Genomes of surface isolates of *Alteromonas macleodii*: the life of a widespread marine opportunistic copiotroph

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Supplementary Table 1. Sequencing details.

		A. macleodii strains		
		673	AD45	BS11
Sequencing technology				
Roche (454)	Total pb	124030529	138685183	121195022
	Average read length (bp)	478	470	456
	Paired End (Reads/Average)	500025/2922	562619/2965	505401/2970
Illumina (Solexa)	Total pb	965804846	965589766	1004556296
	Average read length (bp)	38	38	38

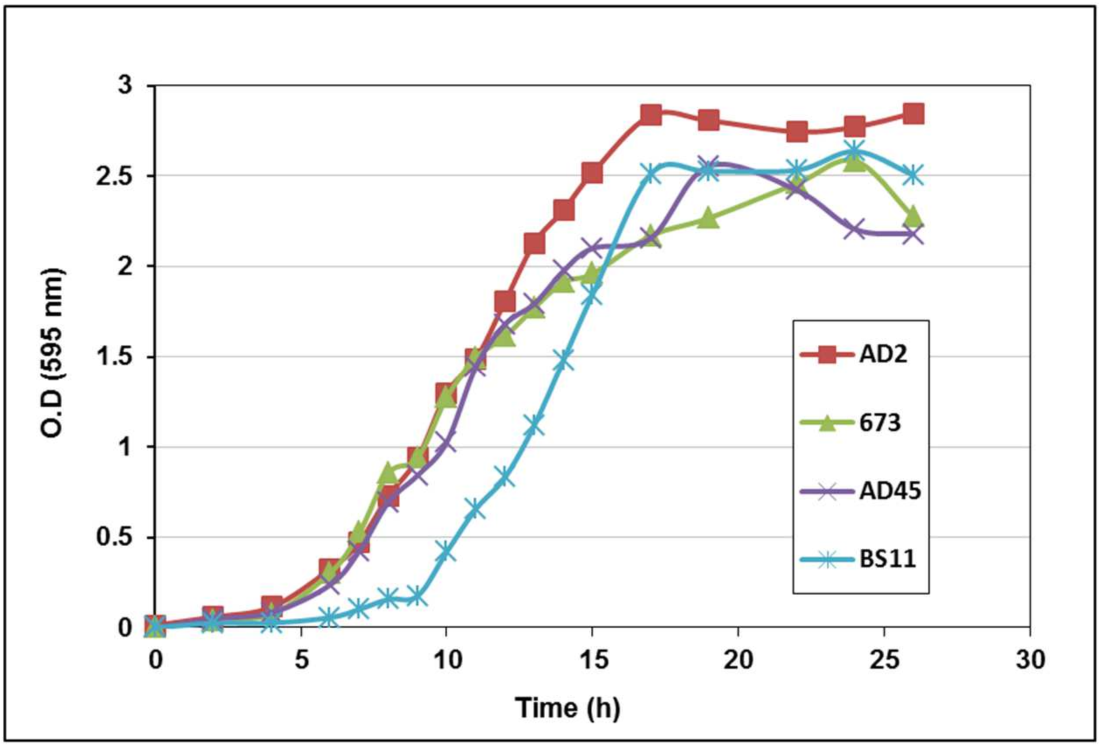
Supplementary Table 2. List of Housekeeping-genes used for the phylogenetic tree.

universal stress protein UspE
Transcriptional regulator
GTP binding protein Era
sodium calcium exchanger
histone deacetylase superfamily protein
hydroxymethylglutaryl CoA lyase
putative ATP synthase F0 A subunit
malate dehydrogenase
putative exopolysaccharide biosynthesis protein
sulfate adenylyltransferase subunit 2
glucose 1 phosphate thymidylyltransferase
glutaminase
chemotaxis protein CheV
diguanylate cyclase
tyrosine recombinase
NAD kinase
putative acyltransferase
methionyl tRNA formyltransferase
rod shape determining protein MreC
putative transcriptional regulator
exopolyphosphatase related protein
MscS Mechanosensitive ion channel
2 methylisocitrate lyase
Zn dependent hydrolase glyoxylase family protein
peptide transport protein ABC superfamily membrane
fused GNAT family acetyltransferase/PaaI related uncharacterized conserved domain
hypothetical protein AmacA2_01913
ribonuclease BN
ABC transporter ATP binding protein
chromosome replication initiation inhibitor protein
K dependent Na /Ca exchanger related protein
flagellar basal body rod protein FlgG
response regulator receiver modulated CheW protein
flagellar biosynthesis sigma factor
recombination associated protein
hypothetical protein AmacA2_03691
DNA adenine methylase
putative transcriptional regulator with periplasmic binding protein domain LysR family
Conserved membrane protein RarD
GumN
porphobilinogen deaminase
tyrosine recombinase
DNA binding transcriptional activator GcvA
SAM dependent methyltransferase
putative transmembrane protein
ABC type amino acid transport/signal transduction system periplasmic component/domain
hypothetical protein AmacA2_09356

