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Supplement of

Planktonic foraminiferal spine versus shell carbonate Na incorporation in relation to salinity

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Supplement

‘Planktonic foraminiferal spine versus shell carbonate Na incorporation in relation to salinity’, Mezger et al. 2019

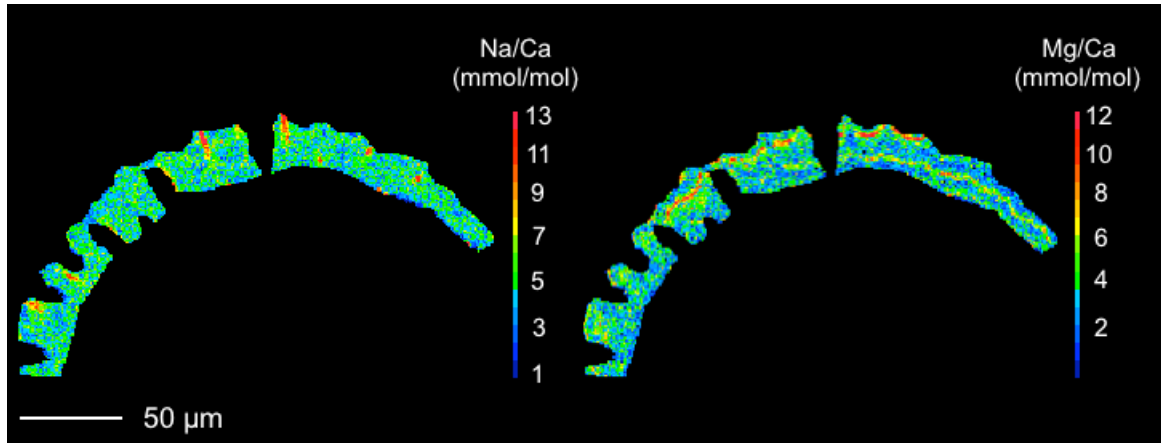


Figure S1. Overview of a cross-section of a *T. sacculifer* shell, measured at the GEOMAR in Kiel (Bertlich et al., 2018). Clearly, Mg is distributed in bands, whereas Na is more concentrated in the spine base regions.

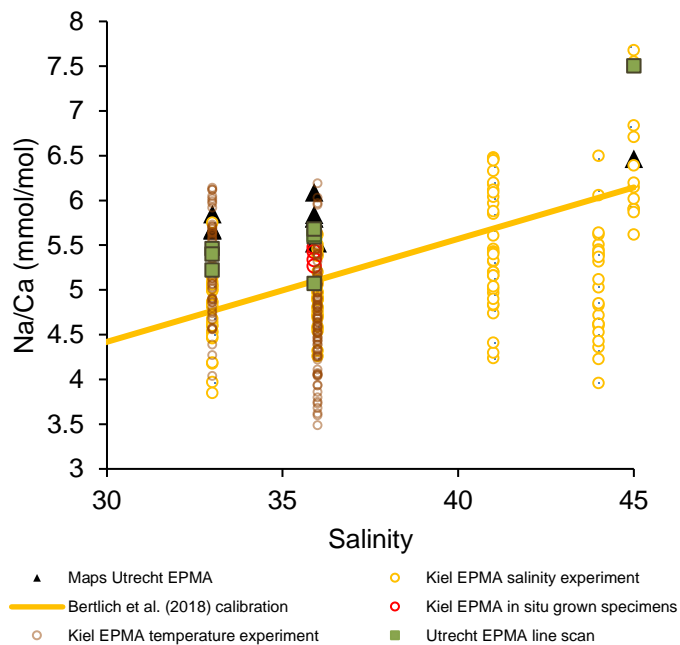


Figure S2. Comparison between Na/Ca map-values for the same embedded *T. sacculifer* specimens measured with EPMA in Kiel (Bertlich et al., 2018), and line-scan and map values measured in Utrecht.

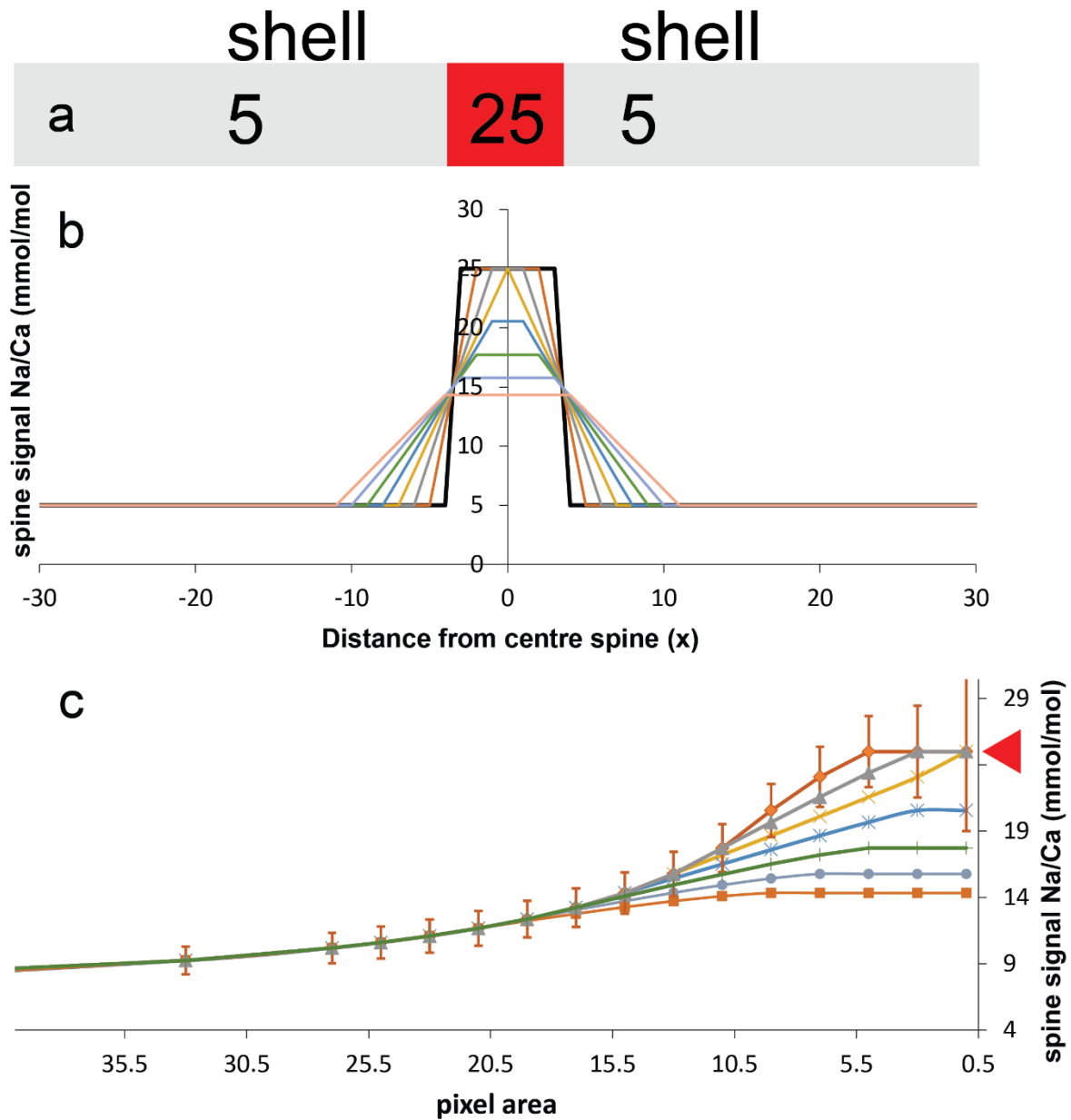


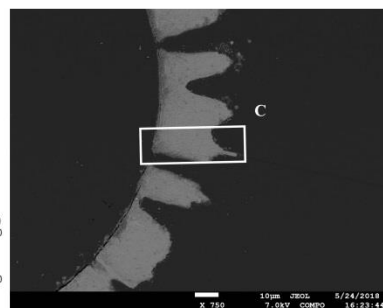
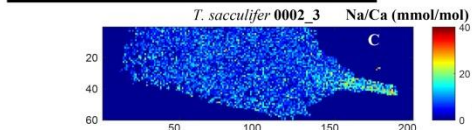
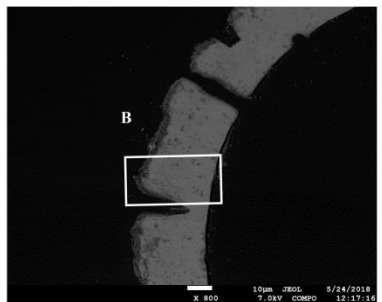
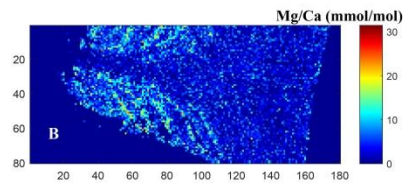
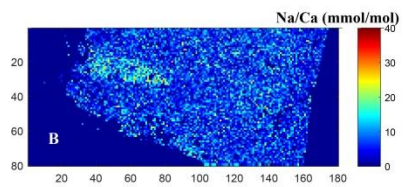
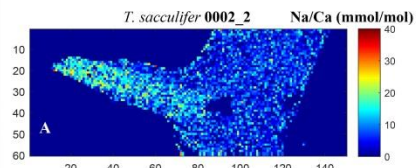
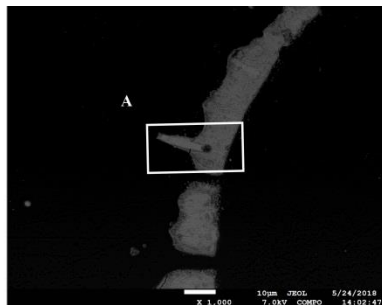
Figure S3. Spine base quantification model, showing: a) a schematic representation of a spinose planktonic foraminiferal shell cross section, including Na/Ca values of a spine (in red: 25 mmol/mol) sandwiched by two layers (in grey: 5 mmol/mol) of calcite with lower Na/Ca; b) the effect of differences 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

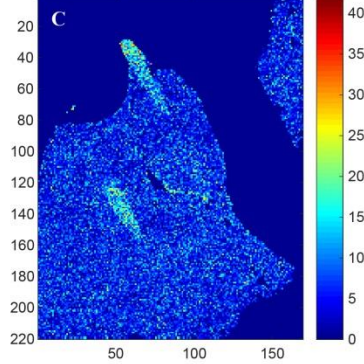
Part 2: Core-tops and plankton pump specimens (Mezger et al., 2018)

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

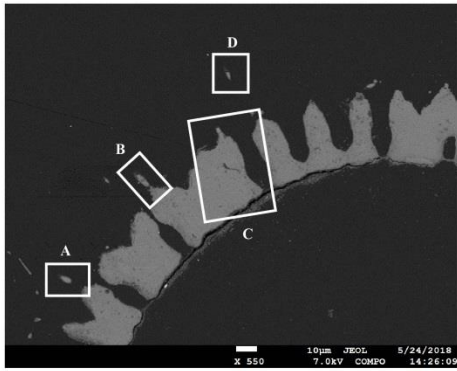
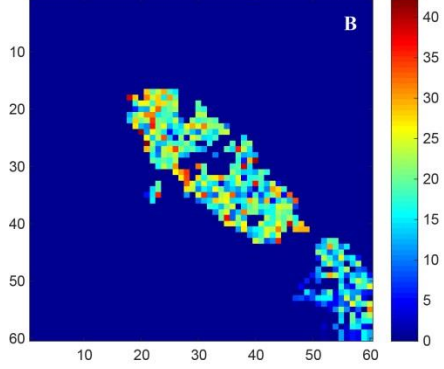
Part 1: Multi-net specimens



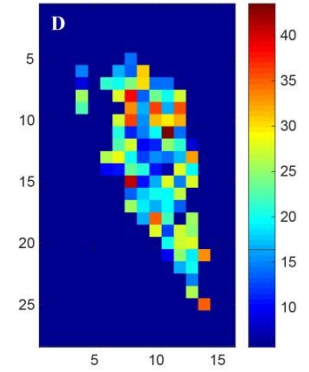
T. sacculifer 0002_4 Na/Ca (mmol/mol)



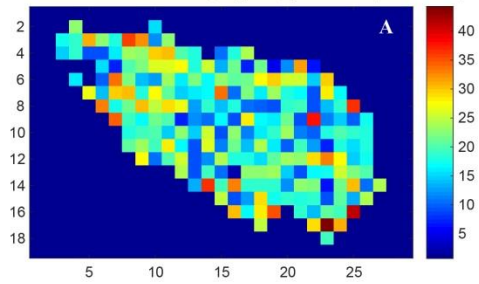
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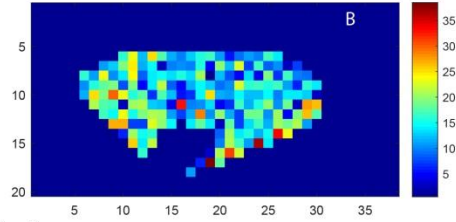
*T. sacculifer*_0002_7 Na/Ca (mmol/mol)



