

Sus scrofa BLAST Anomaly Report

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Overall Statistics

Metric	Value
Total Sequence Analyzed	1
Total Records	468
Total Anomalies	1
Anomaly Rate	0.2%

Analysis Configuration:

Non-anomaly keywords: Sus scrofa

Normal sample size: 5

BatchBLAST ID: blast_res/EBxrtYQbsw

Detailed File Analysis

Filename	Total	Normal	Anomalies	Anomaly %
Danio_rerio_chr3_003.csv	468	467	1	0.2%

Analysis: Danio_rerio_chr3_003.csv

Metric	Value
Total Records	468
Normal Results	467
Anomalous Results	1
Anomaly Percentage	0.2%

Anomaly Groups

Species Group	Count	Percentage
Sus celebensis	1	100.0%

Sample Anomalies

Species Group	Count	Sample Title	Accession
Sus celebensis	1	Sus celebensis mitochondrion, complete genome	NC_024860

Normal Results Sample

Title	Accession	E-value
Sus scrofa breed Chinese Min mitochondrion, complete genome	AF486864	1.32994
Sus scrofa breed Hezuo mitochondrion, partial genome	MN550011	1.32994
Sus scrofa isolate Mali2 mitochondrion, complete genome	PP763947	1.32994
Sus scrofa isolate shg184 mitochondrion, complete genome	EF545575	1.32994
Sus scrofa breed Large White mitochondrion, complete genome	AY574048	1.32994