

Appendix I - Analysis of Metals

A- Statistical Analysis

I. Oneway Analysis of metal burden by sex

The results from these analyses indicate that sex is not a significant factor in burden.

Analysis of Variance (Nickel)

Source	DF	Sum of Squares	Mean Square	F Ratio	Prob > F
Sex	1	0.273	0.273	0.0017	0.9669
Error	127	19990.092	157.402		
C. Total	128	19990.364			

Analysis of Variance (Copper)

Source	DF	Sum of Squares	Mean Square	F Ratio	Prob > F
Sex	1	6.519	6.519	0.0160	0.8994
Error	127	51621.094	406.465		
C. Total	128	51627.613			

Analysis of Variance (Zinc)

Source	DF	Sum of Squares	Mean Square	F Ratio	Prob > F
Sex	1	6234	6233.6	0.0664	0.7970
Error	127	11913901	93810.2		
C. Total	128	11920134			

Analysis of Variance (Strontium)

Source	DF	Sum of Squares	Mean Square	F Ratio	Prob > F
Sex	1	110.451	110.451	0.9546	0.3304
Error	127	14694.767	115.707		
C. Total	128	14805.219			

Analysis of Variance (Silver)

Source	DF	Sum of Squares	Mean Square	F Ratio	Prob > F
Sex	1	0.003206	0.003206	0.0046	0.9461
Error	127	88.589574	0.697556		
C. Total	128	88.592780			

Analysis of Variance (Cadmium)

Source	DF	Sum of Squares	Mean Square	F Ratio	Prob > F
Sex	1	7.0118	7.0118	0.5297	0.4681
Error	127	1681.0866	13.2369		
C. Total	128	1688.0985			

Analysis of Variance (Tin)

Source	DF	Sum of Squares	Mean Square	F Ratio	Prob > F
Sex	1	0.00001491	0.000015	0.8575	0.3562
Error	127	0.00220878	0.000017		
C. Total	128	0.00222369			

Analysis of Variance (Mercury)

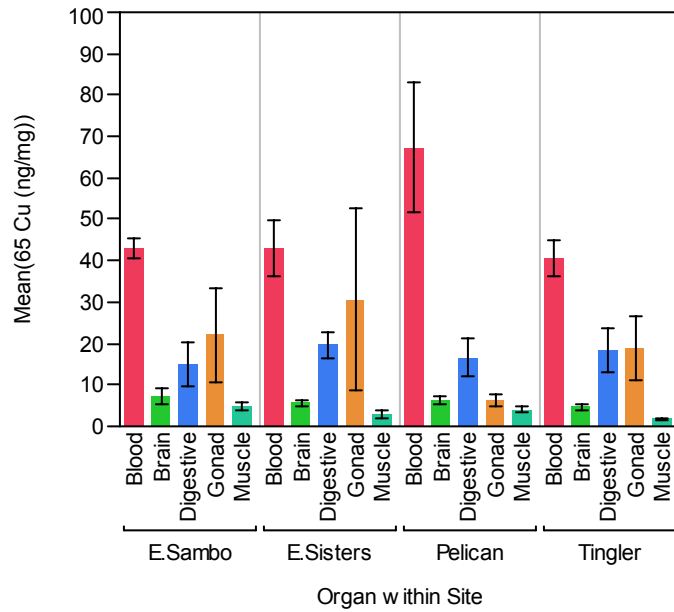
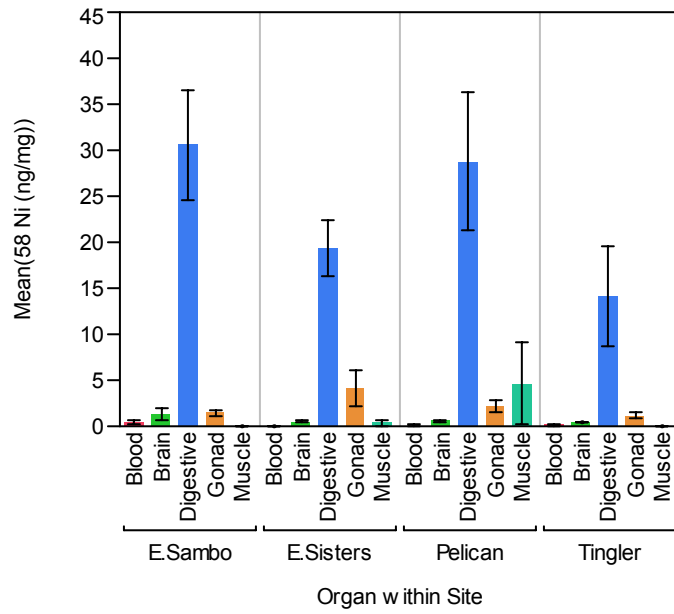
Source	DF	Sum of Squares	Mean Square	F Ratio	Prob > F
Sex	1	0.0190327	0.019033	1.5587	0.2142
Error	127	1.5507775	0.012211		
C. Total	128	1.5698102			

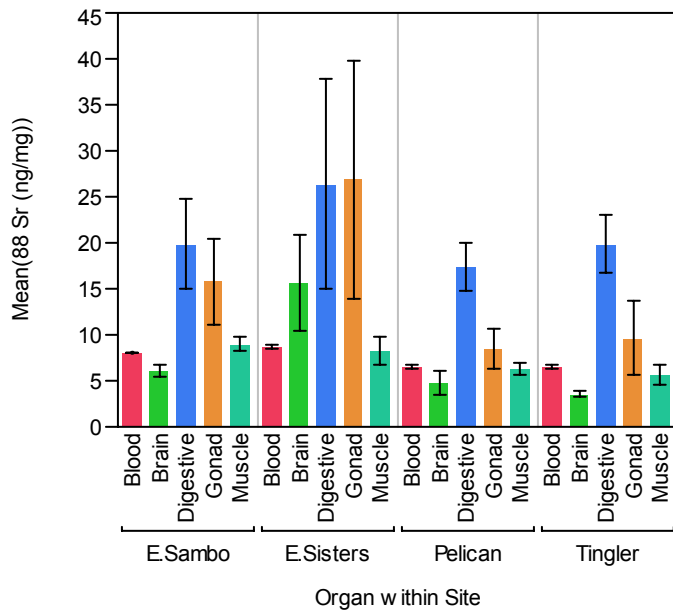
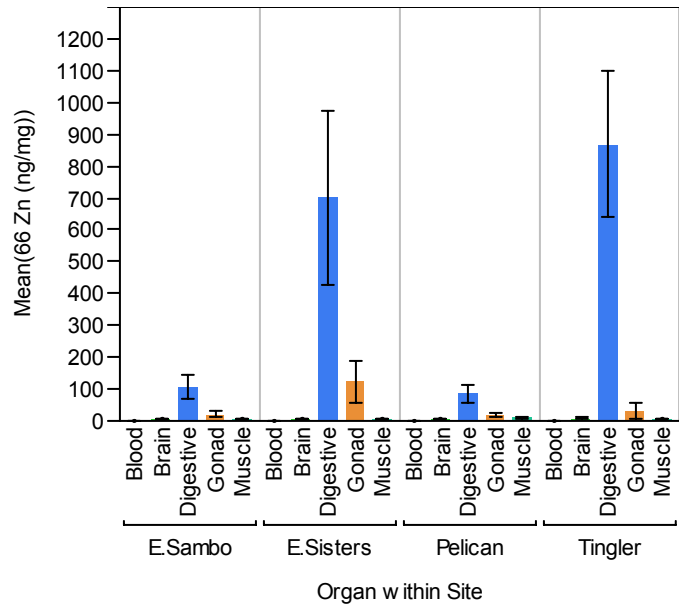
Analysis of Variance (Uranium)

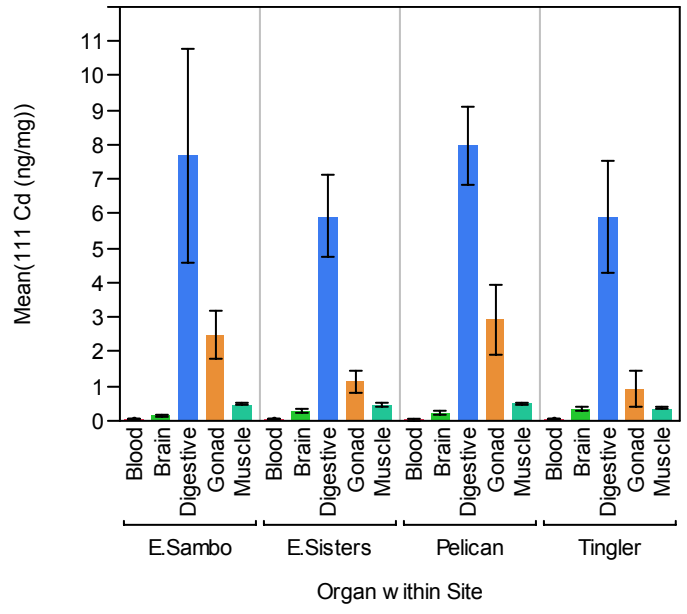
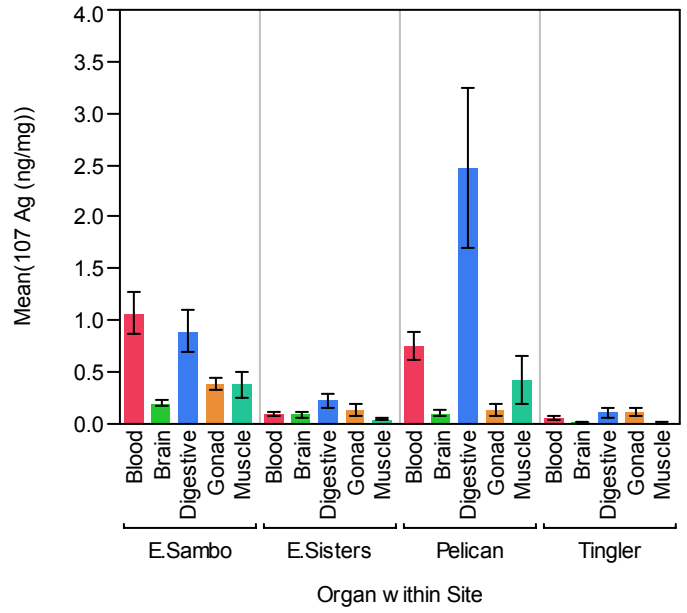
Source	DF	Sum of Squares	Mean Square	F Ratio	Prob > F
Sex	1	3.30372	3.30372	0.5714	0.4511
Error	127	734.25826	5.78156		
C. Total	128	737.56198			

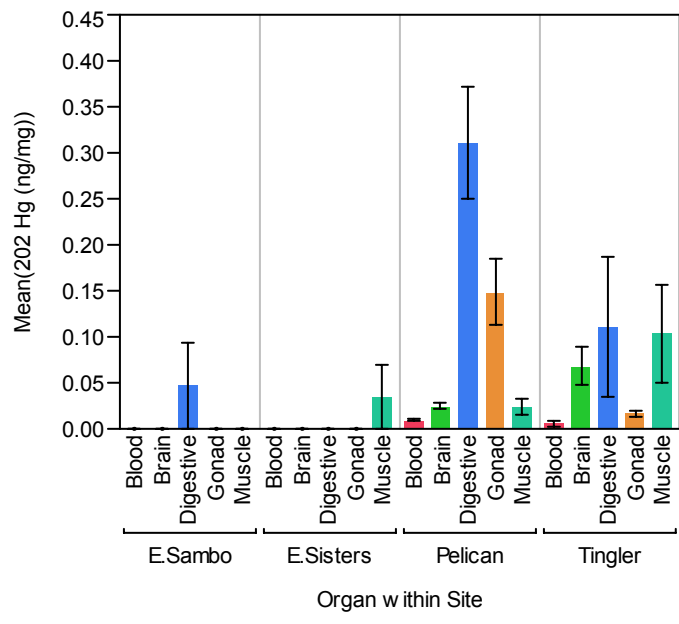
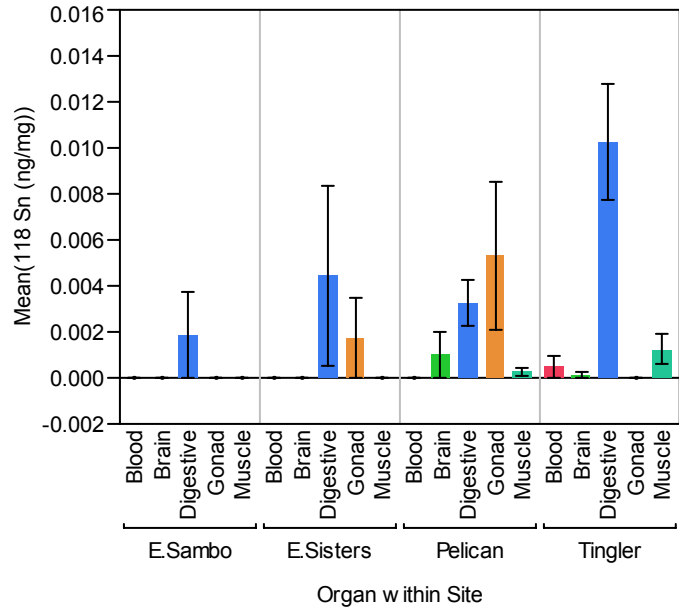
II. ANOVA analysis

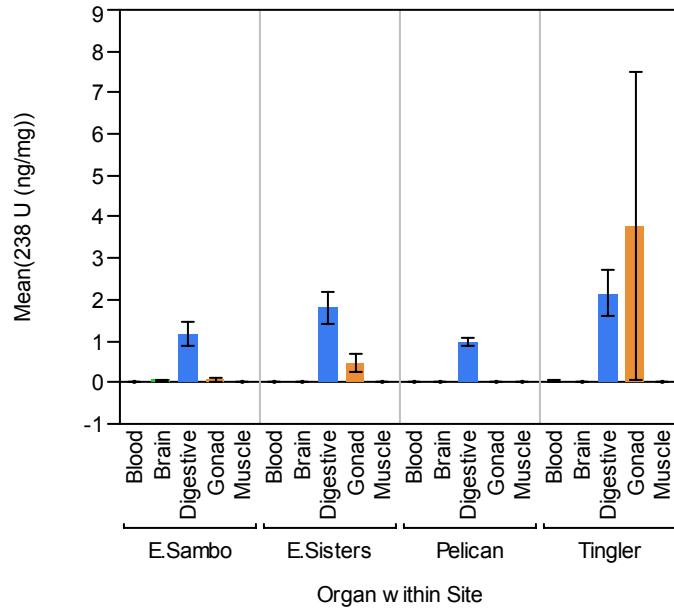
Graphs











Two way Analysis of Variance
 Model: Metal = Site Organ Site*Organ

1. Nickel

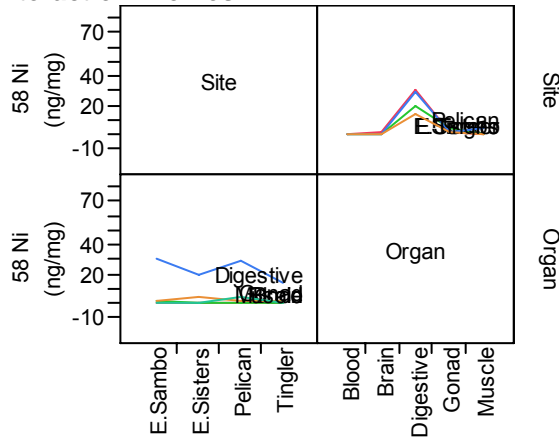
Whole Model Analysis of Variance

Source	DF	Sum of Squares	Mean Square	F Ratio
Model	19	12405.062	652.898	9.3821
Error	109	7585.302	69.590	Prob > F
C. Total	128	19990.364		<.0001

Effect Tests

Source	Nparm	DF	Sum of Squares	F Ratio	Prob > F
Site	3	3	326.024	1.5616	0.2029
Organ	4	4	10325.260	37.0932	<.0001
Site*Organ	12	12	1060.418	1.2698	0.2468

Interaction Profiles



Site Effect

LSMeans Differences Student's t

$\alpha=0.050$ $t=1.98197$

Level		Least Sq Mean
Pelican	A	7.2562417
E.Sambo	A	6.7387762
E.Sisters	A	4.8648033
Tingler	A	3.1795857

Levels not connected by same letter are significantly different.

Organ Effect

LSMeans Differences Student's t

$\alpha=0.050$ $t=1.98197$

Level		Least Sq Mean
Digestive	A	23.187659
Gonad	B	2.252795
Muscle	B	1.273839
Brain	B	0.680195
Blood	B	0.154771

Levels not connected by same letter are significantly different.

Site*Organ Effect

LSMeans Differences Student's t

$\alpha=0.050$ $t=1.98197$

Level			Least Sq Mean	
E.Sambo,Digestive	A		30.556286	
Pelican,Digestive	A		28.785500	
E.Sisters,Digestive		B	19.278600	
Tingler,Digestive		B C	14.130250	
Pelican,Muscle			D	4.603250
E.Sisters,Gonad		C	D	4.138250
Pelican,Gonad			D	2.259333
E.Sambo,Gonad			D	1.450167
E.Sambo,Brain			D	1.264571
Tingler,Gonad			D	1.163429
Pelican,Brain			D	0.564125
E.Sisters,Brain			D	0.467833
Tingler,Brain			D	0.424250
E.Sisters,Muscle			D	0.380000
E.Sambo,Blood			D	0.368000
Tingler,Blood			D	0.122750
Pelican,Blood			D	0.069000
E.Sisters,Blood			D	0.059333

Level		Least Sq Mean
Tingler,Muscle	D	0.057250
E.Sambo,Muscle	D	0.054857

Levels not connected by same letter are significantly different.

