Supplement

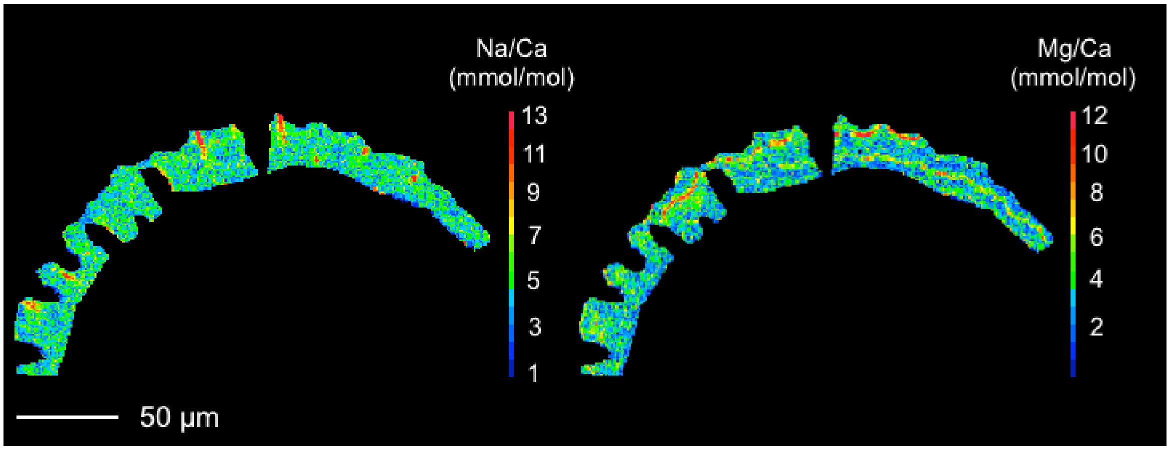


Figure S1. Overview of a cross-section of a *T. sacculifer* shell, measured at the GEOMAR in Kiel (Bertlich et al., 2018). Clearly, Mg is distributed in bands, whereas Na is more concentrated in the spine base regions.

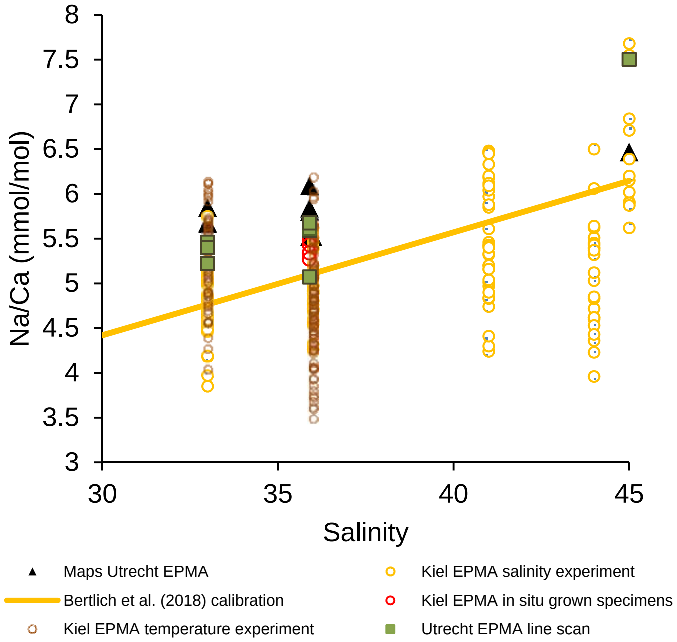


Figure S2. Comparison between Na/Ca map-values for the same embedded *T. sacculifer* specimens measured with EPMA in Kiel (Bertlich et al., 2018), and line-scan and map values measured in Utrecht.

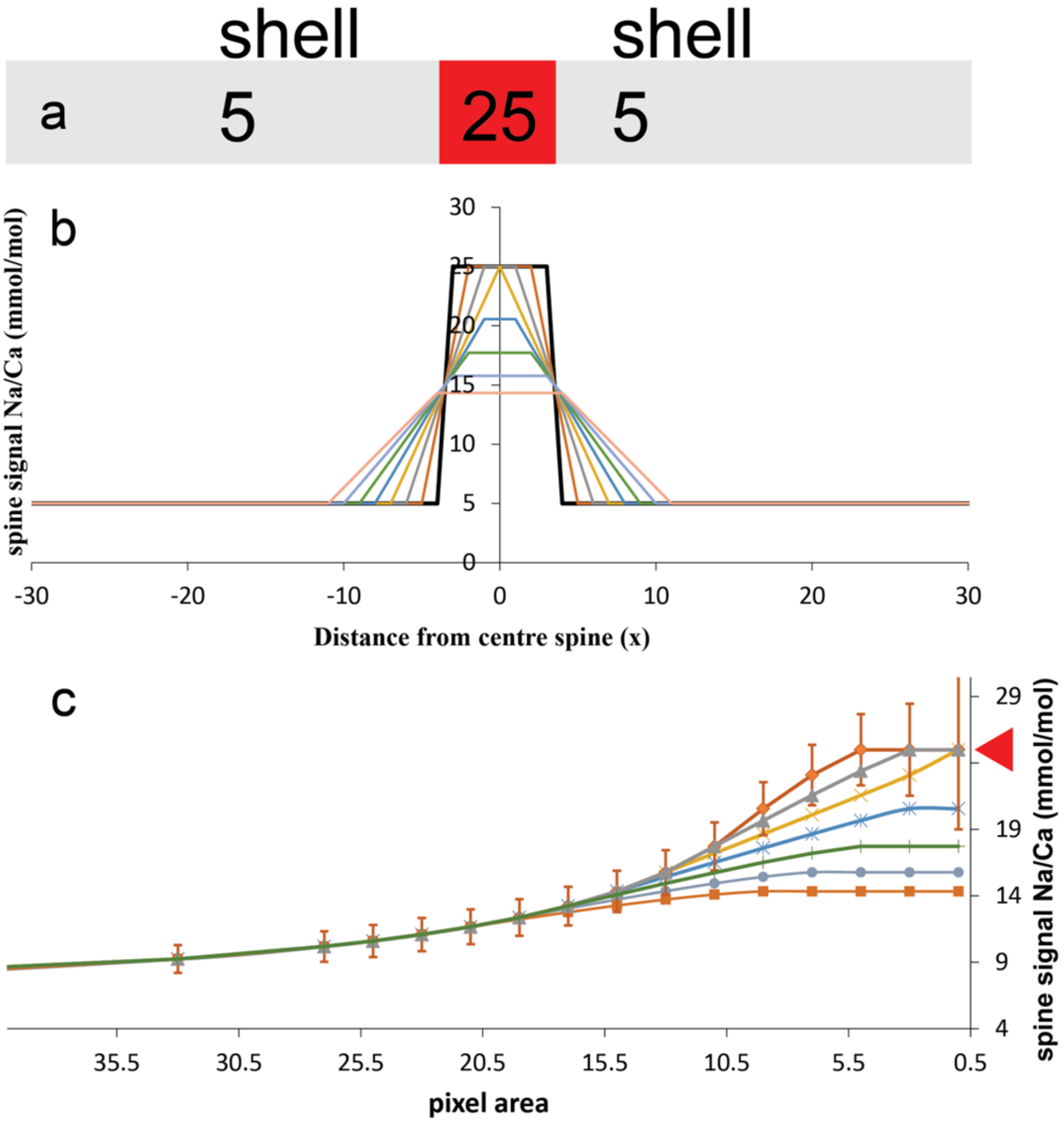


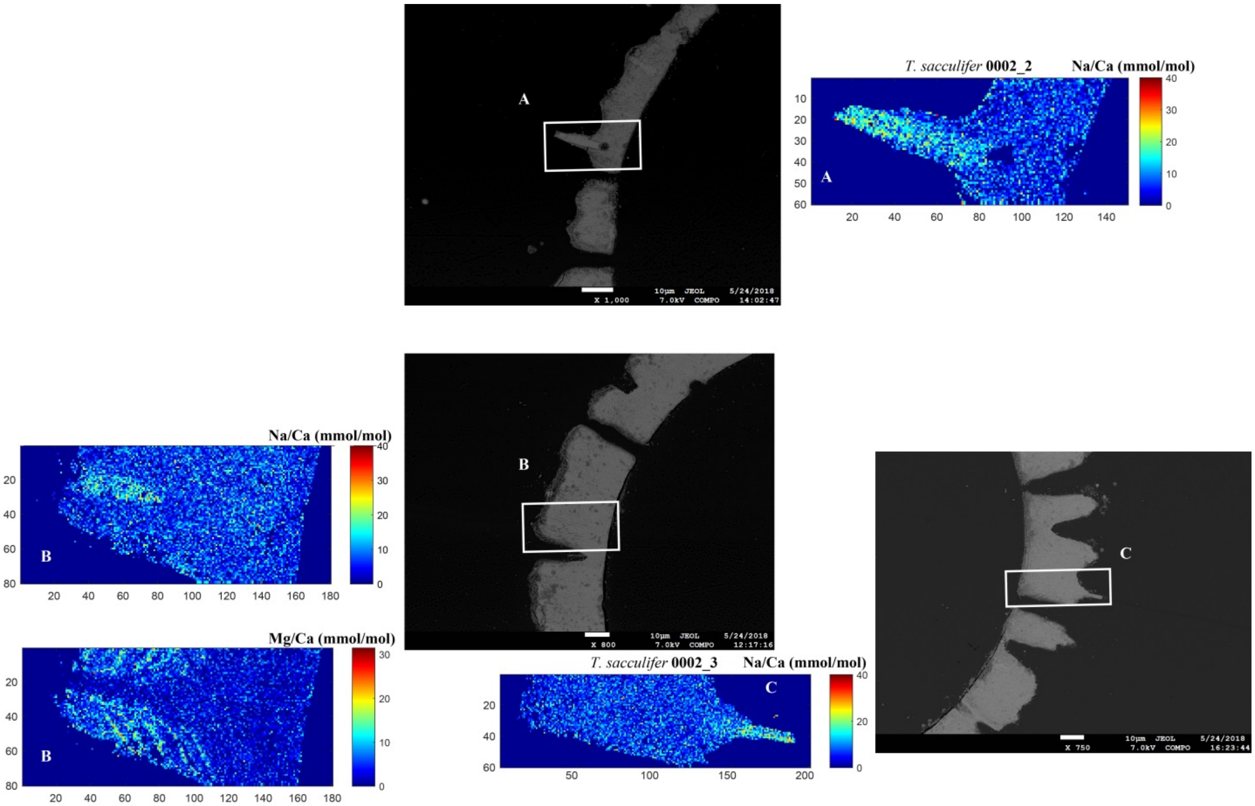
Figure S3. Spine base quantification model, showing: a) a schematic representation of a spinose planktonic foraminiferal shell cross section, including Na/Ca values of a spine (in red: 25 mmol/mol) sandwiched by two layers (in grey: 5 mmol/mol) of calcite with lower Na/Ca; b) the effect of differences in sampling volume on Na/Ca values measured (the 'EPMA-image'), obtained for hypothetical cross section 'a)'. Clearly, when increasing the sampling volume with a step-size of one at the time, the original signal can only be preserved at the center of the spine. However, when the sampling width is too large, the original spine base Na/Ca signal is no longer preserved (Y-axis). The different colors represent different sampling widths and the resulting Na/Ca values measured on the Y-axis, c) the effort to obtain the original spine base (red triangle) value by narrowing the surface area around the center of the spine base in a spine base map, with the same colors indicating the same scenarios described in 'b)'.

