test Chemicals
Exposure Time:	24-hours	**Test Medium:**	Not Applicable

Table 1. Raw Data Summary for % Tail DNA

(Unit: mg/kg)

Dose	1	2	3	4	5
Negative Control	4.1000	6.2000	5.5000	3.8000	4.9000
12.5	7.5000	9.1000	6.8000	11.2000	8.0000
25	14.5000	18.2000	11.5000	20.1000	16.0000
50	22.5000	35.1000	18.9000	40.2000	28.0000
Positive Control	54.1000	58.2000	55.9000	52.8000	56.5000

Step 1. Outlier Detection (Data QA/QC) Analysis

No statistical outliers were detected in the raw data based on Tukey's fences.

*Tukey's fences: Values outside Q1 - 1.5*IQR or Q3 + 1.5*IQR (IQR method).*

Step 2. Descriptive Statistics

Table 2. Descriptive Statistics for % Tail DNA

(Unit: mg/kg)

Dose	N	Mean	SD	SE	CV (%)	Median
Negative Control	5	4.90000	0.98742	0.44159	20.15145	4.90000
12.5	5	8.52000	1.71668	0.76772	20.14886	8.00000
25	5	16.06000	3.32160	1.48546	20.68242	16.00000
50	5	28.94000	8.77343	3.92360	30.31591	28.00000
Positive Control	5	55.50000	2.10357	0.94074	3.79021	55.90000

Abbreviations & Explanations:

- N: Number of replicates.

- Mean: Average response value.

- SD: Standard Deviation of the mean.

- SE: Standard Error of the mean.

- CV (%): Coefficient of Variation.

- Median: 50th percentile of observed values.

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Table 3. Shapiro-Wilk's test for normality on the % Tail DNA

Dose	Statistic	P-value	Result
Negative Control	0.9581	0.7948	Normal Distribution
12.5	0.9298	0.5947	Normal Distribution
25	0.9897	0.9787	Normal Distribution
50	0.9606	0.8124	Normal Distribution
Positive Control	0.9816	0.9432	Normal Distribution

P>0.05 indicates Normal Distribution.

Final decision: The % Tail DNA data follows a normal distribution.

Table 4. Levene's test for homogeneity on the % Tail DNA

Statistic	P-value	Result
5.45121	0.00390	Unequal Variances

P>0.05 indicates Equal Variances.

Final decision: The % Tail DNA data shows unequal variances.

Table 5. Transformed Data Summary for % Tail DNA (Log transformation)

(Unit: mg/kg)

Dose	1	2	3	4	5	Mean	SD
Negative Control	1.6292	1.9741	1.8718	1.5686	1.7750	1.3588	0.7327
12.5	2.1401	2.3125	2.0541	2.5014	2.1972	1.9726	0.8915
25	2.7408	2.9549	2.5257	3.0493	2.8332	2.4803	1.1181
50	3.1570	3.5863	2.9907	3.7184	3.3673	2.9645	1.3465
Positive Control	4.0091	4.0809	4.0413	3.9853	4.0518	3.3614	1.6471

SD: Standard Deviation

Table 6. Shapiro-Wilk's test for normality on the transformed % Tail DNA.

Dose	Statistic	P-value	Result
Negative Control	0.95896	0.80076	Normal Distribution
12.5	0.95750	0.79050	Normal Distribution
25	0.97502	0.90640	Normal Distribution
50	0.96547	0.84546	Normal Distribution
Positive Control	0.98078	0.93877	Normal Distribution

P>0.05 indicates Normal Distribution.

Final decision: The data follows a normal distribution.

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Table 7. Levene's test for homogeneity on the transformed % Tail DNA.

Statistic	P-value	Result
2.30173	0.09413	Equal Variances

P>0.05 indicates Equal Variances.

Final decision: The data shows equal variances.