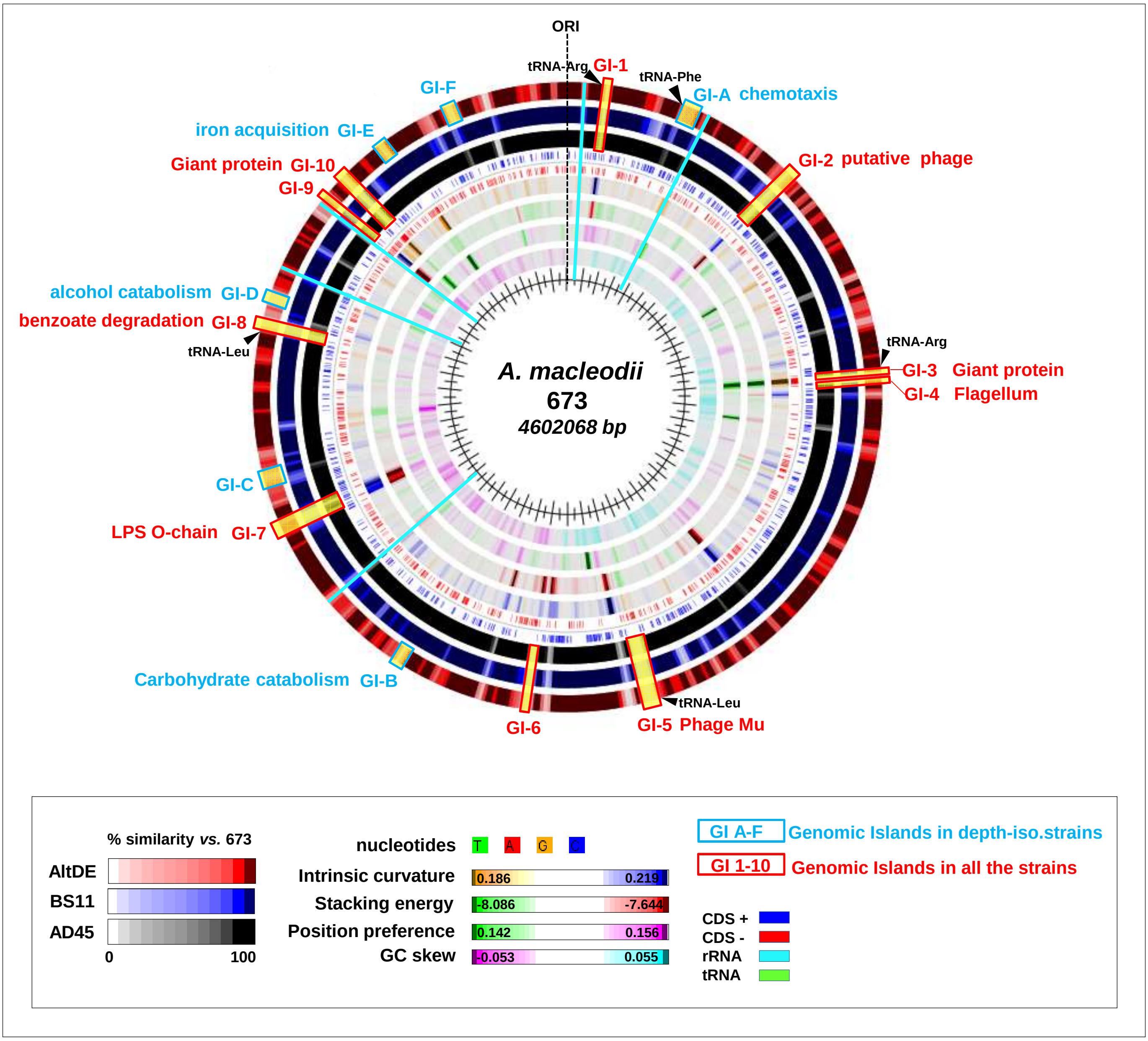
S adenosyl methyltransferase MraW
ribose phosphate pyrophosphokinase
lipoyl synthase
geranyltranstransferase
UDP 3 O [3 hydroxymyristoyl] N acetylglucosamine deacetylase
peptidase M23/M37 family protein
putative flagellar biosynthesis
integral membrane protein
predicted glutathione S transferase
hypothetical protein AmacA2_01513
Phosphatidylserine decarboxylase
molecular chaperone Dna K
RNA polymerase beta subunit rpoB
Succinyl-CoA ligase
hypothetical protein AmacA2_00434
phosphoglucomutase
methionyl-tRNA synthetase
serine hydroxymethyltransferase
β subunit of the DNA gyrase
transcriptional regulator

Supplementary Table-3. Growth of *A. macleodii* in different conditions.