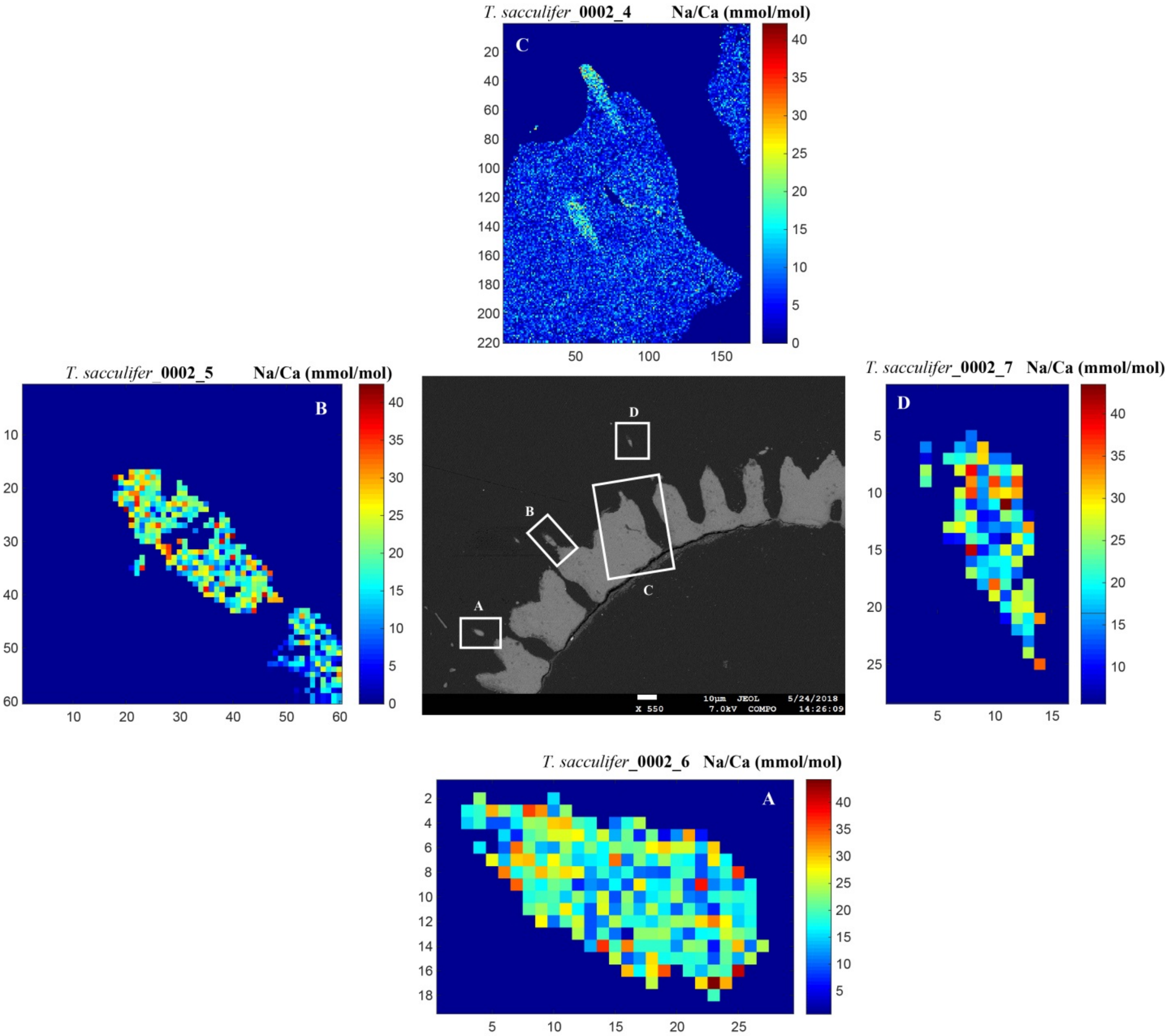
Part 1: Multi-net specimens

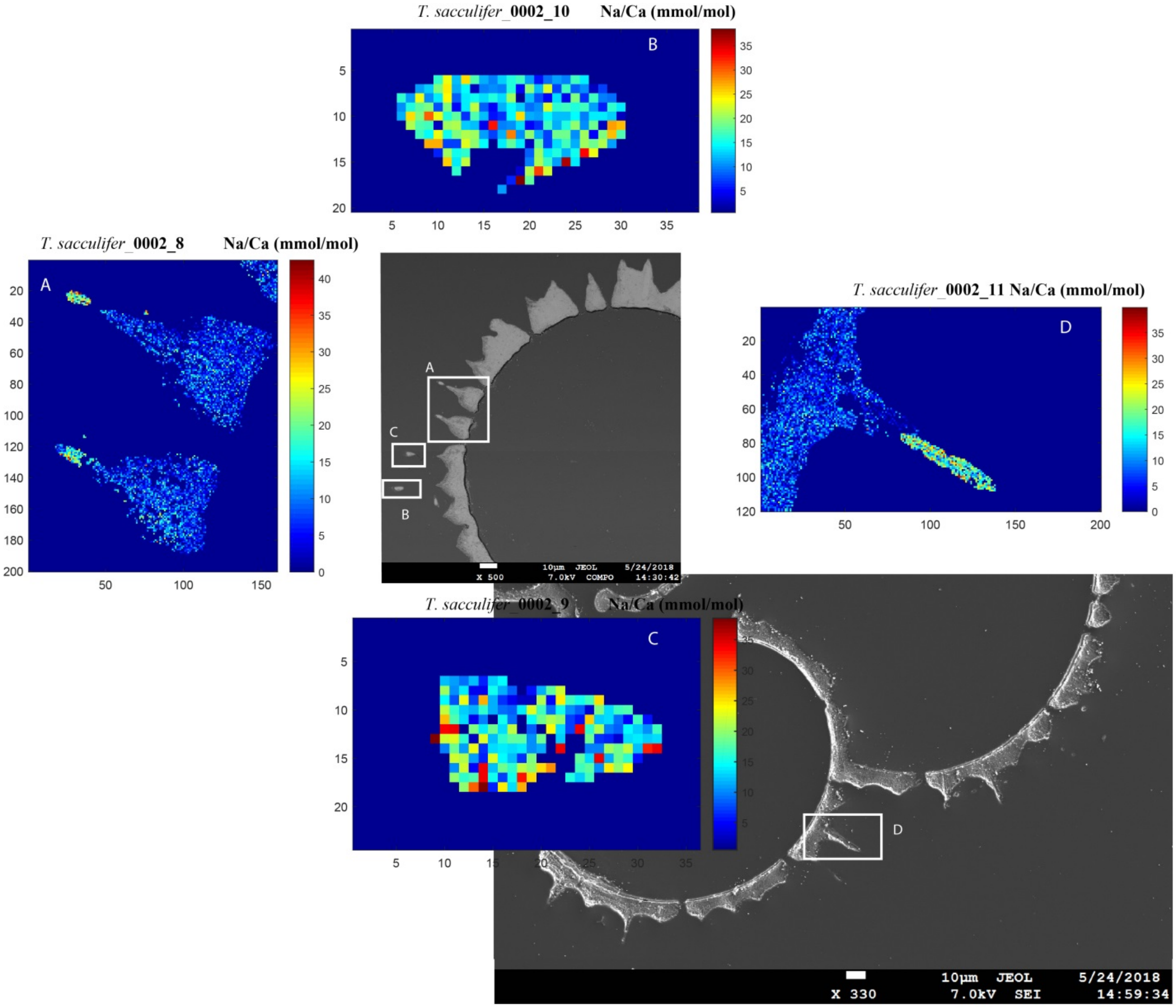
Part 2: Core-tops and plankton pump specimens (Mezger et al., 2018)

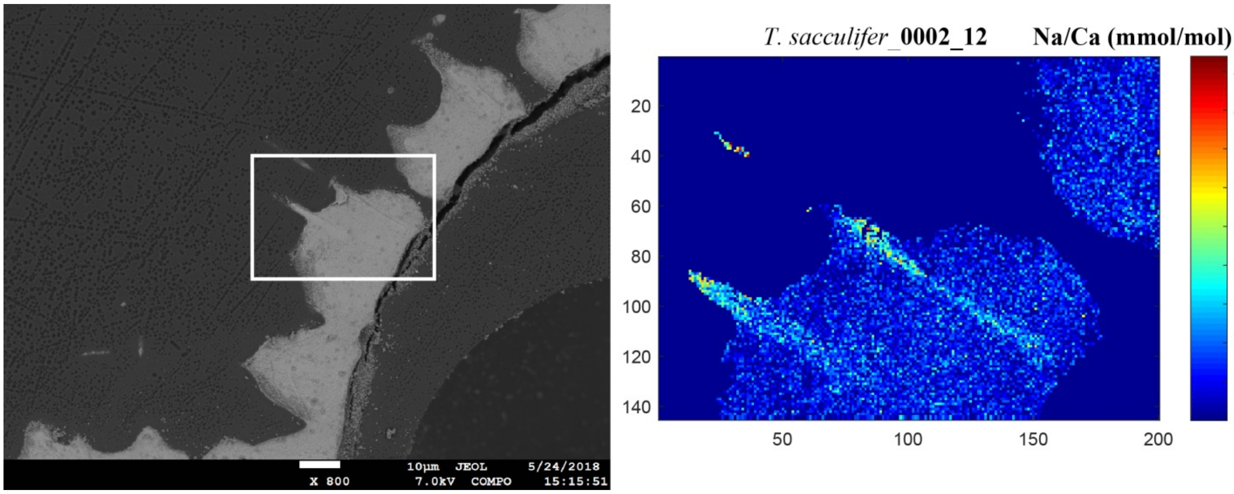
Part 3: Cultured *T. sacculifer* (Bertlich et al., 2018;Bijma et al., 1990)

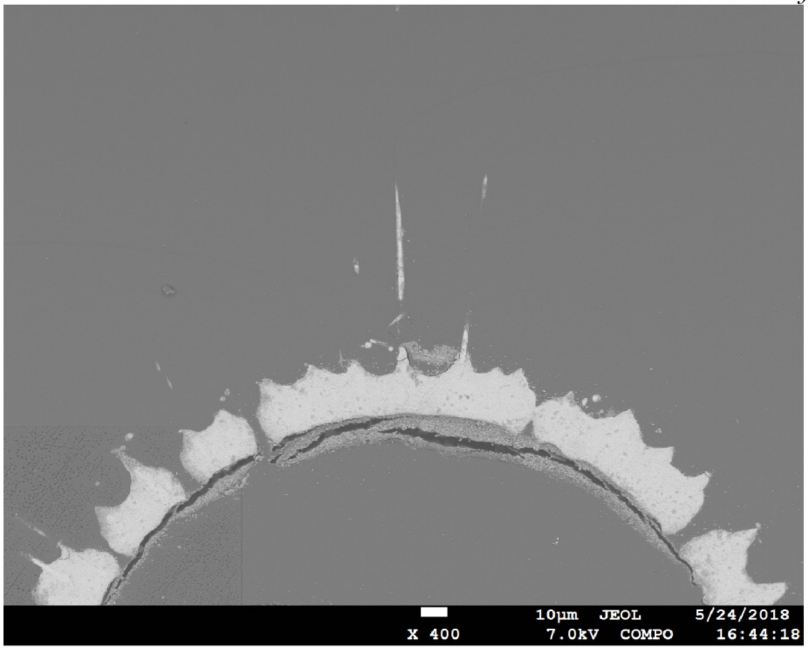
Part 1: Multi-net specimens

A
10µm JEOL 5/24/2018
X 1,000 7.0kV COMPO 14:02:47
T. sacculifer 0002_2
Na/Ca (mmol/mol)
A
B
10µm JEOL 5/24/2018
X 800 7.0kV COMPO 12:17:16
Na/Ca (mmol/mol)
B
Mg/Ca (mmol/mol)
B
T. sacculifer 0002_3
Na/Ca (mmol/mol)
C
C
10µm JEOL 5/24/2018
X 750 7.0kV COMPO 16:23:44

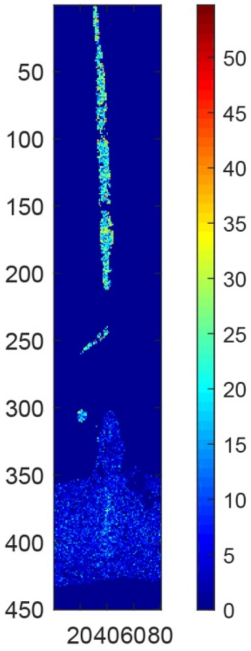

T. sacculifer_0002_4 Na/Ca (mmol/mol)
C
20
40
60
80
100
120
140
160
180
200
220
50
100
150
40
35
30
25
20
15
10
5
0
T. sacculifer_0002_5 Na/Ca (mmol/mol)
B
10
20
30
40
50
60
10
20
30
40
50
60
40
35
30
25
20
15
10
5
0
D
B
C
A
10µm JEOL 5/24/2018
X 550 7.0kV COMPO 14:26:09
T. sacculifer_0002_7 Na/Ca (mmol/mol)
D
5
10
15
20
25
5
10
15
40
35
30
25
20
15
10
T. sacculifer_0002_6 Na/Ca (mmol/mol)
A
2
4
6
8
10
12
14
16
18
5
10
15
20
25
40
35
30
25
20
15
10
5


T. sacculifer_0002_10 Na/Ca (mmol/mol)
B
T. sacculifer_0002_8 Na/Ca (mmol/mol)
A
T. sacculifer_0002_11 Na/Ca (mmol/mol)
D
T. sacculifer_0002_9 Na/Ca (mmol/mol)
C
A
B
C
D
10µm JEOL 5/24/2018
X 500 7.0kV COMPO 14:30:42
10µm JEOL 5/24/2018
X 330 7.0kV SEI 14:59:34

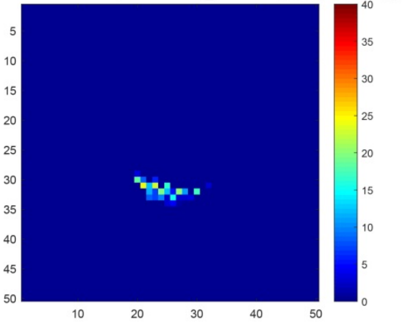

T. sacculifer_0002_12 Na/Ca (mmol/mol)
10µm JEOL 5/24/2018
X 800 7.0kV COMPO 15:15:51

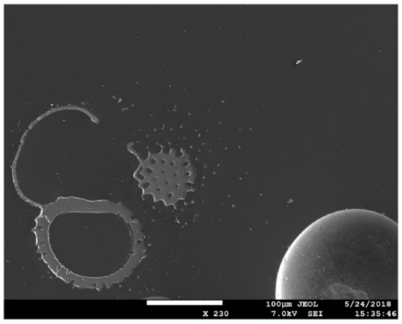


T. sacculifer **0002_13** **Na/Ca (mmol/mol)**

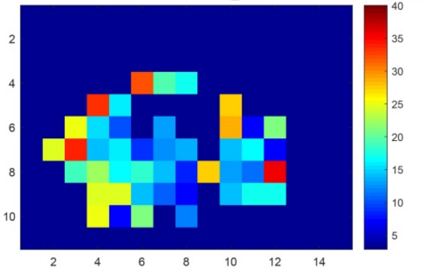


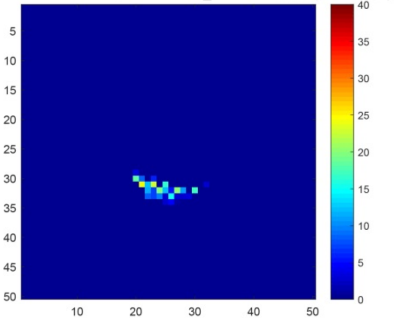
G. ruber **0004_1** **Na/Ca (mmol/mol)**



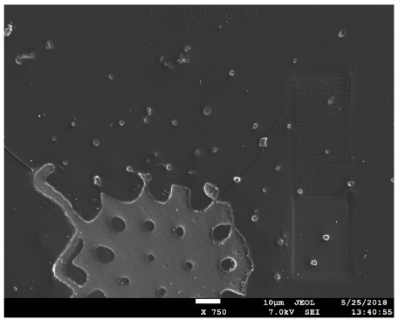


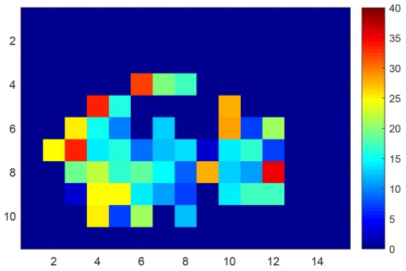
G. ruber **0002_14** **Na/Ca (mmol/mol)**



