APPENDIX C: SORTING AND RE-ANALYSIS FORMS

Date_____

Sorting Form:

SQO Example	
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MACROFAUNA SORTING SHEET

Station	Analytical Laboratory:					
Sorting Laboratory:	Sorted by:					
Date Sorting Begins:	# of Hours to Sort:					
# of Taxa Lots in Sample:	# of Sample Containers:					
Comments:						
QUALITY CONTROL RE-SORT	(for use only if sample subject to QC re-sort)					
Re-sorted by:	Date of Re-sort:					
Re-sort Method (check one) Whole Sample Aliquot						
PERCENT SORTING EFFICENCY =	Whole Sample MethodAliquot Method[A ÷ (A+B)] x 100[A ÷ (A+B x %_{aliquot})] x 100					
A = # of Organisms Originally	A = # of Organisms Originally Sorted =					
B = # of Organisms Found in I	Re-sort =					
Percent Sorting Efficency =						
QUALITY CONTROL ACTIONS: (no action required if Sorting Efficency = 95 % or greater)						
Signed	l:					
	Responsible Supervisor (signature required if sample subject to QC resort)					

Discrepancy Report:

SQC	Example				Date
MAC	ROFAUNAL ANALYSIS QC			DISCREPANCY REPORT	Page 1 of
	Station				
	Analytical Laboratory (Lab A):			Date Analyzed:	·
	Re-Analytical Laboratory (Lab B):			Date Re-Analyz	zed:
Line #	Re-Identification	Re- Count	Orig. Count	Original Identification	Comments
2	2				
3	3				
4	1				
-					
5	3				
)				
10)				
1					
12	2				
13	3				
14	ł				
15	5				
16	3				
17	7				
18	3				
19	3				
20)				
2	3				
22	3				
24	1				
2!	5				
26	3				

Discrep	ancy Report (cont'd)				Date
St	ation				Page 2 of
Line		Re-	Orig.		_
#	Re-Identification	Count	Count	Original Identification	Comments
27					
28					
29					
30					
31					
32					
33					
34					
35					
36					
37					
38					
39					
40					
41					
42					
43					
44					
45					
46					
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48					
49					
50					
51					
52					
53					
54					
55					
56					
57					
58					
59					

Discr	epancy Report (cont'd)				Date
	Station				Page of
Line #	Re-Identification	Re- Count	Orig. Count	Original Identification	Comments

Discrepancy Resolution Report:

SQO MAC	Example ROFAUNAL ANALYSIS QC DISCREI	PANCY RESOLUTION REPORT	Page 1	of		Date
	StationAnalytical Laboratory (Lab A):	Date Analyzed:	Total Taxa I Lab A: Lab B:	# of Rprtd: 	Tota Indv. Lab A: Lab B:	l # of Rprtd:
	Re-Analytical Laboratory (Lab B):	Date Re-Analyzed:	Do	not write ir	ו these columns	
Line ‡	e # refers to Discrepancy Report (a discrepancy may involve multiple line #s)				Effect of Resolution on Orig. Results	
Line #	CC Provide resolution and explanation of all discrepancie	DMMENTARY as (use as many lines as necessary for each discrepancy)	Discrep. Class.	Resol. Code	SPP # (+/-)	Count (+/-)
						-
						_
						-
						1
	Discrepancy Classification: E = Error J = Judgmental Diff. N Resolution Code: 1 = Lab A misID 2 = Lab B misID	N = Nomenclature L = Apparent Specimen Loss 3 = Lab A mis Count 4 = Lab B mis Count	•			<u>.</u>

Station	Page of		not write i	n these colu	imns
Station	Fage 01	D0	not write ii	Effoct of	Posolution
Line # refers to Discrepancy Report (a discrepancy may involve multiple line #s)				on Orig	Results
	ARY	Discen	Resol	SPP #	Count
# Provide resolution and explanation of all discrepancies (use as	many lines as necessary for each discrepancy)	Class.	Code	(+/-)	(+/-)
			0040		
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					1
					
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				ļ	───
					───
					+
					+
					<u> </u>
					1
					1
					1

Infaunal Identification and Enumeration Accuracy Report:						
SQO Example	ACCURACY REPORT	Date				
Station						
Analytical Laboratory (Lab A):	Date Analyzed:					
Re-Analytical Laboratory (Lab B):	Date Re-Analyzed:					
% ERROR OF ANALYSIS: Percent error organism cou to parameters as percent er representatio	is calculated for three aspects of sample analysis. Error i nt may be either + or These provide measures of the d s such as species richness, abundance, and diversity. Ide ror in identification of individual taxa. It provides a measur n of community composition.	in the # of taxa discriminated and total ata quality as relates entification accuracy is expressed re of the quality of the data as a				
<pre># of Taxa Discriminated: [(X-Y)/X] * 100 where X = # of Taxa after discrepancy resolution Y = # of Taxa originally discriminated X = Y= Score:%</pre>	Total Organism Count: [(X-Y)/X] * 100 where X = # in Resolved count Y = # in Original count X = Y= Score:%	Identification Accuracy: [X/Y] * 100 where X = # of Taxa changed Y = # of Taxa after discrepancy resolution X = Y= Score:%				
COMMENTS		·				

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