2. Copper

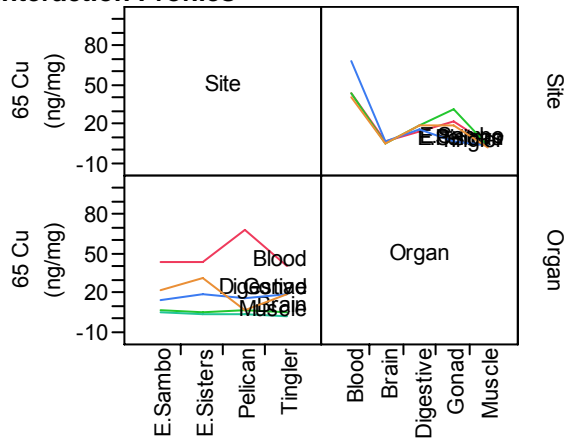
Whole Model Analysis of Variance

Source	DF	Sum of Squares	Mean Square	F Ratio
Model	19	30558.040	1608.32	8.3204
Error	109	21069.572	193.30	
C. Total	128	51627.613		Prob > F <.0001

Effect Tests

Source	Nparm	DF	Sum of Squares	F Ratio	Prob > F
Site	3	3	244.677	0.4219	0.7376
Organ	4	4	28531.686	36.9010	<.0001
Site*Organ	12	12	3254.190	1.4029	0.1754

Interaction Profiles



Site Effect

LSMeans Differences Student's t

$\alpha=0.050$ $t=1.98197$

Level		Least Sq Mean
E.Sisters	A	20.375823
Pelican	A	20.049783
E.Sambo	A	18.372252
Tingler	A	16.813061

Levels not connected by same letter are significantly different.

Organ Effect

LSMeans Differences Student's t

$\alpha=$
 0.050 $t=$
 1.98197

Level		Least Sq Mean
Blood	A	48.418246
Gonad	B	19.426628
Digestive	B	17.429099
Brain	C	5.890234

Level		Least Sq Mean
Muscle	C	3.349443

Levels not connected by same letter are significantly different.

Site*Organ

LSMeans Differences Student's t

$\alpha=0.050$ $t=1.98197$

Level									Least Sq Mean
Pelican,Blood	A								67.238667
E.Sisters,Blood		B							43.030833
E.Sambo,Blood		B							42.845857
Tingler,Blood		B							40.557625
E.Sisters,Gonad		B	C						30.634750
E.Sambo,Gonad			C	D					22.019833
E.Sisters,Digestive			C	D	E	F	G		19.591200
Tingler,Gonad			C	D	E	F			18.755429
Tingler,Digestive			C	D	E				18.393625
Pelican,Digestive			C	D	E	F	G		16.644000
E.Sambo,Digestive			C	D	E	F	G		15.087571
E.Sambo,Brain				D	E	F	G		7.211143
Pelican,Gonad				D	E	F	G		6.296500
Pelican,Brain					E	F	G		6.157250
E.Sisters,Brain					E	F	G		5.589167
E.Sambo,Muscle					E	F	G		4.696857
Tingler,Brain						F	G		4.603375
Pelican,Muscle							G		3.912500
E.Sisters,Muscle							G		3.033167
Tingler,Muscle					E	F	G		1.755250

Levels not connected by same letter are significantly different.

3. Zinc

Whole Model

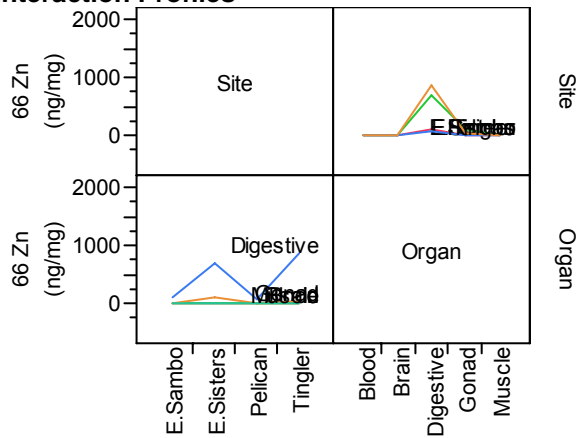
Analysis of Variance

Source	DF	Sum of Squares	Mean Square	F Ratio	Prob > F
Model	19	7362674	387509	9.2680	
Error	109	4557460	41812		
C. Total	128	11920134			<.0001

Effect Tests

Source	Nparm	DF	Sum of Squares	F Ratio	Prob > F
Site	3	3	689451.0	5.4965	0.0015
Organ	4	4	3837956.6	22.9479	<.0001
Site*Organ	12	12	2745366.3	5.4717	<.0001

Interaction Profiles



Site Effect

LSMeans Differences Student's t

$\alpha =$
0.050 t=
1.98197

Level		Least Sq Mean
Tingler	A	183.22844
E.Sisters	A	167.88917
E.Sambo	B	27.85236
Pelican	B	23.67078

Levels not connected by same letter are significantly different.

Organ Effect

LSMeans Differences Student's t

$\alpha =$
0.050 t=
1.98197

Level		Least Sq Mean
Digestive	A	440.65805
Gonad	B	48.65052
Brain	B	6.52341
Muscle	B	6.24155
Blood	B	1.22740

Levels not connected by same letter are significantly different.

Site*Organ Effect

LSMeans Differences Student's t

$\alpha =$
0.050 t=
1.98197

Level		Least Sq Mean
Tingler,Digestive	A	869.17350
E.Sisters,Digestive	A	701.76500
E.Sisters,Gonad	B	123.83600
E.Sambo,Digestive	B	106.40257
Pelican,Digestive	B	85.29112
Tingler,Gonad	B	32.79643
E.Sambo,Gonad	B	21.57350
Pelican,Gonad	B	16.39617
Pelican,Muscle	B	10.14012

Level		Least Sq Mean
Tingler,Brain	B	7.96525
E.Sisters,Brain	B	6.51617
E.Sisters,Muscle	B	5.93300
Pelican,Brain	B	5.84950
E.Sambo,Brain	B	5.76271
Tingler,Muscle	B	4.57150
E.Sambo,Muscle	B	4.32157
Tingler,Blood	B	1.63550
E.Sisters,Blood	B	1.39567
E.Sambo,Blood	B	1.20143
Pelican,Blood	B	0.67700

Levels not connected by same letter are significantly different.

4. Strontium

Whole Model

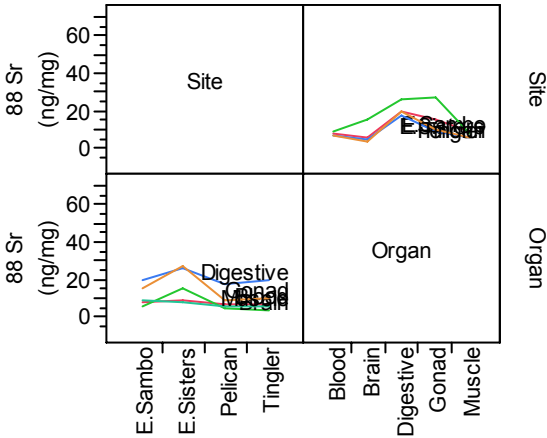
Analysis of Variance

Source	DF	Sum of Squares	Mean Square	F Ratio
Model	19	5595.987	294.526	3.4860
Error	109	9209.231	84.488	Prob > F
C. Total	128	14805.219		<.0001

Effect Tests

Source	Nparm	DF	Sum of Squares	F Ratio	Prob > F
Site	3	3	1271.1215	5.0150	0.0027
Organ	4	4	3870.0912	11.4516	<.0001
Site*Organ	12	12	696.1732	0.6867	0.7611

Interaction Profiles



Site Effect

LSMeans Differences Student's t

$\alpha=0.050$ $t=1.98197$

Level		Least Sq Mean
E.Sisters	A	17.182193
E.Sambo	B	11.749290
Tingler	B	9.042132
Pelican	B	8.708200

Levels not connected by same letter are significantly different.

Organ Effect
LSMeans Differences Student's t

$\alpha=0.050$ $t=1.98197$

Level		Least Sq Mean
Digestive	A	20.875785
Gonad	B	15.205405
Brain	C	7.511699
Blood	C	7.453735
Muscle	C	7.305646

Levels not connected by same letter are significantly different.

Site*Organ Effect
SMeans Differences Student's t

$\alpha=0.050$ $t=1.98197$

Level		Least Sq Mean
E.Sisters,Gonad	A	26.871500
E.Sisters,Digestive	A	26.410800
E.Sambo,Digestive	A	19.860714
Tingler,Digestive	A	19.812750
Pelican,Digestive	A B	17.418875
E.Sambo,Gonad	A B C	15.769167
E.Sisters,Brain	A B C	15.595833
Tingler,Gonad	B C D	9.655286
E.Sambo,Muscle	B C D	8.970000
E.Sisters,Blood	B C D	8.745000
Pelican,Gonad	B C D	8.525667
E.Sisters,Muscle	B C D	8.287833
E.Sambo,Blood	B C D	8.037857
Pelican,Blood	B C D	6.577333
Tingler,Blood	C D	6.454750
Pelican,Muscle	C D	6.261750
E.Sambo,Brain	C D	6.108714
Tingler,Muscle	C D	5.703000
Pelican,Brain	D	4.757375
Tingler,Brain	D	3.584875

Levels not connected by same letter are significantly different.

5. Silver

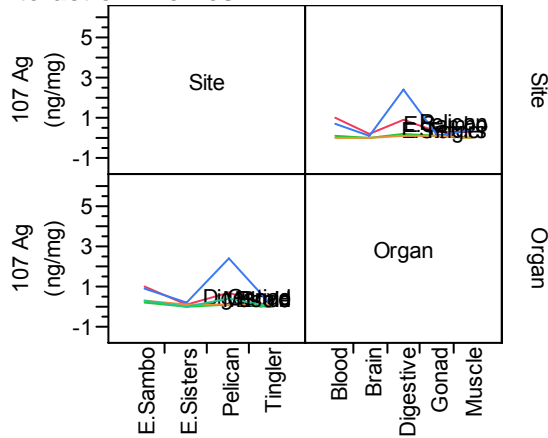
Whole Model
Analysis of Variance

Source	DF	Sum of Squares	Mean Square	F Ratio
Model	19	47.156282	2.48191	6.5287
Error	109	41.436498	0.38015	Prob > F
C. Total	128	88.592780		<.0001

Effect Tests

Source	Nparm	DF	Sum of Squares	F Ratio	Prob > F
Site	3	3	11.055690	9.6941	<.0001
Organ	4	4	11.853957	7.7956	<.0001
Site*Organ	12	12	19.205440	4.2100	<.0001

Interaction Profiles



Site Effect

LSMeans Differences Student's t

$\alpha=0.050$ $t=1.98197$

Level		Least Sq Mean
Pelican	A	0.77589560
E.Sambo	A	0.58662857
E.Sisters	B	0.11811000
Tingler	B	0.05996071

Levels not connected by same letter are significantly different.

Organ Effect

LSMeans Differences Student's t

$\alpha=$
0.050 $t=$
1.98197

Level		Least Sq Mean
Digestive	A	0.92288304
Blood	B	0.49431101
Muscle	B C	0.21271280
Gonad	B C	0.19503914
Brain	C	0.10079762

Levels not connected by same letter are significantly different.

Site*Organ

LSMeans Differences Student's t

$\alpha=$
0.050 $t=$
1.98197

Level		Least Sq Mean
Pelican,Digestive	A	2.4663750
E.Sambo,Blood	B	1.0722857
E.Sambo,Digestive	B C	0.8938571
Pelican,Blood	B C D	0.7510000
Pelican,Muscle	C D	0.4233750
E.Sambo,Gonad	C D	0.3880000
E.Sambo,Muscle	C D	0.3791429
E.Sisters,Digestive	C D	0.2238000
E.Sambo,Brain	D	0.1998571
E.Sisters,Gonad	C D	0.1402500
Pelican,Gonad	D	0.1364780
Tingler,Gonad	D	0.1154286
Tingler,Digestive	D	0.1075000

Level		Least Sq Mean
Pelican,Brain	D	0.1022500
E.Sisters,Blood	D	0.0978333
E.Sisters,Brain	D	0.0893333
Tingler,Blood	D	0.0561250
E.Sisters,Muscle	D	0.0393333
Tingler,Brain	D	0.0117500
Tingler,Muscle	D	0.0090000

Levels not connected by same letter are significantly different.

6. Cadmium

Whole Model

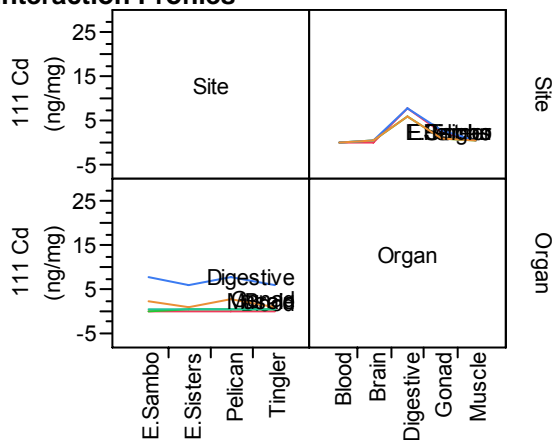
Analysis of Variance

Source	DF	Sum of Squares	Mean Square	F Ratio	Prob > F
Model	19	968.8819	50.9938	7.7283	
Error	109	719.2166	6.5983		Prob > F
C. Total	128	1688.0985			<.0001

Effect Tests

Source	Nparm	DF	Sum of Squares	F Ratio	Prob > F
Site	3	3	15.63667	0.7899	0.5020
Organ	4	4	865.15583	32.7794	<.0001
Site*Organ	12	12	26.45514	0.3341	0.9813

Interaction Profiles



Site Effect

LSMeans Differences Student's t

$\alpha=0.050$ $t=1.98197$

Level		Least Sq Mean
Pelican	A	2.3438833
E.Sambo	A	2.1767286
E.Sisters	A	1.5746467
Tingler	A	1.5225036

Levels not connected by same letter are significantly different.

Organ Effect

LSMeans Differences Student's t

$\alpha=0.050$ $t=1.98197$

Level		Least Sq Mean
Digestive	A	6.8824750
Gonad	B	1.8722440

Level		Least Sq Mean
Muscle	B C	0.4601205
Brain	C	0.2575818
Blood	C	0.0497813

Levels not connected by same letter are significantly different.

Site*Organ Effect

LSMeans Differences Student's t

$\alpha=0.050$ $t=1.98197$

Level		Least Sq Mean
Pelican,Digestive	A	7.9846250
E.Sambo,Digestive	A	7.6890000
E.Sisters,Digestive	A B	5.9354000
Tingler,Digestive	A	5.9208750
Pelican,Gonad	B C	2.9533333
E.Sambo,Gonad	C D	2.4775000
E.Sisters,Gonad	C D	1.1330000
Tingler,Gonad	C D	0.9251429
Pelican,Muscle	C D	0.5071250
E.Sambo,Muscle	C D	0.4858571
E.Sisters,Muscle	C D	0.4830000
Tingler,Muscle	C D	0.3645000
Tingler,Brain	C D	0.3383750
E.Sisters,Brain	C D	0.2866667
Pelican,Brain	C D	0.2340000
E.Sambo,Brain	C D	0.1712857
Tingler,Blood	D	0.0636250
E.Sambo,Blood	D	0.0600000
Pelican,Blood	C D	0.0403333
E.Sisters,Blood	C D	0.0351667

Levels not connected by same letter are significantly different.

7. Tin

Whole Model

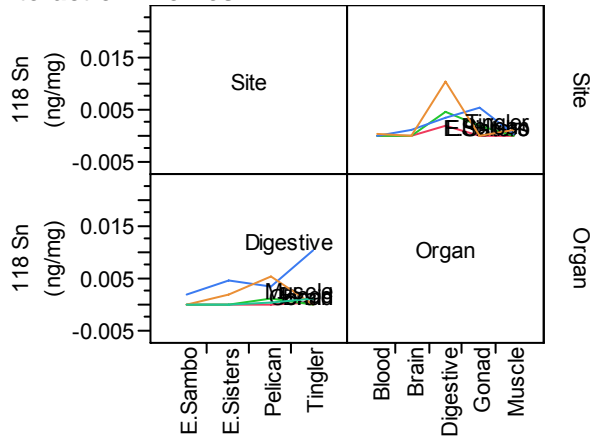
Analysis of Variance

Source	DF	Sum of Squares	Mean Square	F Ratio
Model	19	0.00092942	0.000049	4.1197
Error	109	0.00129427	0.000012	Prob > F
C. Total	128	0.00222369		<.0001

Effect Tests

Source	Nparm	DF	Sum of Squares	F Ratio	Prob > F
Site	3	3	0.00007911	2.2208	0.0898
Organ	4	4	0.00043164	9.0879	<.0001
Site*Organ	12	12	0.00036023	2.5281	0.0056

Interaction Profiles



Site Effect

LSMeans Differences Student's t

$\alpha=0.050$ $t=1.98197$

Level			Least Sq Mean
Tingler	A		0.00242500
Pelican	A	B	0.00196667
E.Sisters	A	B	0.00123000
E.Sambo		B	0.00037143

Levels not connected by same letter are significantly different.

Organ Effect

LSMeans Differences Student's t

$\alpha=0.050$ $t=1.98197$

Level			Least Sq Mean
Digestive	A		0.00493929
Gonad		B	0.00177083
Muscle		B	0.00037500
Brain		B	0.00028125
Blood		B	0.00012500

Levels not connected by same letter are significantly different.

Site*Organ Effect

LSMeans Differences Student's t

$\alpha=0.050$ $t=1.98197$

Level			Least Sq Mean
Tingler,Digestive	A		0.0102500
Pelican,Gonad		B	0.0053333
E.Sisters,Digestive		B C	0.0044000
Pelican,Digestive		B C D	0.0032500
E.Sambo,Digestive		B C D	0.0018571
E.Sisters,Gonad		B C D	0.0017500
Tingler,Muscle		B C D	0.0012500
Pelican,Brain		C D	0.0010000
Tingler,Blood		D	0.0005000
Pelican,Muscle		D	0.0002500
Tingler,Brain		D	0.0001250
E.Sisters,Muscle		D	1.5721e-18
E.Sisters,Blood		D	-1.084e-19
E.Sisters,Brain		D	-1.084e-19
E.Sambo,Muscle		D	-4.337e-19

Level		Least Sq Mean
Tingler,Gonad	D	-4.337e-19
E.Sambo,Blood	D	-1.301e-18
E.Sambo,Brain	D	-1.518e-18
E.Sambo,Gonad	D	-1.952e-18
Pelican,Blood	C D	-4.77e-18

Levels not connected by same letter are significantly different.