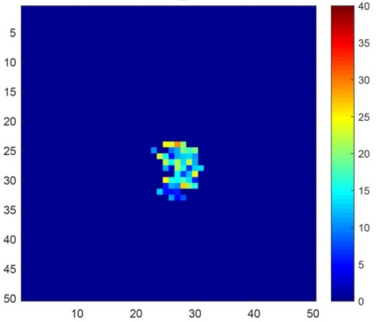


G. ruber **0004_1** **Na/Ca (mmol/mol)**

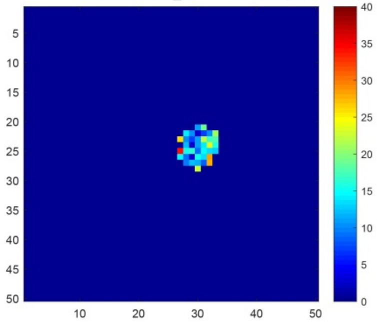




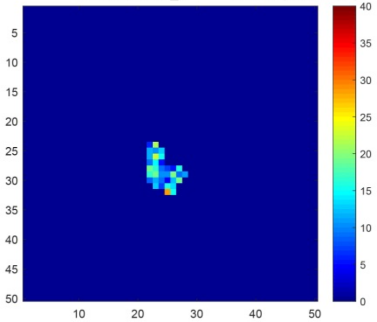
G. ruber **0002_14** **Na/Ca (mmol/mol)**



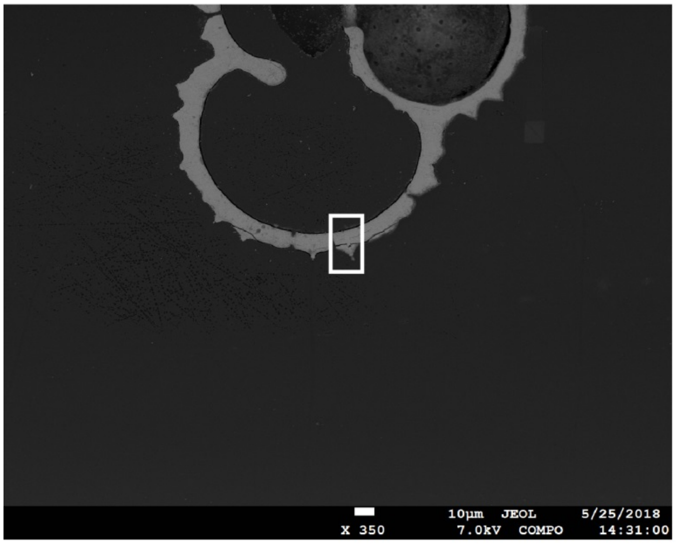
G. ruber **0004_4** **Na/Ca (mmol/mol)**

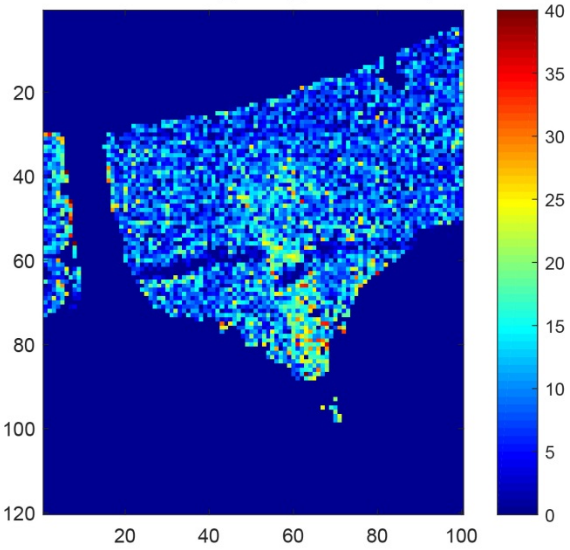


G. ruber **0004_5** **Na/Ca (mmol/mol)**

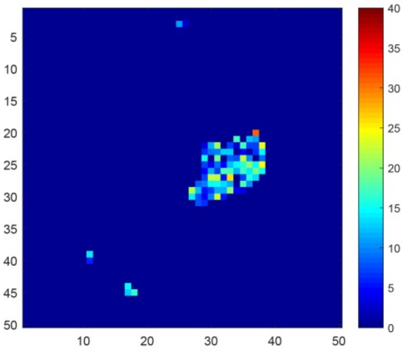


G. ruber **0004_6** **Na/Ca (mmol/mol)**

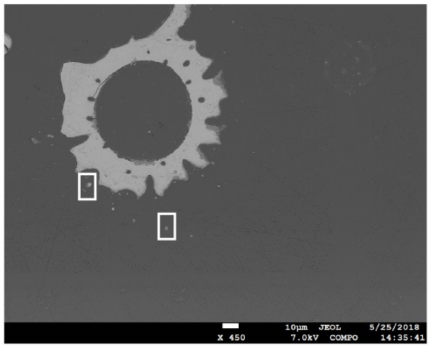


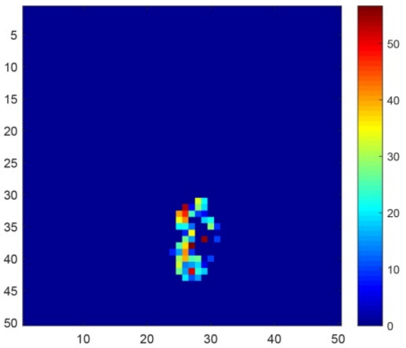


*G. ruber*_**0004_7** **Na/Ca (mmol/mol)**



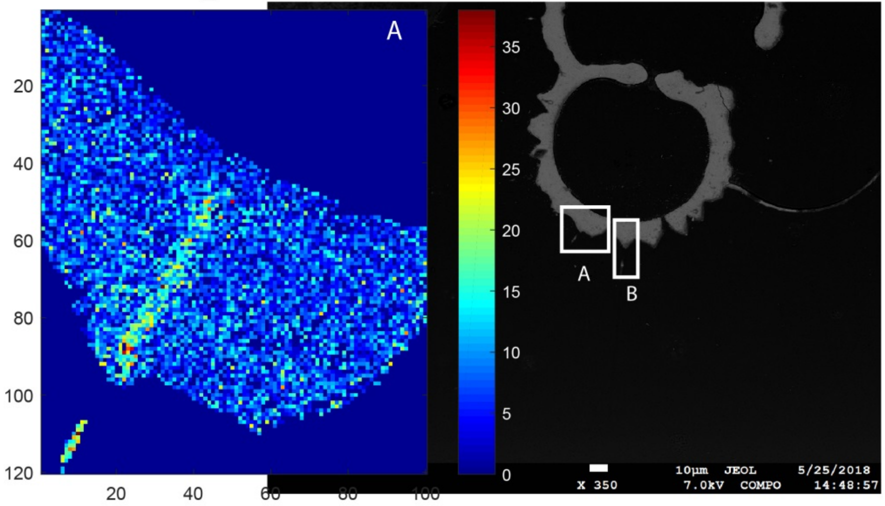
*G. ruber*_**0004_10** **Na/Ca (mmol/mol)**



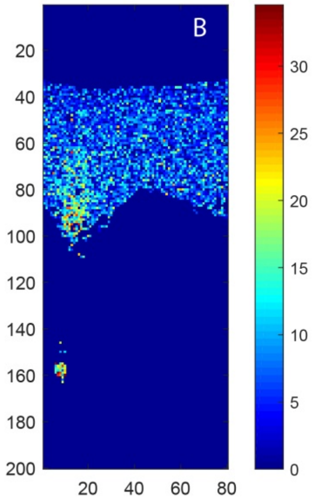


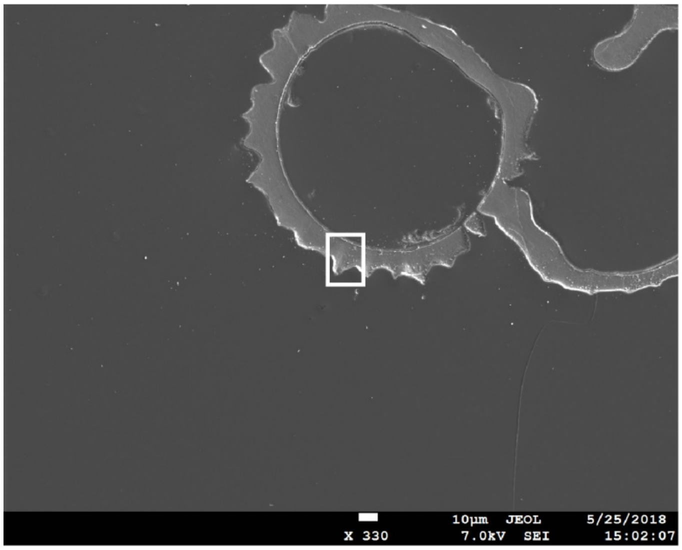
*G. ruber*_**0004_11** **Na/Ca (mmol/mol)**

