

(A) Schematic representation of the early development of the wild type gametophyte (wt GA), the wild type sporophyte (wt SP) and the *imm* mutant sporophyte (*imm* SP). Grey, initial cell; blue, basal tissues consisting of narrow rhizoid cells or round filament cells; red, apical (upright) filaments consisting of cylindrical cells. Note the immediate asymmetrical division of the wild type gametophyte and the *imm* sporophyte germlings and the production of a characteristic straight rhizoid by the *imm* mutant sporophyte. In the wild type sporophyte apical organs develop only once an extensive basal system has been deployed (indicated by the double diagonal lines). Asterisks indicate the stages shown in panels B-E. (B) Three-day-old wild type partheno-sporophyte germling after introduction of siRNAs targeting the *IMM* transcript. The straight rhizoid and the immediate emergence of an upright filament are phenotypes typical of the *imm* mutant. (C) Three-day-old wild type partheno-sporophyte germling after introduction of control *GFP* siRNA. Note the absence of a rhizoid in the wild type. (D) Three-day-old *imm* partheno-sporophyte showing the straight rhizoid typical of this mutant. (E) Six-day-old wild type gametophyte showing the wavy rhizoid typical produced by this generation. Arrow heads indicate rhizoids. Size bar = 20 μ M.

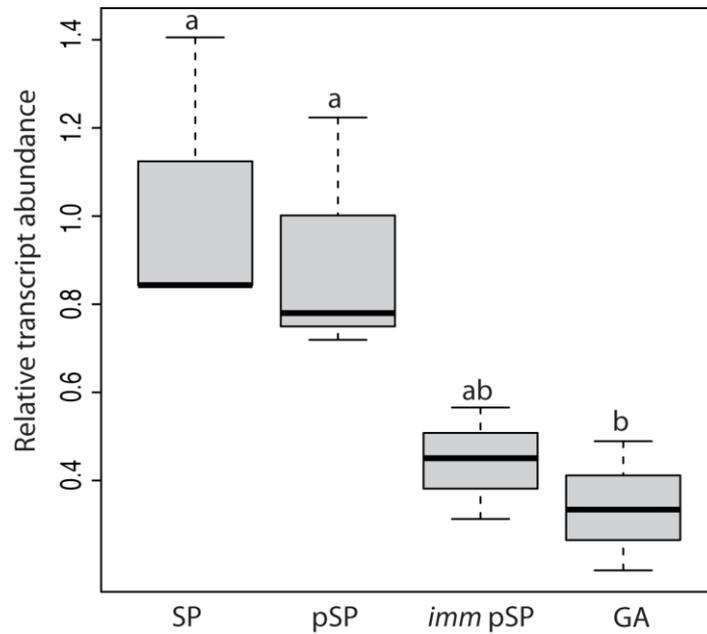


Fig. 3. Boxplot showing a quantitative reverse transcriptase polymerase chain reaction analysis of *IMM* transcript abundance at different stages of the *Ectocarpus* sp. life cycle.

The dark bar indicates the median. SP, wild type diploid sporophyte; pSP, wild type partheno-sporophyte; *imm* pSP, partheno-sporophyte of the *imm* mutant; GA wild type gametophyte; a and b indicate statistically different samples (t test, $P < 0.05$).