8. Mercury

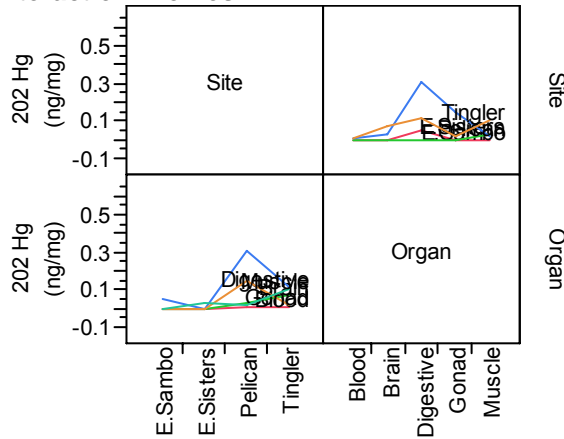
Whole Model Analysis of Variance

Source	DF	Sum of Squares	Mean Square	F Ratio	Prob > F
Model	19	0.8076197	0.042506	6.0788	
Error	109	0.7621905	0.006993		Prob > F
C. Total	128	1.5698102			<.0001

Effect Tests

Source	Nparm	DF	Sum of Squares	F Ratio	Prob > F
Site	3	3	0.18679918	8.9046	<.0001
Organ	4	4	0.19018562	6.7996	<.0001
Site*Organ	12	12	0.32736639	3.9014	<.0001

Interaction Profiles



Site Effect

LSMeans Differences Student's t

$\alpha=0.050$ $t=1.98197$

Level		Least Sq Mean
Pelican	A	0.10333333
Tingler	A	0.06111429
E.Sambo	B	0.00942857
E.Sisters	B	0.00686667

Levels not connected by same letter are significantly different.

Organ Effect

LSMeans Differences Student's t

$\alpha=0.050$ $t=1.98197$

Level		Least Sq Mean
Digestive	A	0.11728571
Gonad	B	0.04130952
Muscle	B	0.04033333
Brain	B	0.02328125

Level		Least Sq Mean
Blood	B	0.00371875

Levels not connected by same letter are significantly different.

Site*Organ Effect

LSMeans Differences Student's t

$\alpha=0.050$ $t=1.98197$

Level		Least Sq Mean
Pelican,Digestive	A	0.3108750
Pelican,Gonad	B	0.1486667
Tingler,Digestive	B C	0.1111250
Tingler,Muscle	B C D	0.1037500
Tingler,Brain	B C D	0.0682500
E.Sambo,Digestive	C D	0.0471429
E.Sisters,Muscle	C D	0.0343333
Pelican,Brain	D	0.0248750
Pelican,Muscle	D	0.0232500
Tingler,Gonad	D	0.0165714
Pelican,Blood	C D	0.0090000
Tingler,Blood	D	0.0058750
E.Sisters,Blood	D	6.245e-17
E.Sisters,Brain	D	3.1225e-17
E.Sisters,Gonad	D	2.2118e-17
E.Sambo,Blood	D	2.0817e-17
E.Sambo,Gonad	D	1.9082e-17
E.Sambo,Muscle	D	-1.041e-17
E.Sambo,Brain	D	-2.429e-17
E.Sisters,Digestive	D	-1.249e-16

Levels not connected by same letter are significantly different.

9. Uranium

Whole Model

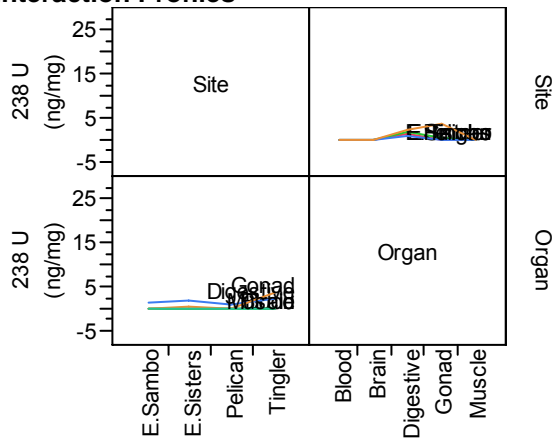
Analysis of Variance

Source	DF	Sum of Squares	Mean Square	F Ratio	Prob > F
Model	19	130.40473	6.86341	1.2322	
Error	109	607.15725	5.57025		
C. Total	128	737.56198			0.2458

Effect Tests

Source	Nparm	DF	Sum of Squares	F Ratio	Prob > F
Site	3	3	20.229445	1.2106	0.3094
Organ	4	4	52.238509	2.3445	0.0592
Site*Organ	12	12	49.125663	0.7349	0.7146

Interaction Profiles



Site Effect

LSMeans Differences Student's t

$\alpha=0.050$ $t=1.98197$

Level		Least Sq Mean
Tingler	A	1.1978714
E.Sisters	A	0.4568926
E.Sambo	A	0.2544778
Pelican	A	0.2055750

Levels not connected by same letter are significantly different.

Organ Effect

LSMeans Differences Student's t

$\alpha=0.050$ $t=1.98197$

Level		Least Sq Mean
Digestive	A	1.5179574
Gonad	A B	1.0799465
Brain	B	0.0266031
Blood	B	0.0176050
Muscle	B	0.0014090

Levels not connected by same letter are significantly different.

Site*Organ Effect

LSMeans Differences Student's t

$\alpha=0.050$ $t=1.98197$

Level		Least Sq Mean
Tingler,Gonad	A	3.773857
Tingler,Digestive	A B	2.156500
E.Sisters,Digestive	A B	1.786208
E.Sambo,Digestive	B	1.153121
Pelican,Digestive	B	0.976000
E.Sisters,Gonad	B	0.465921
E.Sambo,Gonad	B	0.061341
E.Sambo,Brain	B	0.047696
Tingler,Blood	B	0.037125
Pelican,Brain	B	0.024625
Pelican,Gonad	B	0.018667
Tingler,Brain	B	0.017625

Level		Least Sq Mean
E.Sisters,Brain	B	0.016467
E.Sisters,Blood	B	0.015730
E.Sambo,Blood	B	0.010231
Pelican,Blood	B	0.007333
Tingler,Muscle	B	0.004250
Pelican,Muscle	B	0.001250
E.Sisters,Muscle	B	0.000136
E.Sambo,Muscle	B	-1.11e-16

Levels not connected by same letter are significantly different.

III. Analysis considering proximity to shore

Initial one-way ANOVA analysis of metal burden as a function of proximity to shore indicated that zinc and silver has significant differences between locations.

Zinc

Analysis of Variance

Source	DF	Sum of Squares	Mean Square	F Ratio	Prob > F
Inshore/Offshore	1	778557	778557	8.8746	0.0035
Error	127	11141577	87729		
C. Total	128	11920134			

Means for Oneway Anova

Level	Number	Mean	Std Error	Lower 95%	Upper 95%
Inshore	62	183.311	37.616	108.9	257.75
Offshore	67	27.820	36.185	-43.8	99.42

Std Error uses a pooled estimate of error variance

Silver

Analysis of Variance

Source	DF	Sum of Squares	Mean Square	F Ratio	Prob > F
Inshore/Offshore	1	12.318500	12.3185	20.5108	<.0001
Error	127	76.274280	0.6006		
C. Total	128	88.592780			

Means for Oneway Anova

Level	Number	Mean	Std Error	Lower 95%	Upper 95%
Inshore	62	0.085258	0.09842	-0.1095	0.28002
Offshore	67	0.703759	0.09468	0.5164	0.89111

Std Error uses a pooled estimate of error variance

To followup, a multiple ANOVA was performed with organ and location (inshore/offshore) as the factors for Zinc and Silver

Zinc

Analysis of Variance

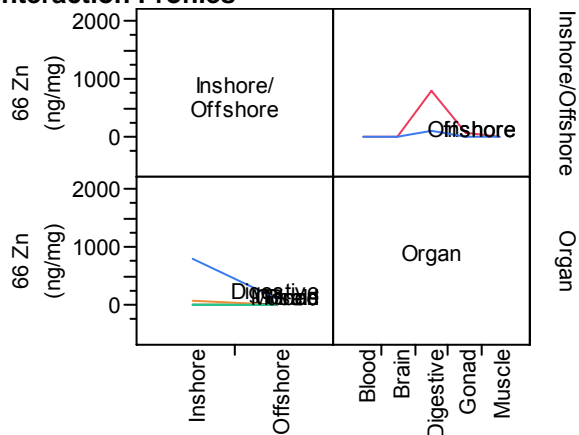
Source	DF	Sum of Squares	Mean Square	F Ratio	Prob > F
Model	9	7253461	805940	20.5514	
Error	119	4666673	39216		

Source	DF	Sum of Squares	Mean Square	F Ratio
C. Total	128	11920134		<.0001

Effect Tests

Source	Nparm	DF	Sum of Squares	F Ratio	Prob > F
Inshore/Offshore	1	1	720839.7	18.3814	<.0001
Organ	4	4	4167448.5	26.5674	<.0001
Inshore/Offshore*Organ	4	4	2664624.7	16.9870	<.0001

Interaction Profiles



Shore

LSMeans Differences Student's t

$\alpha=0.050$ $t=1.9801$

Level		Least Sq Mean
Inshore	A	176.99053
Offshore	B	25.68117

Levels not connected by same letter are significantly different.

Organ

LSMeans Differences Student's t

$\alpha=0.050$ $t=1.9801$

Level		Least Sq Mean
Digestive	A	449.96437
Gonad	B	42.44328
Brain	B	6.57661
Muscle	B	6.40660
Blood	B	1.28841

Levels not connected by same letter are significantly different.

Shore*Organ

LSMeans Differences Student's t

$\alpha=0.050$ $t=1.9801$

Level		Least Sq Mean
Inshore,Digestive	A	804.78562
Offshore,Digestive	B	95.14313
Inshore,Gonad	B	65.90173
Offshore,Gonad	B	18.98483
Offshore,Muscle	B	7.42480
Inshore,Brain	B	7.34421
Offshore,Brain	B	5.80900
Inshore,Muscle	B	5.38840
Inshore,Blood	B	1.53271
Offshore,Blood	B	1.04410

Levels not connected by same letter are significantly different.

Silver

Whole Model

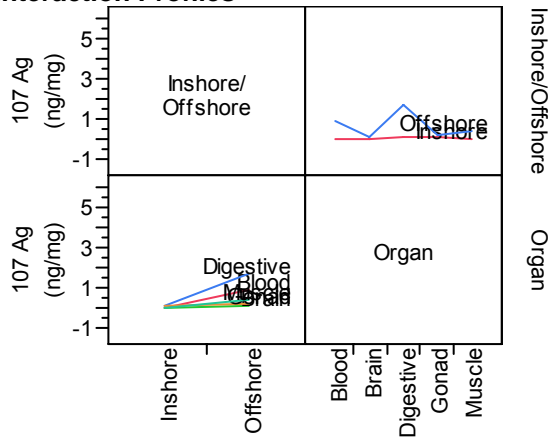
Analysis of Variance

Source	DF	Sum of Squares	Mean Square	F Ratio
Model	9	37.403020	4.15589	9.6611
Error	119	51.189761	0.43017	Prob > F
C. Total	128	88.592780		<.0001

Effect Tests

Source	Nparm	DF	Sum of Squares	F Ratio	Prob > F
Inshore/Offshore	1	1	12.089818	28.1050	<.0001
Organ	4	4	13.031146	7.5733	<.0001
Inshore/Offshore*Organ	4	4	10.512132	6.1093	0.0002

Interaction Profiles



Shore Effect

LSMeans Differences Student's t

$\alpha=0.050$ $t=1.9801$

Level	Least Sq Mean
Offshore A	0.70424113
Inshore B	0.08457706

Levels not connected by same letter are significantly different.

Organ Effect

LSMeans Differences Student's t

$\alpha=0.050$ $t=1.9801$

Level	Least Sq Mean
Digestive A	0.94238205
Blood B	0.52495000
Muscle B C	0.21496667
Gonad B C	0.19334677
Brain C	0.09640000

Levels not connected by same letter are significantly different.

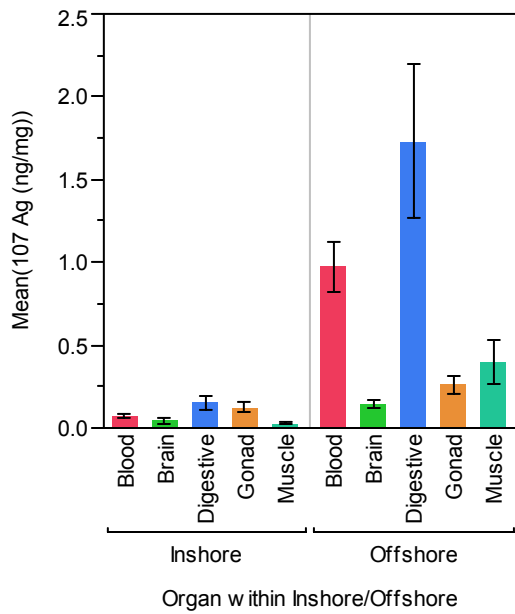
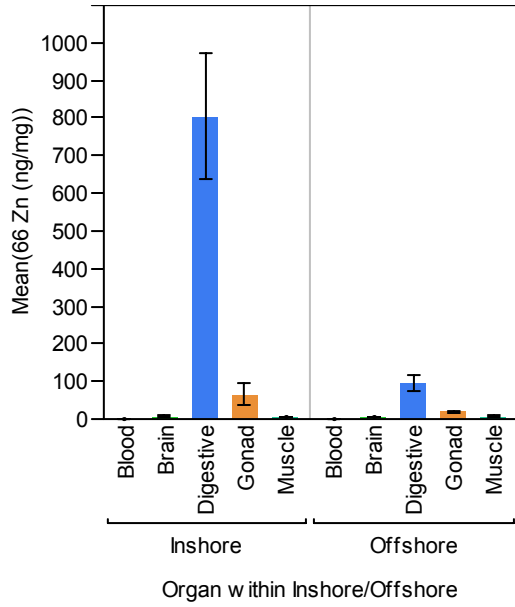
Shore*Organ

LSMeans Differences Student's t

$\alpha=0.050$ $t=1.9801$

Level	Least Sq Mean
Offshore,Digestive	A 1.7325333
Offshore,Blood	B 0.9759000
Offshore,Muscle	C 0.4027333
Offshore,Gonad	C 0.2622390
Inshore,Digestive	C 0.1522308
Offshore,Brain	C 0.1478000
Inshore,Gonad	C 0.1244545
Inshore,Blood	C 0.0740000
Inshore,Brain	C 0.0450000
Inshore,Muscle	C 0.0272000

Levels not connected by same letter are significantly different.



Appendix II –Tables of Chemistry of Water Samples from POCIS and SPMD collectors. SPMD concentrations were converted using the U.S. Geological Survey methods found at the following URL:
<http://www.cerc.usgs.gov/research/spmd.htm>

Results in Site Waters, pg/L

<i>Analyte</i>	<i>Offshore</i>	<i>Nearshore</i>
<i>alpha-BHC</i>	ND	ND
<i>Hexachlorobenzene</i>	ND	ND
<i>beta-BHC</i>	ND	ND
<i>gamma-BHC</i>	ND	ND
<i>delta-BHC</i>	ND	ND
<i>Heptachlor</i>	ND	ND
<i>Aldrin</i>	ND	ND
<i>Heptachlor Epoxide</i>	<5.32	ND
<i>Oxychlorane</i>	ND	ND
<i>trans-Chlordane</i>	ND	ND
<i>o,p-DDE</i>	ND	ND
<i>Endosulfan I</i>	ND	ND
<i>cis-Chlordane</i>	0.27	0.11
<i>trans-Nonachlor</i>	ND	ND
<i>p,p-DDE</i>	ND	ND
<i>Dieldrin</i>	ND	ND
<i>o,p-DDD</i>	ND	ND
<i>Endrin</i>	ND	ND
<i>Endosulfan II</i>	ND	ND
<i>p,p-DDD</i>	ND	5.02
<i>o,p-DDT</i>	ND	ND
<i>cis,-Nonachlor</i>	<1.93	<1.28
<i>Endrin Aldehyde</i>	ND	ND
<i>Endosulfan Sulfate</i>	ND	ND
<i>p,p-DDT</i>	ND	ND
<i>Endrin Ketone</i>	ND	ND
<i>Methoxychlor</i>	ND	ND
<i>Mirex</i>	ND	ND
<i>Kepone</i>	ND	ND
<i>Toxaphene</i>	ND	ND
PAH		
<i>Naphthalene</i>	ND	ND
<i>Acenaphthylene</i>	ND	ND
<i>Acenaphthene</i>	ND	ND
<i>Fluorene</i>	ND	ND

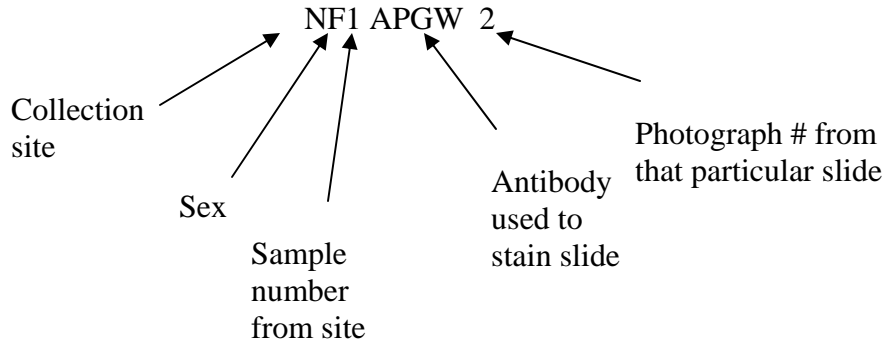
<i>Phenanthrene</i>	ND	ND
<i>Anthracene</i>	ND	ND
<i>Fluoranthene</i>	ND	ND
<i>Pyrene</i>	ND	ND
<i>Chrysene</i>	2.52	3.88
<i>Benz[a]anthracene</i>	3.21	12.68
<i>Benzo[b]fluoranthene</i>	ND	15.13
<i>Benzo[k]fluoranthene</i>	ND	6.24
<i>Benzo[a]pyrene</i>	ND	6.11
<i>Indeno[1,2,3-cd]pyrene</i>	ND	7.40
<i>Dibenz[a,h]anthracene</i>	ND	ND
<i>Benzo[g,h,i]perylene</i>	ND	ND
Total PCBs	ND	ND