*G. ruber*_**0004_12 Na/Ca (mmol/mol)**

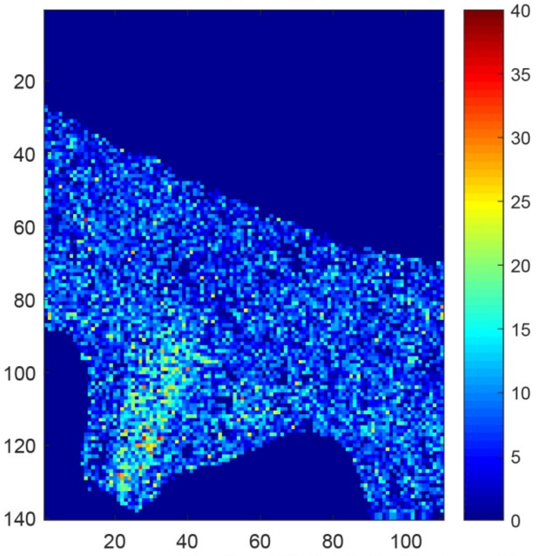


*G. ruber*_**0004_13 Na/Ca (mmol/mol)**

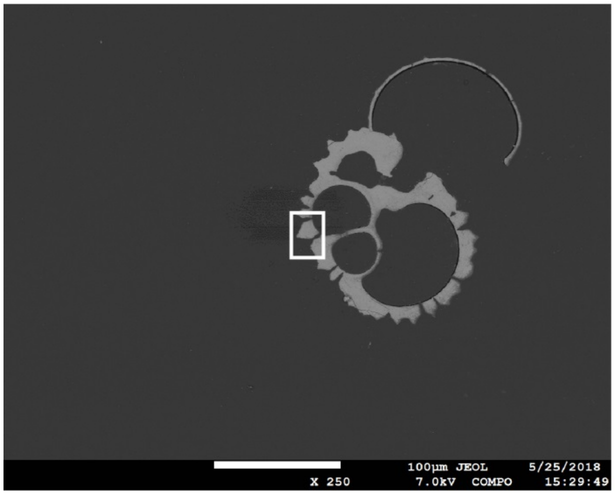


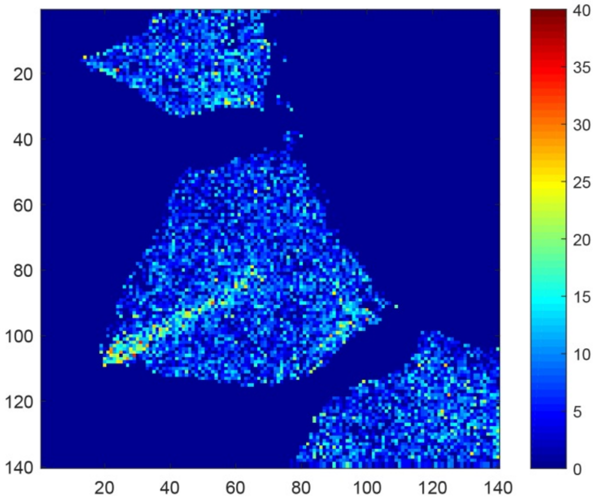


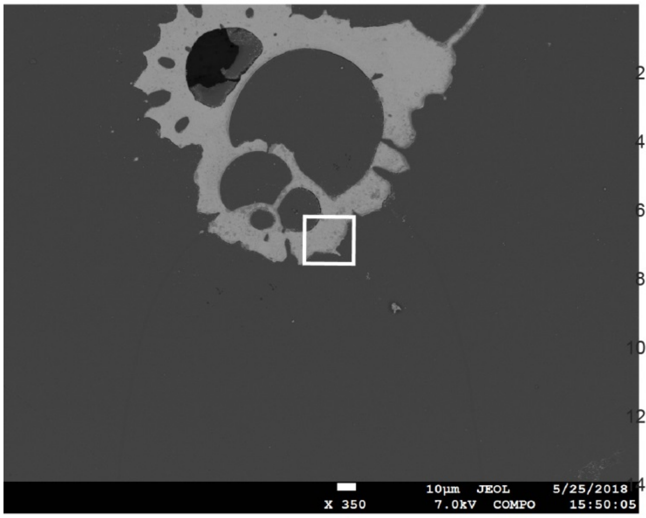
*G. ruber*_**0004_14 Na/Ca (mmol/mol)**



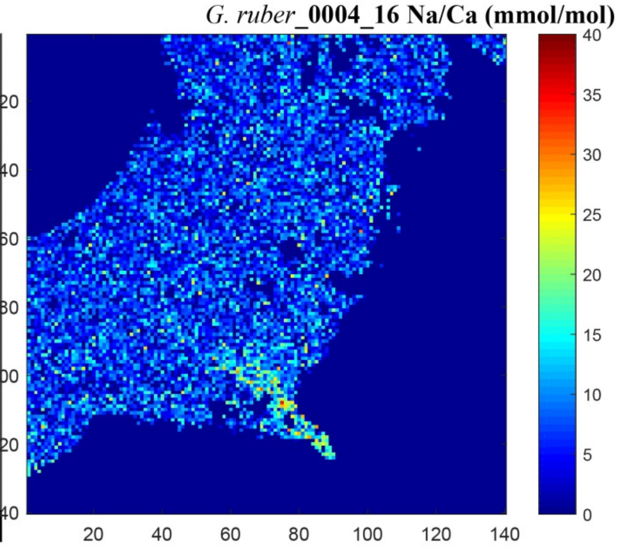
*G. ruber*_**0004_15 Na/Ca (mmol/mol)**



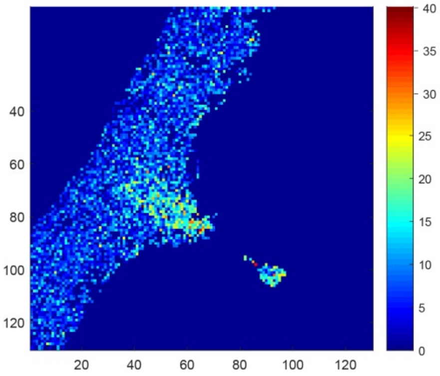




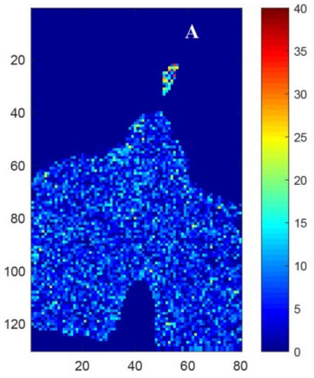
*G. ruber*_**0004_16 Na/Ca (mmol/mol)**



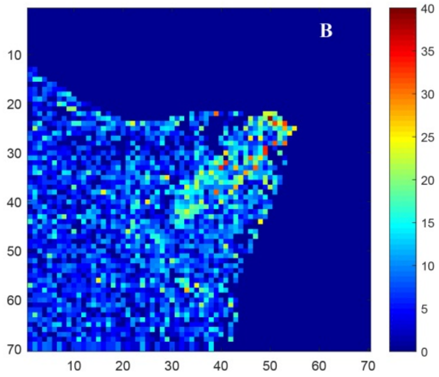
*G. ruber*_**0004_17 Na/Ca (mmol/mol)**



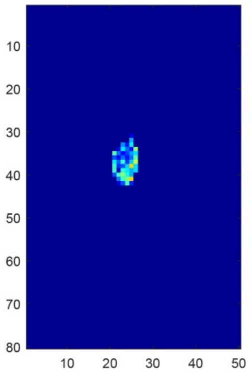
*G. ruber*_**0004_18 Na/Ca (mmol/mol)**

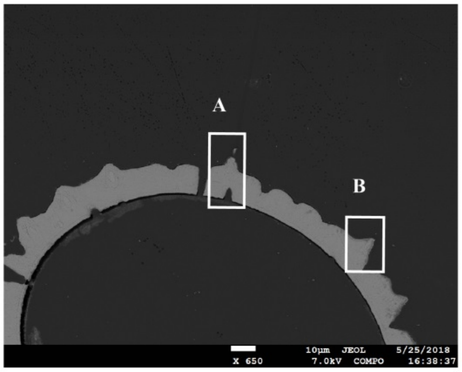


*G. ruber*_**0004_19 Na/Ca (mmol/mol)**

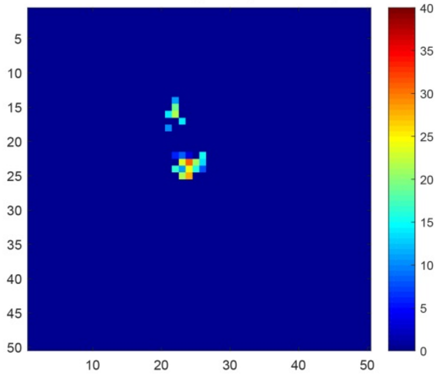


*G. ruber*_**0004_20 Na/Ca (mmol/mol)**

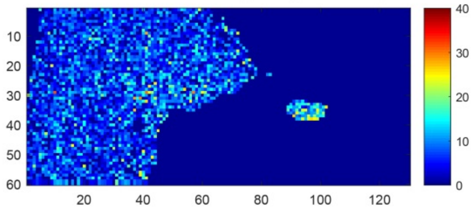


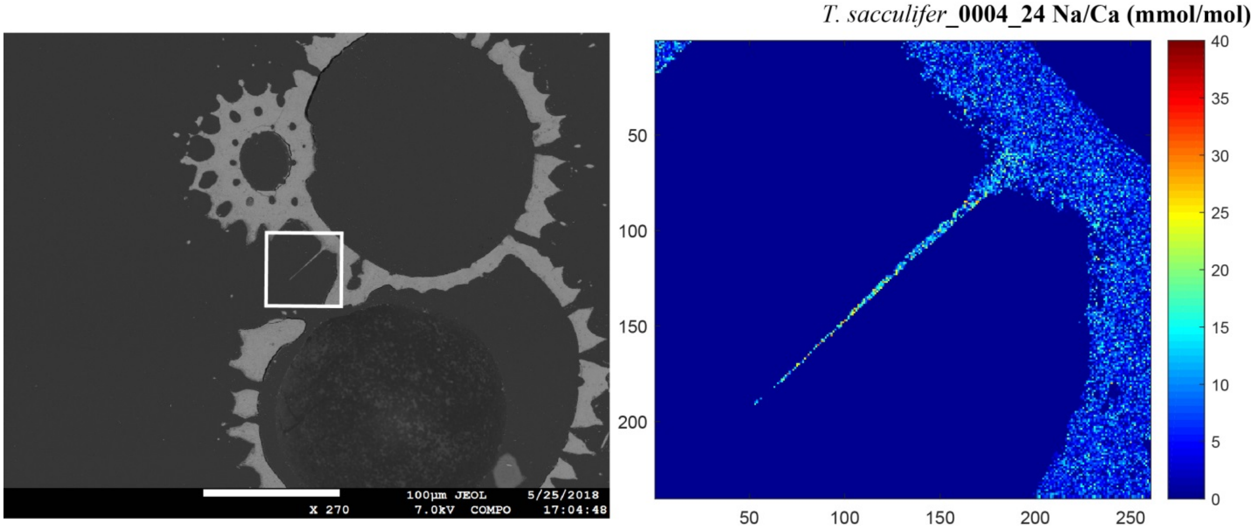


*G. ruber*_**0004_21 Na/Ca (mmol/mol)**



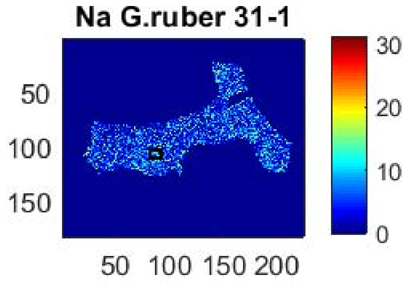
*G. ruber*_**0004_22 Na/Ca (mmol/mol)**

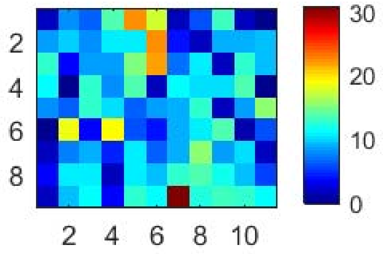


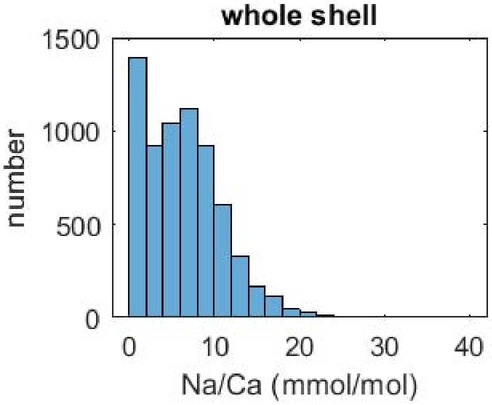


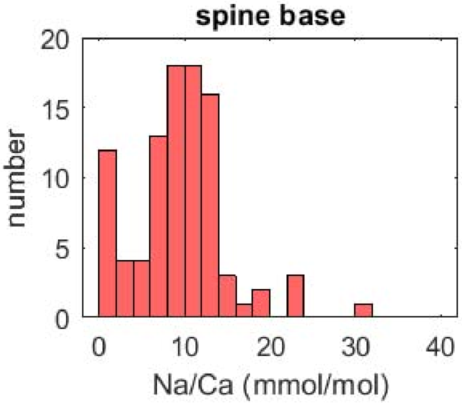
*T. sacculifer*_**0004_24 Na/Ca (mmol/mol)**

Part 2: Plankton pumps and core-tops

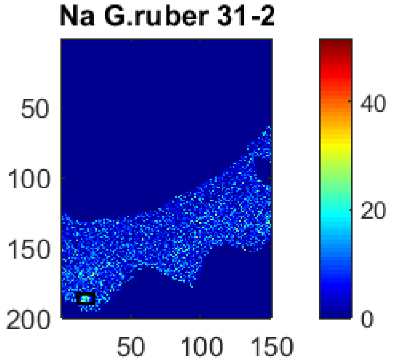


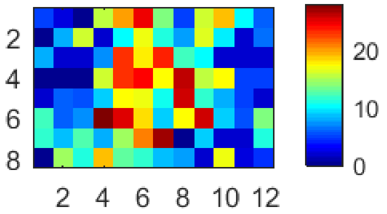


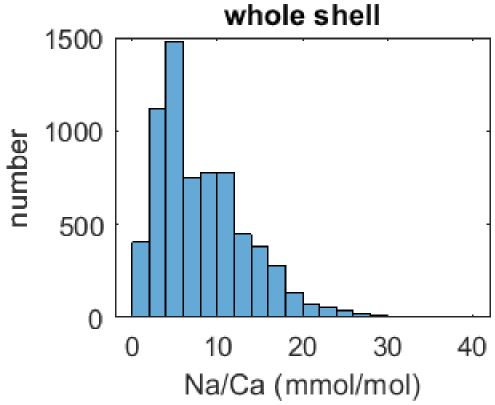


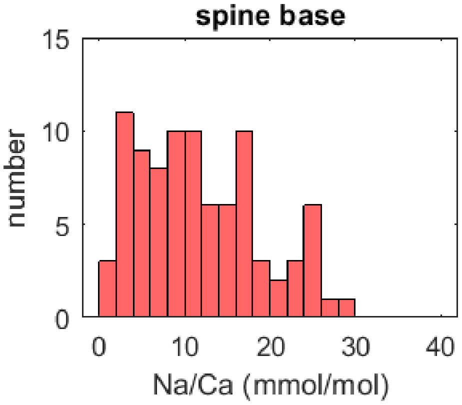


31_1	min	max	mean	median	SD	SE
shell	1.24	30.19	6.31	5.79	4.13	0.05
spine base	1.35	29.77	9.23	8.89	5.10	0.52

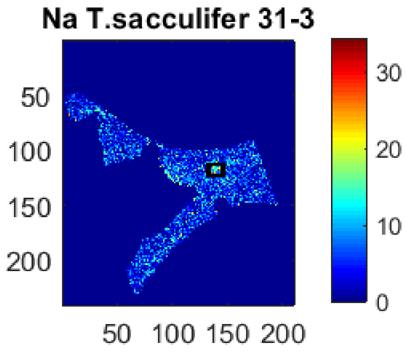


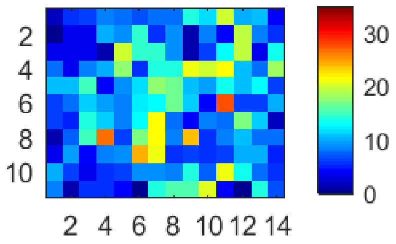


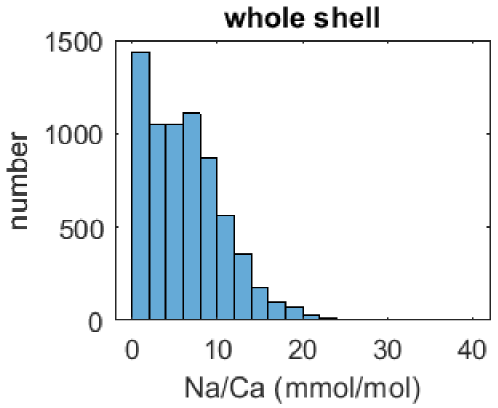


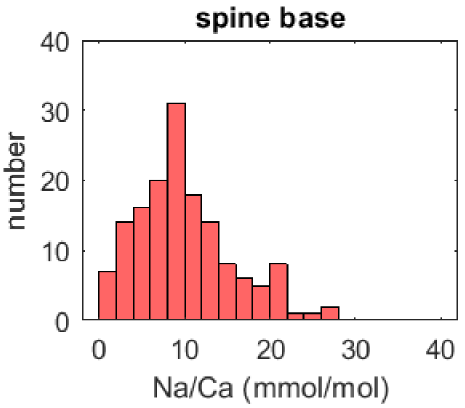


31_2	**min**	**max**	**mean**	**median**	**SD**	**SE**
shell	1.67	51.81	8.21	7.59	5.44	0.07
spine base	1.92	28.01	11.69	10.65	7.24	0.77

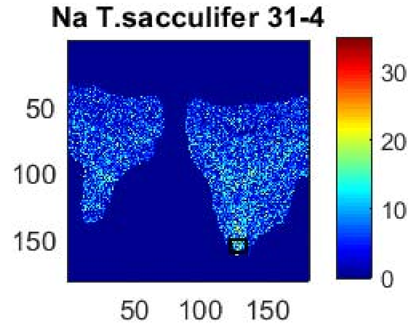

Na T.sacculifer 31-3

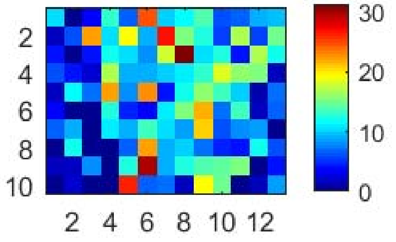


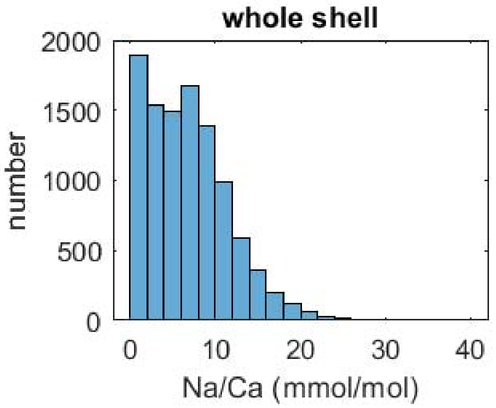

whole shell

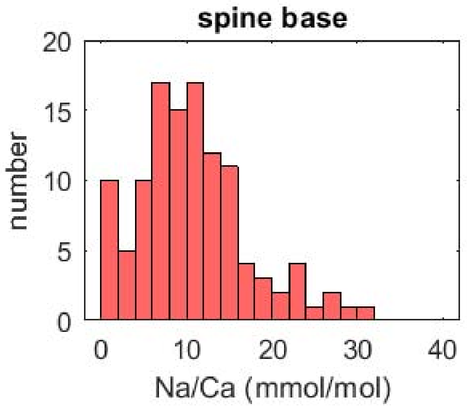

spine base

31_3	min	max	mean	median	SD	SE
shell	1.3	42.9	6.502	5.8893	4.3	0.1
spine base	1.5	27.5	10.1	8.7396	5.6	0.5