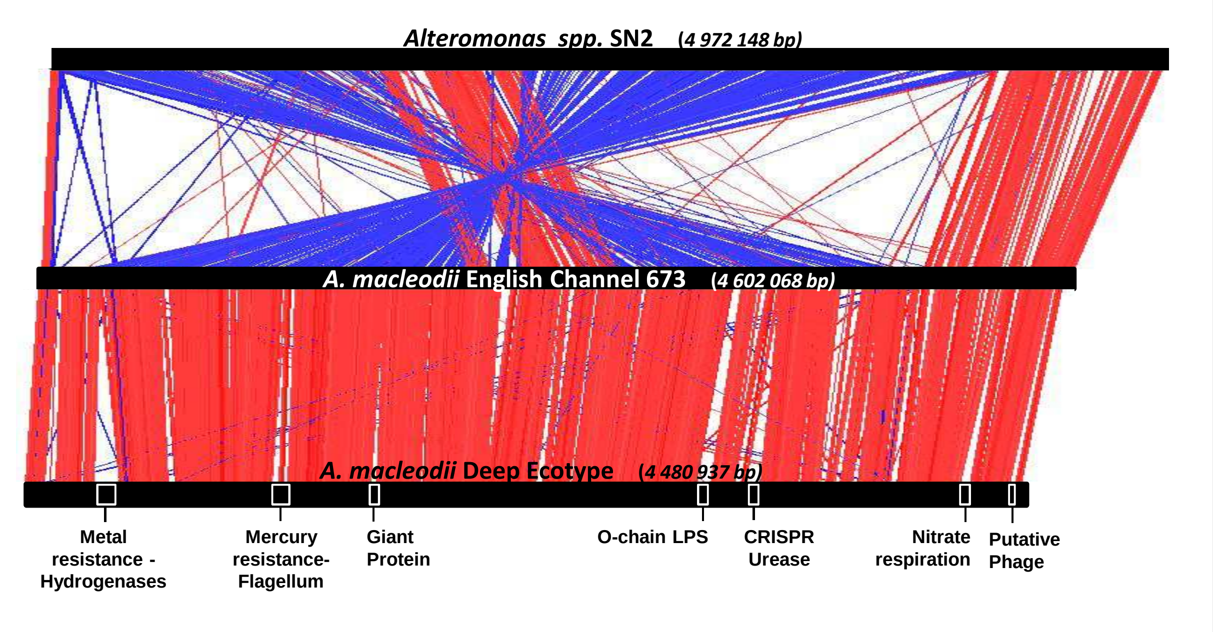
A. macleodii	Temperature (ºC)		Salinity (%NaCl)		Minimum Inhibitory Concentration	
strains	min	max	min	max	$Zn(CH_3COO)$ (Mm)	$HgCl_2$ (mM)
AltDE	10	42	0,50	20	5	0,1
673	10	45	0,50	19	5	0,05
AD45	10	43	0,50	18	5	0,05
BS11	10	42	0,25	18	5	0,05