Statistical Analysis Procedure & Decision Tree

The statistical analysis for '% Tail DNA' was conducted based on the following decision steps:

1. Assumption Verification (Normality & Homogeneity):

- *Since the raw data did not meet the assumption(s) of Homogeneity of Variance, data transformation was attempted to stabilize variance and normalize the distribution.*

2. Data Transformation Strategy:

- *A Log transformation was selected and applied.*
- *Logarithmic transformation reduces skewness in positive data and stabilizes variance when it increases with the mean. It was chosen because it yielded the highest combined score for Normality and Homogeneity among all candidates.*
- *The transformed data successfully met the required statistical assumptions (Normality and Homogeneity of Variance). Thus, Parametric Tests were performed on the transformed data.*

3. Final Selected Test Method:

- *Because after applying data transformation, the transformed data successfully met the required statistical assumptions (Normality and Homogeneity of Variance), the Dunnett Test (Parametric) was selected as the post-hoc test.*
- *Prior to this post-hoc analysis, an Omnibus Test (One-Way ANOVA) was performed to confirm if any statistically significant differences exist among the dose groups ($p < 0.05$).*
- *The selected method is appropriate for comparing multiple treatment groups against a single control group to determine the NOEC/LOEC (No Observed Effect Concentration/Lowest Observed Effect Concentration) or NOAEL/LOAEL (No Observed Adverse Effect Level/Lowest Observed Adverse Effect Level).*

Table 8. One-Way ANOVA on the transformed % Tail DNA data.

F-statistic	P-value	Result
105.9828	0.0000	Significant differences among doses

P<0.05 indicates a statistically significant difference among groups.

Table 9. Post Hoc Analytical Method: Dunnett's Multiple Comparison Test on the transformed % Tail DNA.

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Control	Dose	P-value	Result
Negative Control	12.5	0.0032	Significant difference from Negative Control
Negative Control	25	0.0000	Significant difference from Negative Control
Negative Control	50	0.0000	Significant difference from Negative Control
Negative Control	Positive Control	0.0000	Significant difference from Negative Control

P<0.05 indicates a statistically significant difference from the Negative Control.

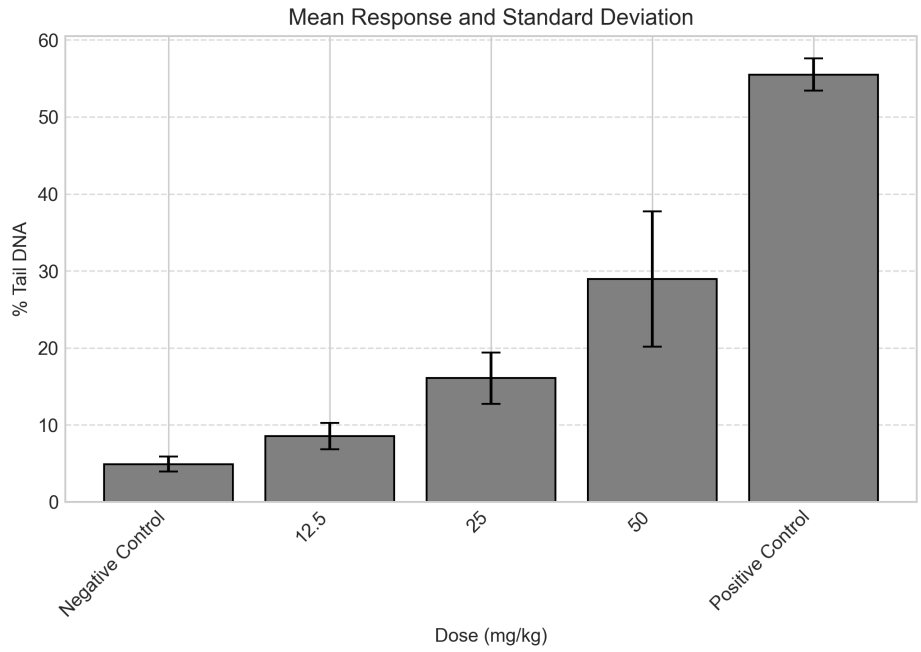

Figure 1. Dose-response trend for % Tail DNA. Bars represent the mean and Standard Deviation (SD).

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