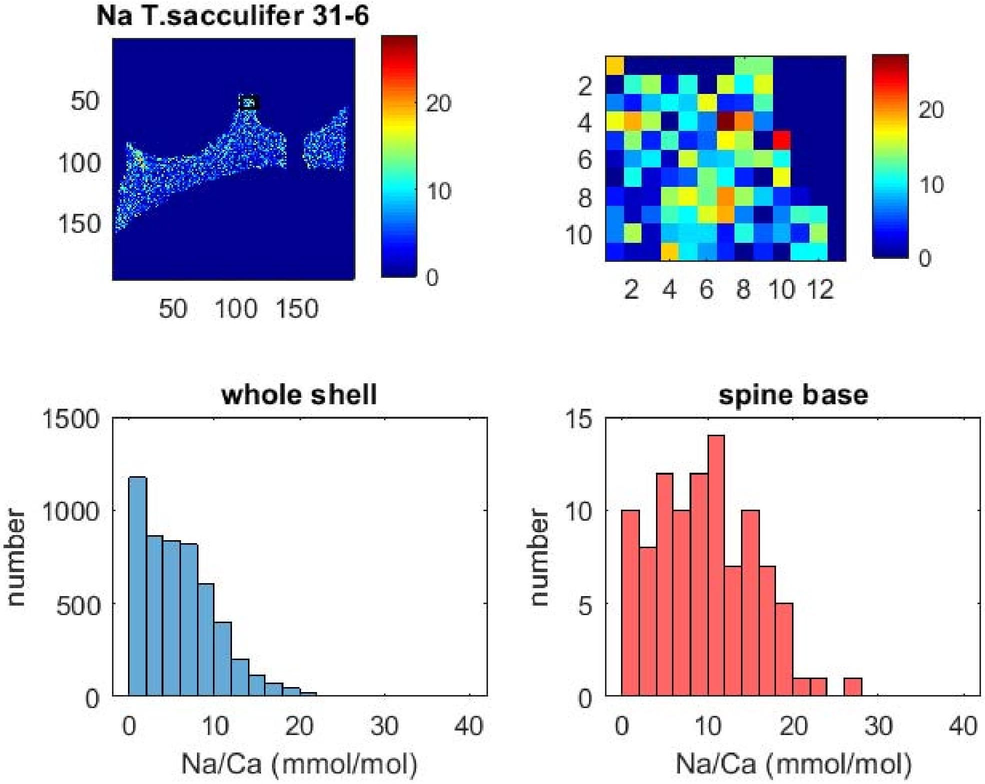




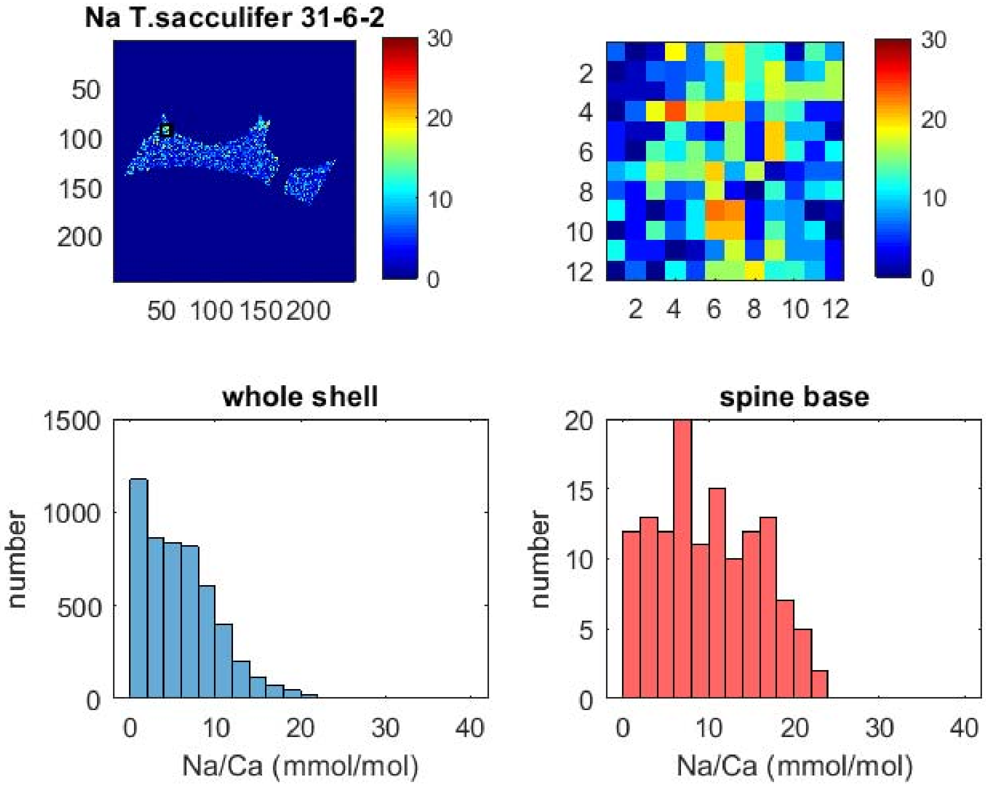




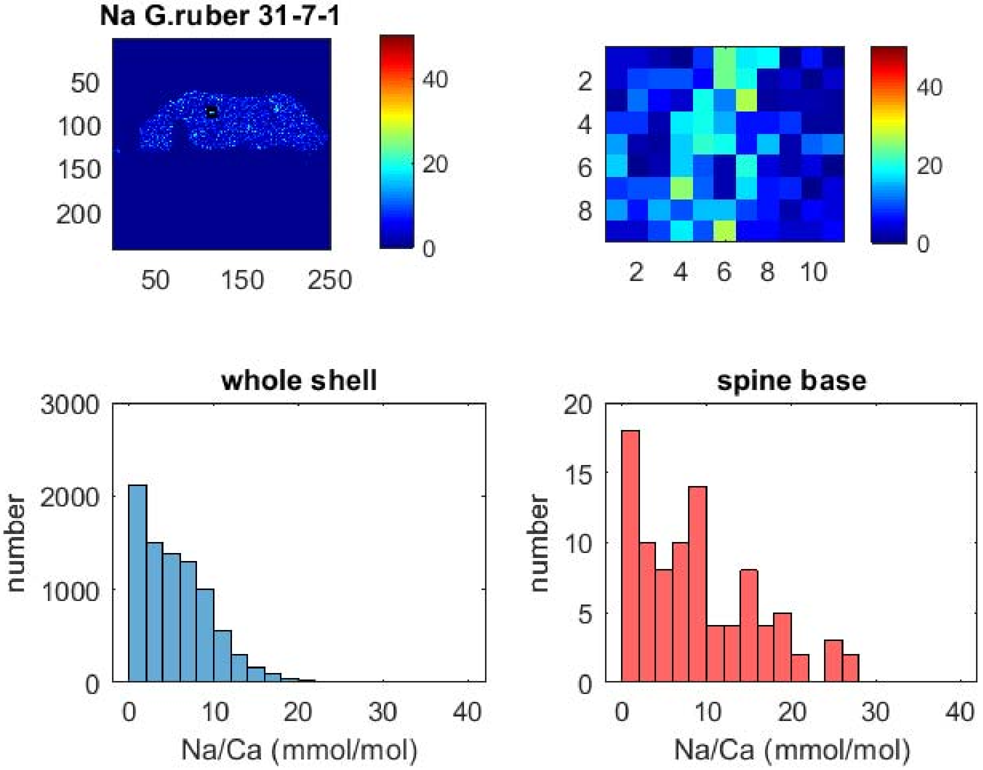
31_4	min	max	mean	median	SD	SE
shell	1.30	52.31	6.94	6.14	4.57	0.04
spine base	1.41	31.37	10.66	10.04	6.40	0.60



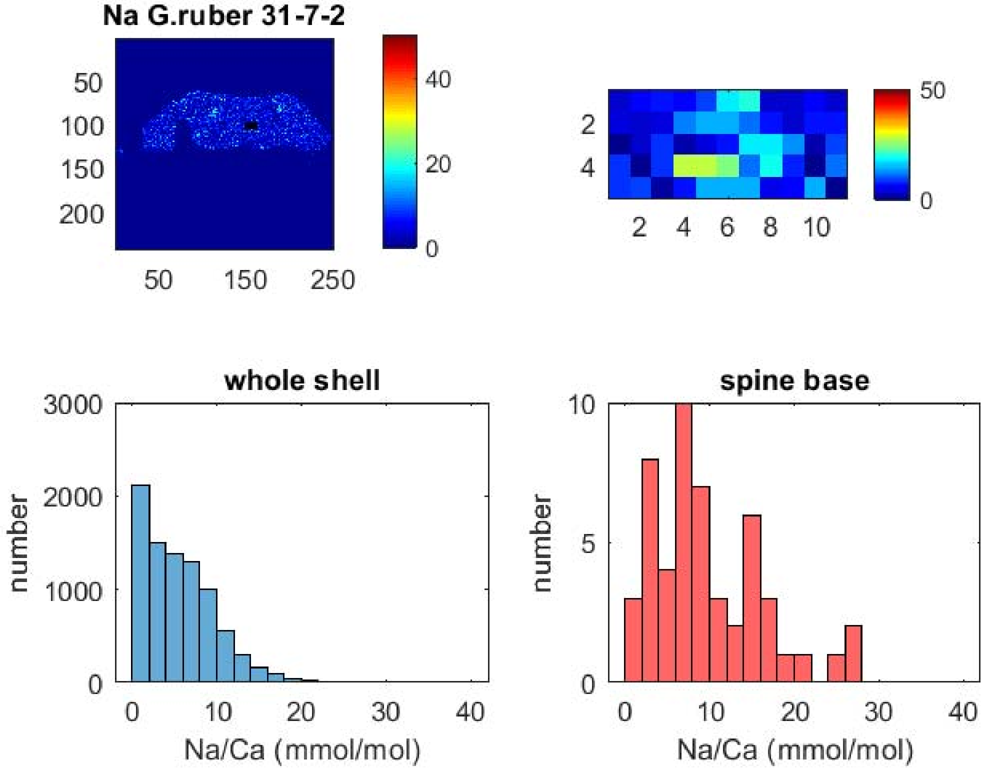
31_6	**min**	**max**	**mean**	**median**	**SD**	**SE**
shell	1.29	27.74	6.14	5.61	4.15	0.06
spine base	1.55	27.36	9.69	9.71	5.60	0.57



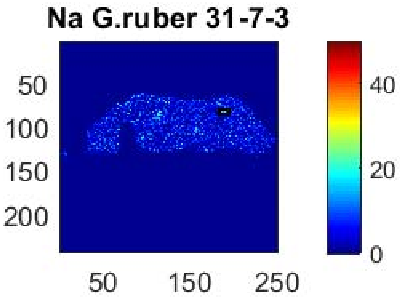
31_6	**min**	**max**	**mean**	**median**	**SD**	**SE**
shell	1.29	27.74	6.14	5.61	4.15	0.06
spine base	1.50	23.88	10.12	9.25	5.87	0.51

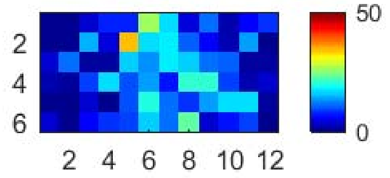


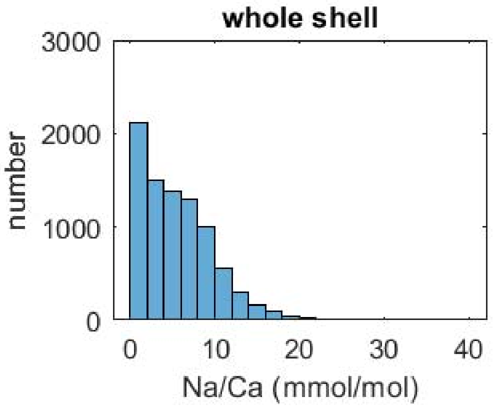
31_7_1	**min**	**max**	**mean**	**median**	**SD**	**SE**
shell	1.3	50.4	5.755	4.4945	3.9	0
spine base	1.4	26.9	9.243	7.7357	6.9	0.7

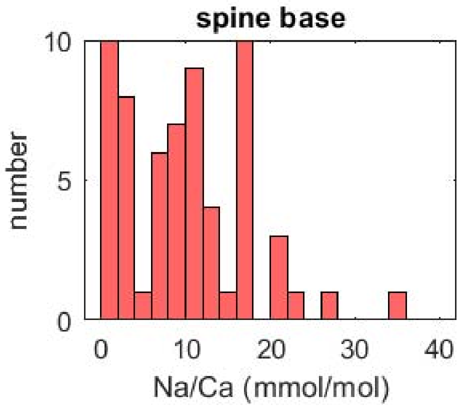


31_7_2	min	max	mean	median	SD	SE
shell	1.3	50.4	5.755	4.4945	3.9	0
spine base	1.4	27.6	9.74	8.0704	6.5	0.9