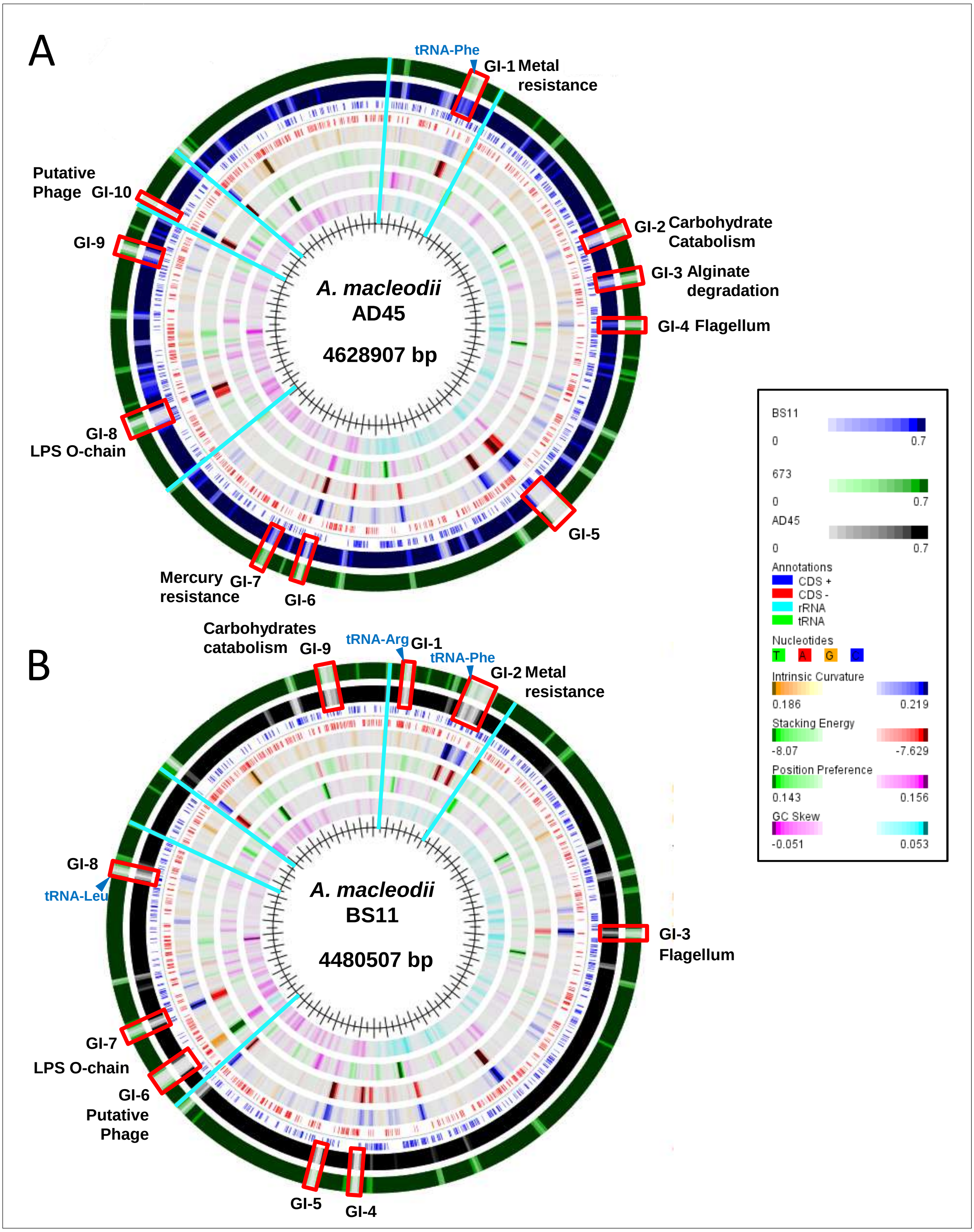
Supplementary Figure 1. Growth of *A. macleodii* strains AltDE, AD45, BS11, ATCC and 673 in marine broth at 20ºC. Cultures were carried out in 250 ml erlenmeyer flasks with 50 ml medium and orbitally shaken at 200 rpm.



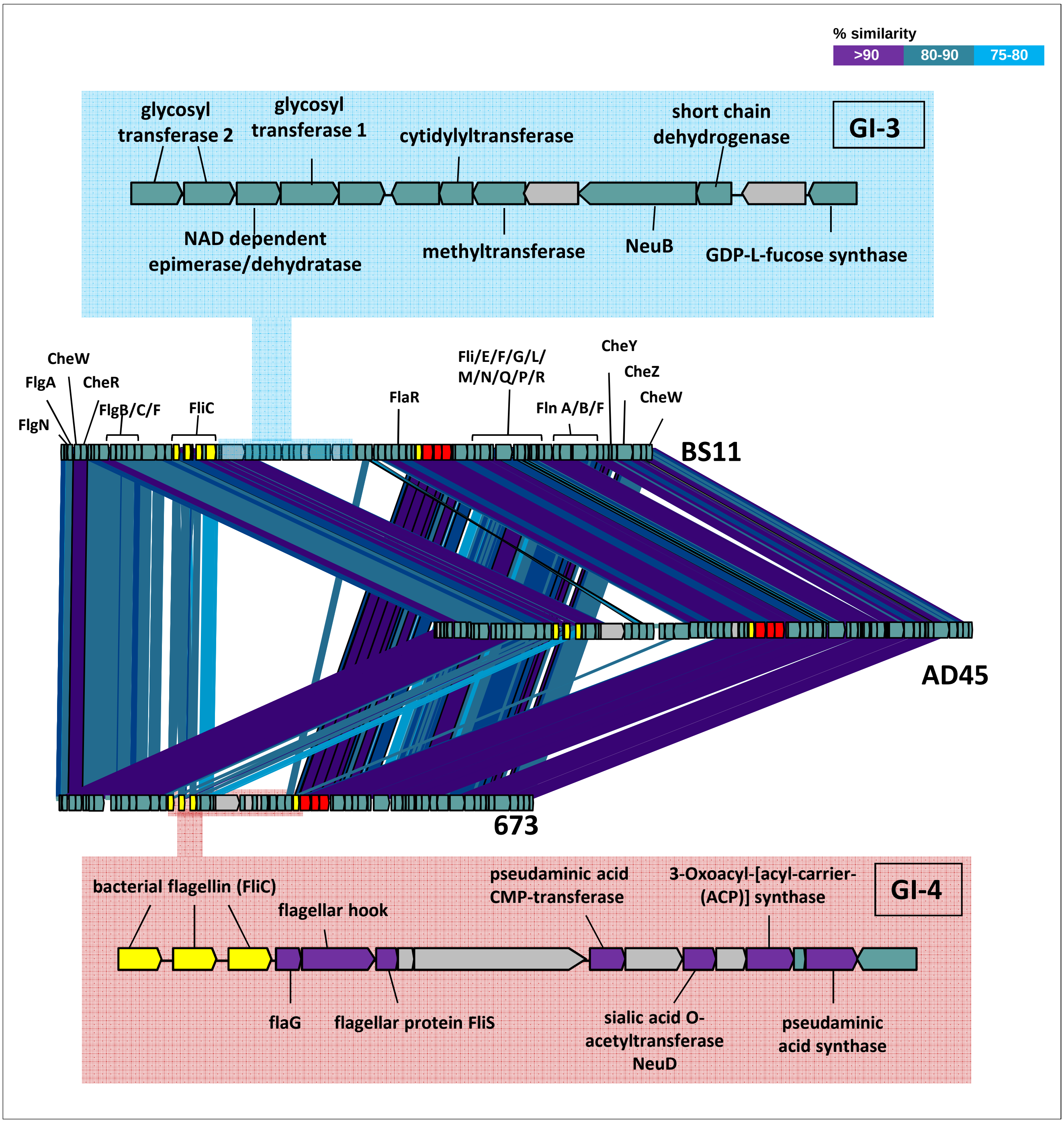
Supplementary Figure 2: Circular representations of the *A. macleodii* 673 genome using genome atlas (http://www.cbs.dtu.dk/index.shtml). Rings from outside to inside: Circles 1,2 and 3: Circular representation of the *A. macleodii* strains chromosome, AltDE, BS11 and AD45 (outside to inside). Circle 4: CDs from the 673 genome in the positive strand. Circle 5: CDS from the 673 genome in the negative strand. Circle 6: Intrinsic curvature. Circle 7: Stacking energy. Circle 8: Position preference. Circle 9: GC skew. Red squares indicates genomic island of 673 compare with all the strains. Blue squares indicates genomic island present in all the surface strains but not in AltDE.