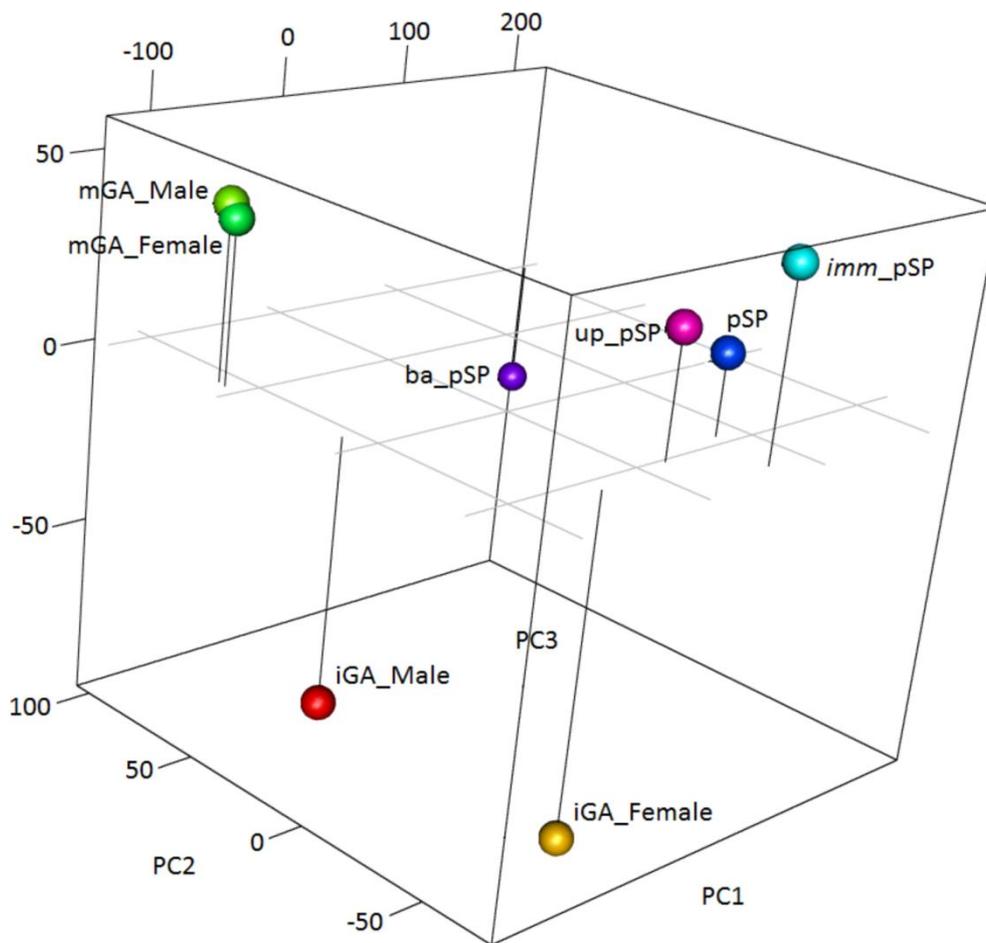


Fig. 4. Comparison of the *imm* partheno-sporophyte transcriptome with those of different tissues and life cycle stages of wild type *Ectocarpus* sp..

Principal component analysis was used to compare gene transcription patterns across samples (see Methods for details). The three dimensions PC1, PC2 and PC3 represent 51.9%, 15.4% and 12.2% of the variance respectively. *imm* pSP, *imm* partheno-sporophyte; pSP, wild type partheno-sporophyte; up_pSP, upright filaments of wild type partheno-sporophyte; ba_pSP, basal system of wild type partheno-sporophyte; iGA_Female, immature wild type female gametophyte; iGA_Male, immature wild type male gametophyte; mGA_Female, mature wild type female gametophyte; mGA_Male, mature wild type male gametophyte.