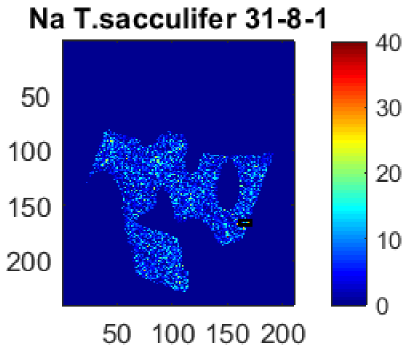


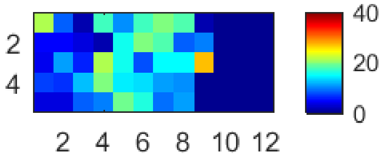


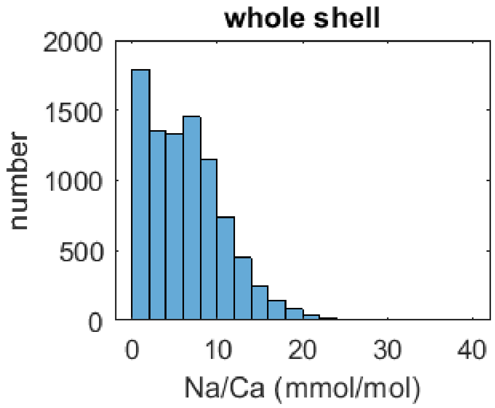


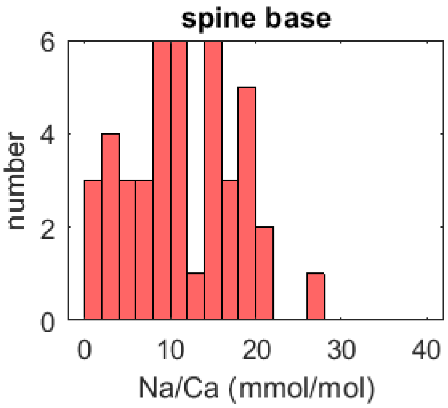


31_7_3	**min**	**max**	**mean**	**median**	**SD**	**SE**
shell	1.3	50.4	5.755	4.4945	3.9	0
spine base	1.4	34.3	10.2	9.1379	7	0.9

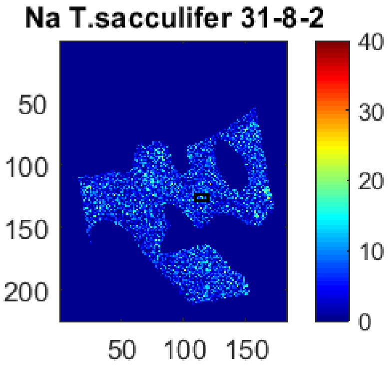

Na T.sacculifer 31-8-1

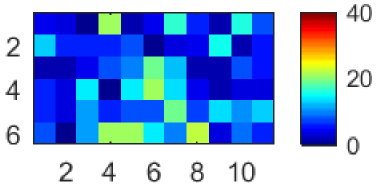


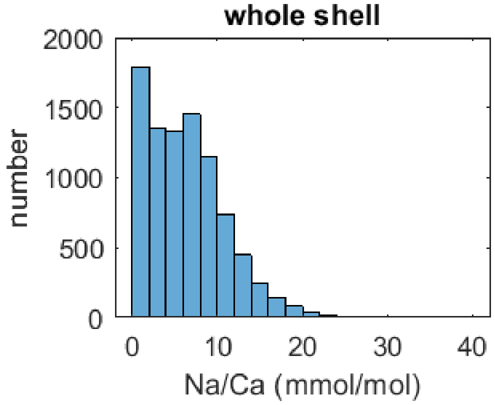

whole shell

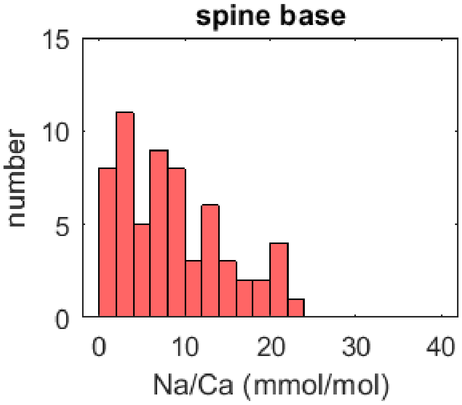

spine base

31_8_1	**min**	**max**	**mean**	**median**	**SD**	**SE**
shell	1.2	41.6	6.511	5.9515	4.3	0
spine base	1.4	26.9	11.55	10.723	6.4	1

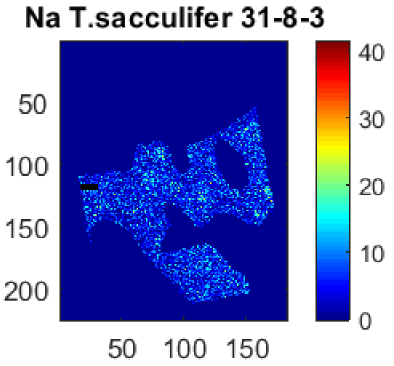


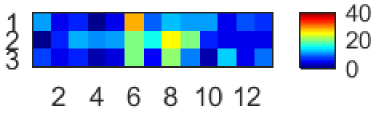


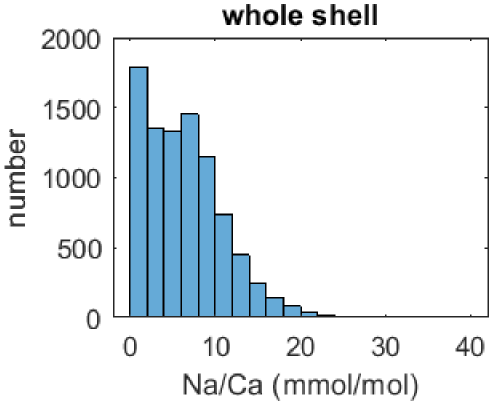


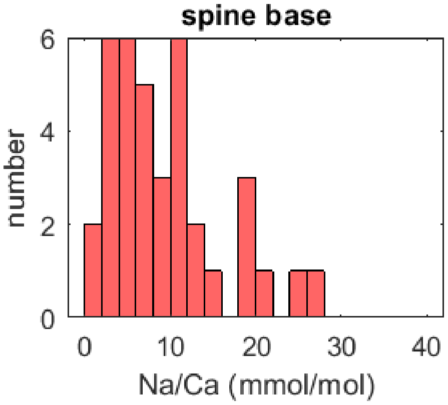


31_8_2	min	max	mean	median	SD	SE
shell	1.2	41.6	6.511	5.9515	4.3	0
spine base	1.4	22.1	8.685	7.325	5.9	0.7

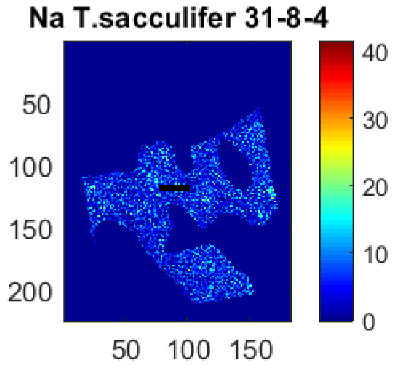


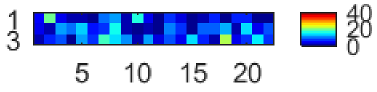


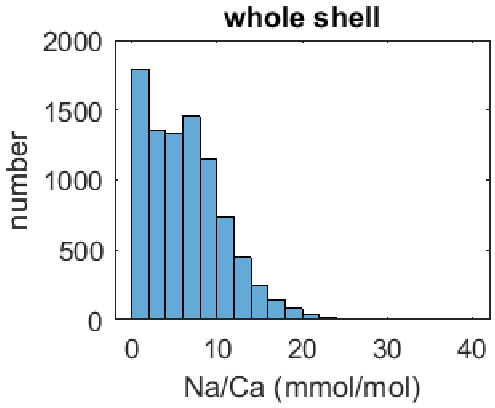


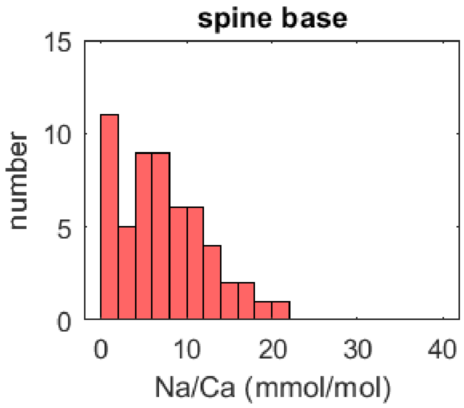


31_8_3	**min**	**max**	**mean**	**median**	**SD**	**SE**
shell	1.2	41.6	6.511	5.9515	4.3	0
spine base	1.6	27.9	9.535	7.6289	6.6	1.1

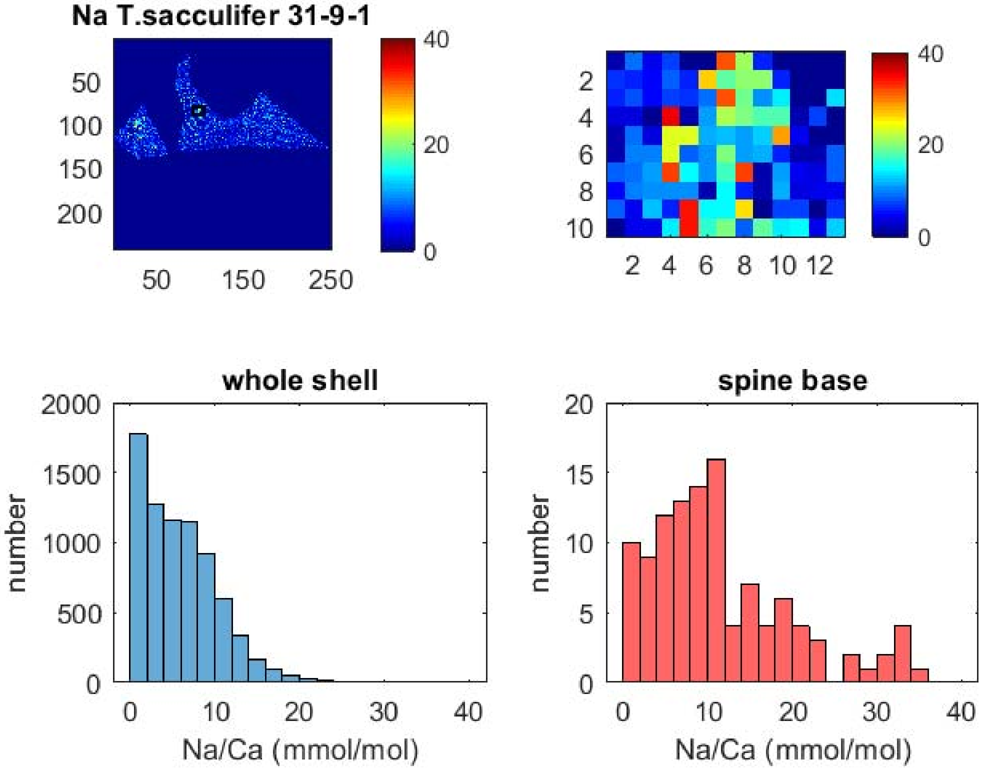




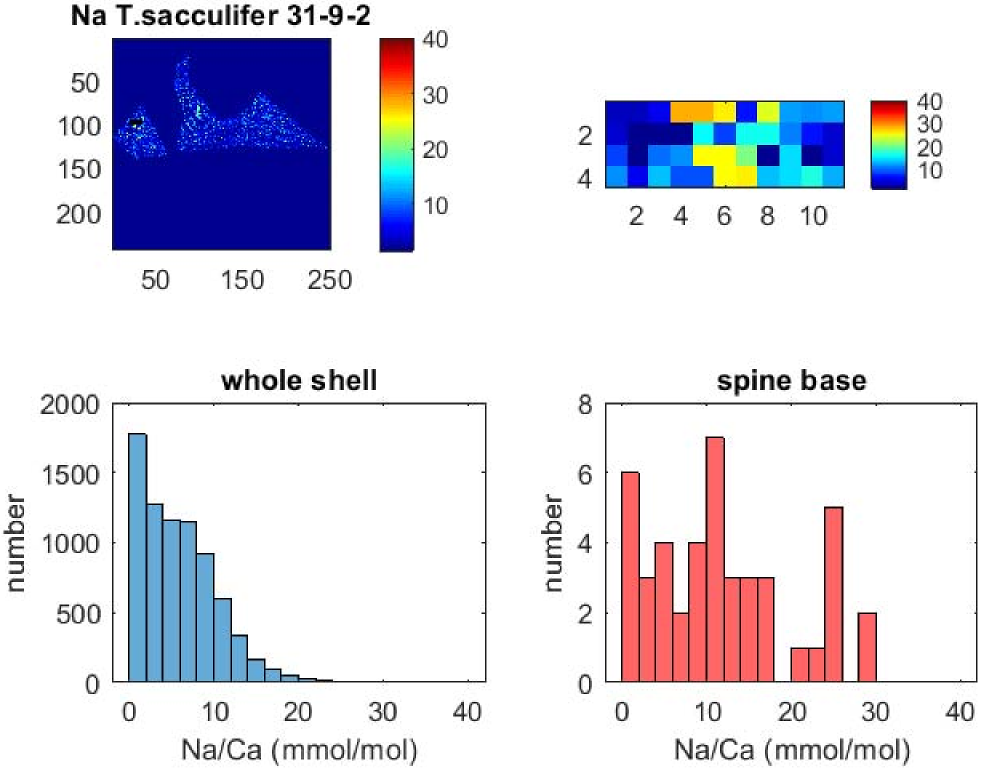




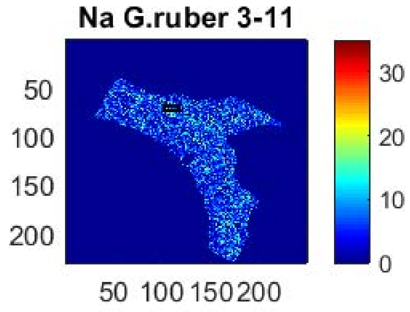
31_8_4	**min**	**max**	**mean**	**median**	**SD**	**SE**
shell	1.2	41.6	6.511	5.9515	4.3	0
spine base	1.4	21.6	7.46	6.4506	4.9	0.7

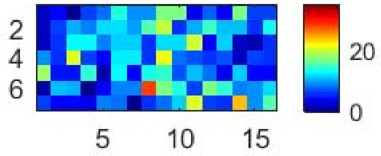


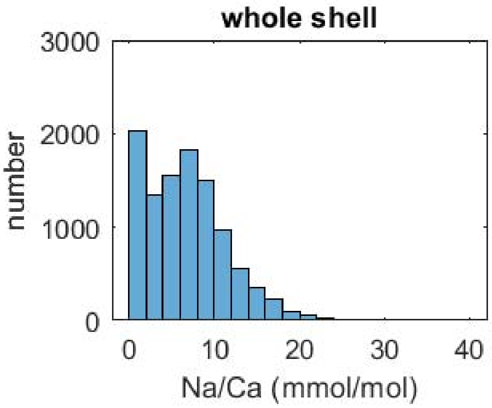
31_9_1	min	max	mean	median	SD	SE
shell	1.2	132	6.165	5.6414	4.6	0.1
spine base	1.5	35.2	11.61	9.6704	8.4	0.8