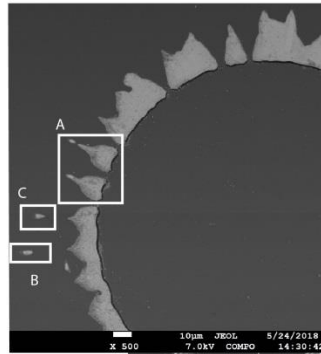
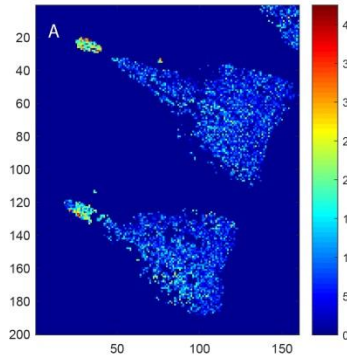
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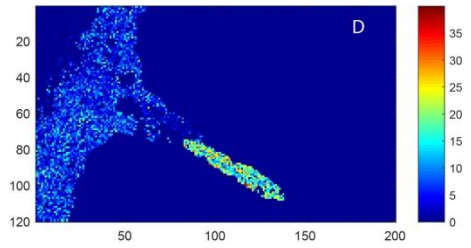
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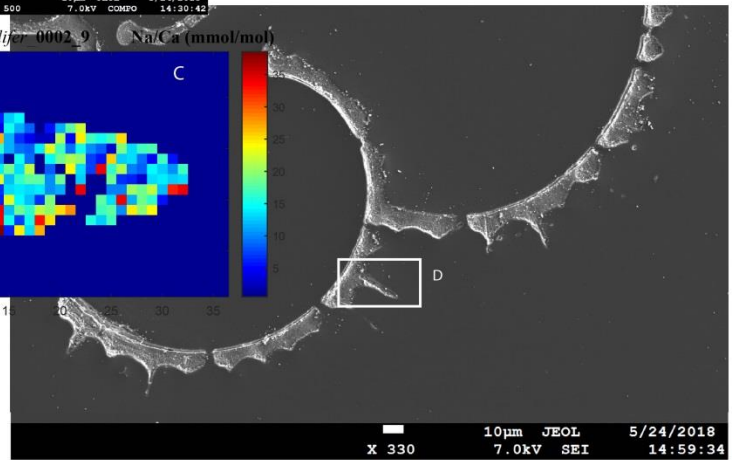
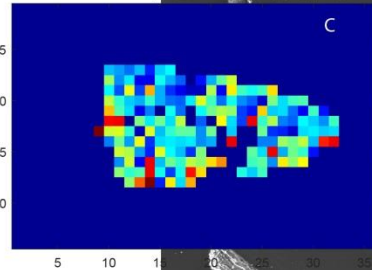
*T. sacculifer*_0002_8 Na/Ca (mmol/mol)



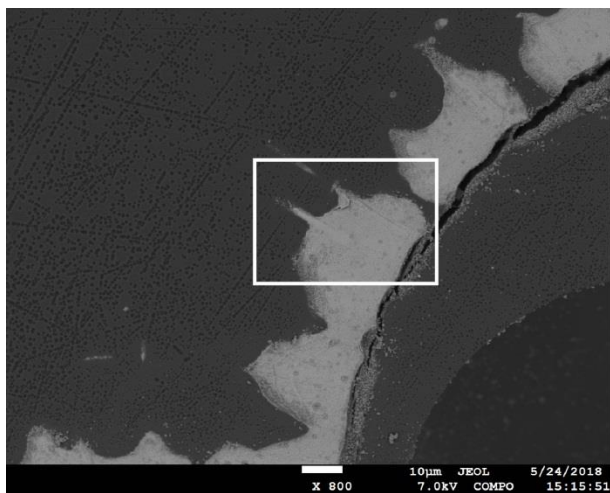
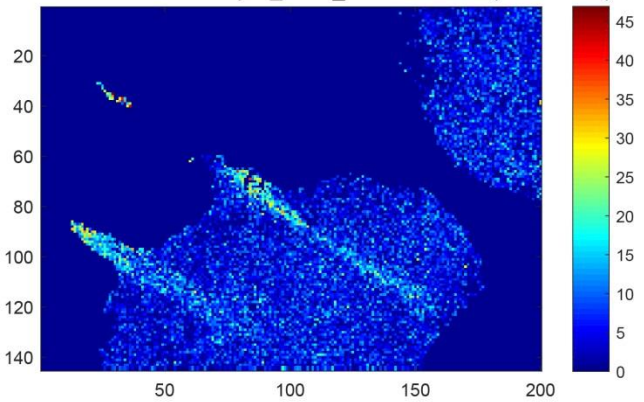
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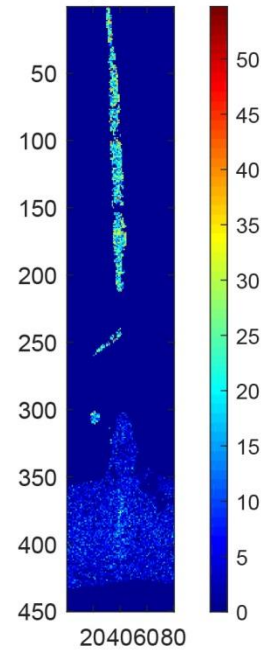
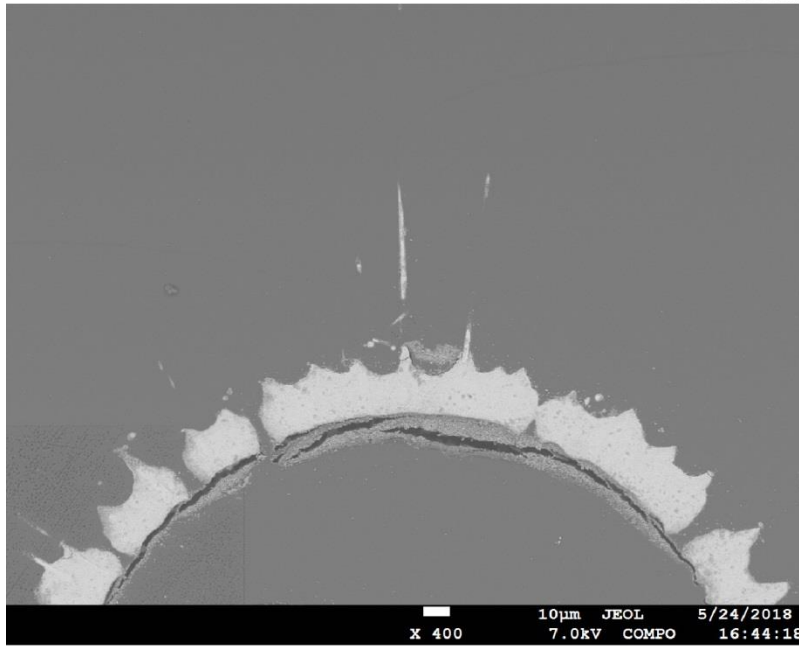
*T. sacculifer*_0002_9 Na/Ca (mmol/mol)



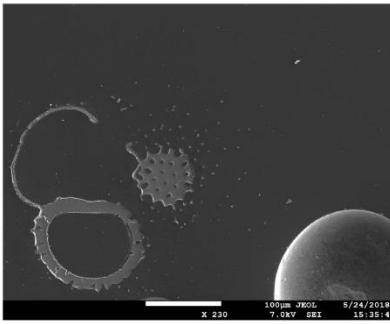
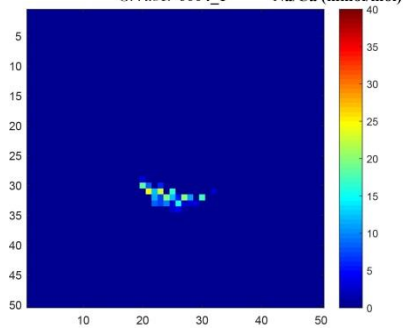
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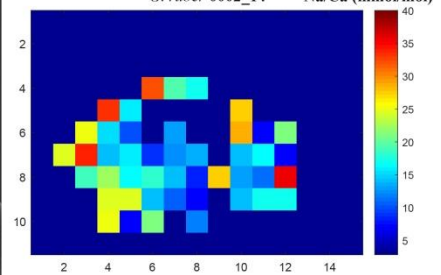
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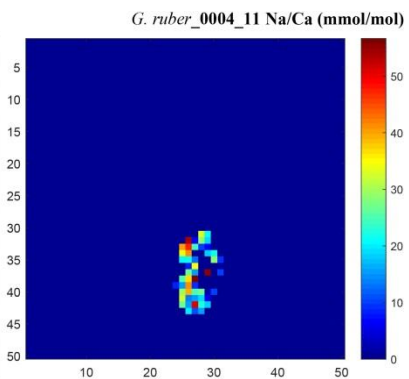
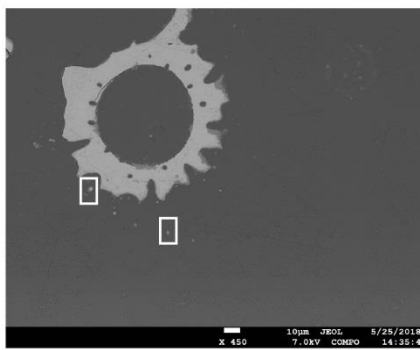
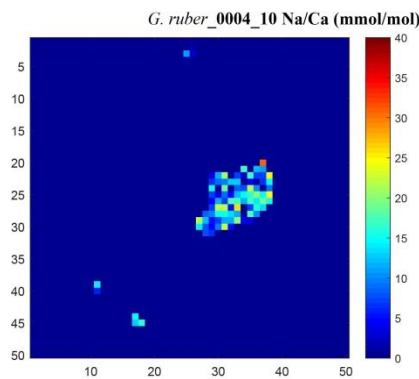
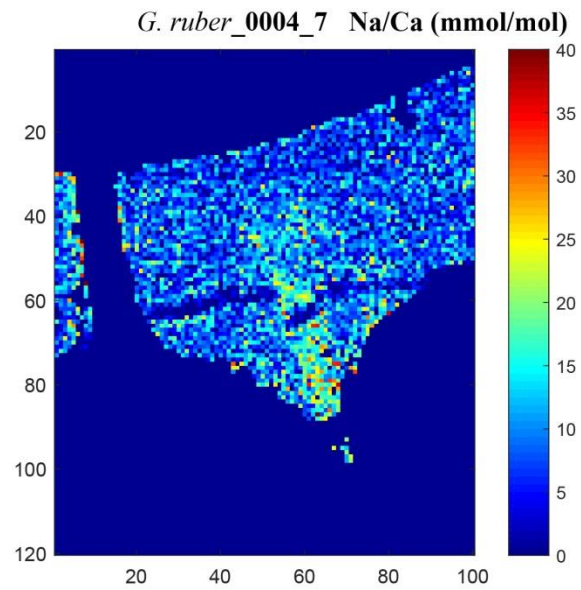
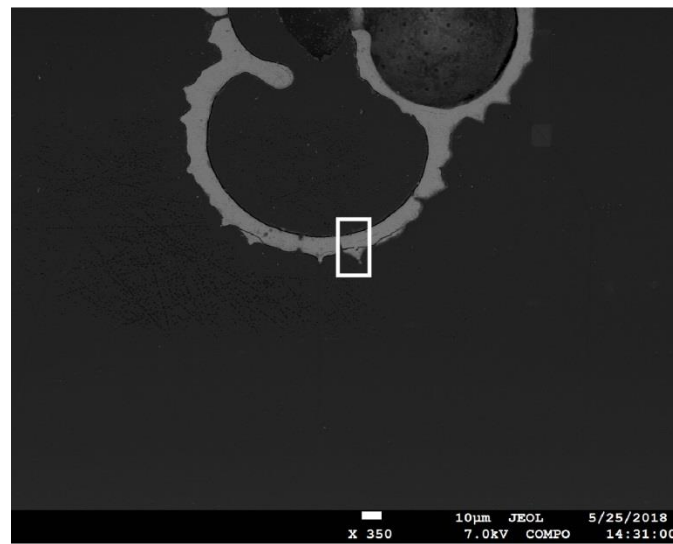
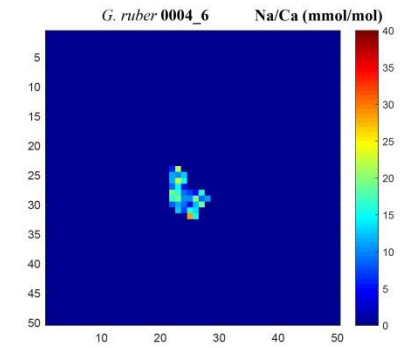
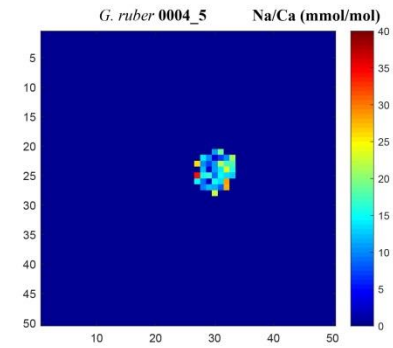
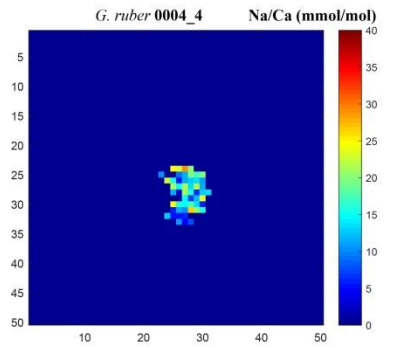
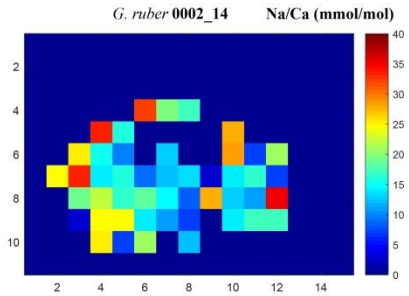
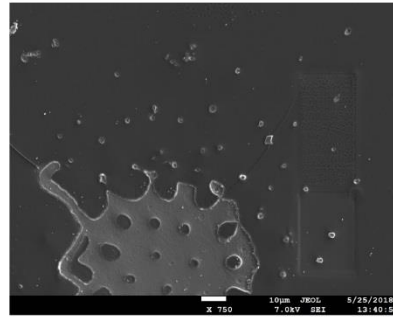
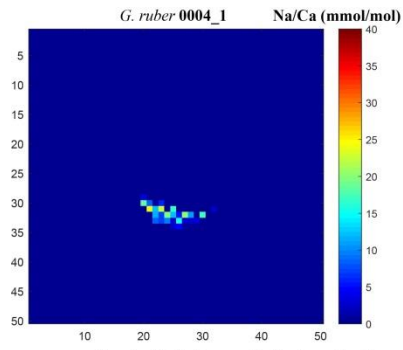