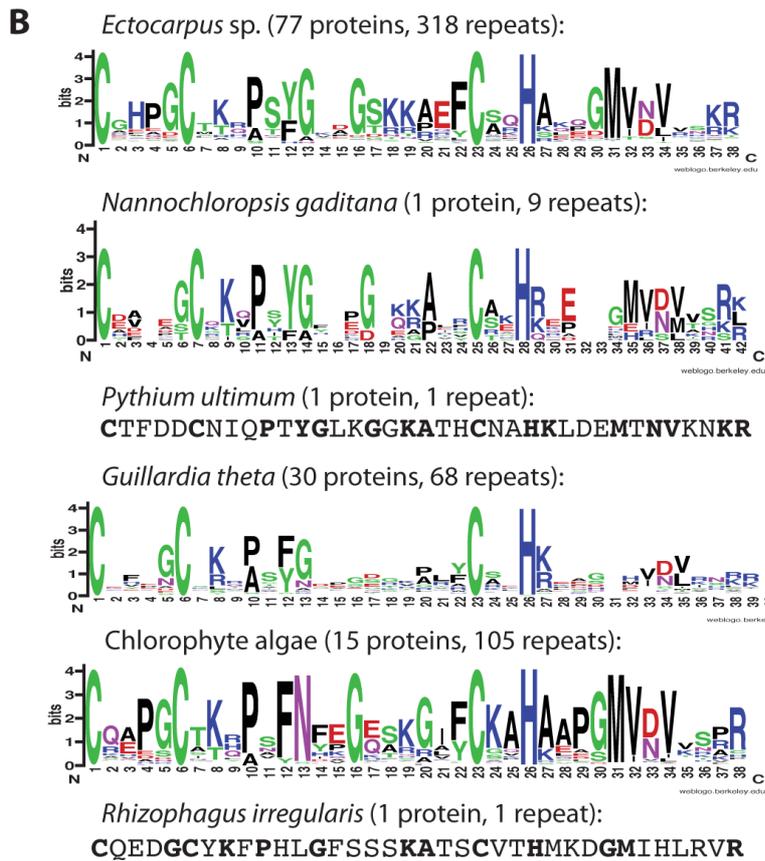
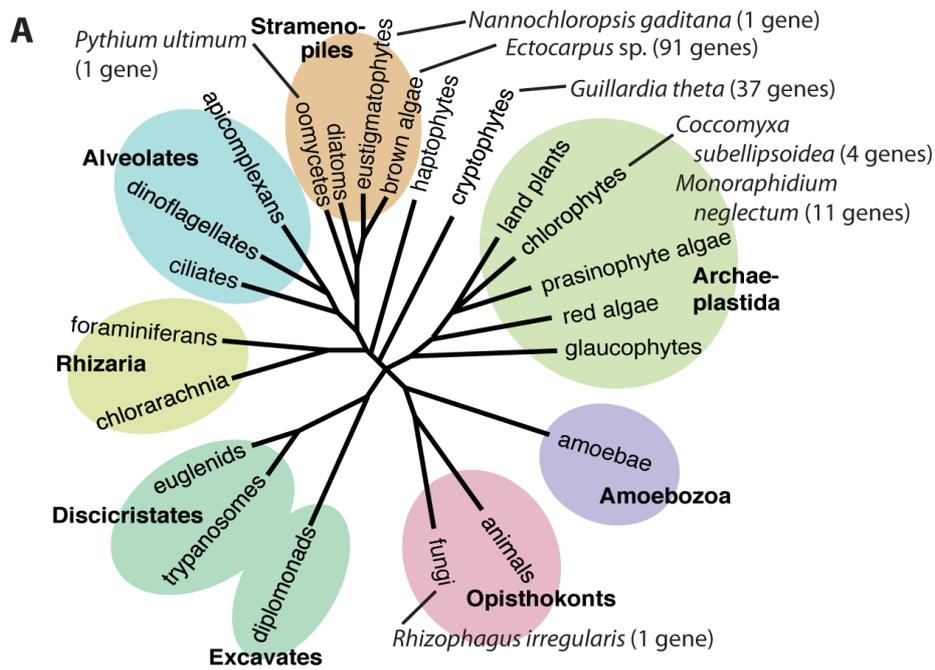


Fig. 5. Distribution of EsV-1-7 domain genes across the eukaryotic supergroups.

(A) Schematic tree of the eukaryotes showing the phylogenetic position of species that possess EsV-1-7 domain genes. (B) Amino acid sequence logos or individual sequences of EsV-1-7 repeats from diverse eukaryotic species. For *Ectocarpus* sp. and *Guillardia theta*, divergent repeats were eliminated to generate more representative logos. Note that the *Rhizophagus irregularis* homologue was the only gene on a short sequence scaffold (2,177 bp), so its assignment to this species requires further verification.

