## **Supplementary Information**



**Figure S1.** DS of Crude S.I.-SP and their FGSP Proportion in Relation to the Habitats Baltic Sea and Atlantic Ocean. The boxplots of B-SP represent the DS of the B05-SP and B06-SP batches; the boxplots of A-SP represent the DS of the A05-SP and A09-SP batches.



**Figure S2.** Size Exclusion Chromatogram of Fraction F3 of A09-SP (*i.e.*, Sulfated Galactofucan) (red line:  $M_r$  (MALLS); blue line:  $M_{HV}$  (RI)). A09-SP-F3 revealed a single peak with a mean  $M_r$  of 416,000 ± 28,000 (MALLS) and 449,000 ± 15,000 (RI), respectively. The further peaks at about 28 mL are due to solvent effects.

Glycosyl Residue	Position of	<b>Deduced Position</b>	A09-SP-F3	A09-SP-F3
	<b>O-Methyl Group</b>	of Substitution	(native)	(Desulfated)
Fucosyl	2,3,4	terminal	-	42.6
	2,3	4	-	1.2
	2,4	3	-	33.4
	3,4	2	23.8	2.2
	2	3,4	35.3	-
	4	2,3	15.5	3.8
		2,3,4	8.5	-
Total Fucose			<u>83.1</u>	<u>83.1</u>
Galactosyl	2,3,4,6	terminal	-	1.5
	2,4,6	3	3.3	3.7
	2,3,6	4	-	3.7
	2,3,4	6	-	5.3
	2,6	3,4	2.5	-
	2,4	3,6	8.5	-
	2,3	4,6	-	2.3
	2	3,4,6	2.3	-
Total Galactose			<u>16.6</u>	<u>16.6</u>
Xylosyl	2,3,4	terminal	<1	<1
	2,3/3,4	4/2	<1	<1

Table S1. Methylation Analysis Data of Native and Desulfated A09-SP-F3<sup>a,b,c</sup>.

<sup>a</sup> The numbers indicate % (mol/mol) of partially methylated alditol acetates (PMAA); <sup>b</sup> Due to degradation and especially loss of fucose during desulfation, the fucose data of desulfated A09-SP-F3 have been upscaled to 83.1% and those for galactose and xylose accordingly downscaled for simpler interpretation. However, the methylation data on desulfated A09-SP-F3 have to be treated with caution; <sup>c</sup> All monosaccharides showed to be present in pyranose form.

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