





**S1 Fig.A: Nucleotide alignment of the brown algal PKS III coding sequences.**

**Nucleotide alignment of the *Fucus vesiculosus* cDNA sequence with Fucus EST sequences.**

qPCR forward primer (FvePKS\_FWp), qPCR reverse primer (FvePKS\_RVp), partial cDNA sequence cloned from *F. vesiculosus*(FvePKS\_clo), *F. vesiculosus* EST of GH706741 GenBank accession (FvePKS\_GH7), *F. serratus* EST of GH701018 GenBank accession (FsePKS\_GH7). The positions sharing a conservation of 100, 80 and 60% are respectively shaded in black, dark grey and light grey.





**S1 Fig. B: Nucleotide alignment of the brown algal PKS III coding sequences.**

*Fucus serratus* GH701018 (FsePKS), partial cDNA sequence cloned from *Fucus vesiculosus*(FvePKS), *Sargassum binderi* HM245964 (SbiPKS), *Ectocarpus siliculosus* Esi0024\_0032 ORCAE Id (EsiPKS1). The positions sharing a conservation of 100, 75 and 50% are respectively shaded in black, dark grey and light grey.



**S1 Fig.C: Protein sequence alignment of the brown algal PKS III with a bacterial counterpart.**

*Mycobacterium tuberculosis* P9WPF0 (MtuPKS18), translated sequence of *Fucus serratus* GH701018 (FsePKS), translated sequence of *Fucus vesiculosus*(FvePKS), *Sargassum binderi* ADK13089 (SbiPKS), *Ectocarpus siliculosus* Esi0024\_0032 (EsiPKS1), translated sequence of *Saccharina japonica* contig\_6991 (SjaPKS), translated sequence of *Saccharina latissima* contig\_4304 (SjaPKS). The residues sharing 100, 80 and 60% identity are respectively shaded in black, dark grey and light grey.