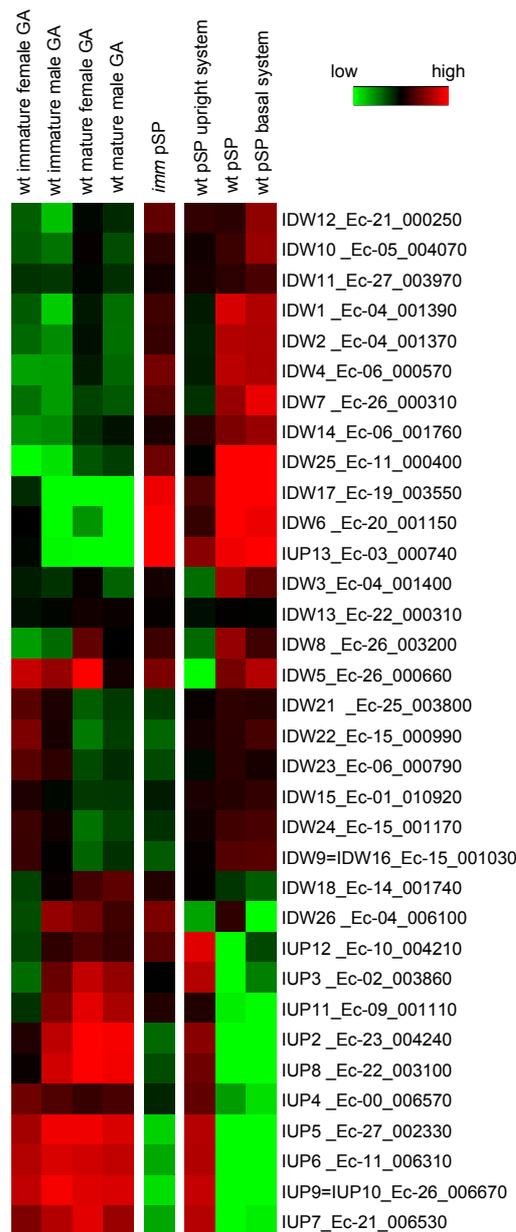


Fig. S1. Heat map representing abundances of transcripts of the *immediate upright* up-regulated (IUP) and *immediate upright* down-regulated (IDW) genes identified by Peters et al. (2008) at different stages of the life cycle and in different tissues.

Expression levels are based on log₂ transformed TPMs. Gametophyte samples are on the left of the *imm* mutant partheno-sporophyte sample and sporophyte samples on the right. Note the similarity between transcript abundances in gametophyte samples and in sporophyte upright filaments. wt, wild type; *imm*, *imm* mutant; GA, gametophyte; pSP, partheno-sporophyte. Samples are whole organism unless otherwise stated. Gene identifiers (LocusIDs) have the format Ec-00_000000.

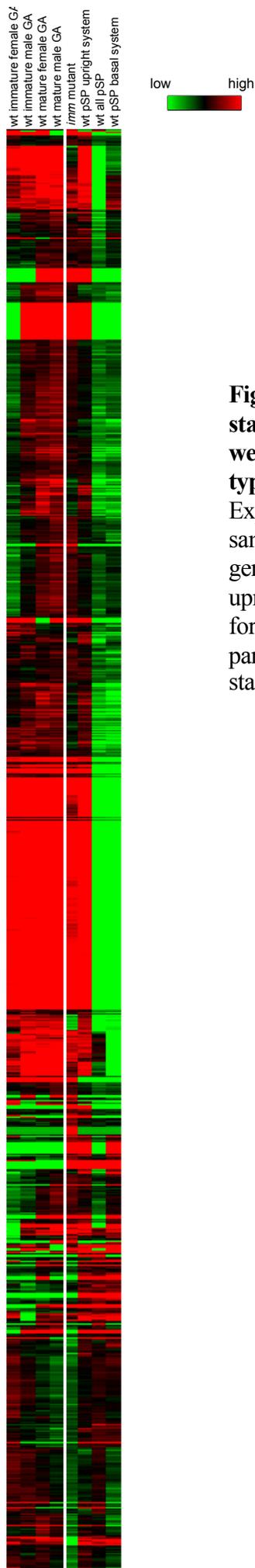


Fig. S2. Heat map representing transcript abundances at different stages of the life cycle and in different tissues for 1,087 genes that were significantly differentially expressed between the *imm* and wild type partheno-sporophytes.