G. ruber 0004_1 Na/Ca (mmol/mol)

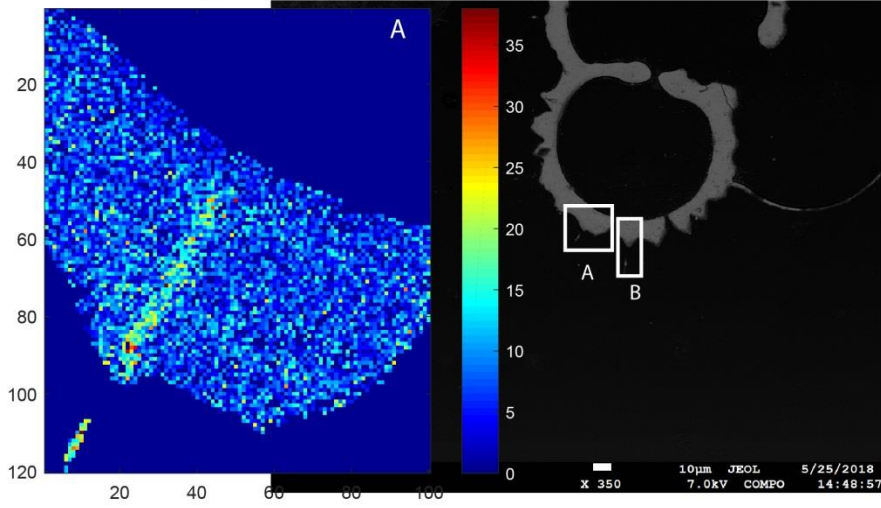


G. ruber 0002_14 Na/Ca (mmol/mol)

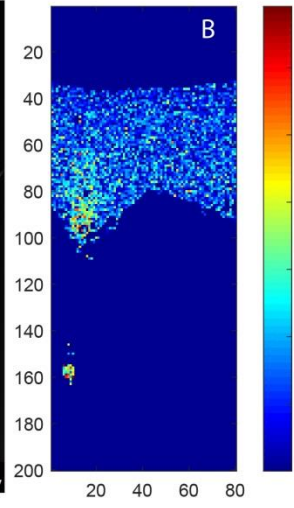




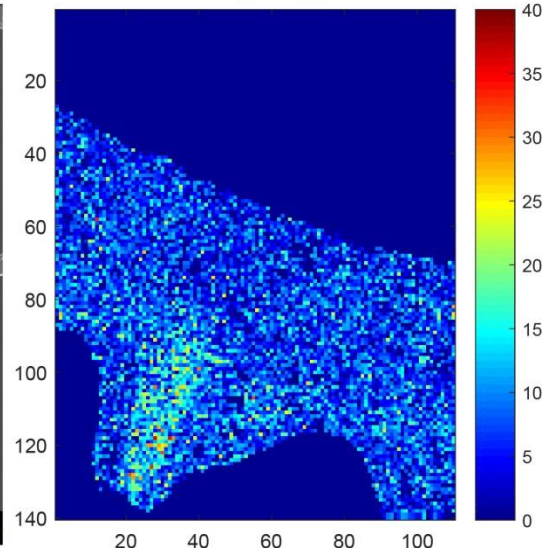
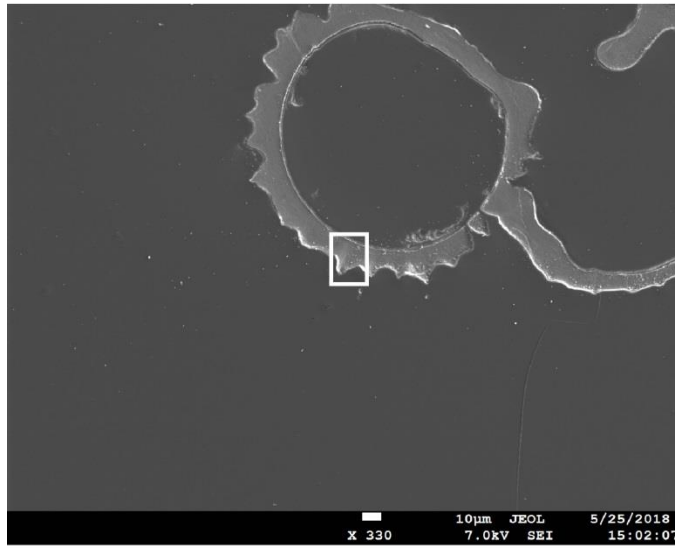
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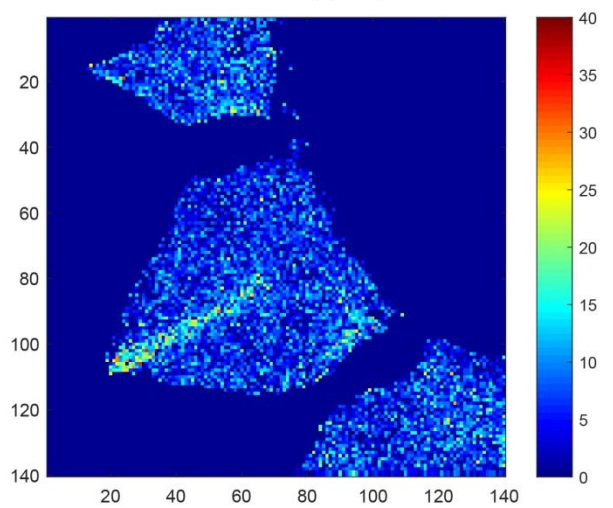
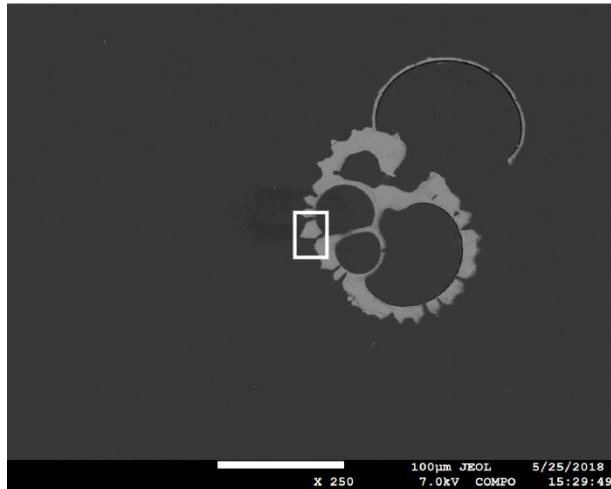
G. ruber_0004_13 Na/Ca (mmol/mol)

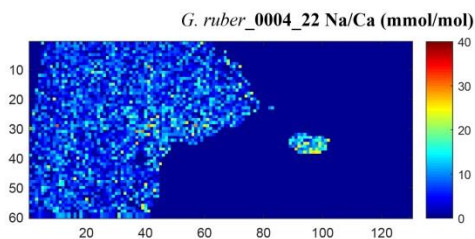
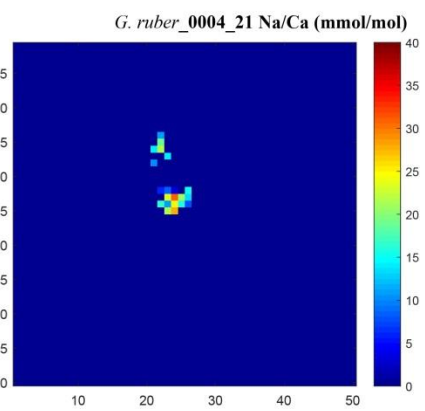
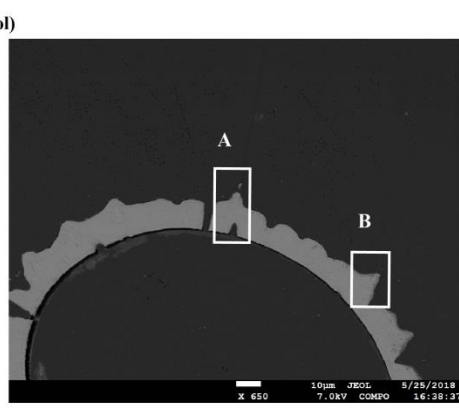
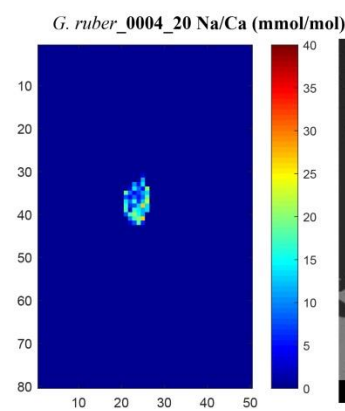
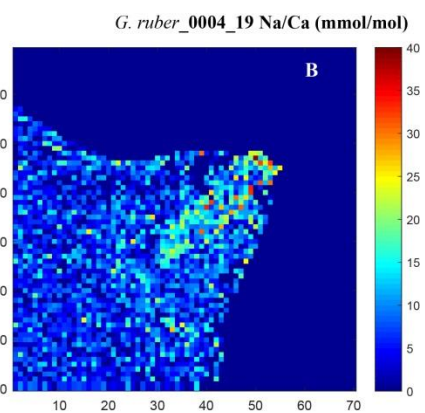
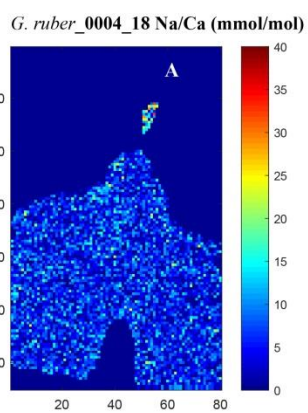
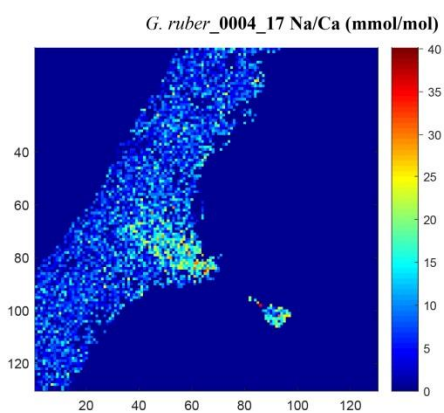
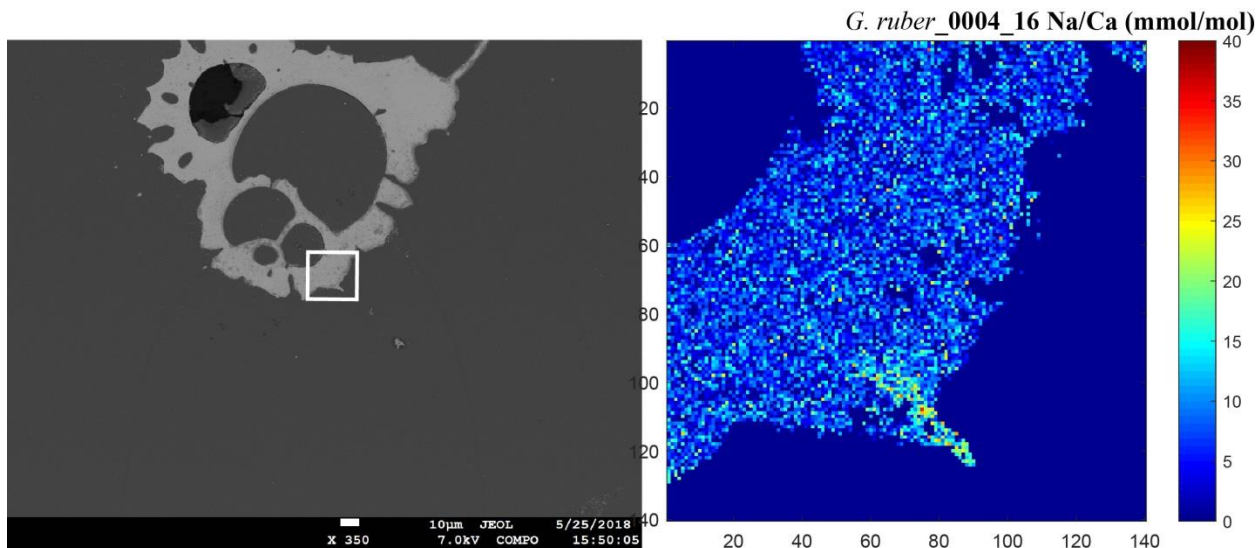