ND, analyzed for but not detected (below limit of detection)

BQL, below limit of quantitation (estimated values italicized)

Appendix III - Immunohistochemistry of ELH and APGWamide

All slides were photographed using FITC = Fluorescein Isothiocyanate Microscopy.
Designations for all photographs follow the identification scheme:



N= Nearshore

O= Offshore

F= Female

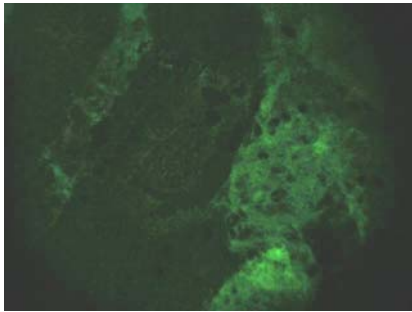
M= Male

APGW= Anti-APGWamide staining

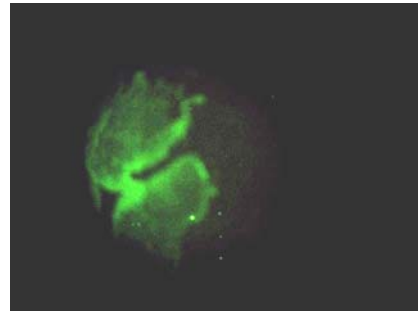
ELH= Anti-ELH staining (Egg Laying Hormone)

Anti-APGWamide staining
All exposures at 10X (unless noted) using FITC

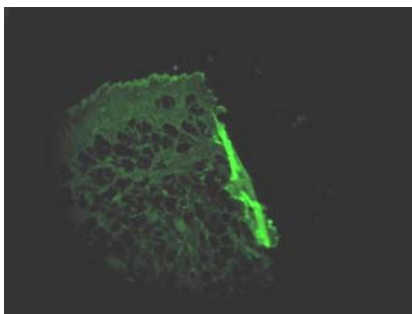
Date: 3-14-2008



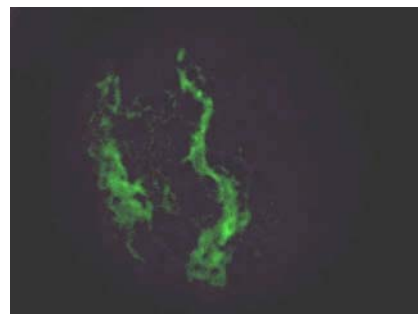
OM1 APGW 1



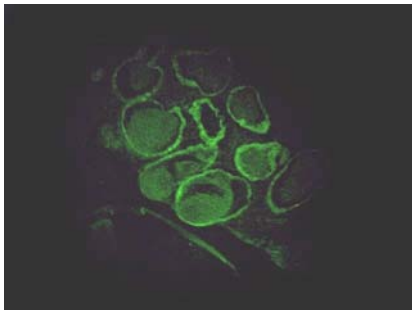
OM1 APGW 3



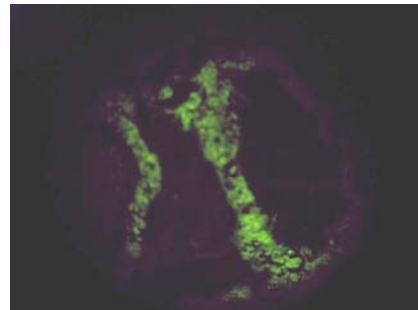
OM1 APGW 4



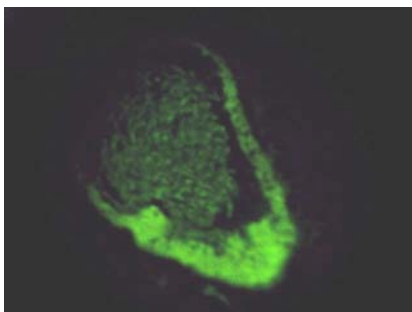
OM1 APGW 6



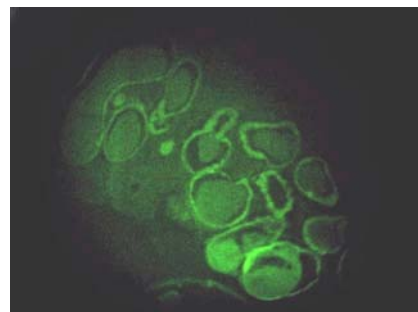
OM2 APGW 2



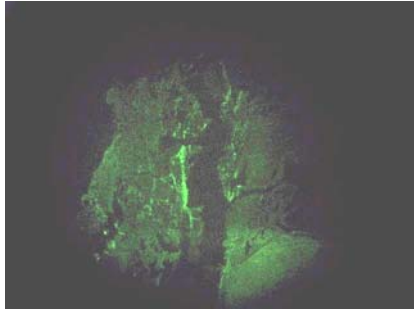
OM2 APGW 3 (20X)



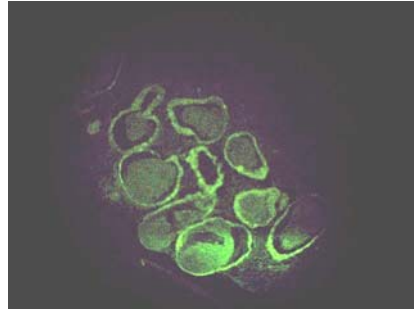
OM2 APGW 4 (20X)



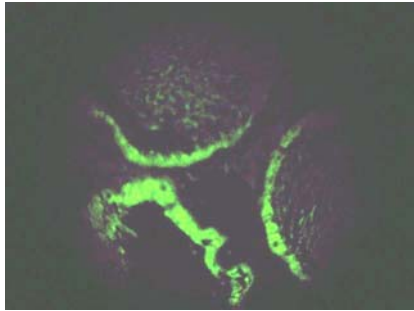
OM2 APGW 5



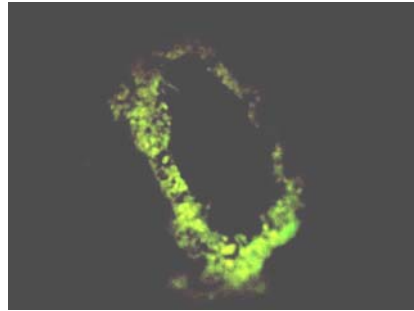
OM2 APGW 6



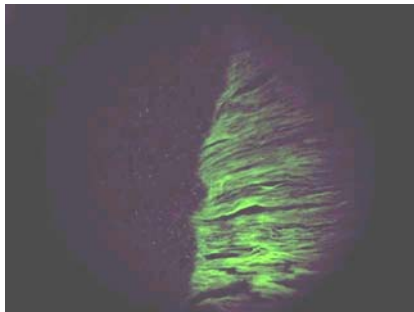
OM2 APGW 8



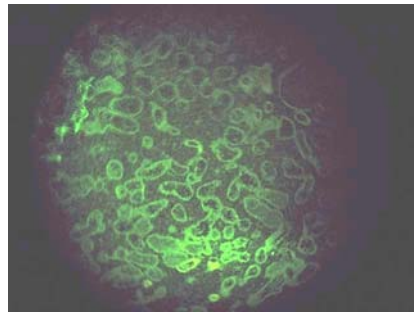
OM2 APGW 9 (20X)



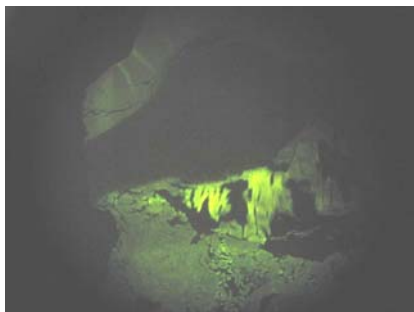
OM2 APGW 10 (20X)



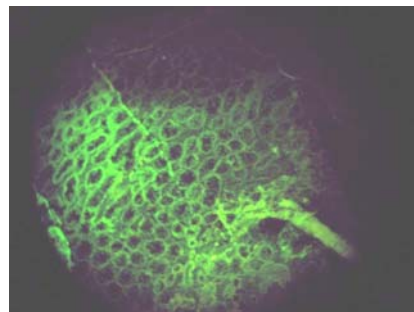
OM2 APGW 11



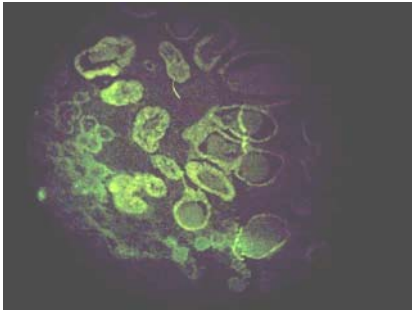
OM2 APGW 13



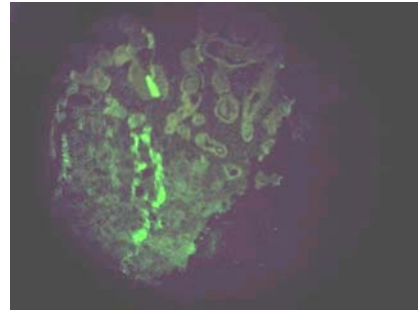
OM3 APGW 1



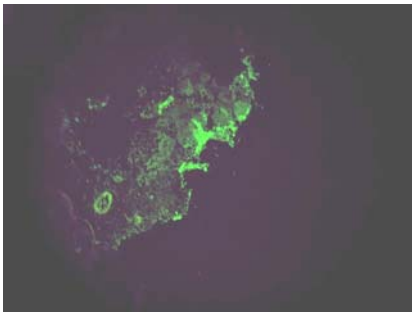
OM3 APGW 3



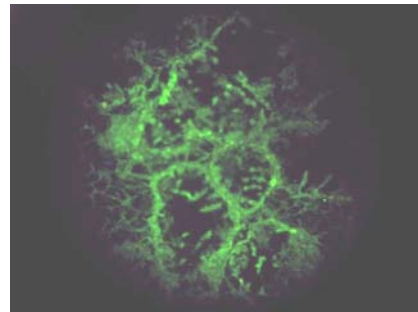
OM3 APGW 5



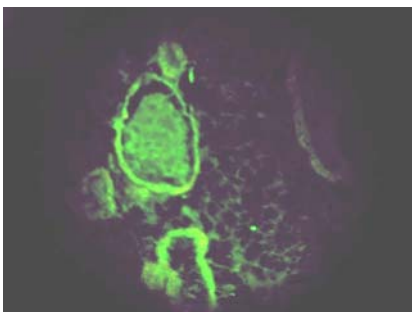
OM4 APGW 1



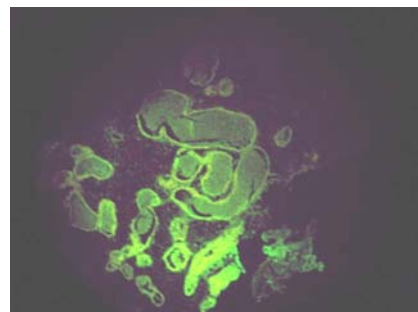
OM4 APGW 2



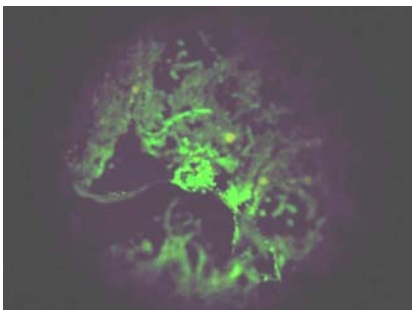
OM4 APGW 3 (20X)



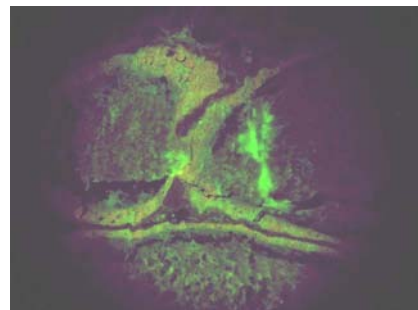
OM4 APGW 4 (20X)



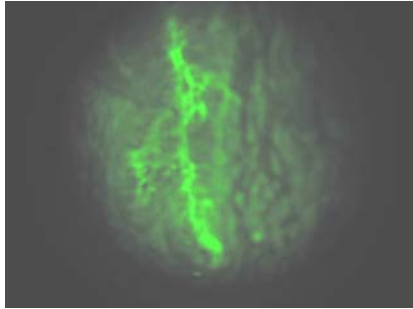
OM4 APGW 5



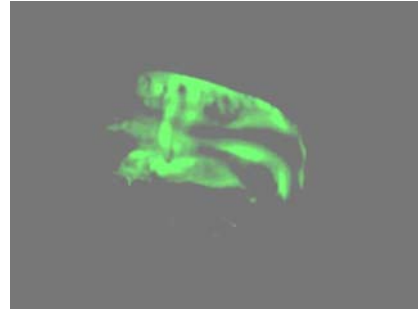
OM4 APGW 6



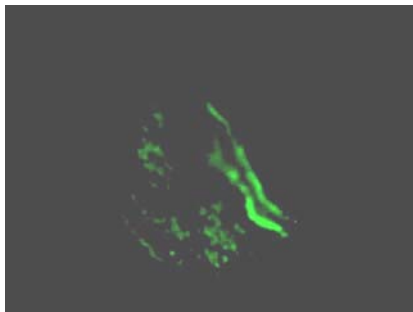
OM4 APGW 8



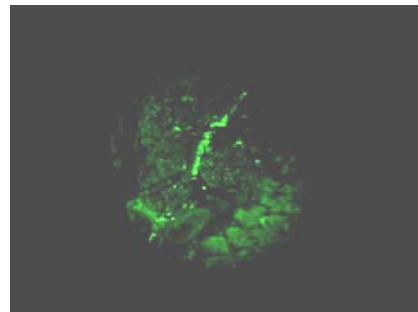
OF1-1 APGW 3



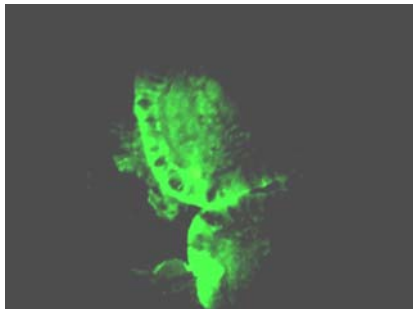
OF1-1 APGW 7 (20X)



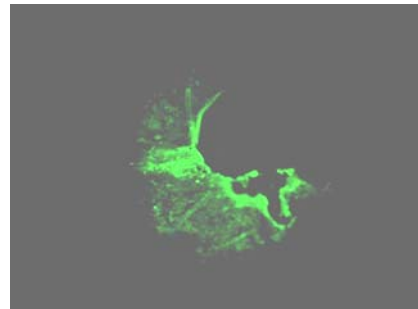
OF1-1 APGW 9



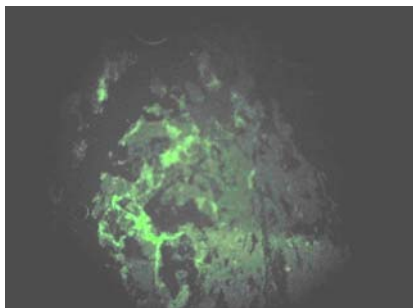
OF1-1 APGW 10



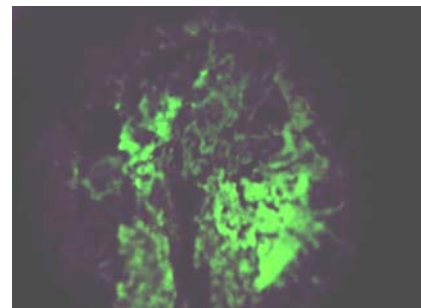
OF1-1 APGW 11 (40X)