Expression levels are based on log₂ transformed TPMs. Gametophyte samples are on the left and sporophyte samples on the right. Note that genes that are upregulated in the gametophyte generation also tend to be upregulated in sporophyte upright filaments. Gene names were omitted for clarity. wt, wild type; *imm*, *imm* mutant; GA, gametophyte; pSP, partheno-sporophyte. Samples are whole organism unless otherwise stated.

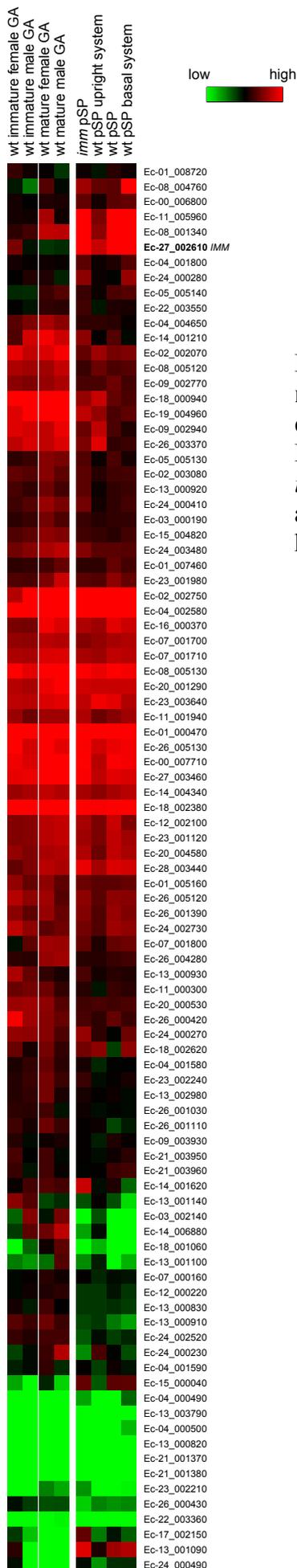


Fig. S3. Heat map representing abundances of transcripts of the members of the *Ectocarpus* sp. EsV-1-7 domain gene family at different stages of the life cycle and in different tissues.

Expression levels are based on log₂ transformed TPMs. wt, wild type; *imm*, *imm* mutant; GA, gametophyte; pSP, partheno-sporophyte. Samples are whole organism unless otherwise stated. Gene identifiers (LocusIDs) have the format Ec-00_000000.

