

# sus scrofa BLAST Anomaly Report

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## Overall Statistics

Metric	Value
Total Sequence Analyzed	2
Total Records	1,179
Total Anomalies	0
Anomaly Rate	0.0%

**Analysis Configuration:**  
Non-anomaly keywords: b, o, s, , t, a, u, r, u, s,  
Normal sample size: 5  
BatchBLAST ID: blast\_res/OVRBgaxyjs

## Detailed File Analysis

Input Sequence Name	Total	Normal	Anomalies	Anomaly %
reverse journal.	711	711	0	0.0%
forward journal.	468	468	0	0.0%

Analysis: reverse journal.

Metric	Value
Total Records	711
Normal Results	711
Anomalous Results	0
Anomaly Percentage	0.0%

No anomalies detected in this file.

Normal Results Sample

Title	Accession	E-value
Liolaemus silvai isolate H15ICho NADH dehydrogenase subunit 2 gene, partial cds;...	OQ625496	1.33027
Sus scrofa isolate Banda13 mitochondrion, complete genome	PP763968	0.381129
Sus scrofa isolate Banda5 mitochondrion, complete genome	PP763960	0.381129
Sus scrofa breed Chinese Yushanhei mitochondrion, complete genome	AF486871	0.381129
Sus scrofa breed Hezuo mitochondrion, complete genome	KT943507	0.381129

## Analysis: forward journal.

Metric	Value
Total Records	468
Normal Results	468
Anomalous Results	0
Anomaly Percentage	0.0%

No anomalies detected in this file.

### *Normal Results Sample*

Title	Accession	E-value
Sus scrofa breed Fengjing mitochondrion, complete genome	MH603005	1.32994
Sus scrofa mitochondrion, complete genome	MN624263	1.32994
Sus scrofa isolate Doom6 mitochondrion, complete genome	PP763929	0.0312772
Sus scrofa isolate Huainan13 mitochondrion, complete genome	MK858169	1.32994
Sus scrofa isolate Russia_CO mitochondrion, complete genome	KX982631	1.32994

## Cross-File Anomaly Patterns

No cross-file anomaly patterns detected.