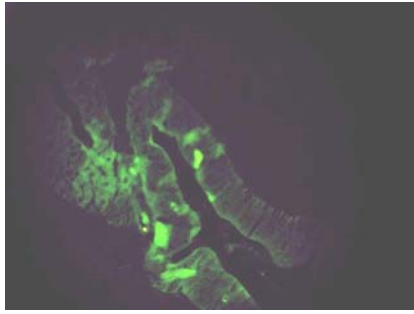
OF1-1 APGW 12



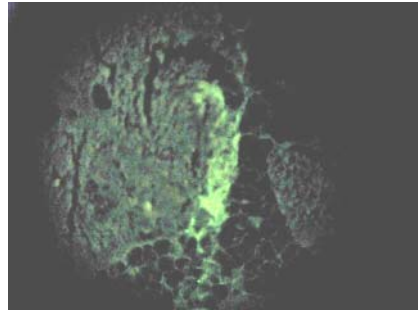
OF1-2 APGW 1



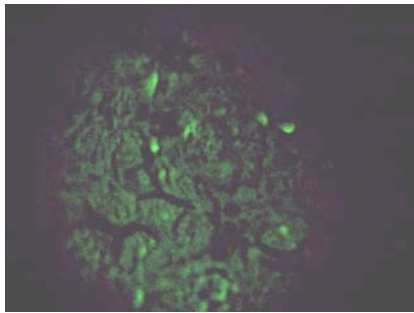
OF1-2 APGW 6



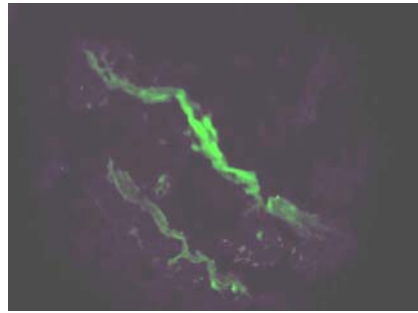
OF3 APGW 3



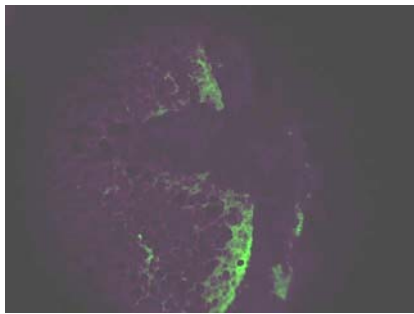
OF3 APGW 4



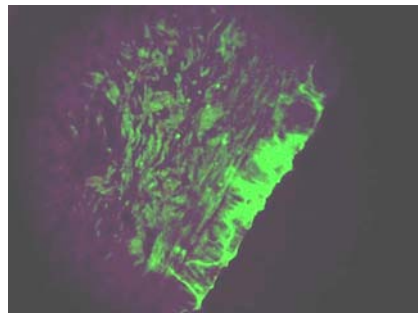
OF3 APGW 5



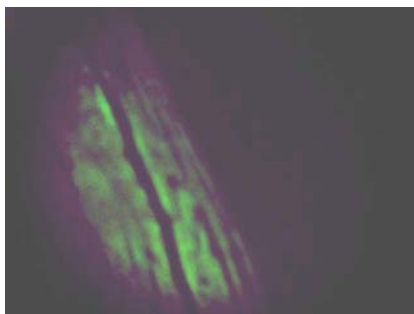
OF4 APGW 1



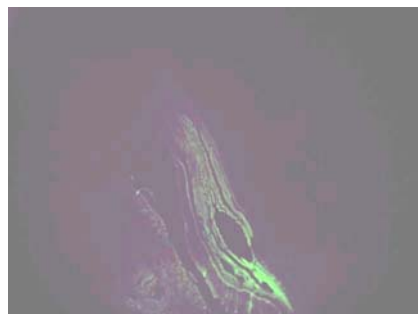
OF4 APGW 2



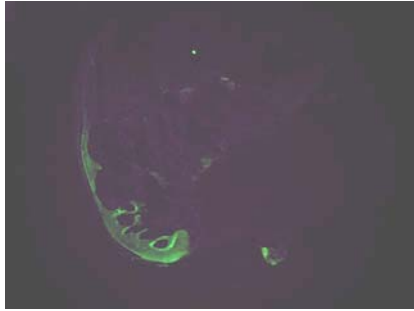
OF4 APGW 4



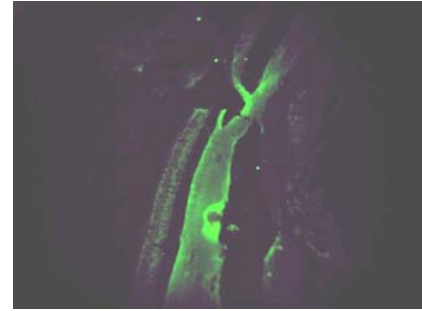
OF4 APGW 5



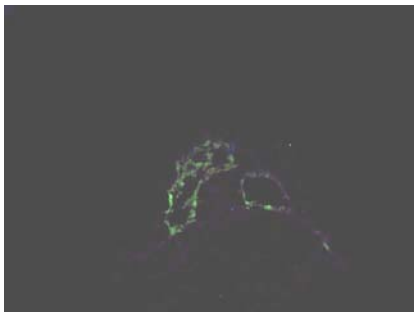
OF4 APGW 7



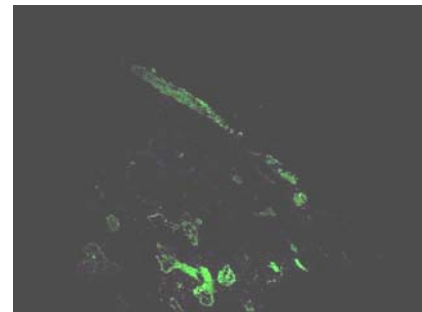
NM1 APGW 1



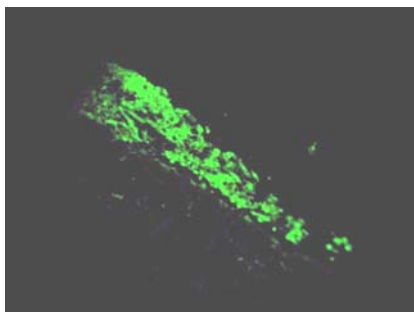
NM1 APGW 2



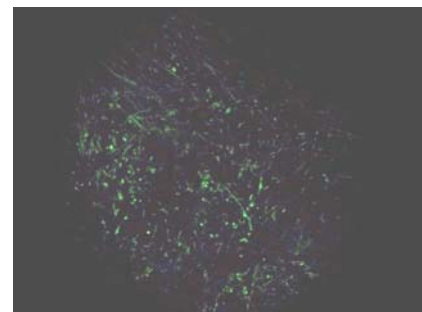
NM1 APGW 4



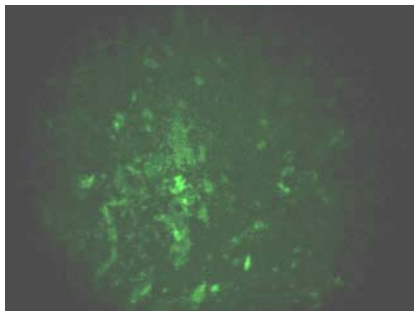
NM2 APGW 2



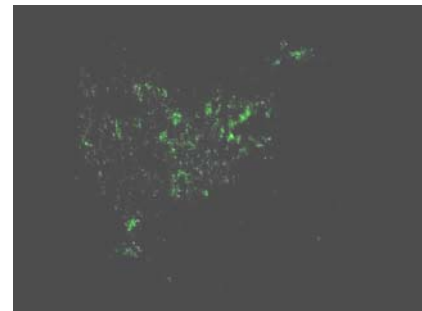
NM2 APGW 3 (20X)



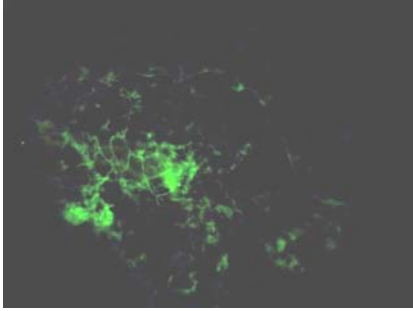
NM2 APGW 5



NM3 APGW 1



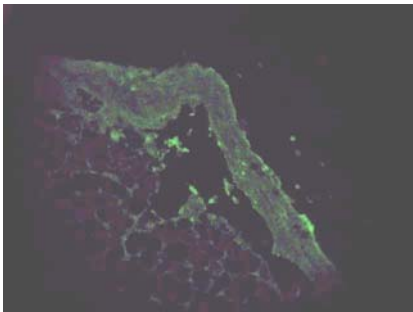
NM3 APGW 3



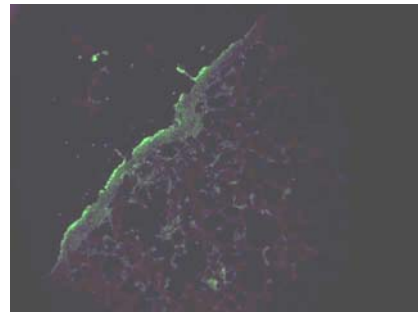
NM3 APGW 6



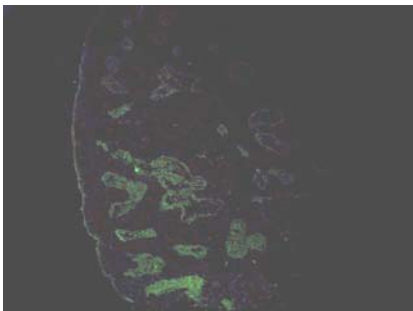
NM3 APGW 7



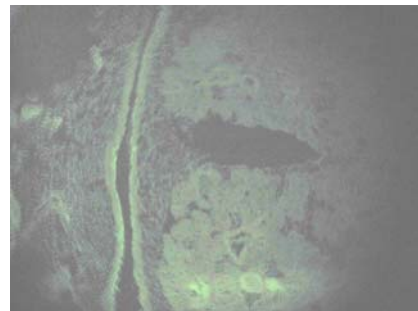
NM3 APGW 8



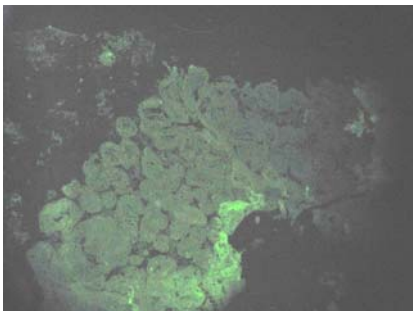
NM3 APGW 10



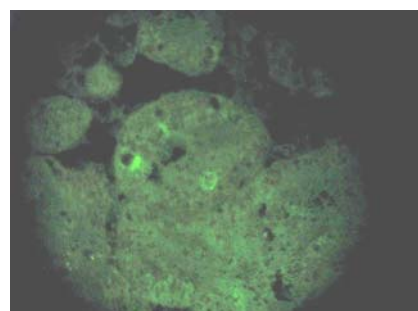
NM4 APGW 1



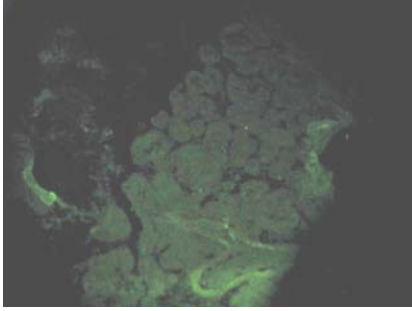
NM4 APGW 4



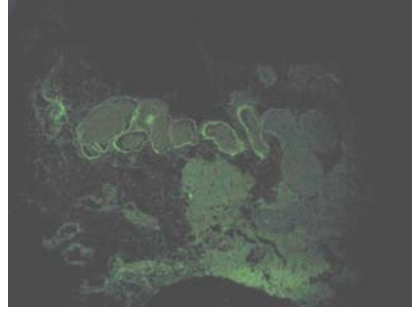
NM4 APGW 5



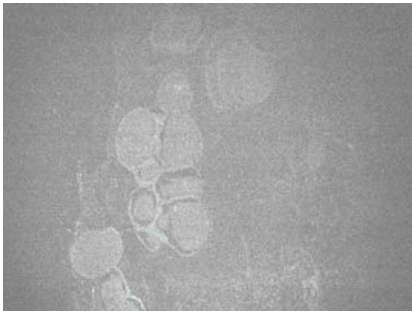
NM4 APGW 7



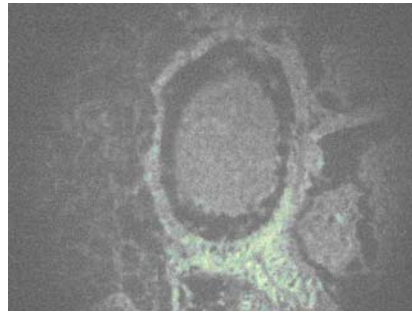
NM4 APGW 10



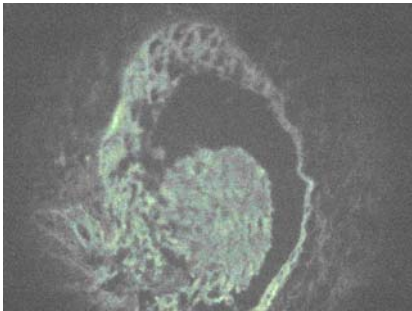
NM4 APGW 11



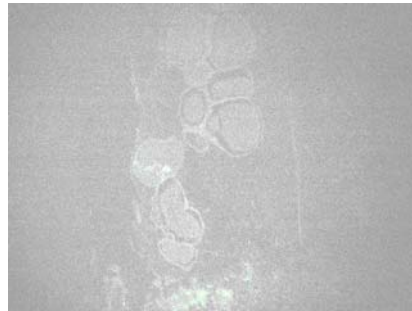
NM5 APGW 2



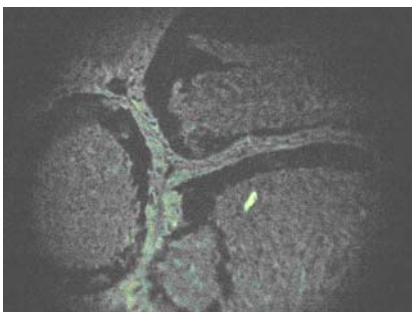
NM5 APGW 3 (20X)



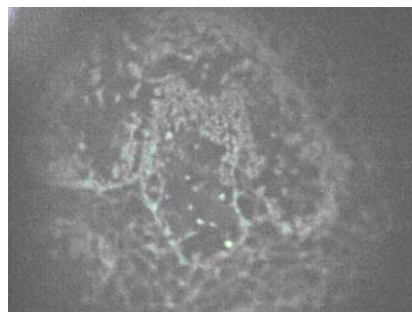
NM5 APGW 4 (20X)



NM5 APGW 5



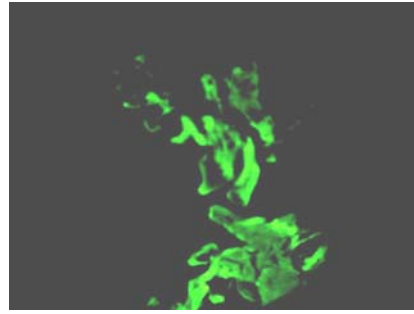
NM5 APGW 6 (20X)



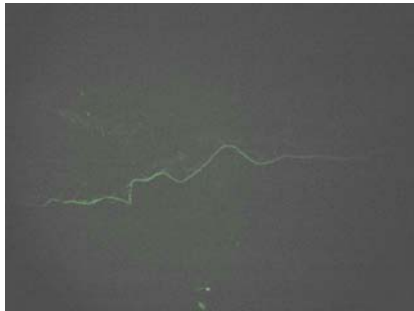
NM5 APGW 7 (20X)



NF1 APGW 2



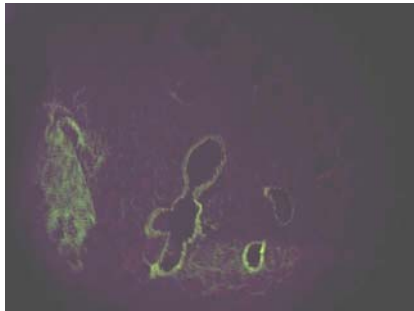
NF1 APGW 3



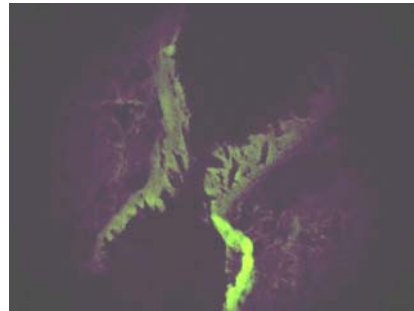
NF1 APGW 6



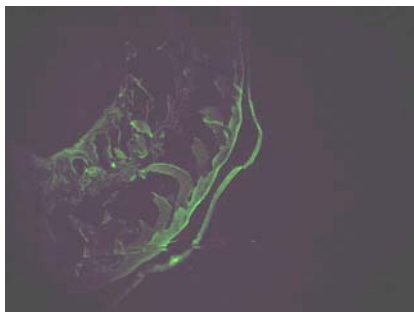
NF1 APGW 7



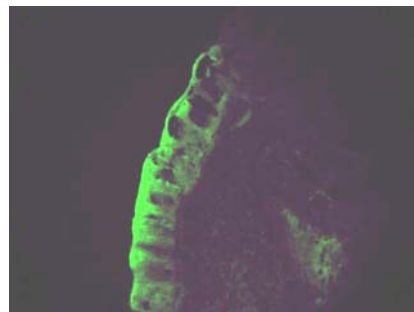
NF2 APGW 1



NF2 APGW 2 (20X)



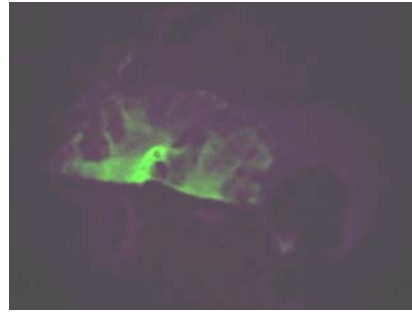
NF2 APGW 5



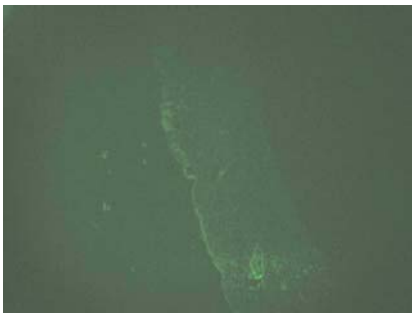
NF2 APGW 7 (20X)



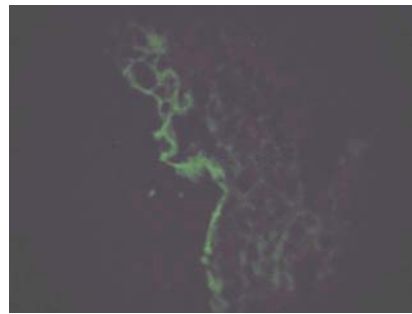
NF3 APGW 1



NF3 APGW 3

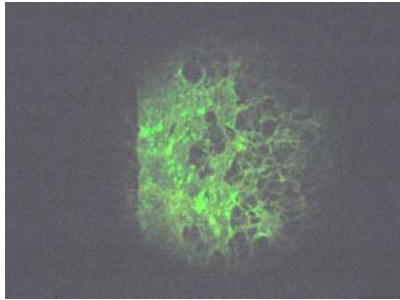


NF3 APGW 4

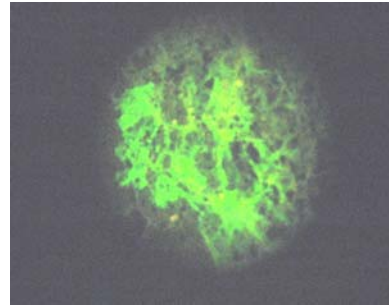


NF3 APGW 5

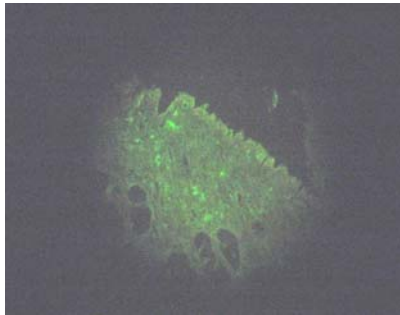
Anti-ELH staining
All exposures at 10X (unless noted) using FITC