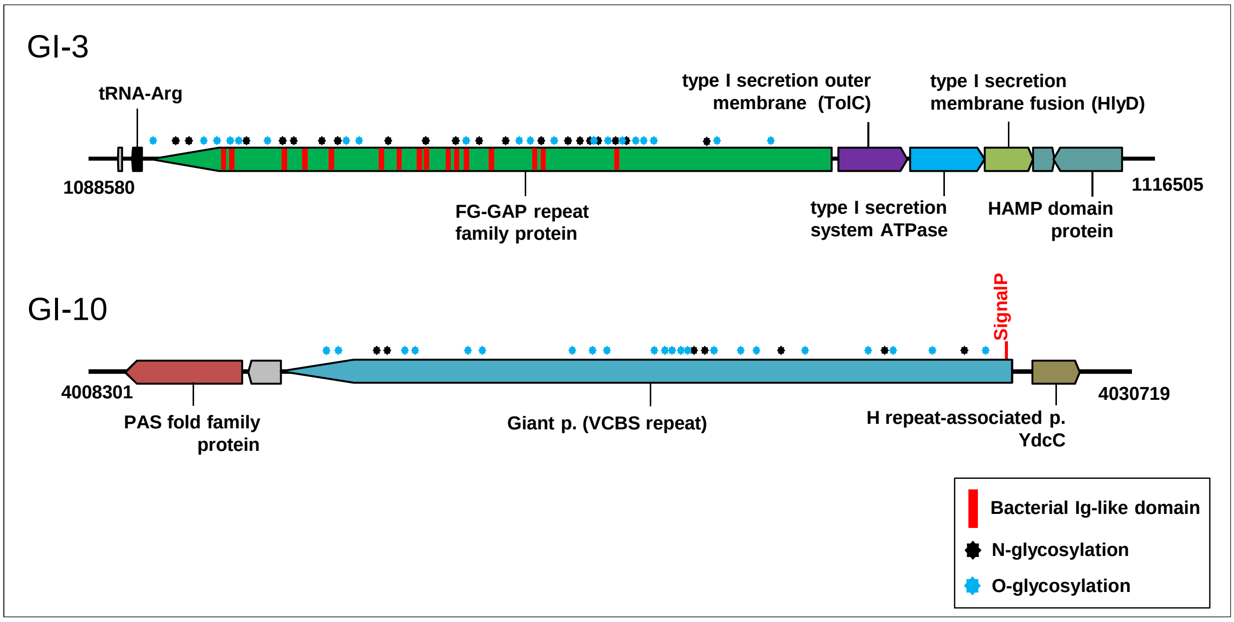
Supplementary Figure 3: Genome comparison of *A. macleodii* 673 versus *Alteromonas* sp. SN2 and *A. macleodii* Deep Ecotype. Chromosomes were compared using ACT. Red lines connect homologous regions present in the same orientation while the blue lines connect regions of inverted orientation. White square indicates GI as described in (Ivars et al, 2008) for AltDE.