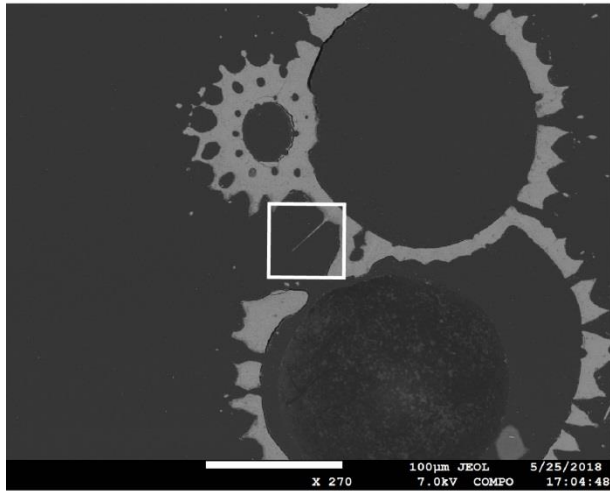
G. ruber_0004_14 Na/Ca (mmol/mol)



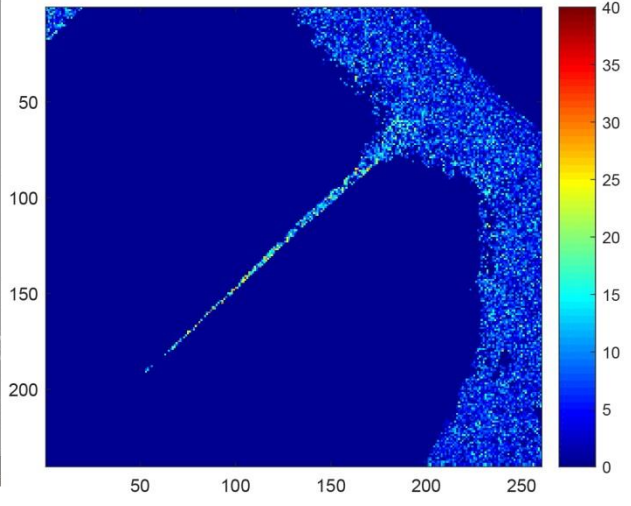
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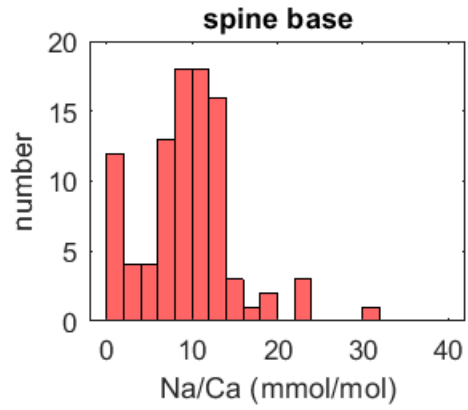
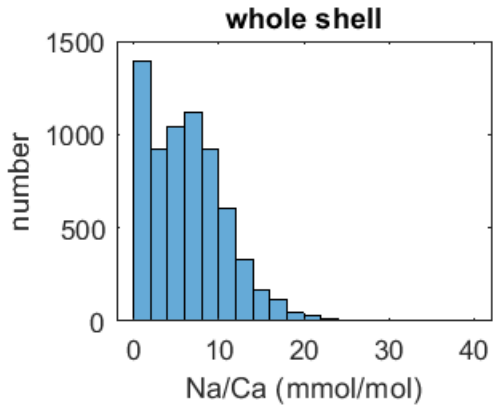
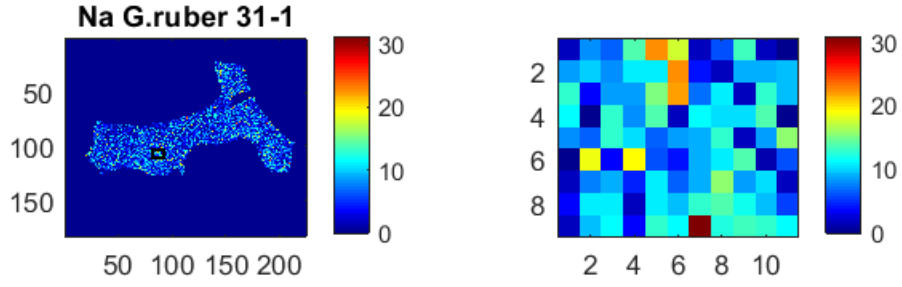




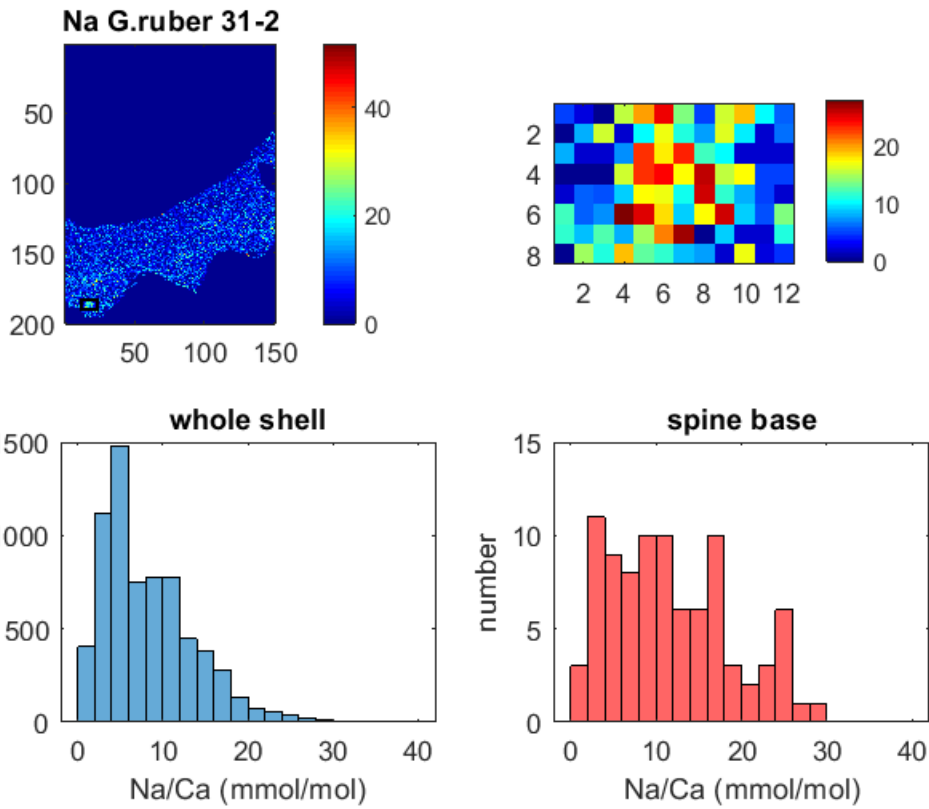
T. sacculifer_0004_24 Na/Ca (mmol/mol)



Part 2: Plankton pumps and core-tops

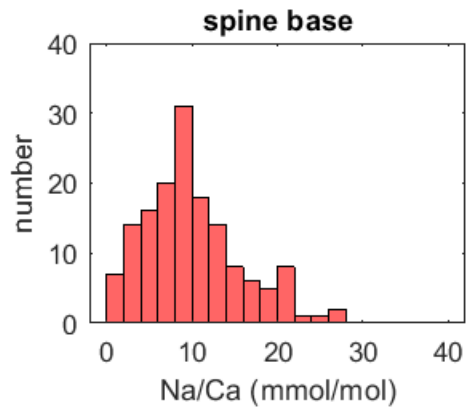
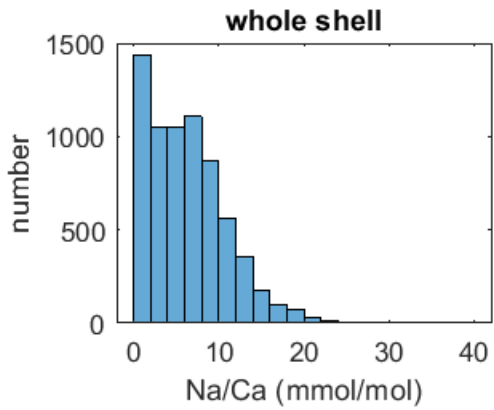
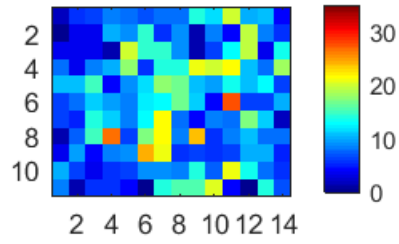
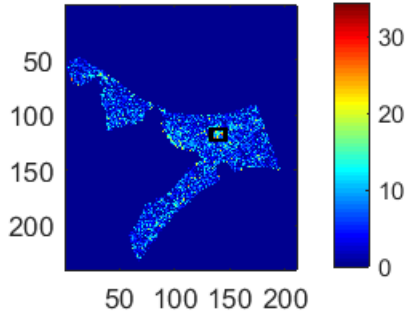


31_1	min	max	mean	median	SD	SE
shell	1.24	30.19	6.31	5.79	4.13	0.05
spine base	1.35	29.77	9.23	8.89	5.10	0.52



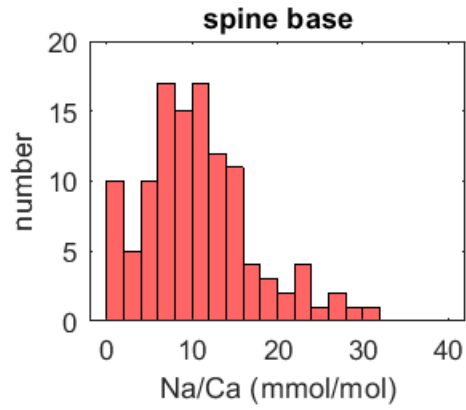
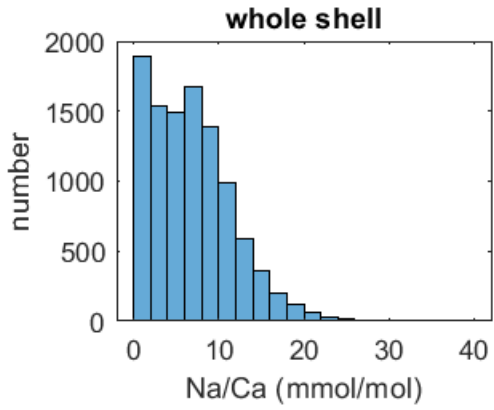
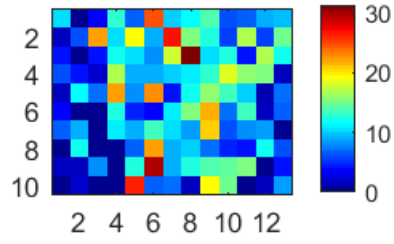
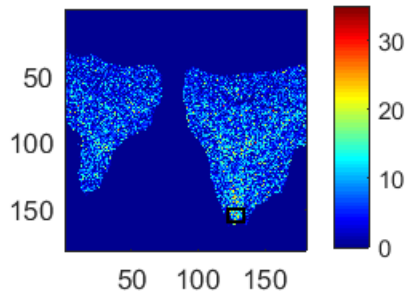
31_2	min	max	mean	median	SD	SE
shell	1.67	51.81	8.21	7.59	5.44	0.07
spine base	1.92	28.01	11.69	10.65	7.24	0.77