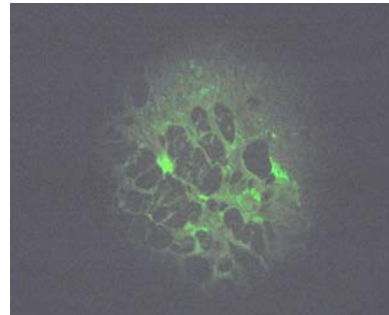
OM1 ELH 1



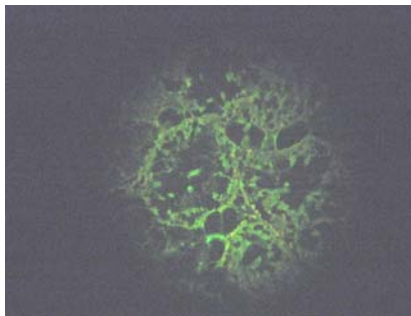
OM1 ELH 2 (20X)



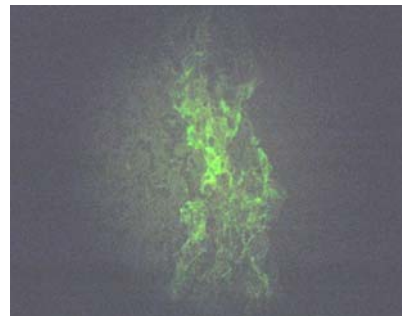
OM1 ELH 8



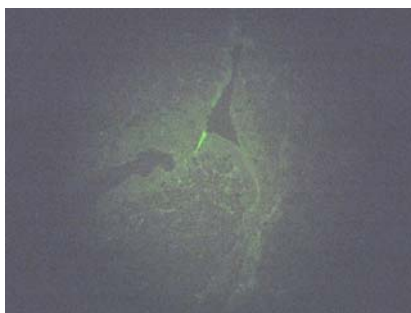
OM1 ELH 9 (20X)



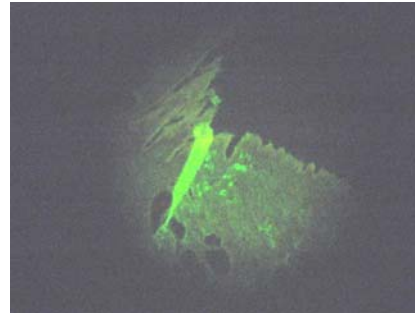
OM1 ELH 16 (20X)



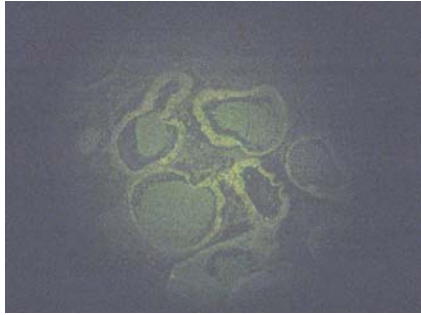
OM1 ELH 17



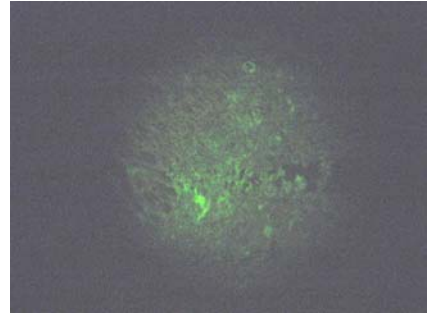
OM1 ELH 19



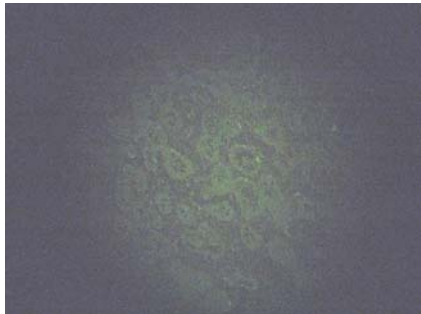
OM1 ELH 20 (20X)



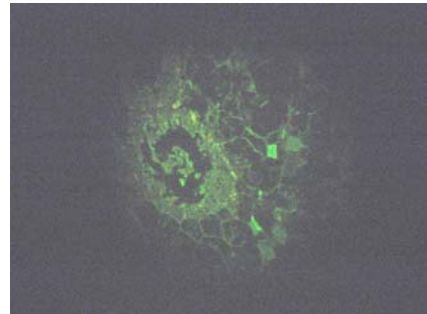
OM2 ELH 2 (20X)



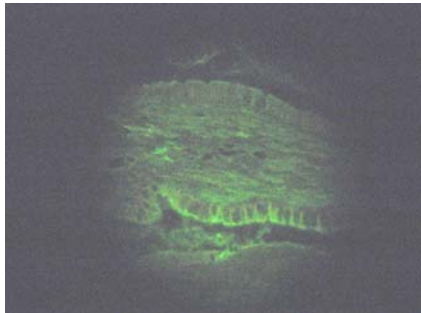
OM2 ELH 7



OM2 ELH 8



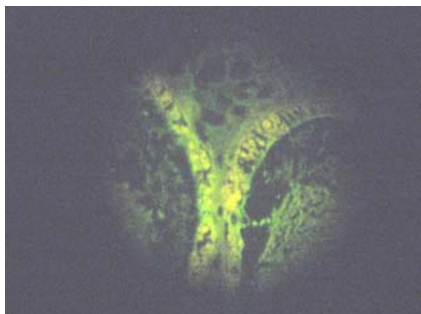
OM2 ELH 9 (20 X)



OM2 ELH 13



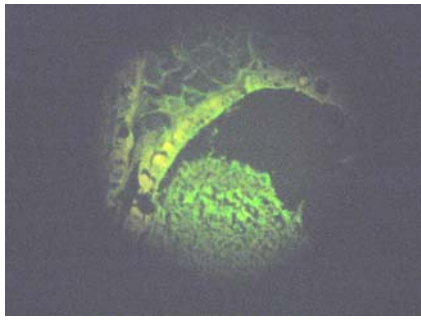
OM2 ELH 15 (20X)



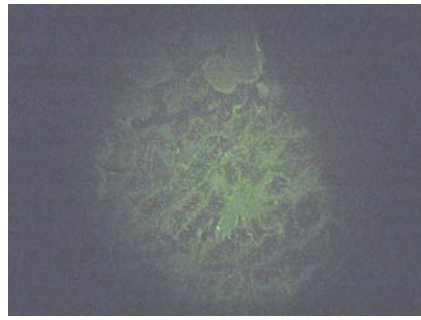
OM2 ELH 17 (100X)



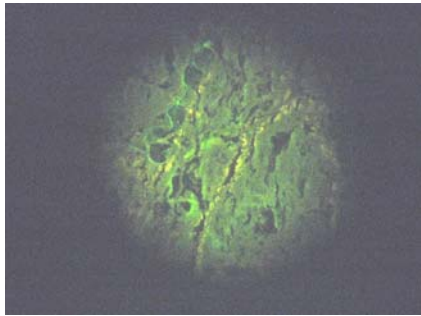
OM3 ELH 1 (20X)



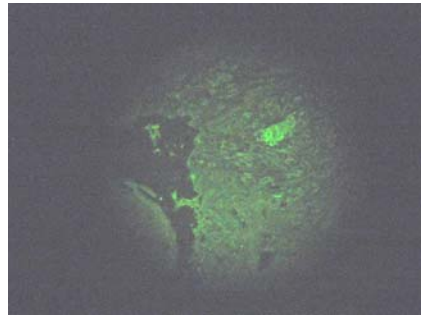
OM3 ELH 2 (100X)



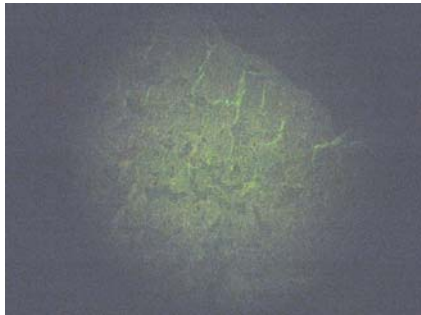
OM3 ELH 3



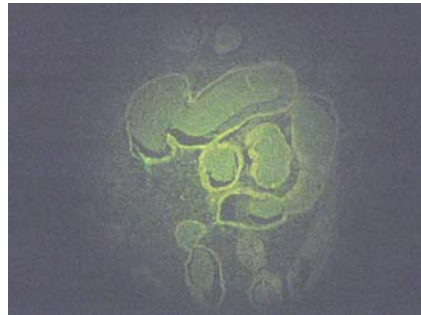
OM3 ELH 5



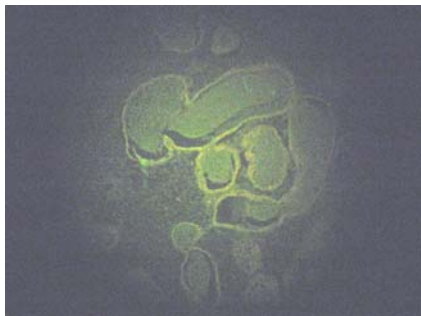
OM3 ELH 7



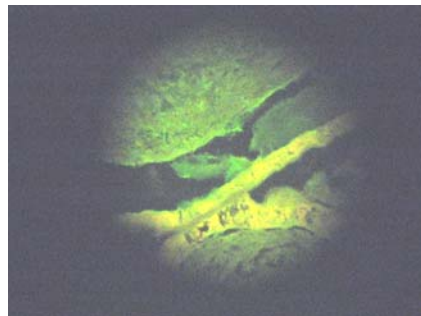
OM3 ELH 10



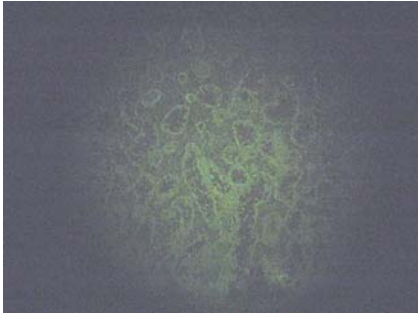
OM4 ELH 1



OM4 ELH 2



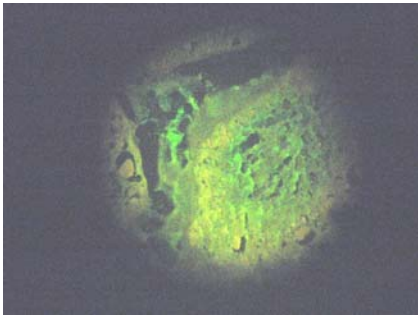
OM4 ELH 3



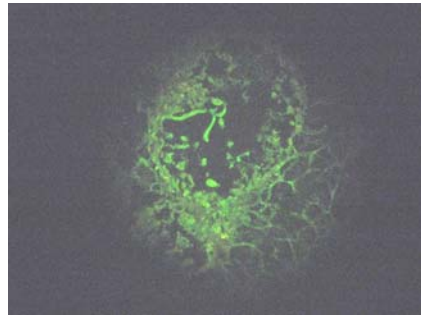
OM4 ELH 6



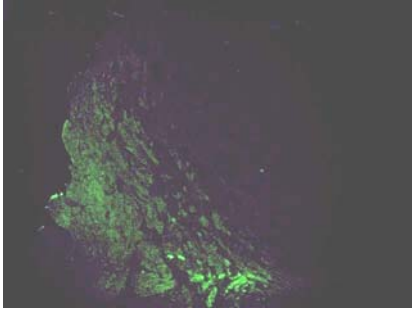
OM4 ELH 14



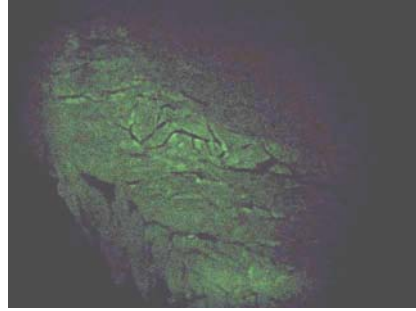
OM4 ELH 15



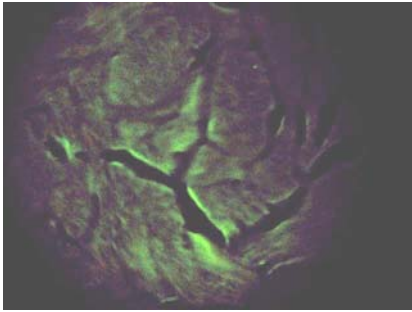
OM4 ELH 17 (20X)



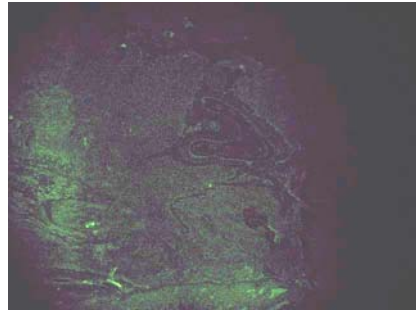
OF1-1 ELH 1



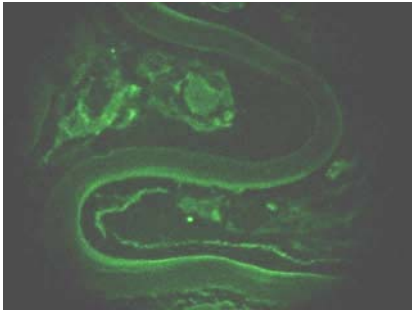
OF1-1 ELH 3



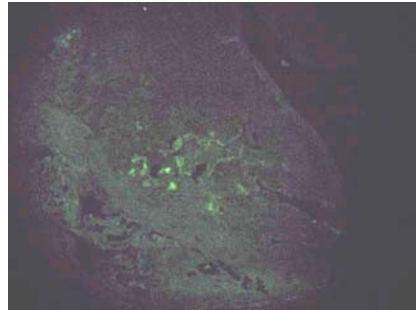
OF1-1 ELH 5 (20X)



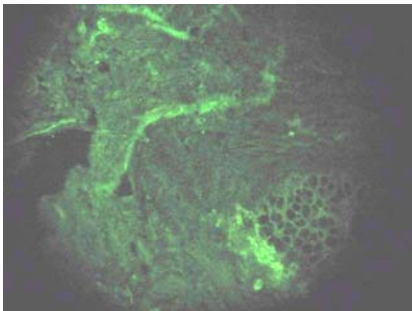
OF1-1 ELH 9



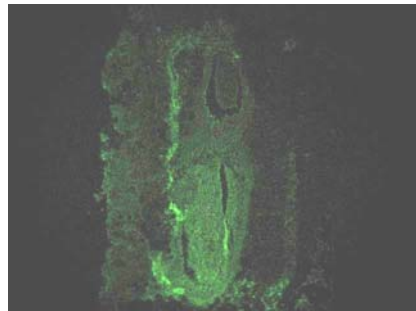
OF1-1 ELH 11 (20X)