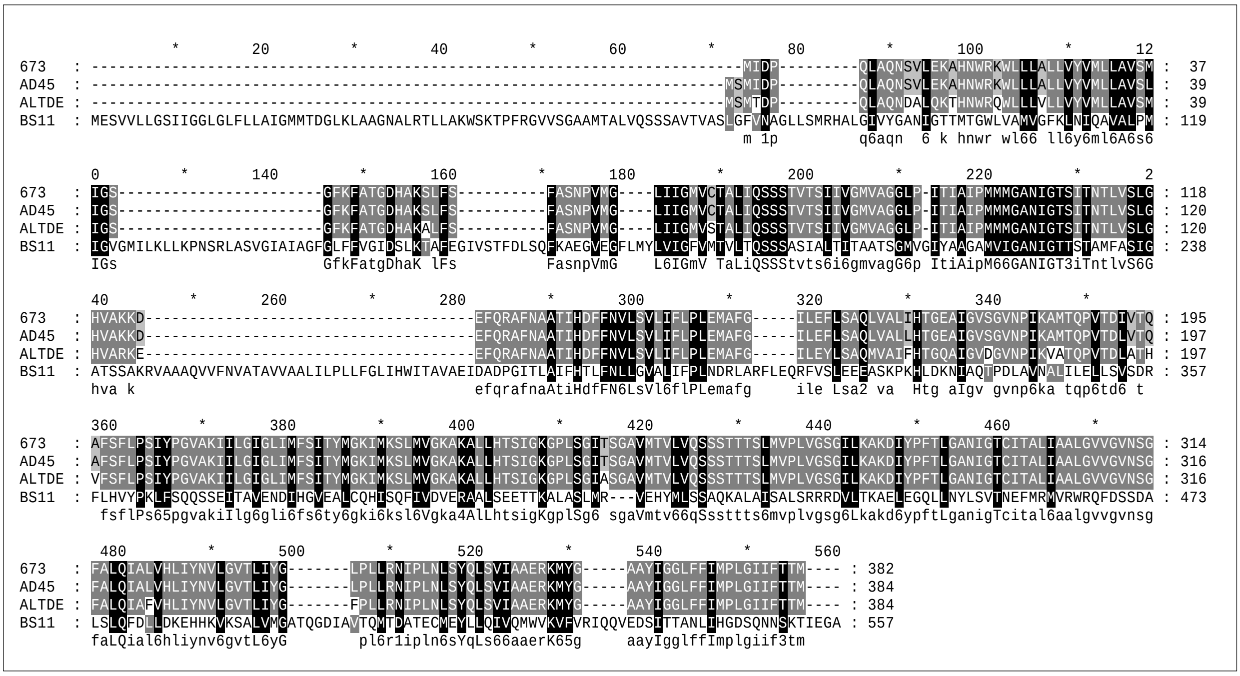
Supplementary Figure 4. Circular representations of *the A. macleodii* AD45 and BS11 genome using genome atlas (http://www.cbs.dtu.dk/index.shtml). (A) AD45 genome as a reference. Rings from the outside to inside: Circles 1 and 2: Circular representation of the A. macleodii strains chromosome 673 and BS11 respectively. (B) BS11 genome as a reference. Rings from the outside to inside: Circles 1 and 2: Circular representation of the A. macleodii strains chromosome 673 and AD45 respectively. Rests of the circles are common. Circle 3: CDS in the positive strand in blue. Circle 4: CDS in the negative strand in red. Circle 5: Intrinsic curvature. Circle 6: Stacking energy. Circle 7: Position preference. Circle 8: GC skew. Red squares indicates genomic island.



Supplementary Figure 5: Schematic representation comparing the flagellum gene clusters of *A. maclodii* AltDE, 673, AD45 and BS11 strains**.** The hypervariable region GI4 in 673 and GI3 of BS11 have been enlarged to indicate individual genes.



Supplementary Figure 6. Schematic representations fo the giant proteins found in *A. macleodii* 673 GI3 and GI10.



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                 *        20         *        40         *        60         *        80         *       100         *       12
673   : -------------------------------------------------------------------------MIDP---------QLAQNSVLEKAHNWRKWLLLALLVYVMLLAVSM :  37
AD45  : -----------------------------------------------------------------------MSMIDP---------QLAQNSVLEKAHNWRKWLLLALLVYVMLLAVSL :  39
ALTDE : -----------------------------------------------------------------------MSMTDP---------QLAQNDALQKTHNWRQWLLLVLLVYVMLLAVSM :  39
BS11  : MESVVLLGSIIGGLGLFLLAIGMMTDGLKLAAGNALRTLLAKWSKTPFRGVVSGAAMTALVQSSSAVTVASLGFVNAGLLSMRHALGIVYGANIGTTMTGWLVAMVGFKLNIQAVALPM : 119
                                                                                 m 1p         q6aqn  6 k hnwr wl66 ll6y6ml6A6s6