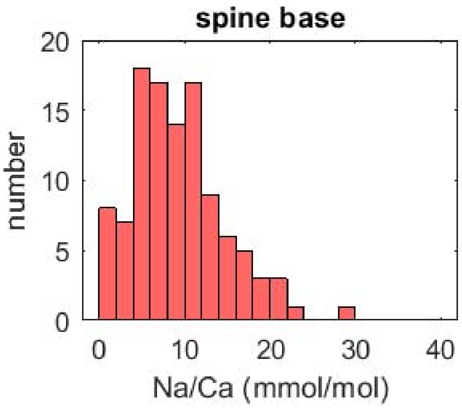


31_9_2	**min**	**max**	**mean**	**median**	**SD**	**SE**
shell	1.2	132	6.165	5.6414	4.6	0.1
spine base	1.5	28.4	11.99	11.255	8.2	1.2



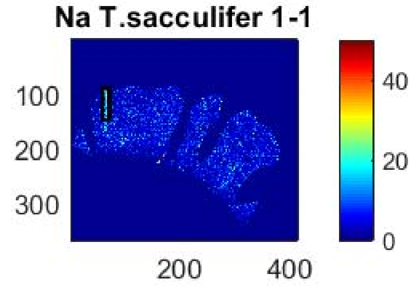


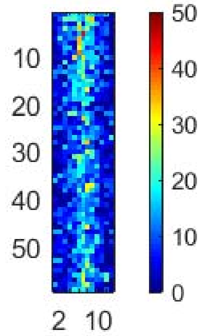


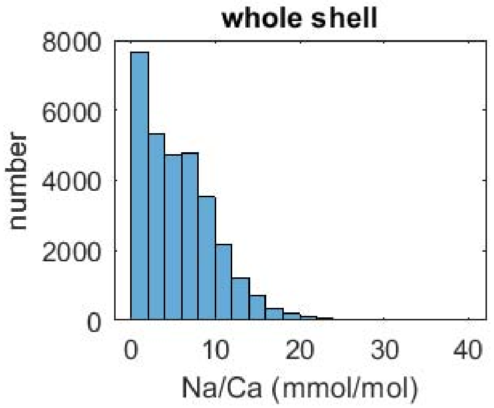


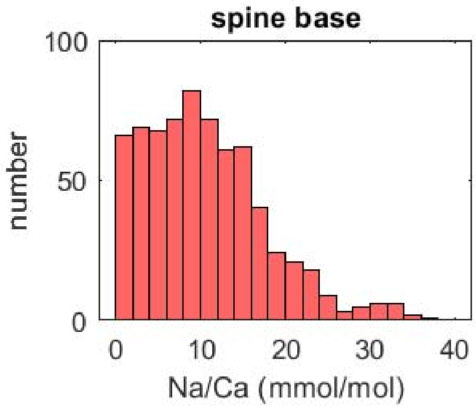
3_11	**min**	**max**	**mean**	**median**	**SD**	**SE**
shell	1.4	38.4	6.852	6.1887	4.4	0
spine base	1.5	28.4	9.345	8.4687	5.3	0.5

Part 3: Cultured *T. sacculifer* specimens

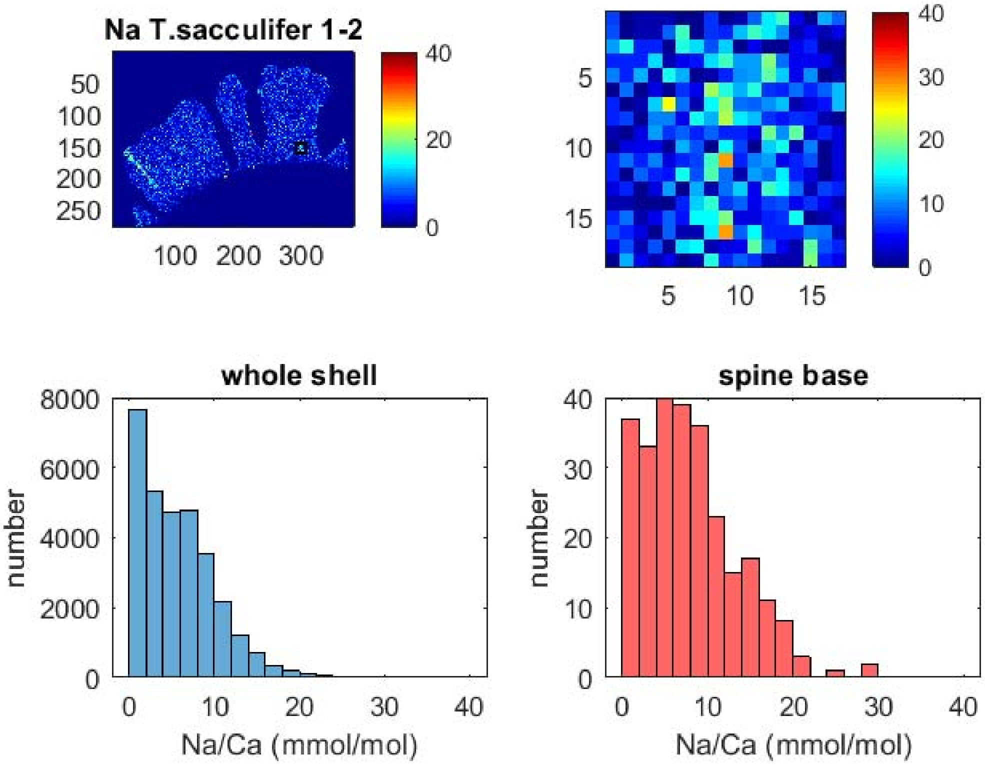




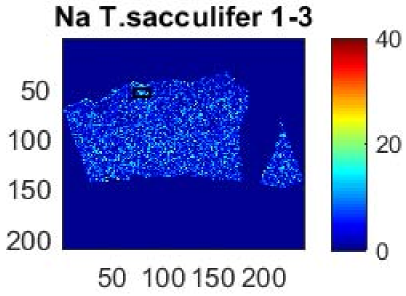


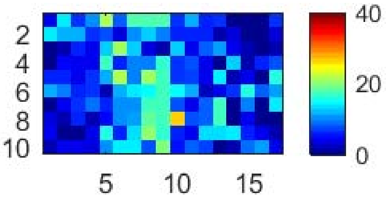


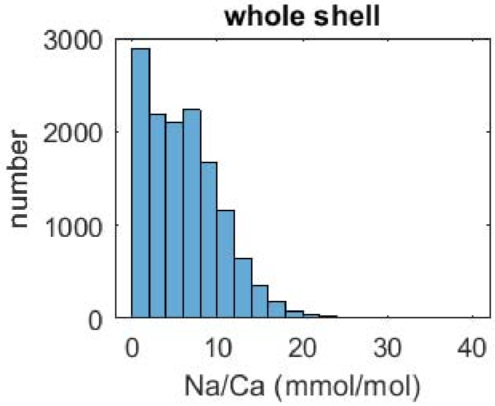
1_1	min	max	mean	median	SD	SE
shell	1.3	108	5.969	5.3616	4.4	0
spine base	1.3	43	10.74	9.7348	7.1	0.3

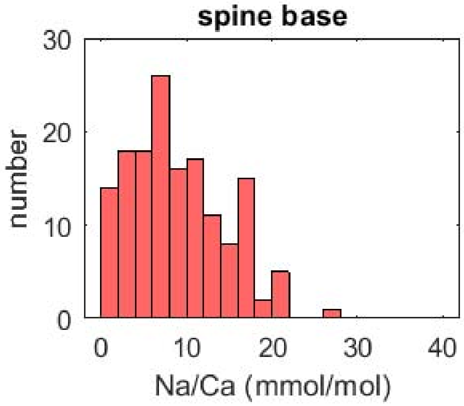


1_1_2	min	max	mean	median	SD	SE
shell	1.3	108	5.969	5.3616	4.4	0
spine base	1.4	28.7	8.159	6.5566	5.3	0.3

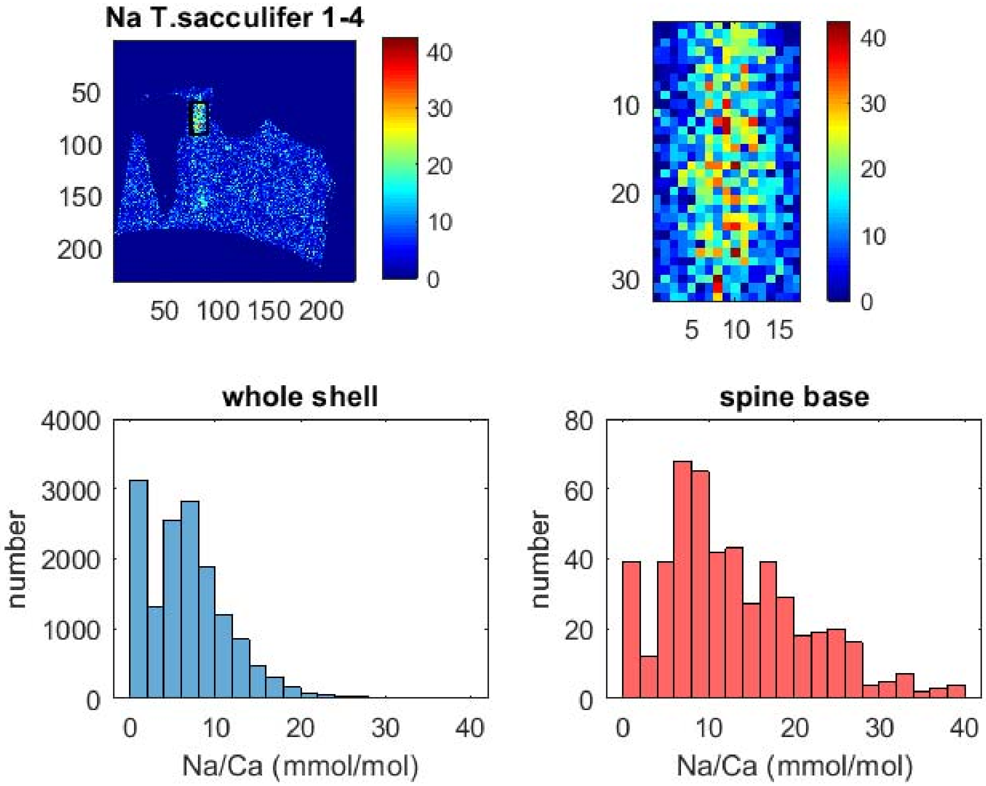




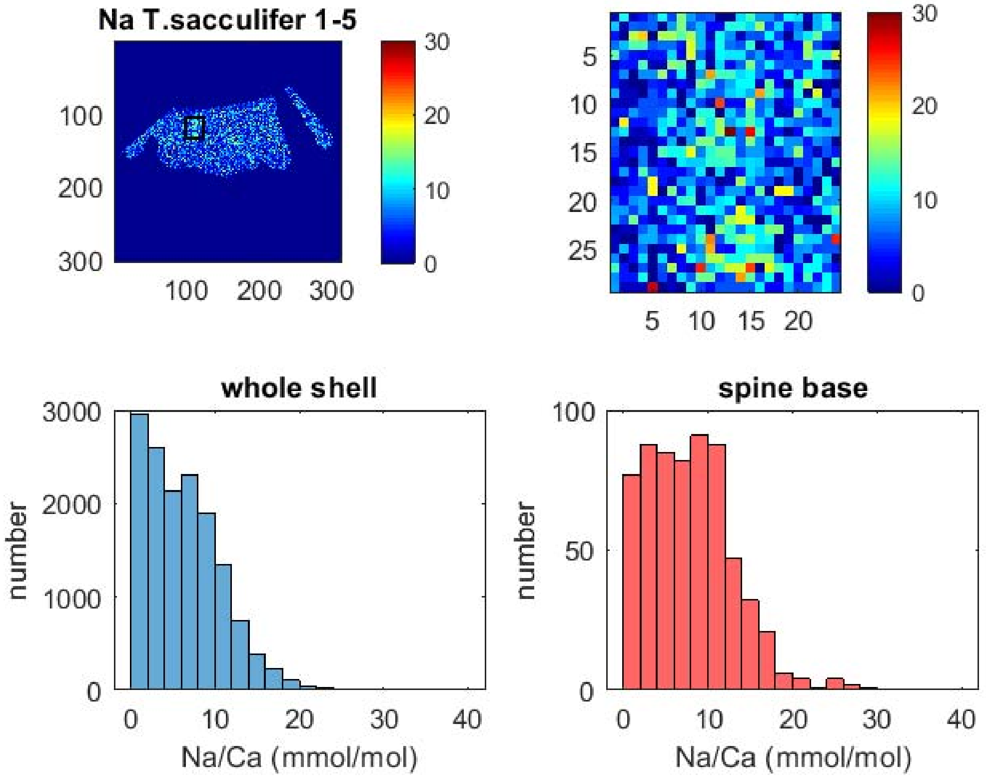




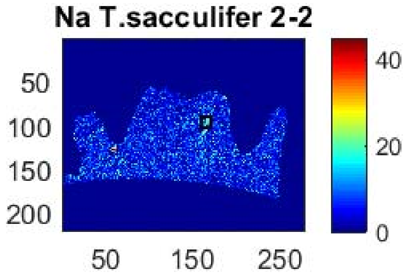
1_3	min	max	mean	median	SD	SE
shell	1.3	114	6.321	5.8649	4.3	0
spine base	1.4	26.7	9.052	7.9622	5.5	0.4