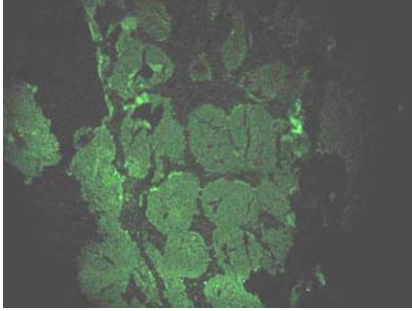
OF1-1 ELH 12



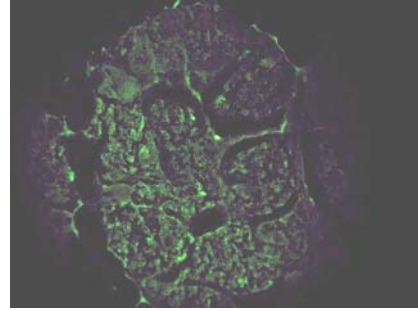
OF1-1 ELH 14



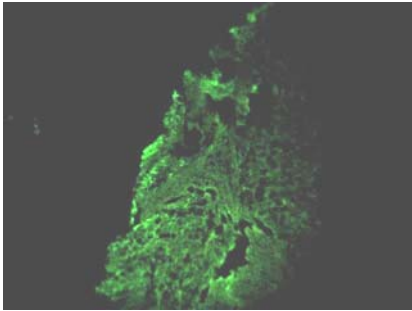
OF1-2 ELH 1



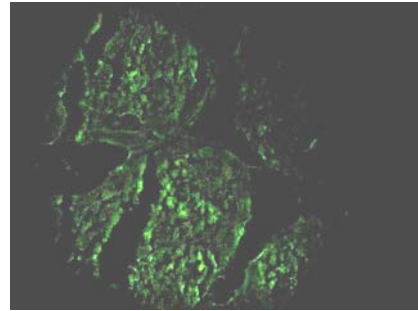
OF1-2 ELH 3



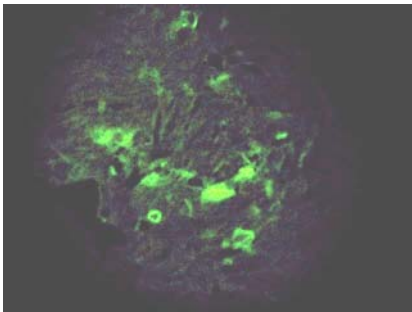
OF1-2 ELH 4



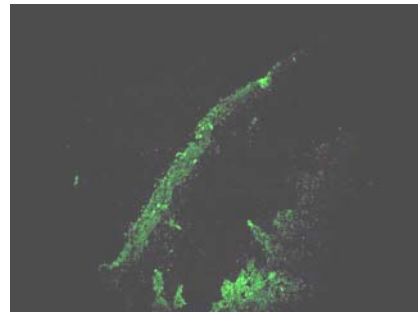
OF1-2 ELH 7



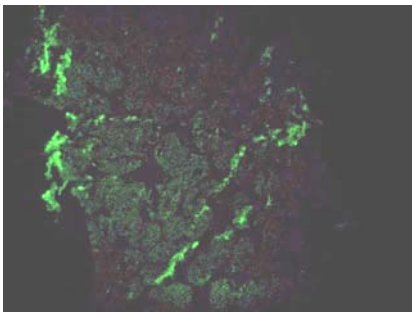
OF2 ELH 3



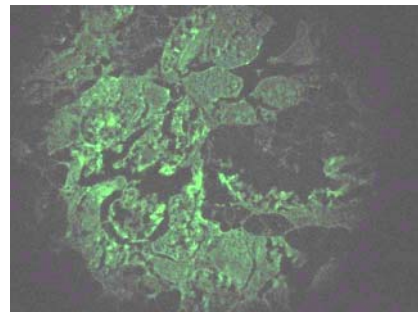
OF2 ELH 6



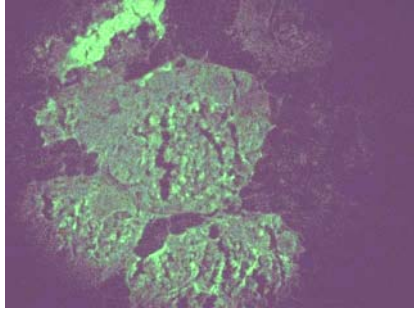
OF2 ELH 7



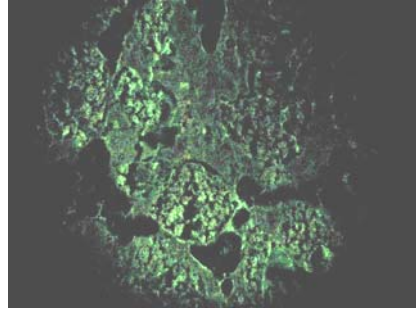
OF2 ELH 10



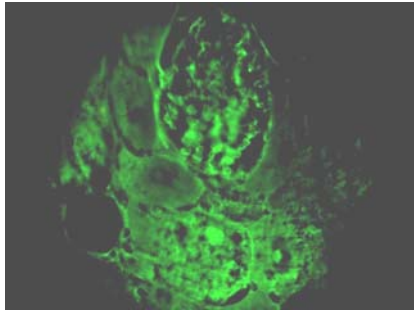
OF2 ELH 12



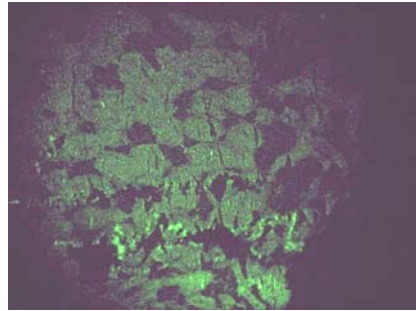
OF2 ELH 13



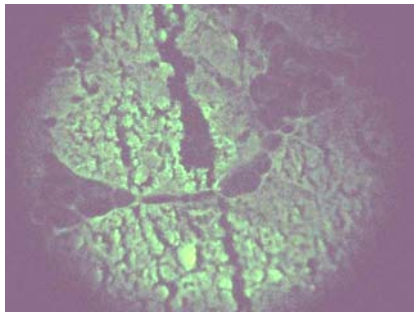
OF2 ELH 16



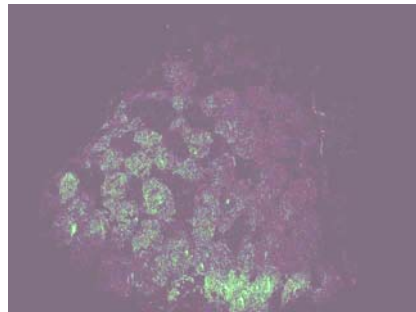
OF2 ELH 17 (100X)



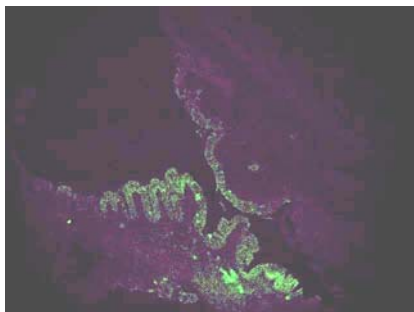
OF3 ELH 2



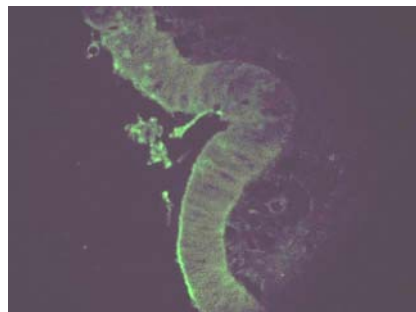
OF3 ELH 3



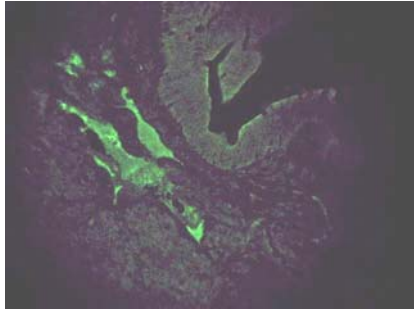
OF3 ELH 4



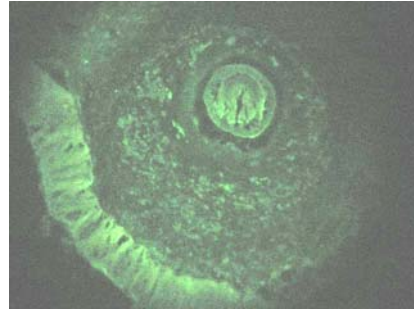
OF3 ELH 36



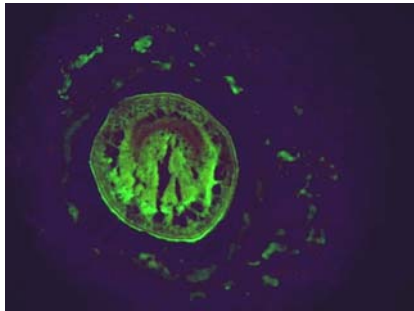
OF3 ELH 7



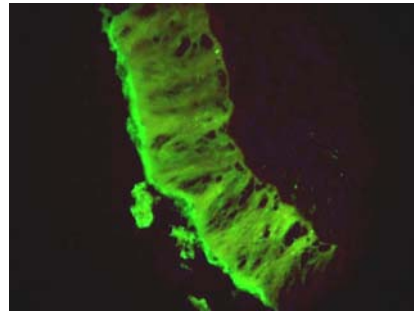
OF3 ELH 9



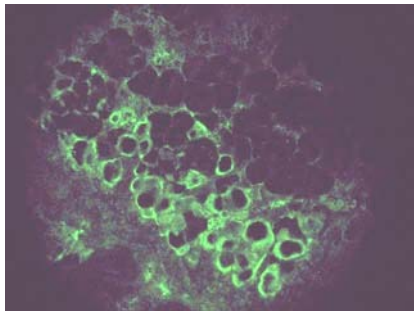
OF3 ELH 12 (20X)



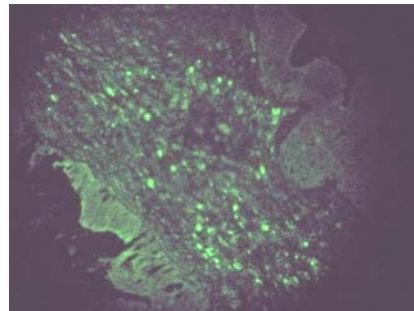
OF3 ELH 13-1 (100X)



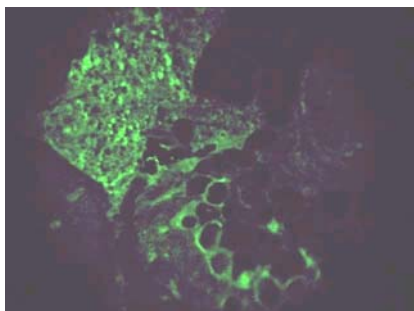
OF3 ELH 13-2 (100X)



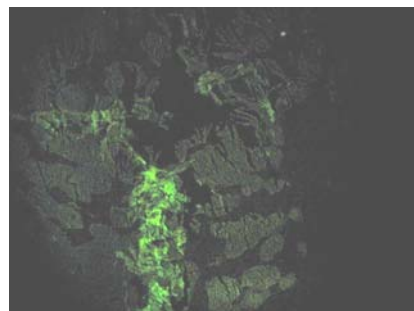
OF3 ELH 15



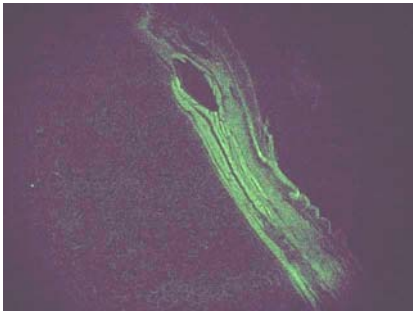
OF3 ELH 16



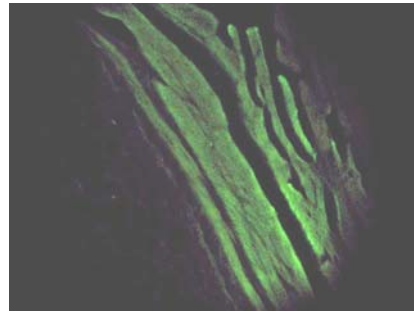
OF3 ELH 22



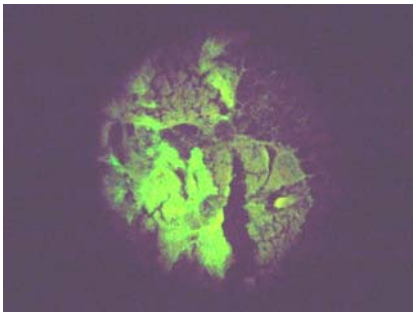
OF4 ELH 3



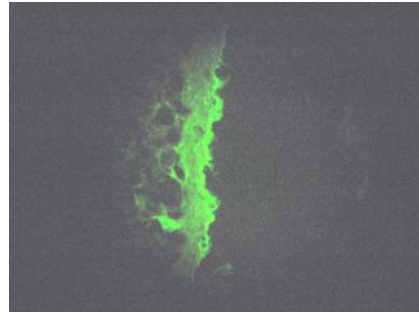
OF4 ELH 4



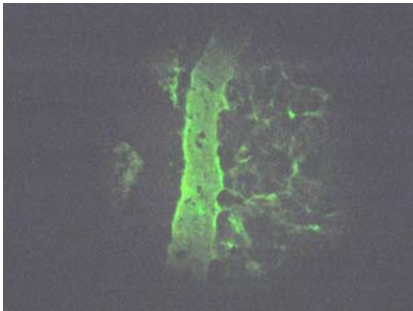
OF4 ELH 6 (20X)



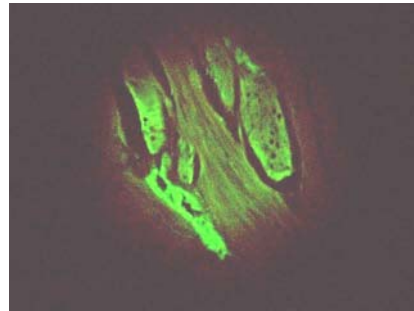
OF4 ELH 12



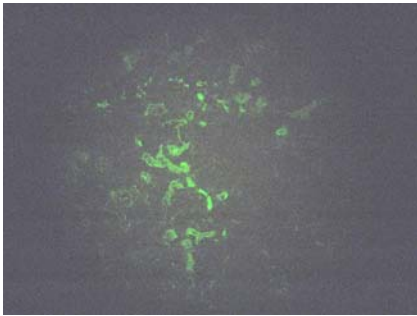
OF4 ELH 16 (20X)



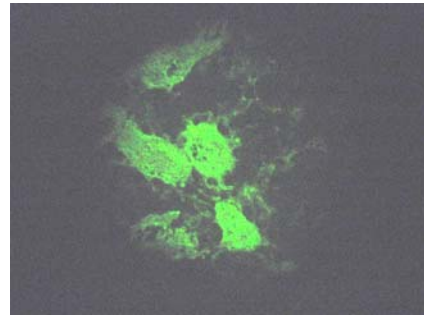
OF4 ELH 17 (20X)



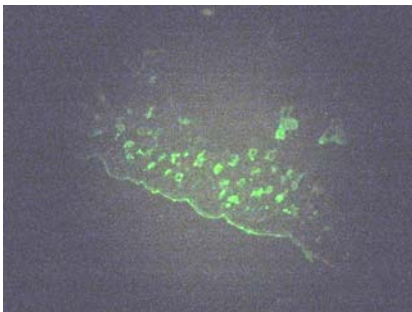
OF4 ELH 21 (100X)



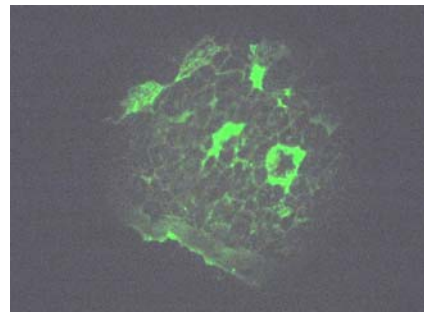
NM1 ELH 1



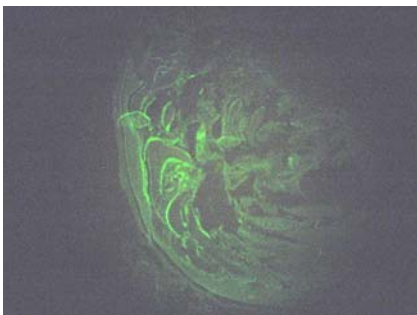
NM1 ELH 3



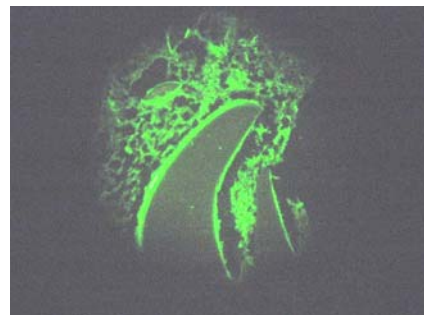
NM1 ELH 5



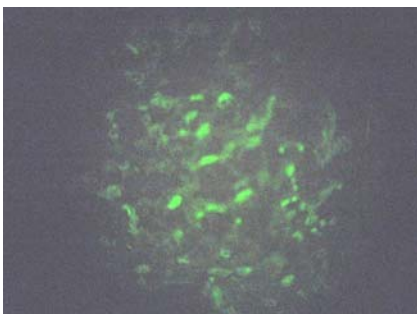
NM1 ELH 7 (20X)



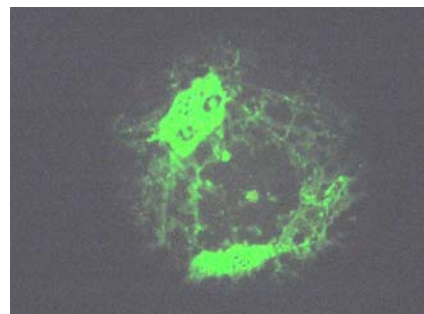
NM1 ELH 14



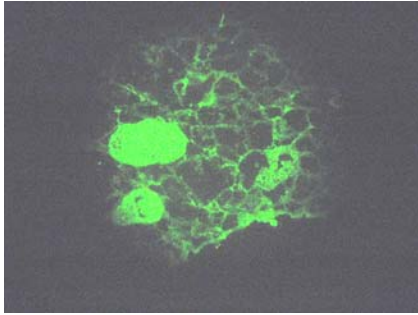
NM1 ELH 15 (20X)



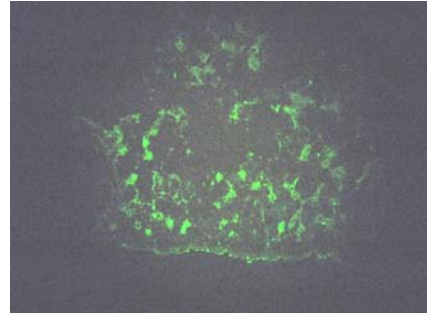
NM1 ELH 19



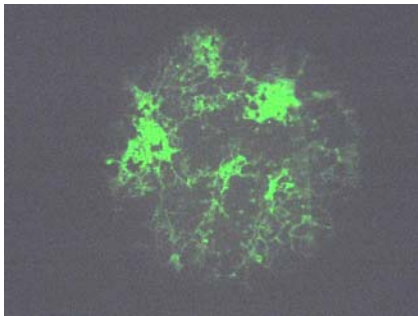
NM1 ELH 21 (20X)



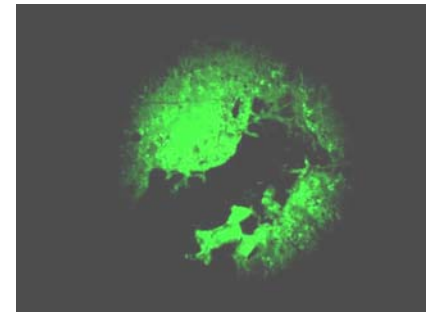
NM1 ELH 22 (20X)



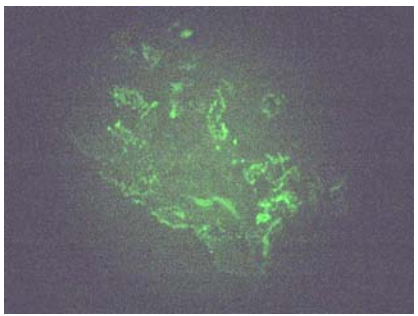
NM1 ELH 27



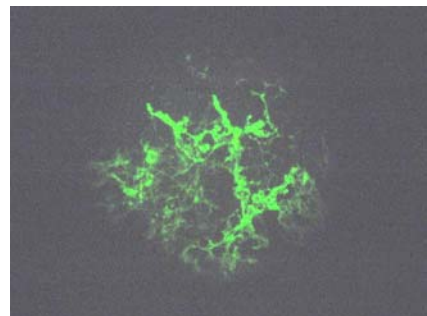
NM1 ELH 28 (20X)