        0         *       140         *       160         *       180         *       200         *       220         *       2
673   : IGS-----------------------GFKFATGDHAKSLFS----------FASNPVMG----LIIGMVCTALIQSSSTVTSIIVGMVAGGLP-ITIAIPMMMGANIGTSITNTLVSLG : 118
AD45  : IGS-----------------------GFKFATGDHAKSLFS----------FASNPVMG----LIIGMVCTALIQSSSTVTSIIVGMVAGGLP-ITIAIPMMMGANIGTSITNTLVSLG : 120
ALTDE : IGS-----------------------GFKFATGDHAKALFS----------FASNPVMG----LIIGMVSTALIQSSSTVTSIIVGMVAGGLP-ITIAIPMMMGANIGTSITNTLVSLG : 120
BS11  : IGVGMILKLLKPNSRLASVGIAIAGFGLFFVGIDSLKTAFEGIVSTFDLSQFKAEGVEGFLMYLVIGFVMTVLTQSSSASIALTITAATSGMVGIYAAGAMVIGANIGTTSTAMFASIG : 238
        IGs                       GfkFatgDhaK lFs          FasnpVmG    L6IGmV TaLiQSSStvts6i6gmvagG6p ItiAipM66GANIGT3iTntlvS6G

        40         *       260         *       280         *       300         *       320         *       340         *
673   : HVAKKD-------------------------------------EFQRAFNAATIHDFFNVLSVLIFLPLEMAFG-----ILEFLSAQLVALIHTGEAIGVSGVNPIKAMTQPVTDIVTQ : 195
AD45  : HVAKKD-------------------------------------EFQRAFNAATIHDFFNVLSVLIFLPLEMAFG-----ILEFLSAQLVALLHTGEAIGVSGVNPIKAMTQPVTDLVTQ : 197
ALTDE : HVARKE-------------------------------------EFQRAFNAATIHDFFNVLSVLIFLPLEMAFG-----ILEYLSAQMVAIFHTGQAIGVDGVNPIKVATQPVTDLATH : 197
BS11  : ATSSAKRVAAAQVVFNVATAVVAALILPLLFGLIHWITAVAEIDADPGITLAIFHTLFNLLGVALIFPLNDRLARFLEQRFVSLEEEASKPKHLDKNIAQTPDLAVNALILELLSVSDR : 357
        hva k                                      efqrafnaAtiHdfFN6LsVl6flPLemafg     ile Lsa2 va  Htg aIgv gvnp6ka tqp6td6 t

        360         *       380         *       400         *       420         *       440         *       460         *
673   : AFSFLPSIYPGVAKIILGIGLIMFSITYMGKIMKSLMVGKAKALLHTSIGKGPLSGITSGAVMTVLVQSSSTTTSLMVPLVGSGILKAKDIYPFTLGANIGTCITALIAALGVVGVNSG : 314
AD45  : AFSFLPSIYPGVAKIILGIGLIMFSITYMGKIMKSLMVGKAKALLHTSIGKGPLSGITSGAVMTVLVQSSSTTTSLMVPLVGSGILKAKDIYPFTLGANIGTCITALIAALGVVGVNSG : 316
ALTDE : VFSFLPSIYPGVAKIILGIGLIMFSITYMGKIMKSLMVGKAKALLHTSIGKGPLSGIASGAVMTVLVQSSSTTTSLMVPLVGSGILKAKDIYPFTLGANIGTCITALIAALGVVGVNSG : 316
BS11  : FLHVYPKLFSQQSSEITAVENDIHGVEALCQHISQFIVDVERAALSEETTKALASLMR---VEHYMLSSAQKALAISALSRRRDVLTKAELEGQLLNYLSVTNEFMRMVRWRQFDSSDA : 473
         fsflPs65pgvakiIlg6gli6fs6ty6gki6ksl6Vgka4AlLhtsigKgplSg6 sgaVmtv66qSsstts6mvplvgsg6Lkakd6ypftLganigTcital6aalgvvgvnsg

