

Table S1: Assembly results and annotation success of *Zostera marina* transcriptome sequencing against *A. thaliana* and *O. sativa* orthologous genes (BLASTX, e-val < 10<sup>-4</sup>). There were 27,400 and 56,800 genes in the reference proteomes for *A. thaliana* and *O. sativa*, respectively

<i>Zostera marina</i>		# contigs in assembly	Median length contigs (bp)	reference proteome#	# annotated contigs	annotated contigs [%]	# unique genes found	average # of contigs mapping to unique reference gene
Assembly	# reads				contigs			
big clone	866,838	35,918	614	<i>A. thaliana</i>	24,813	69.08	11,135	2.2
Northern population	540,973	39,445	493		30,073	76.24	8,673	3.5
Southern population	571,965	41,707	483		32,484	77.89	8,579	3.8
mapping assembly	1,979,776	40,689	547		29,147	71.63	11,544	2.5
big clone	See above	See above	See above	<i>O. sativa</i>	26,023	72.45	11,400	2.3
Northern population	See above	See above	See above		30,178	76.51	8,811	3.4
Southern population	See above	See above	See above		32,190	77.18	8,722	3.7
mapping assembly	See above	See above	See above		30,329	74.54	11,720	2.6

#Orthologous genes were identified via BLASTX (e ≤ 0.0001) against the respective reference proteome.