Na T.sacculifer 31-3



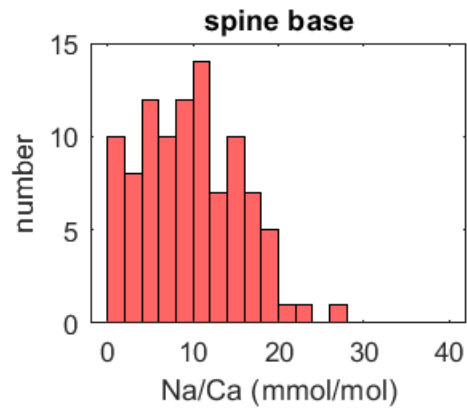
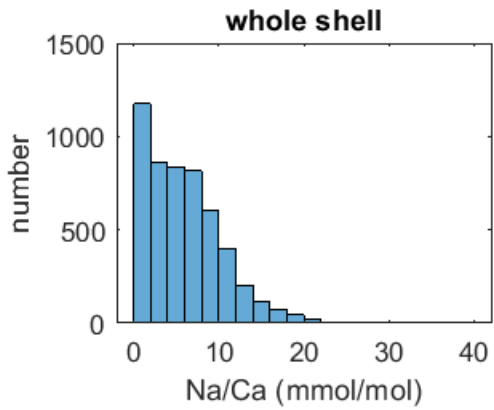
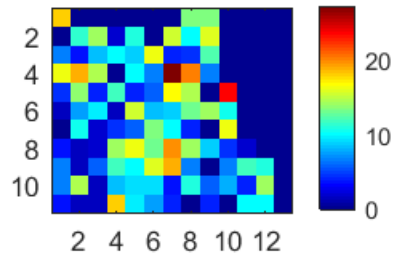
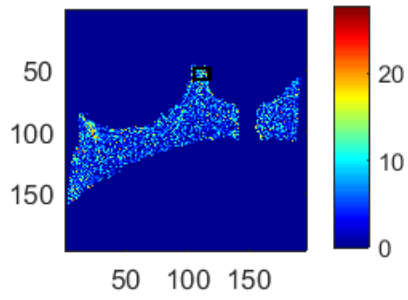
31_3	min	max	mean	median	SD	SE
shell	1.3	42.9	6.502	5.8893	4.3	0.1
spine base	1.5	27.5	10.1	8.7396	5.6	0.5

Na T.sacculifer 31-4



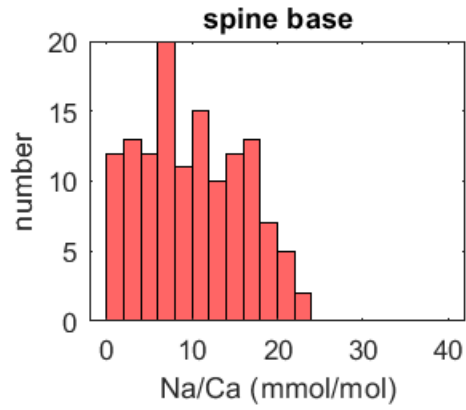
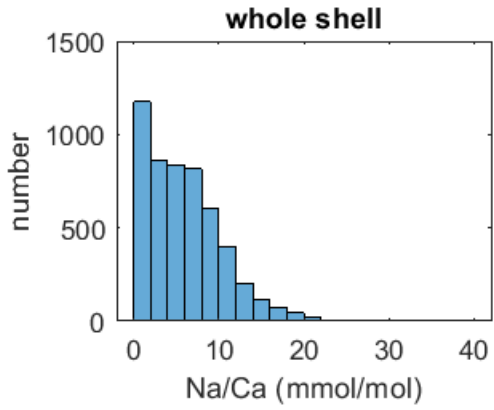
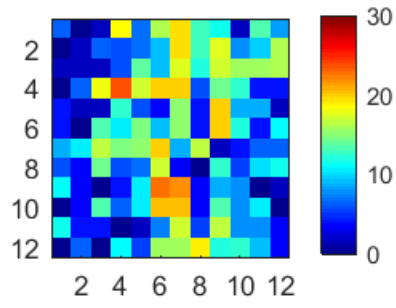
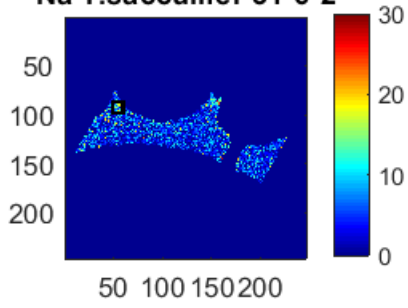
31_4	min	max	mean	median	SD	SE
shell	1.30	52.31	6.94	6.14	4.57	0.04
spine base	1.41	31.37	10.66	10.04	6.40	0.60

Na T.sacculifer 31-6



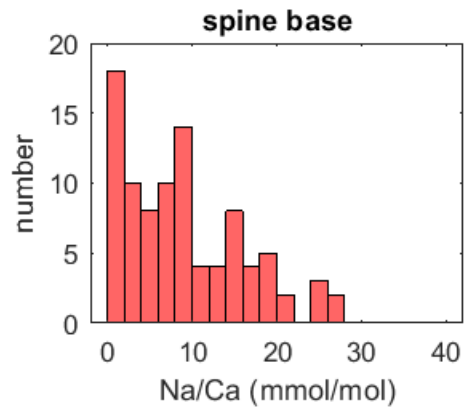
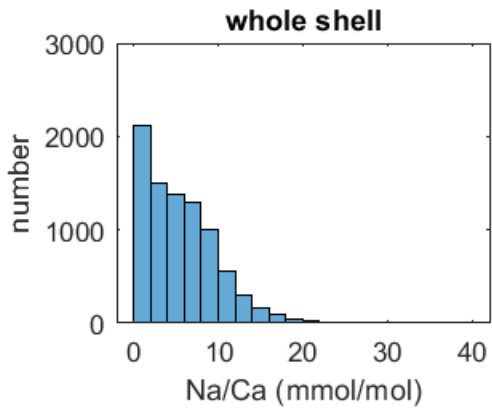
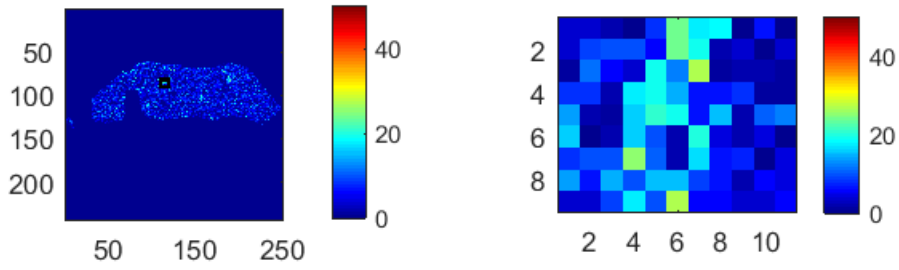
31_6	min	max	mean	median	SD	SE
shell	1.29	27.74	6.14	5.61	4.15	0.06
spine base	1.55	27.36	9.69	9.71	5.60	0.57

Na T.sacculifer 31-6-2

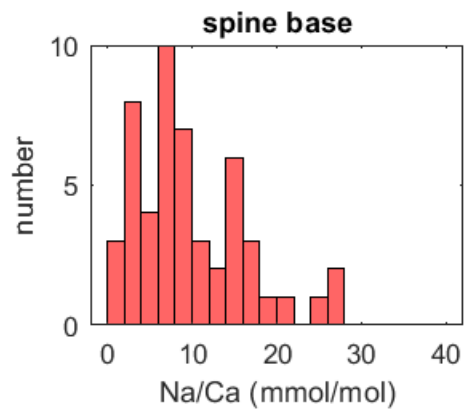
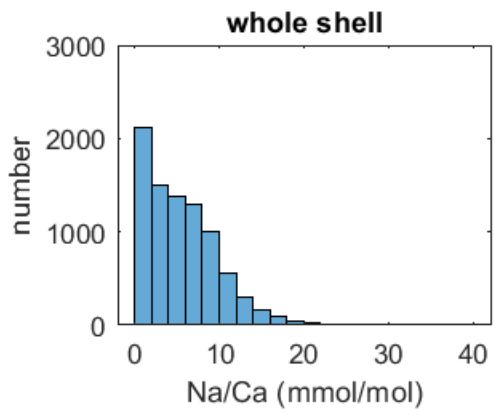
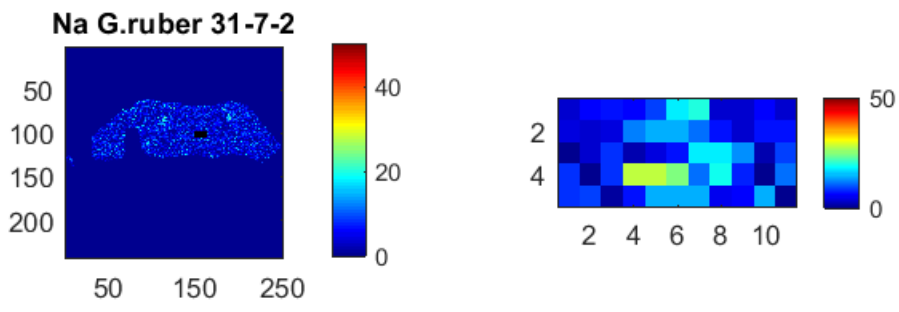


31_6	min	max	mean	median	SD	SE
shell	1.29	27.74	6.14	5.61	4.15	0.06
spine base	1.50	23.88	10.12	9.25	5.87	0.51

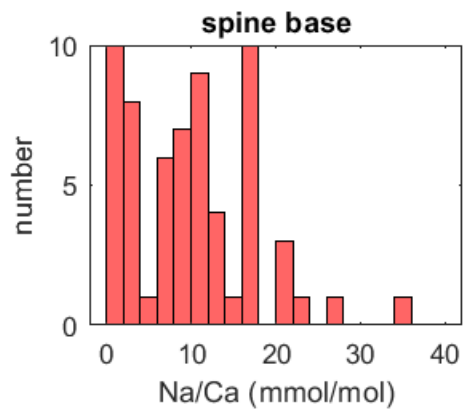
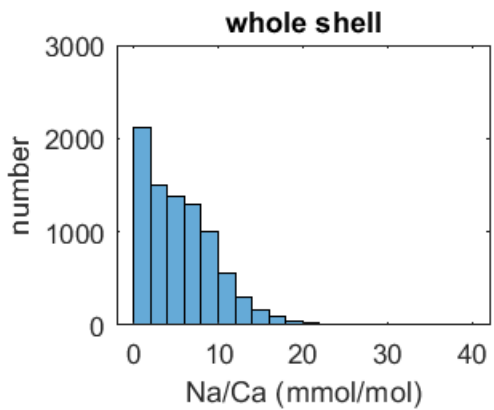
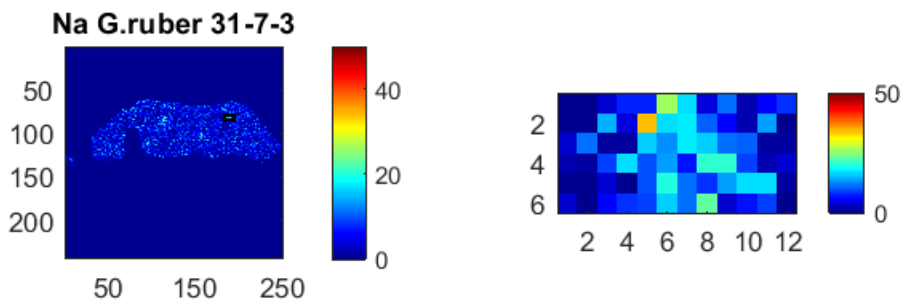
Na G.ruber 31-7-1



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

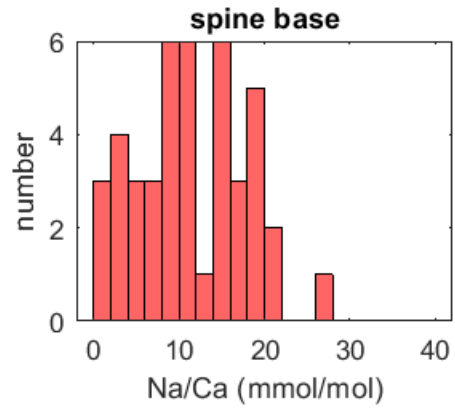
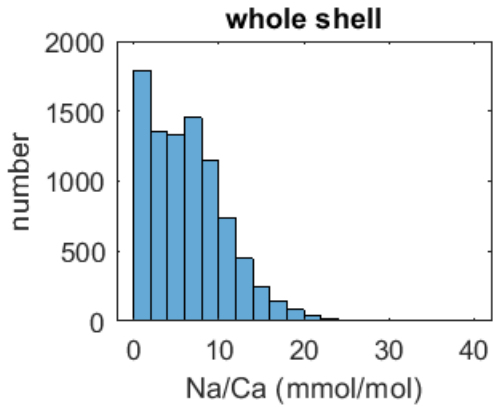
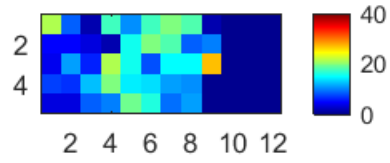
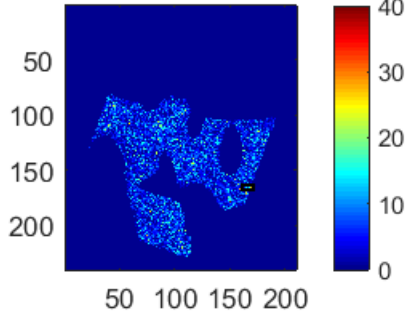