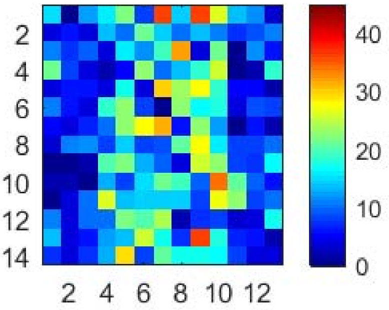


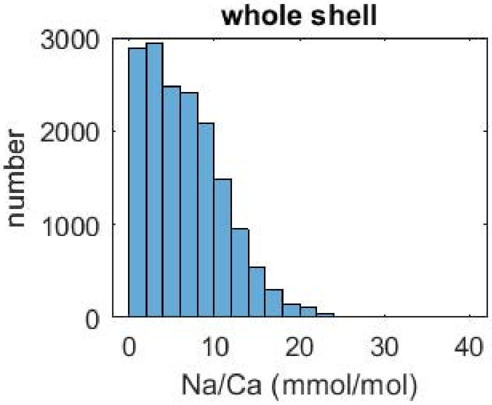
1_4	**min**	**max**	**mean**	**median**	**SD**	**SE**
shell	1.3	42.4	6.899	6.2465	4.8	0
spine base	1.4	42.4	13.14	11.275	8.4	0.4

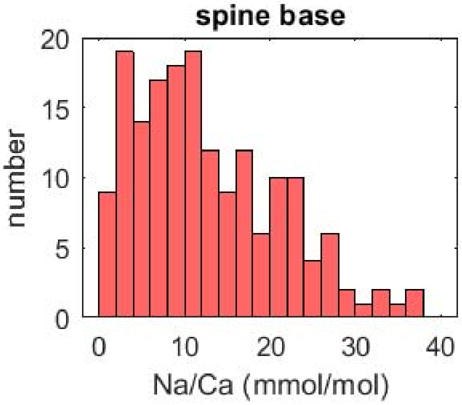


1_5	min	max	mean	median	SD	SE
shell	1.3	29.8	6.474	5.9071	4.2	0
spine base	1.3	29.8	8.057	7.6801	4.9	0.2

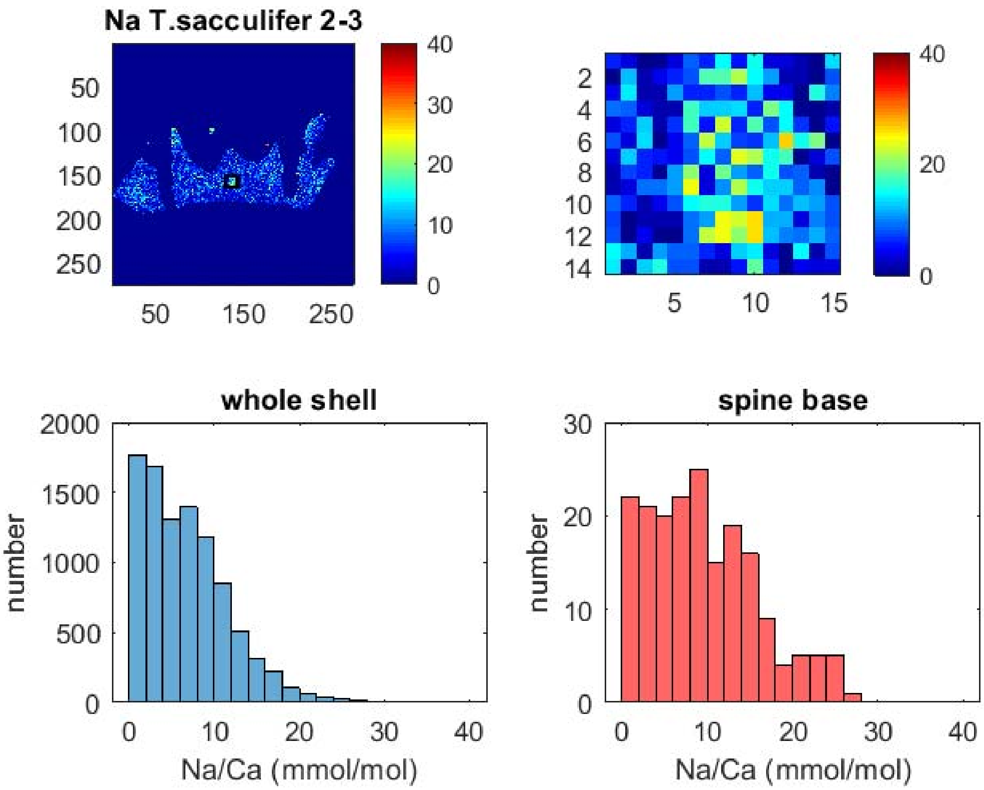




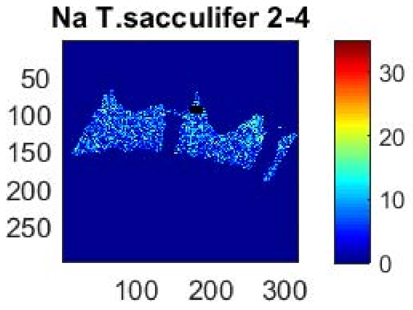


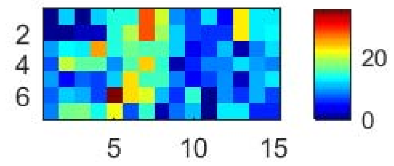


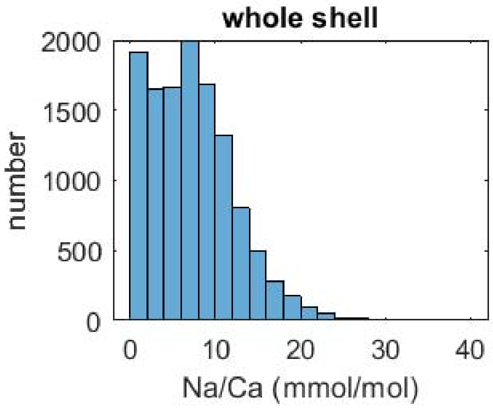
2_2	**min**	**max**	**mean**	**median**	**SD**	**SE**
shell	1.2	60	6.865	5.9637	4.6	0
spine base	1.5	36.5	12.84	10.85	8.3	0.6

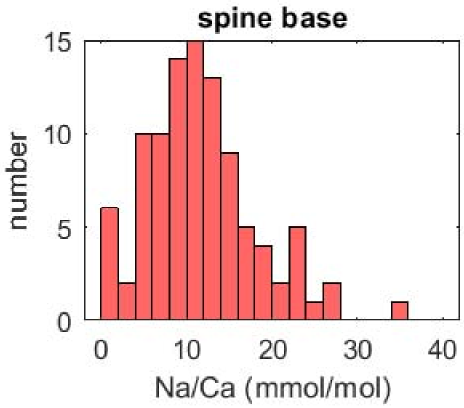


2_3	min	max	mean	median	SD	SE
shell	1.2	55.1	6.965	5.9897	4.9	0
spine base	1.3	26.5	9.728	8.3395	6.2	0.5

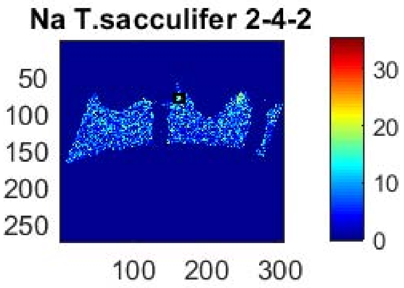


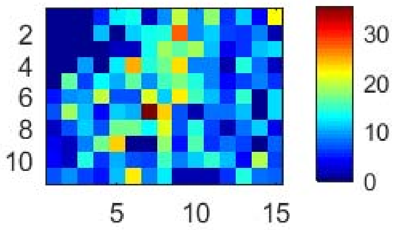


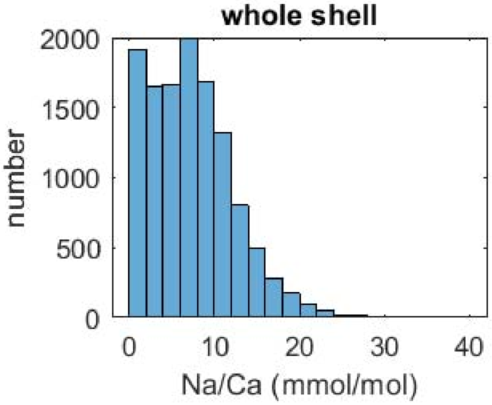


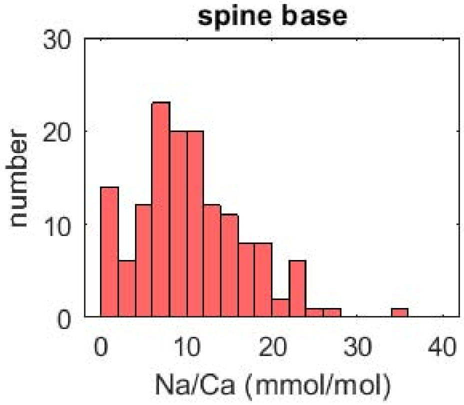


2_4_1	min	max	mean	median	SD	SE
shell	1.3	35.6	7.446	6.4843	4.7	0
spine base	1.4	35.6	11.69	11.014	6.4	0.6

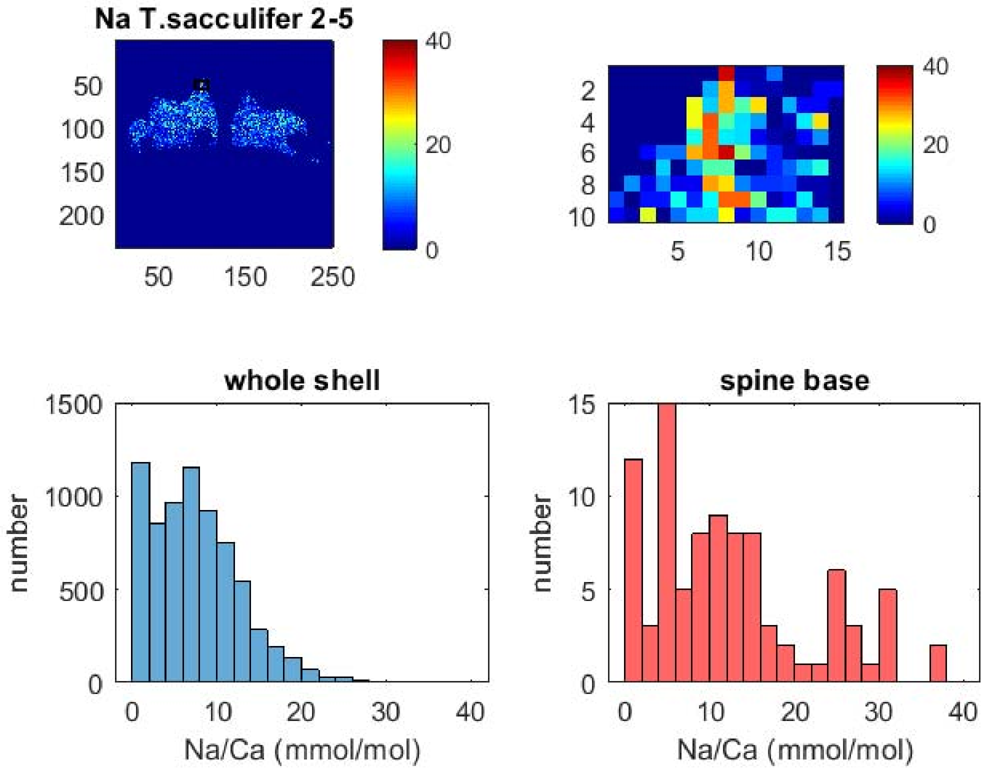




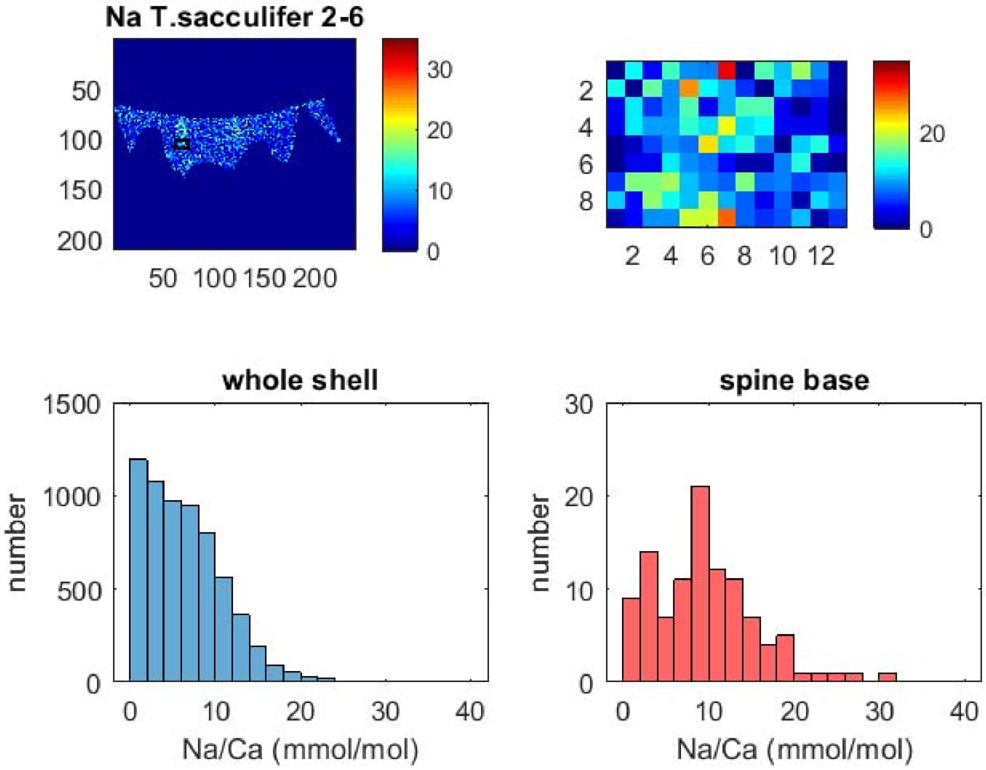




2_4_2	**min**	**max**	**mean**	**median**	**SD**	**SE**
shell	1.3	35.6	7.446	6.4843	4.7	0
spine base	1.4	35.6	10.59	9.3772	6.2	0.5



2_5	min	max	mean	median	SD	SE
shell	1.2	50	7.683	6.6361	5.1	0.1
spine base	1.4	36.7	12.58	10.56	9.4	1



2_6	min	max	mean	median	SD	SE
shell	1.2	36.6	6.68	5.9224	4.4	0.1
spine base	1.4	31	9.85	8.9016	5.9	0.6

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