         480         *       500         *       520         *       540         *       560
673   : FALQIALVHLIYNVLGVTLIYG-------LPLLRNIPLNLSYQLSVIAAERKMYG-----AAYIGGLFFIMPLGIIFTTM---- : 382
AD45  : FALQIALVHLIYNVLGVTLIYG-------LPLLRNIPLNLSYQLSVIAAERKMYG-----AAYIGGLFFIMPLGIIFTTM---- : 384
ALTDE : FALQIAFVHLIYNVLGVTLIYG-------FPLLRNIPLNLSYQLSVIAAERKMYG-----AAYIGGLFFIMPLGIIFTTM---- : 384
BS11  : LSLQFDLLDKEHHKVKSALVMGATQGDIAVTQMTDATECMEYLLQIVQMWVKVFVRIQQVEDSITTANLIHGDSQNNSKTIEGA : 557
        faLQial6hliynv6gvtL6yG        pl6r1ipln6sYqLs66aaerK65g     aayIgglffImplgiif3tm
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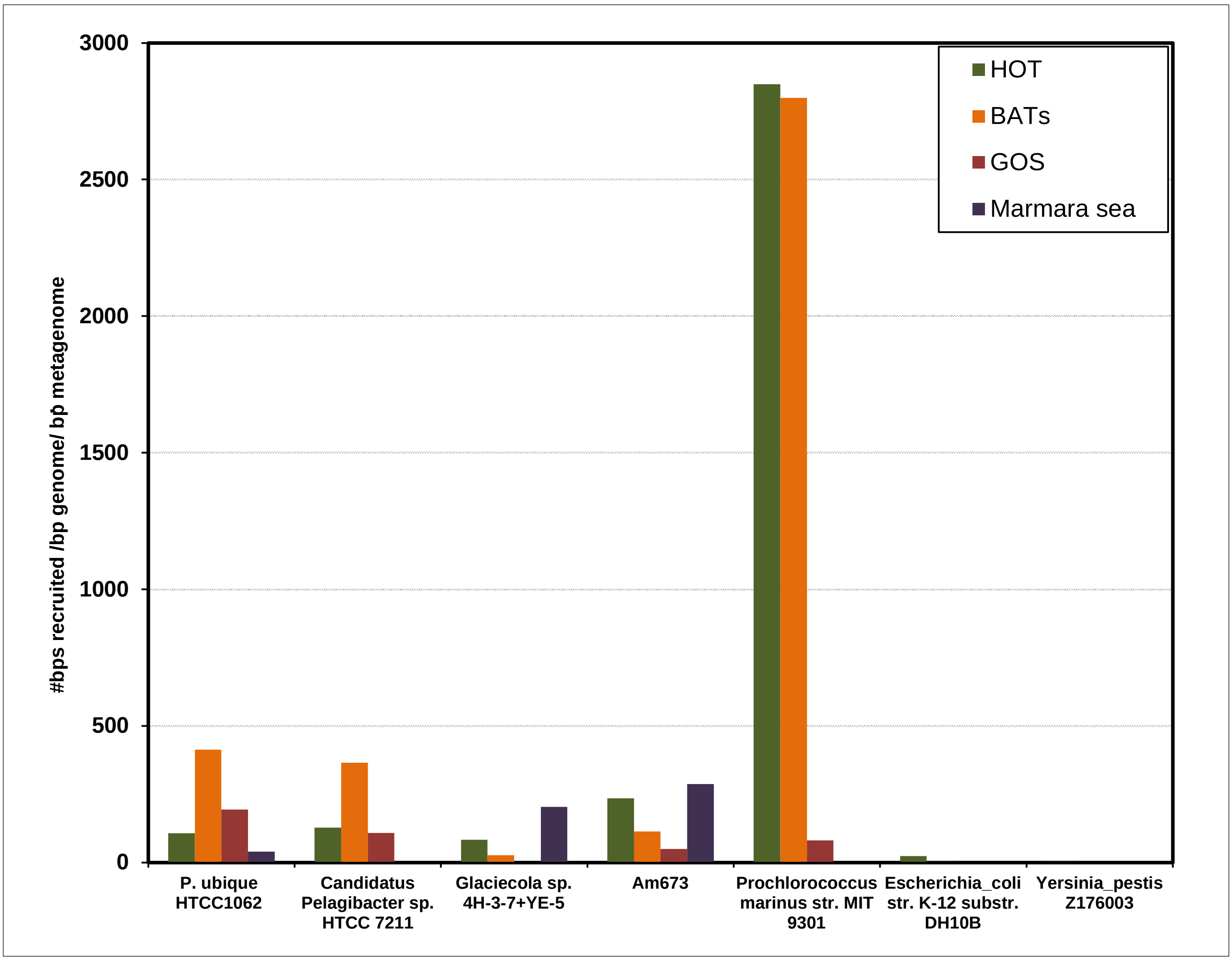
Supplementary Figure 7. Amino acid sequence alignment of the Na+/Pi cotransporter family protein in the genomes indicated. Multiple sequences were aligned using CLUSTALW.



Supplementary Figure 8. Reads recruitment of some representative genomes of marine bacteria in HOT, BATS, GOS and Marmara Sea metagenomes. Genomes used were *Candidatus Pelagibacter ubique* strains HTCC 1062 and HTCC 7211, *Prochlorococcus marinus* MIT9301, *Glaciecola sp*. 4H-7+YE-5 and *A. macleodii 673. Yersinia pestis* Z176003 and *Escherichia coli* K12-DH10B genomes were used as negative controls.