31_7_2	min	max	mean	median	SD	SE
shell	1.3	50.4	5.755	4.4945	3.9	0
spine base	1.4	27.6	9.74	8.0704	6.5	0.9



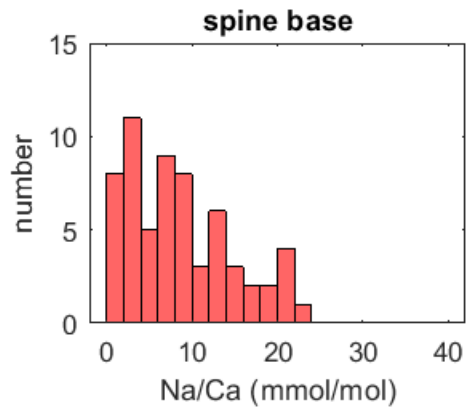
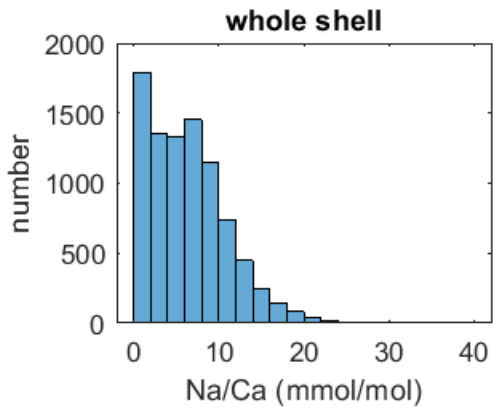
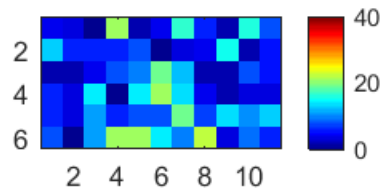
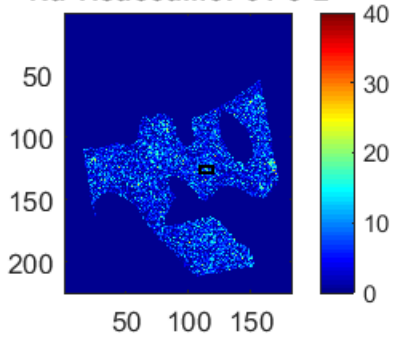
31_7_3	min	max	mean	median	SD	SE
shell	1.3	50.4	5.755	4.4945	3.9	0
spine base	1.4	34.3	10.2	9.1379	7	0.9

Na T.sacculifer 31-8-1



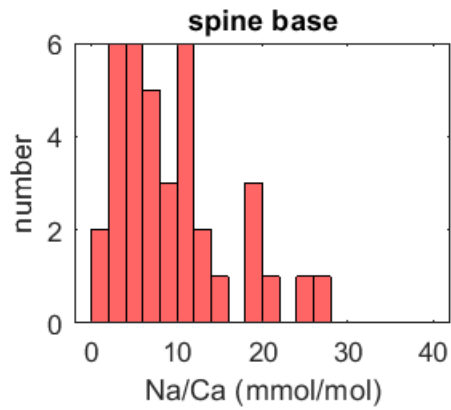
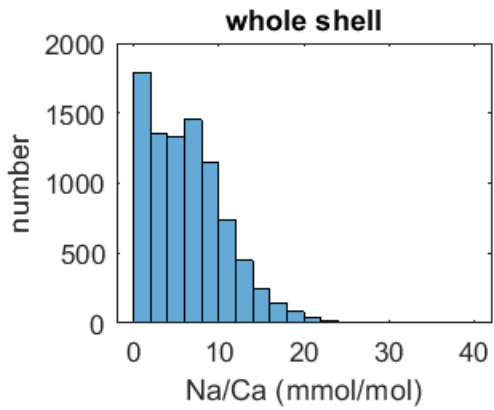
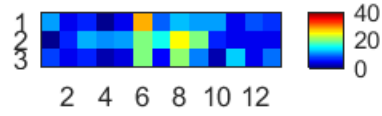
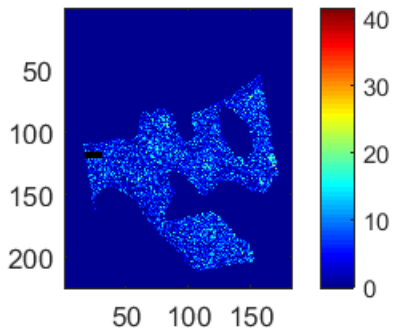
31_8_1	min	max	mean	median	SD	SE
shell	1.2	41.6	6.511	5.9515	4.3	0
spine base	1.4	26.9	11.55	10.723	6.4	1

Na T.sacculifer 31-8-2



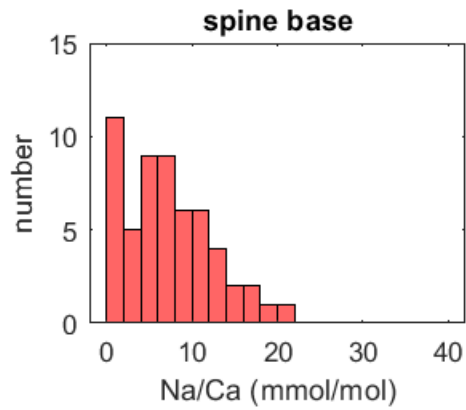
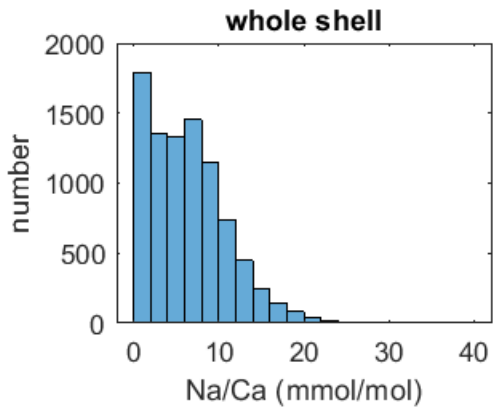
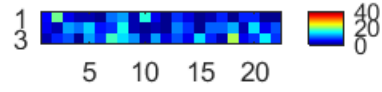
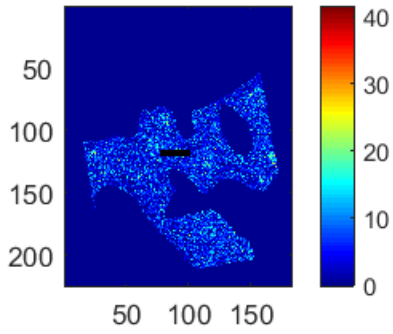
31_8_2	min	max	mean	median	SD	SE
shell	1.2	41.6	6.511	5.9515	4.3	0
spine						
base	1.4	22.1	8.685	7.325	5.9	0.7

Na T.sacculifer 31-8-3



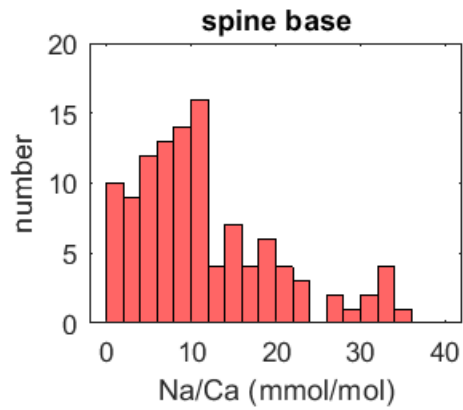
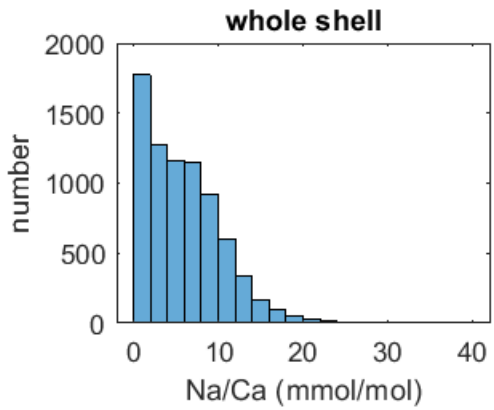
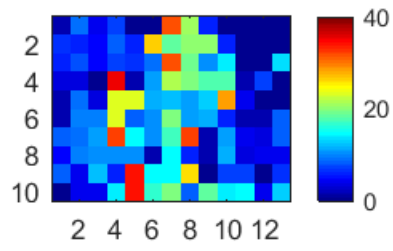
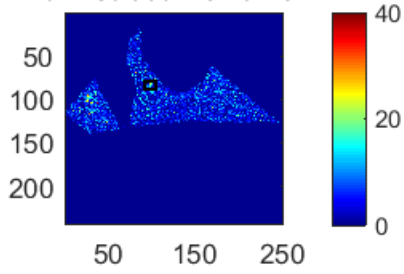
31_8_3	min	max	mean	median	SD	SE
shell	1.2	41.6	6.511	5.9515	4.3	0
spine base	1.6	27.9	9.535	7.6289	6.6	1.1

Na T.sacculifer 31-8-4



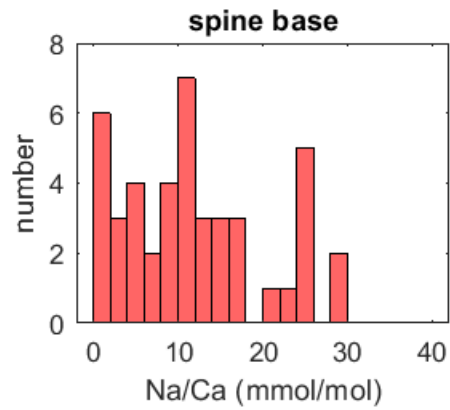
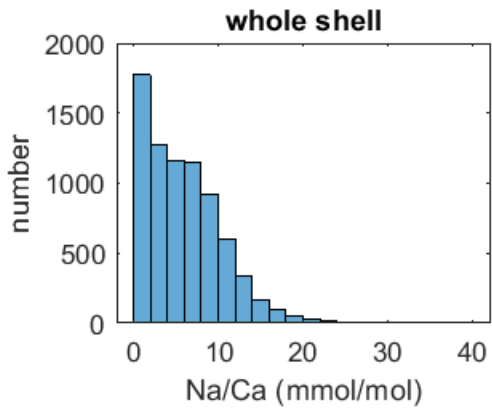
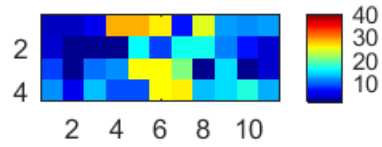
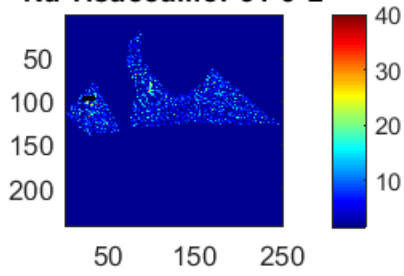
31_8_4	min	max	mean	median	SD	SE
shell	1.2	41.6	6.511	5.9515	4.3	0
spine base	1.4	21.6	7.46	6.4506	4.9	0.7

Na T.sacculifer 31-9-1

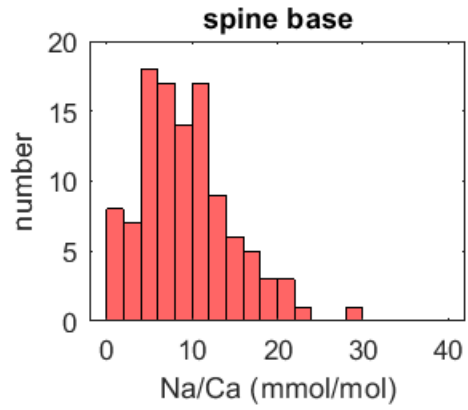
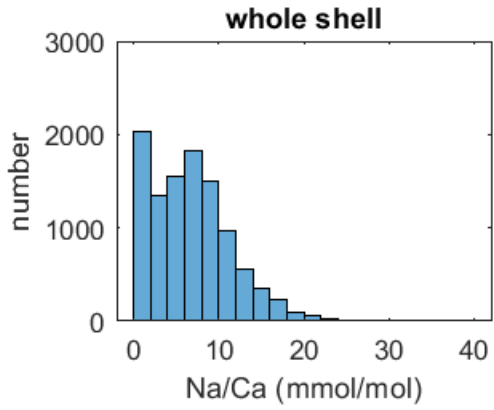
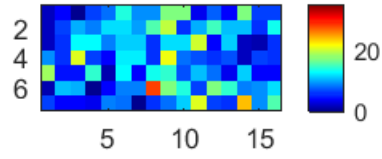
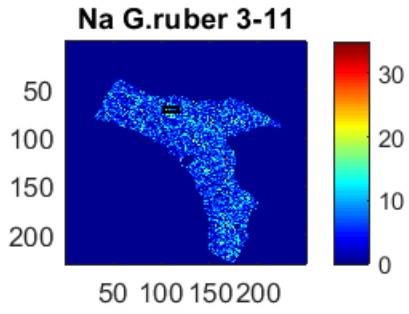