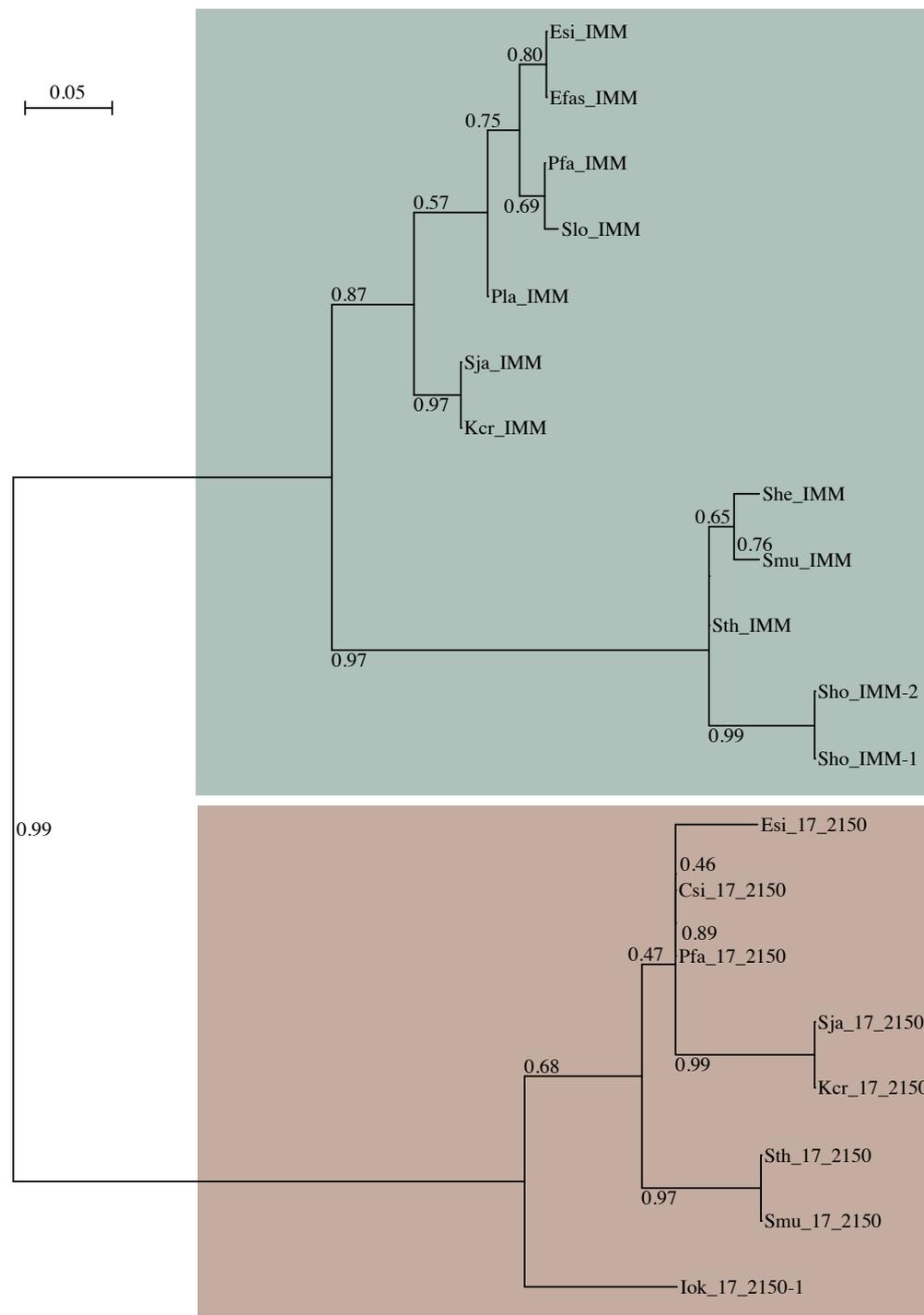


Fig. S4. Unrooted maximum likelihood tree based on an alignment of IMM and Ec-17_002150 orthologues from diverse brown algal species.

The tree was generated from a Muscle alignment with the MEGA7 maximum likelihood algorithm using the JTT+G model and 1000 bootstrap replicates. Bootstrap support values are indicated at each node. Ec-17_002150 is the most similar gene to *IMM* in the *Ectocarpus* sp. genome. IMM, IMM orthologue; 17_2150, Ec-17_002150 orthologue; Esp, *Ectocarpus* sp.; Efas, *Ectocarpus fasciculatus*; Slo, *Scytosiphon lomentaria*; Pfa, *Petalonia fascia*; Pla, *Punctaria latifolia*; Sja, *Saccharina japonica*; Kcr, *Kjellmaniella crassifolia*; Sho, *Sargassum horneri*; Sth, *Sargassum thunbergi*; She, *Sargassum hemiphyllum*; Smu, *Sargassum muticum*; Csi, *Colpomenia sinuosa*; Iok, *Ishige okamurai*.