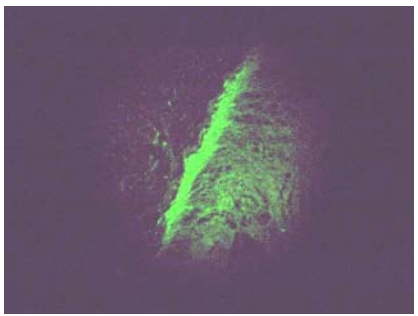
NM1 ELH 31



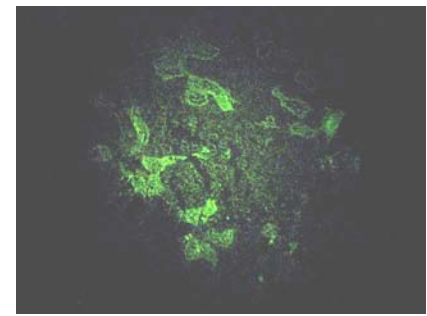
NM2 ELH 2



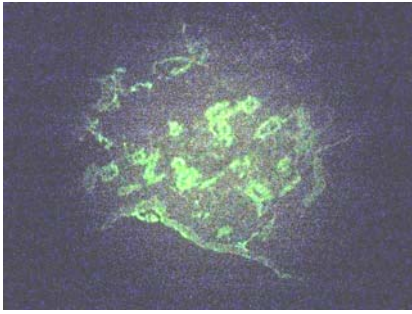
NM2 ELH 3 (20X)



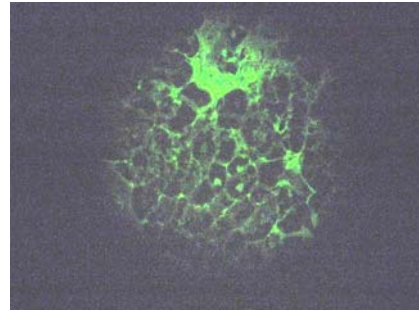
NM2 ELH 6



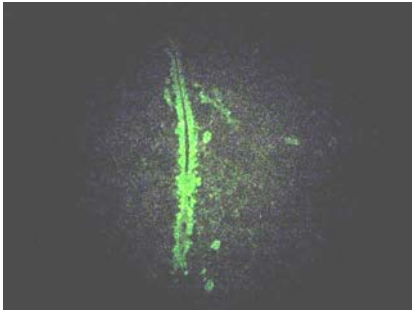
NM2 ELH 8



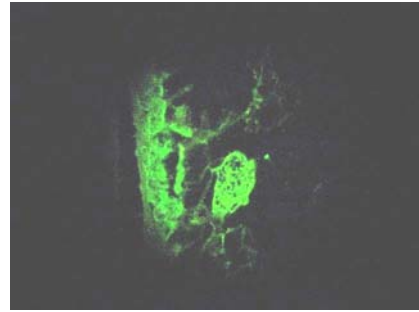
NM2 ELH 11



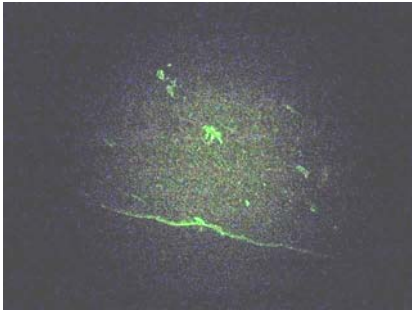
NM2 ELH 13 (20X)



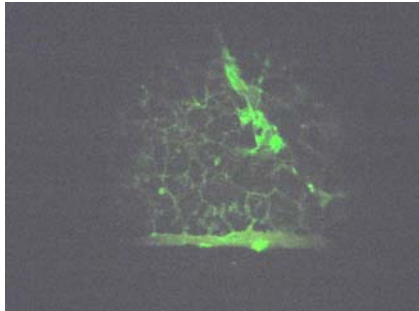
NM3 ELH 1



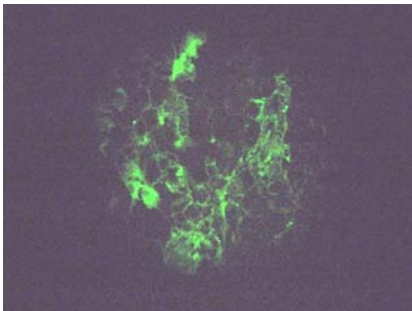
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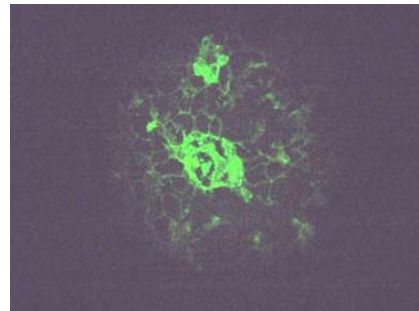
NM3 ELH 5



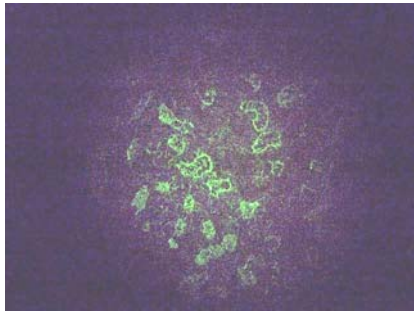
NM3 ELH 6



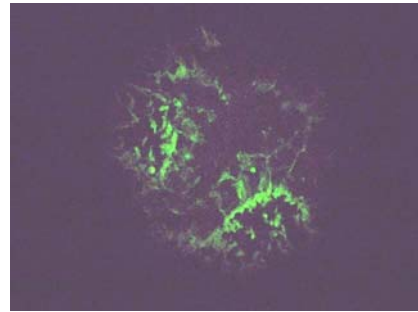
NM3 ELH 9



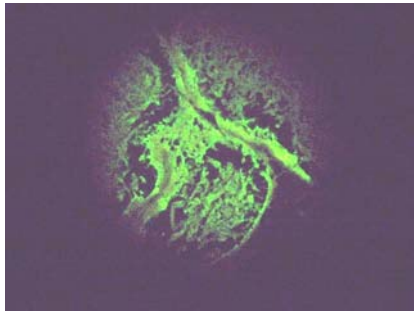
NM3 ELH 10 (20X)



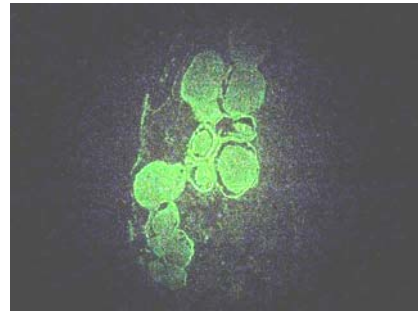
NM4 ELH 2



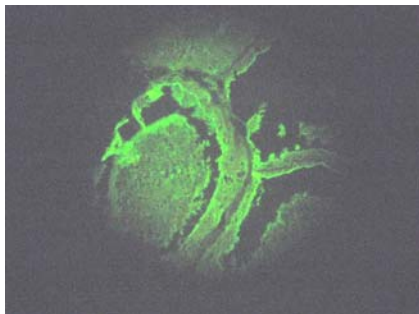
NM4 ELH 4(20X)



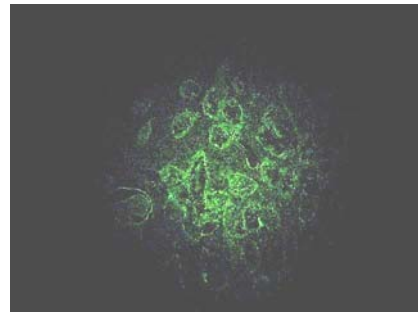
NM4 ELH 11 (20X)



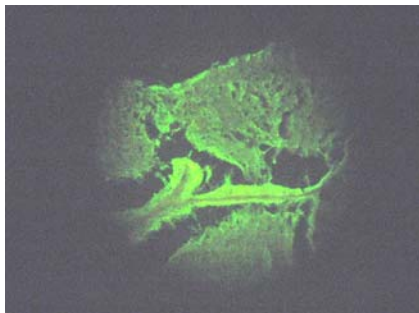
NM5 ELH 2



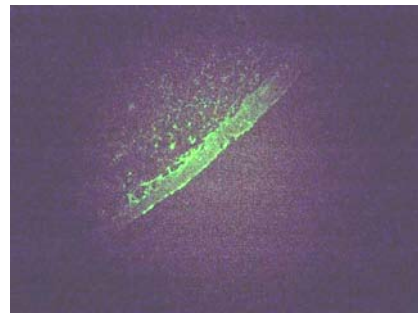
NM5 ELH 3(100X)



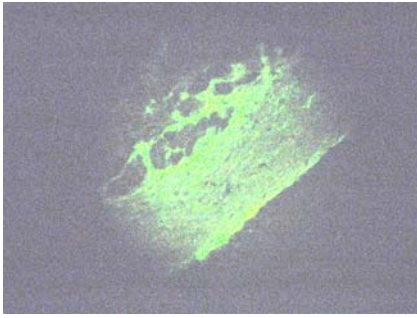
NM5 ELH 5



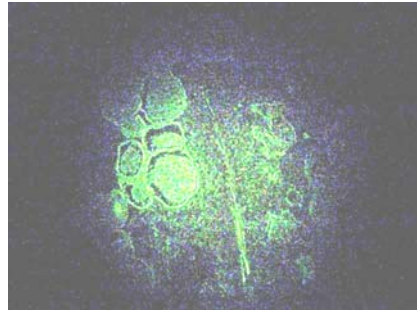
NM5 ELH 7 (20X)



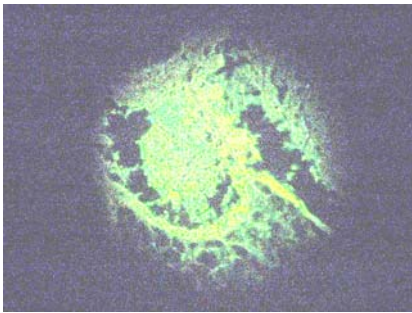
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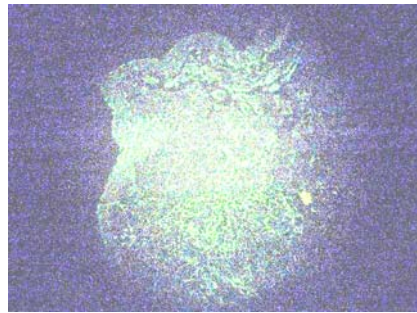
NM5 ELH 10 (20X)



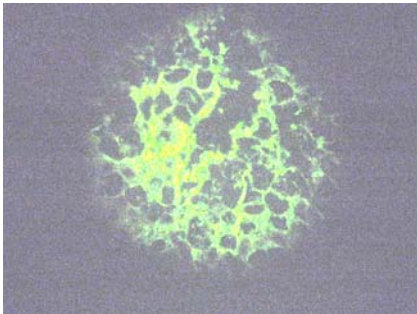
NM5 ELH 12



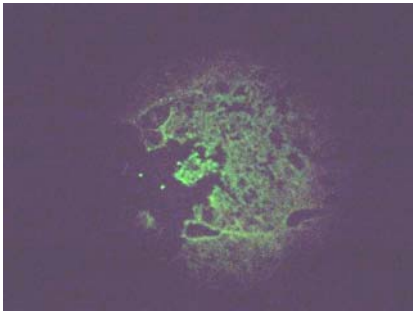
NM5 ELH 13 (20X)



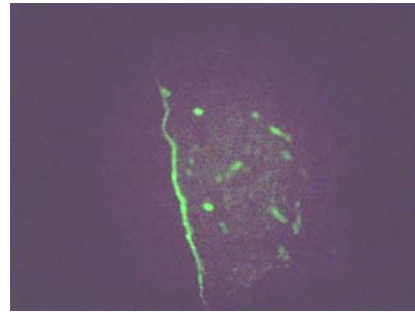
NM5 ELH 14



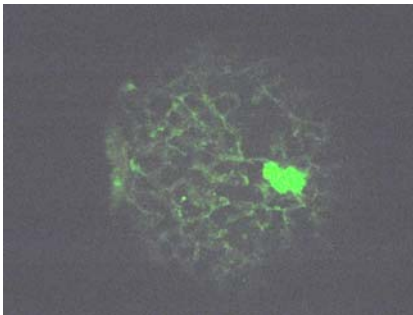
NM5 ELH 15 (20X)



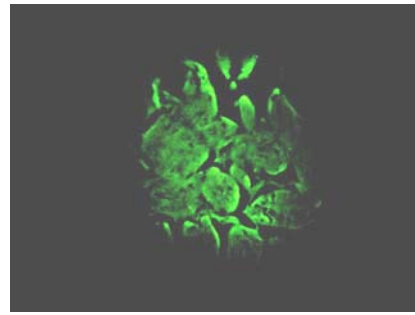
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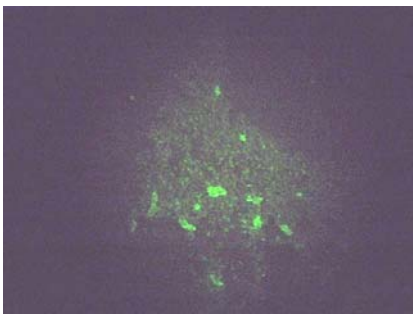
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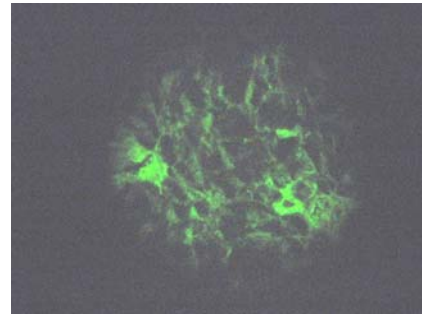
NF1 ELH 6



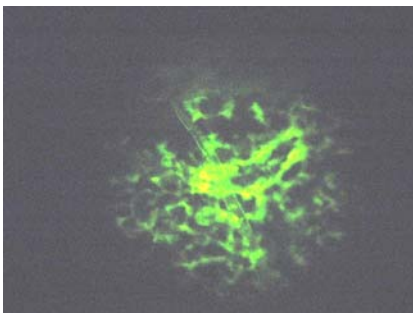
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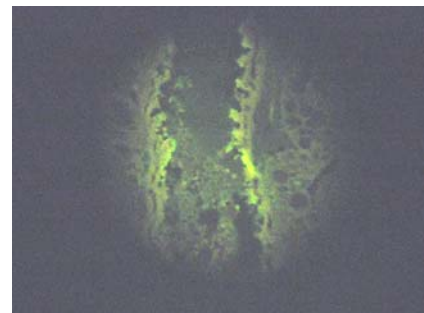
NF1 ELH 10



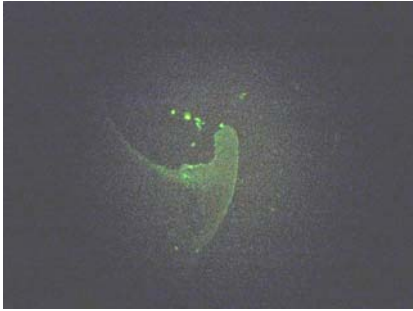
NF1 ELH 11



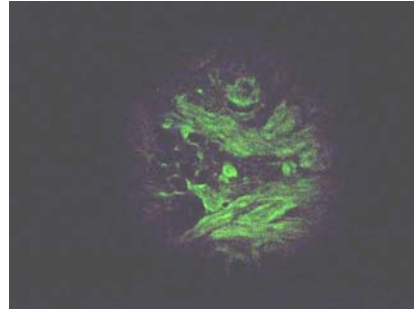
NF1 ELH 12 (20X)



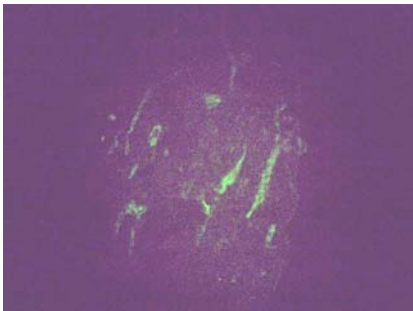
NF2 ELH 2 (20X)



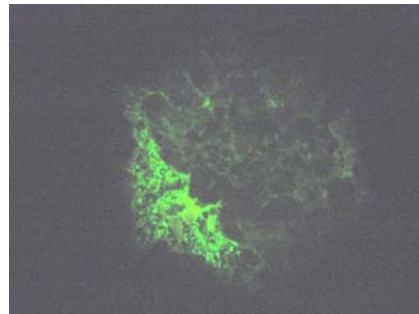
NF3 ELH 1



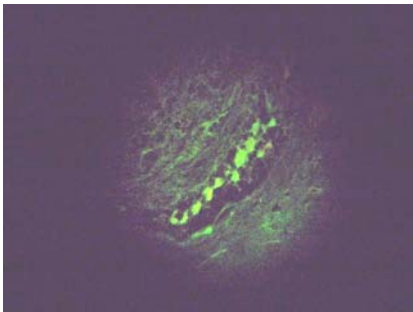
NF3 ELH 5



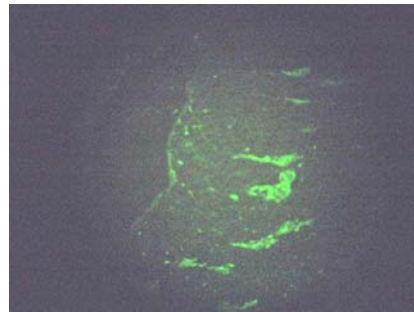
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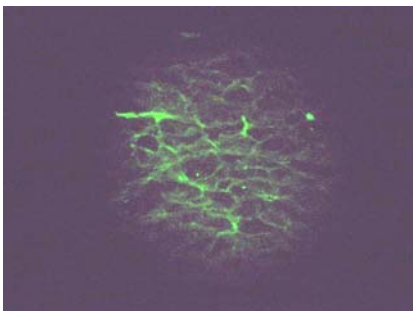
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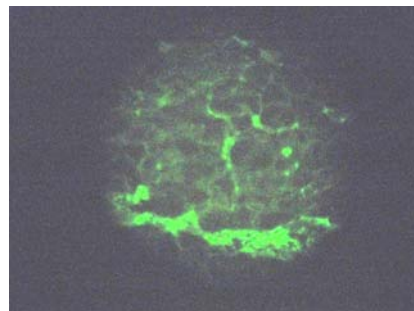
NF3 ELH 10



NF3 ELH 12



NF3 ELH 13



NF3 ELH 14

***Appendix IV – An Annotated Library of Queen Conch
Expressed Sequence Tags***

See Supplemental CD