31_9_1	min	max	mean	median	SD	SE
shell	1.2	132	6.165	5.6414	4.6	0.1
spine base	1.5	35.2	11.61	9.6704	8.4	0.8

Na T.sacculifer 31-9-2

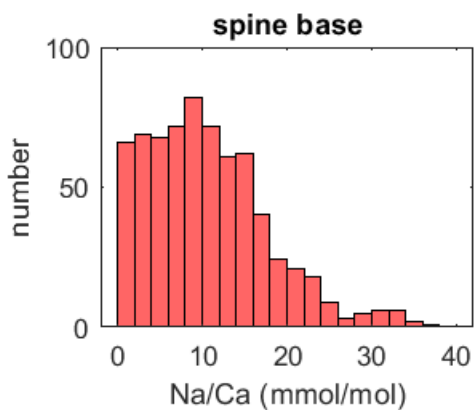
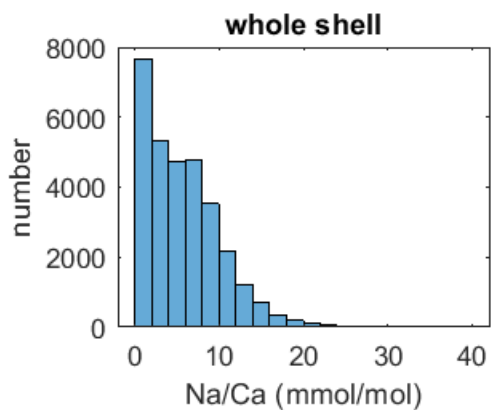
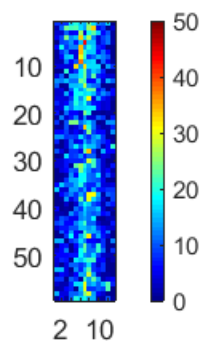
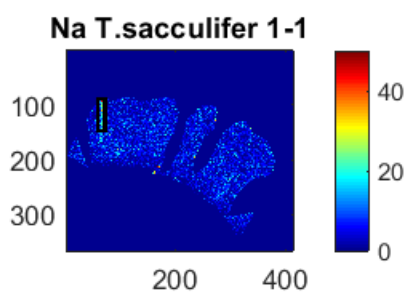


31_9_2	min	max	mean	median	SD	SE
shell	1.2	132	6.165	5.6414	4.6	0.1
spine base	1.5	28.4	11.99	11.255	8.2	1.2

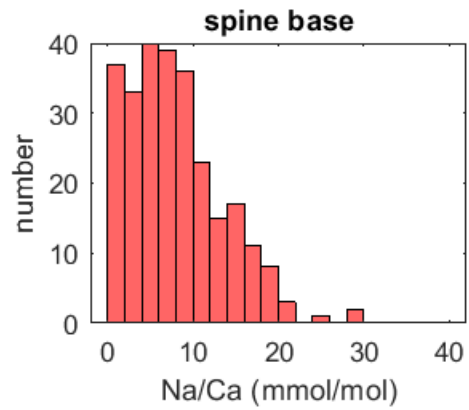
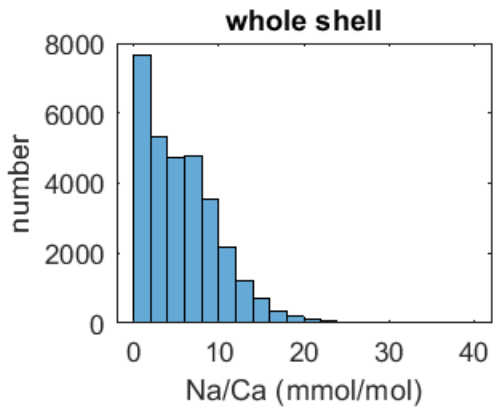
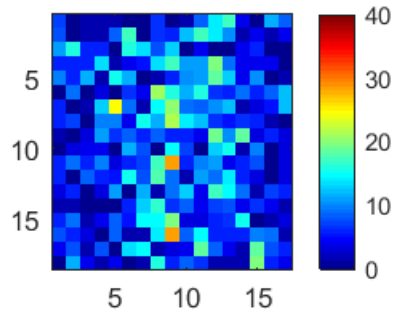
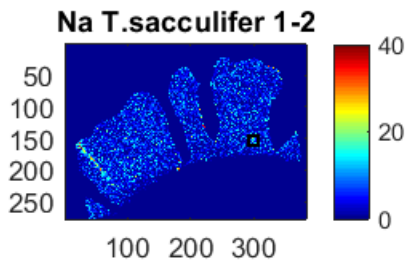


3_11	min	max	mean	median	SD	SE
shell	1.4	38.4	6.852	6.1887	4.4	0
spine base	1.5	28.4	9.345	8.4687	5.3	0.5

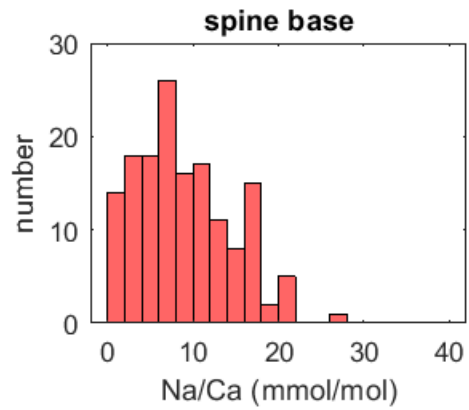
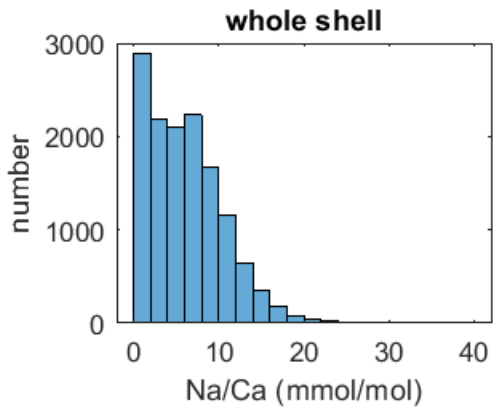
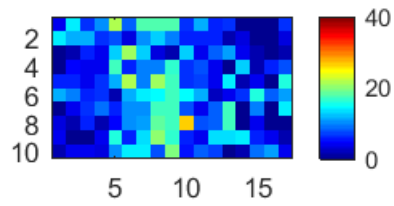
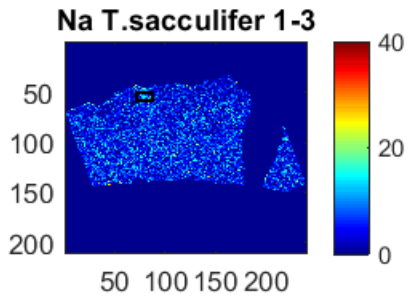
Part 3: Cultured *T. sacculifer* specimens



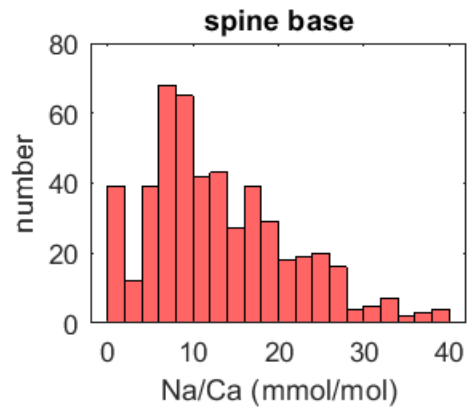
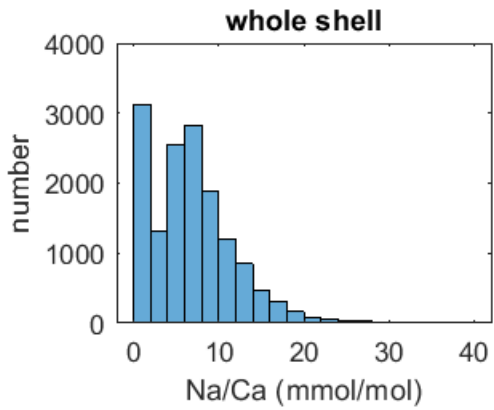
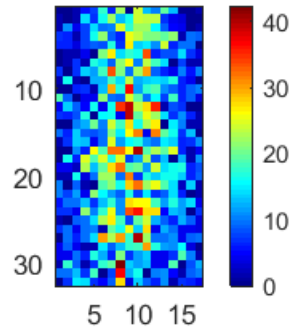
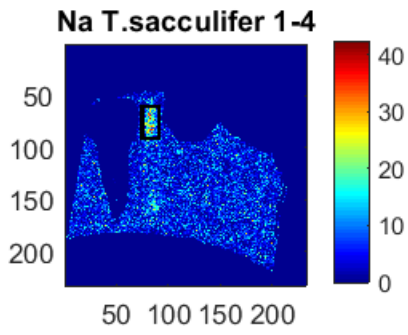
1_1	min	max	mean	median	SD	SE
shell	1.3	108	5.969	5.3616	4.4	0
spine base	1.3	43	10.74	9.7348	7.1	0.3



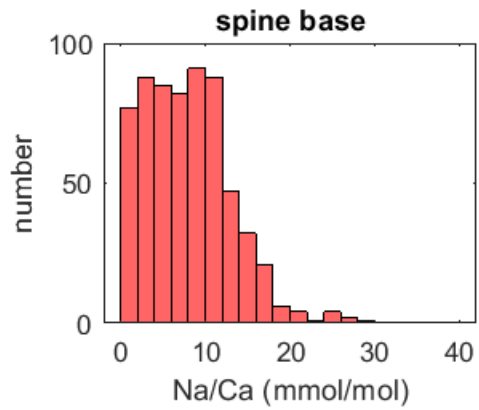
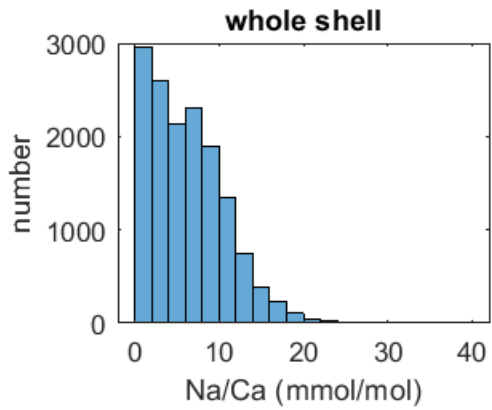
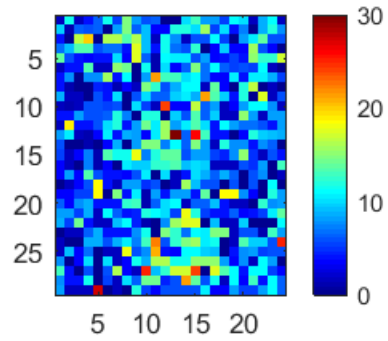
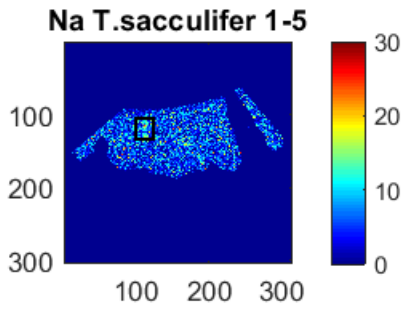
1_1_2	min	max	mean	median	SD	SE
shell	1.3	108	5.969	5.3616	4.4	0
spine base	1.4	28.7	8.159	6.5566	5.3	0.3