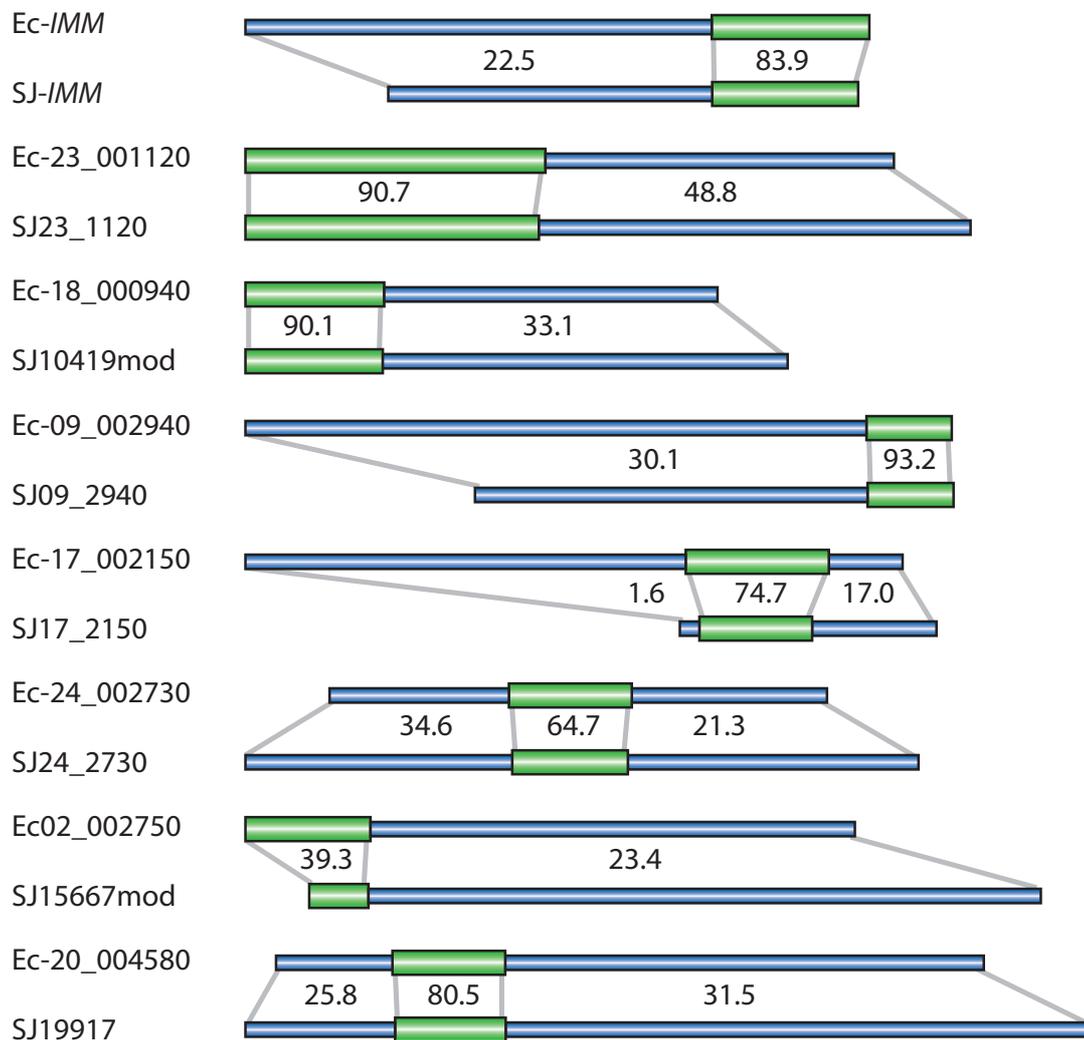


Fig. S5. Comparison of eight representative orthologous pairs of *Ectocarpus* sp. and *S. japonica* EsV-1-7 family proteins showing the weak conservation of regions outside the EsV-1-7 repeat domains.

Ectocarpus sp. (Ec) and *S. japonica* (SJ) predicted proteins are represented by blue cylinders, with the EsV-1-7 repeat regions indicated by a thicker, green cylinder. Grey lines delineate equivalent domains in pairs of orthologues. Global percent amino acid identities between domains are indicated.

Table S1. List of the genetic markers used to map the *IMM* locus.

Table S2. List of the genes that were significantly differentially expressed between the *imm* and wild type sporophyte generations.

Table S3. Results of a GOslim ($p < 0.05$) search for enriched gene ontology categories in the list of genes that were significantly upregulated in the *imm* sporophyte compared with the wild type sporophyte (TPM > 1, fold change > 2).

Table S4. Results of a GOslim ($p < 0.05$) search for enriched gene ontology categories in the list of genes that were significantly downregulated in the *imm* sporophyte compared with the wild type sporophyte (TPM > 1, fold change > 2).

Table S5. Characteristics of the 91 members of the *Ectocarpus* sp. EsV-1-7 domain gene family.

Table S6. EsV-1-7 domain genes in other species.

Table S7. siRNA molecules used for the RNA interference experiments.

Table S8. *Ectocarpus* RNA-seq data used in this study.

[Click here to Download Tables S1-S8](#)