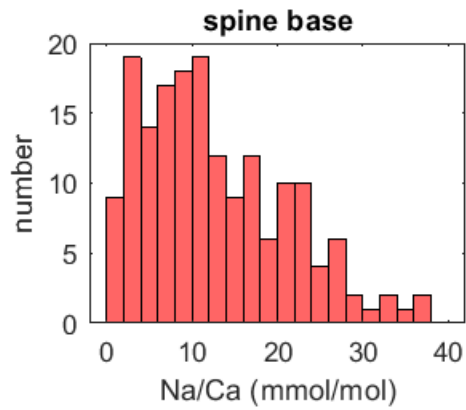
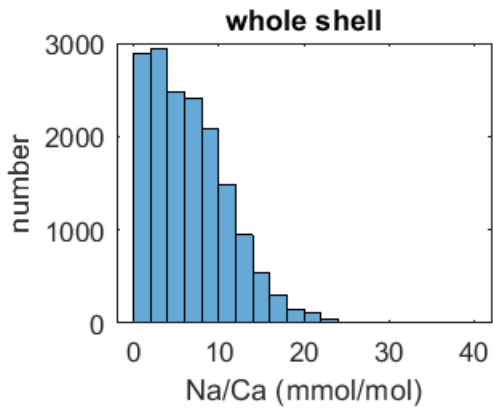
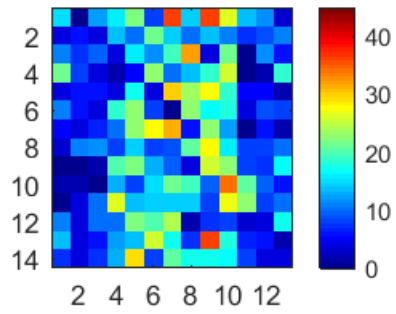
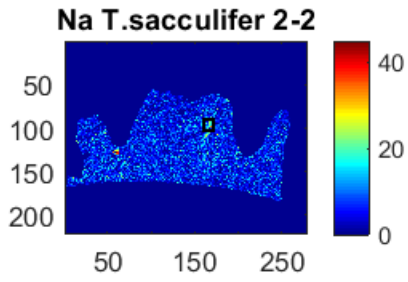
1_3	min	max	mean	median	SD	SE
shell	1.3	114	6.321	5.8649	4.3	0
spine base	1.4	26.7	9.052	7.9622	5.5	0.4



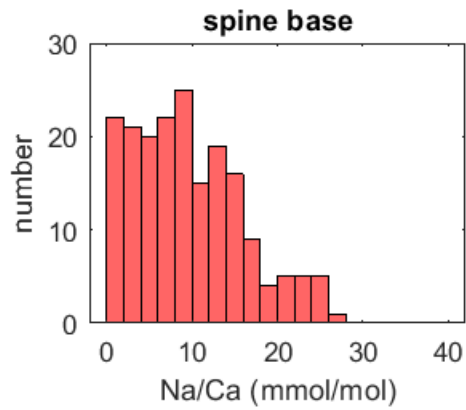
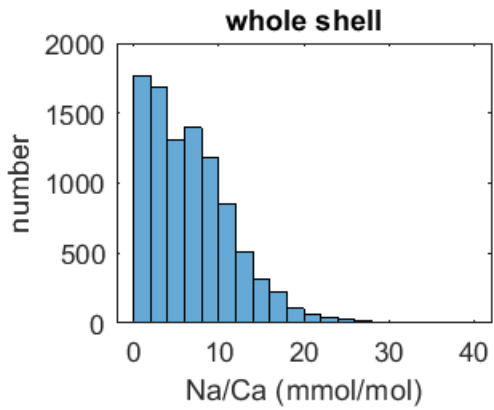
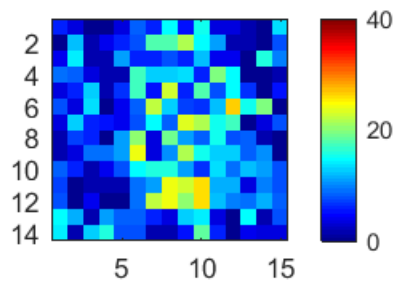
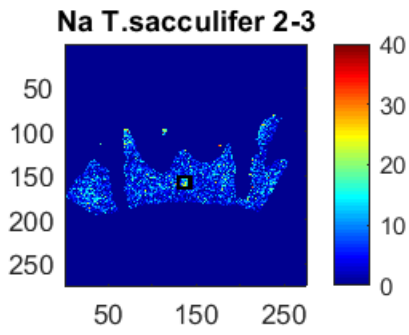
1_4	min	max	mean	median	SD	SE
shell	1.3	42.4	6.899	6.2465	4.8	0
spine base	1.4	42.4	13.14	11.275	8.4	0.4



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

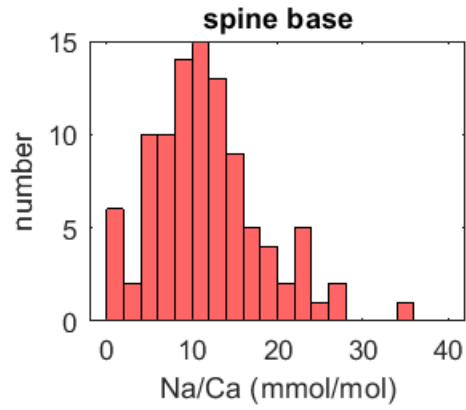
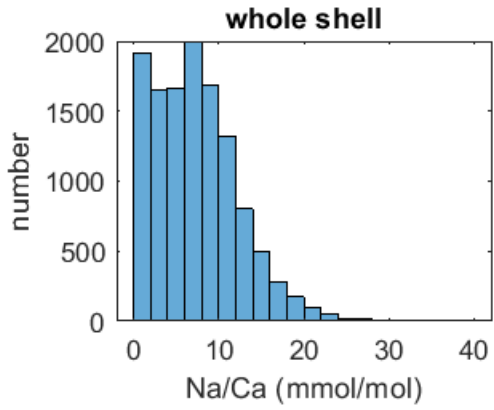
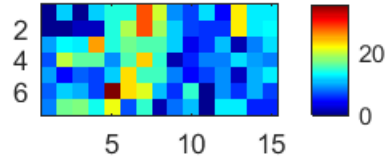
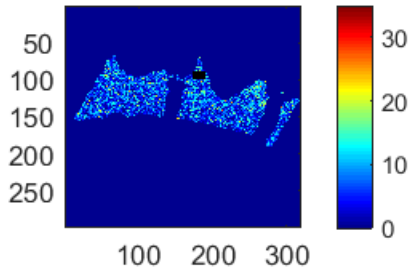


<u>2_2</u>	<u>min</u>	<u>max</u>	<u>mean</u>	<u>median</u>	<u>SD</u>	<u>SE</u>
shell	1.2	60	6.865	5.9637	4.6	0
spine base	1.5	36.5	12.84	10.85	8.3	0.6



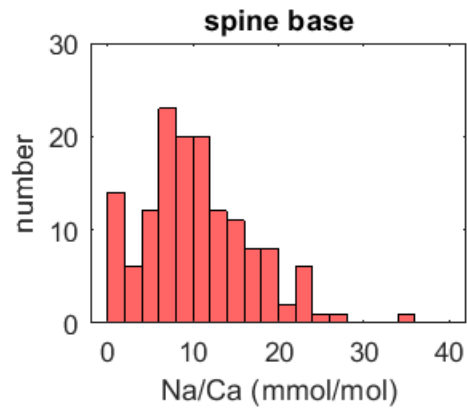
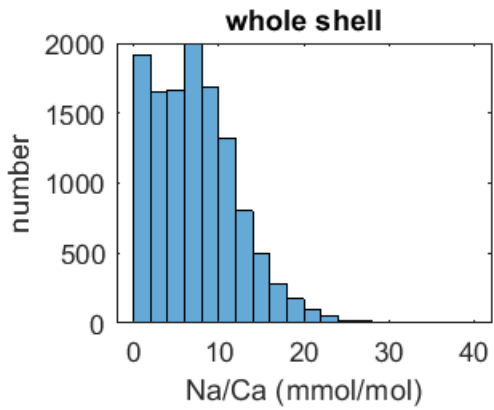
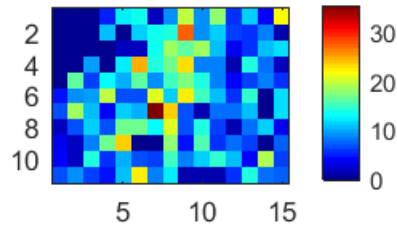
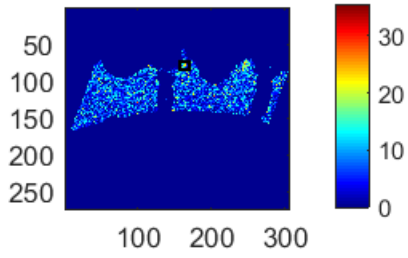
2_3	min	max	mean	median	SD	SE
shell	1.2	55.1	6.965	5.9897	4.9	0
spine base	1.3	26.5	9.728	8.3395	6.2	0.5

Na T.sacculifer 2-4

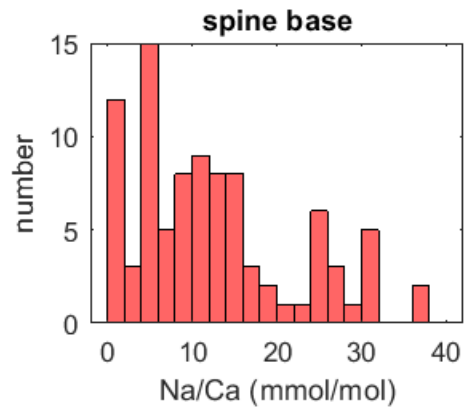
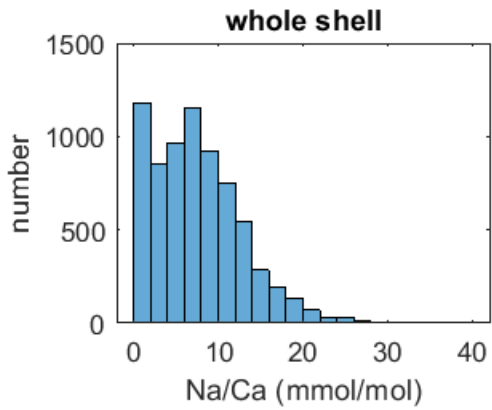
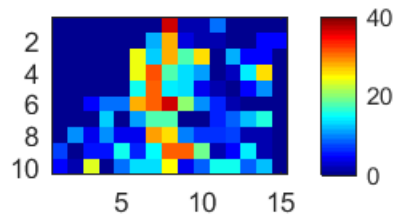
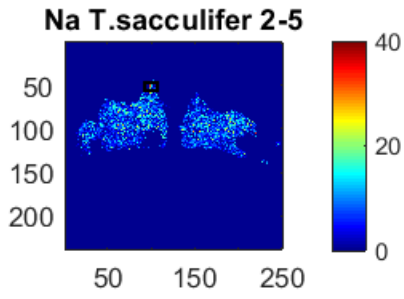


2_4_1	min	max	mean	median	SD	SE
shell	1.3	35.6	7.446	6.4843	4.7	0
spine base	1.4	35.6	11.69	11.014	6.4	0.6

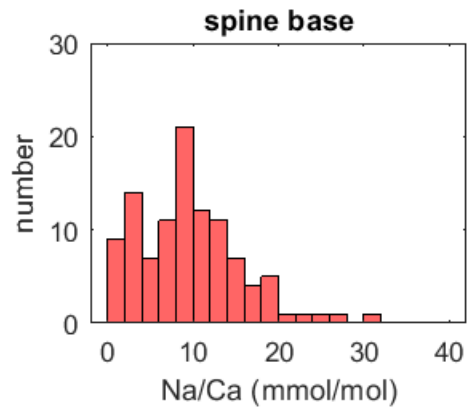
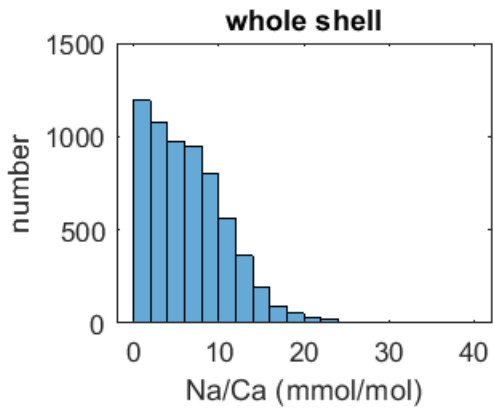
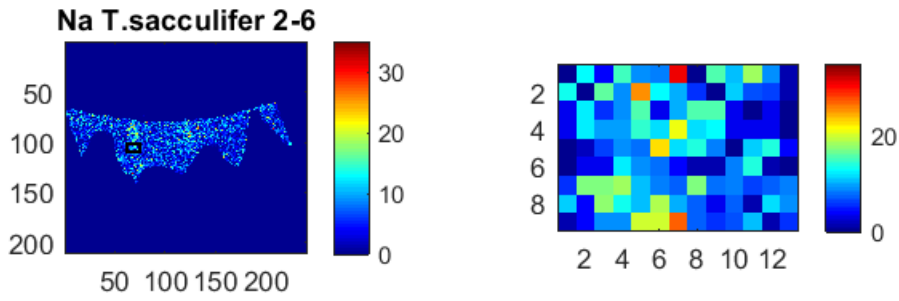
Na T.sacculifer 2-4-2



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



<u>2_5</u>	<u>min</u>	<u>max</u>	<u>mean</u>	<u>median</u>	<u>SD</u>	<u>SE</u>
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



<u>2_6</u>	<u>min</u>	<u>max</u>	<u>mean</u>	<u>median</u>	<u>SD</u>	<u>SE</u>
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