

Supporting Information

Re-annotation, improved large-scale assembly and establishment of a catalogue of non-coding loci for the genome of the model brown alga *Ectocarpus*

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The following Supporting Information is available for this article:

Fig. S1 Classification of *Ectocarpus* lncRNAs.

Fig. S2 Classification of *S. japonica* lncRNAs.

Fig. S3 Comparisons of structural characteristics of the sex-determining and pseudoautosomal regions of the sex chromosome with both a representative autosome and with all autosomes for both the v1 and v2 versions of the *Ectocarpus* genome annotation. (a) percent of sequence that is transposon, (b) number of genes per Mbp, (c) gene size, (d) coding region size, (e) percent GC, (f) percent GC3, (g) cumulative intron size, (h) number of exons.

Fig. S4 Suppressed transcription from a viral genome inserted into chromosome 6.

(Tables S1–S9 see separate Excel file)

Table S1 *Ectocarpus* RNA-seq data used in this study. Reads were cleaned using the Fastx toolkit.

Table S2 Correspondences between v1 and v2 LocusIDs.

Table S3 List of the rRNA loci in the assembled *Ectocarpus* genome.

Table S4 List of predicted snoRNA loci in the *Ectocarpus* genome.

Table S5 *Ectocarpus* orthologues of core protein components of snoRNPs.

Table S6 List of predicted lncRNA loci in the *Ectocarpus* genome.

Table S7 List of predicted lncRNA loci in the *S. japonica* genome.

Table S8 Comparisons of pairs of orthologous lncRNA loci from *Ectocarpus* and *S. japonica*.

Orthologous loci were detected by comparing FEELnc-predicted lncRNA loci from *Ectocarpus* and *S. japonica* using Blastn with a cut off of 10^{-4} .

Table S9 List of 341,426 sequence variants between the genome of the reference male strain Ec32 and the female outcrossing line Ec568.

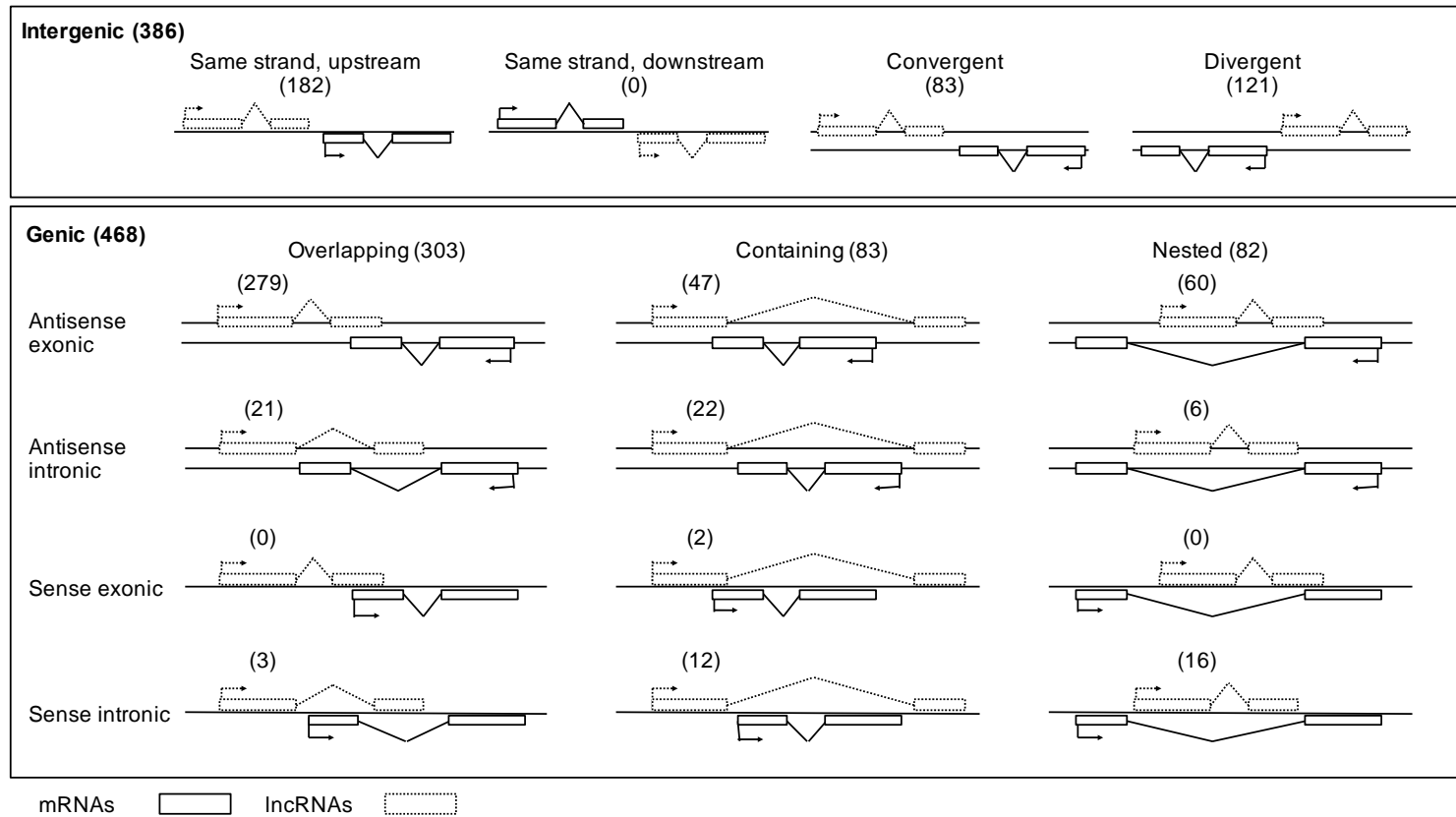


Fig. S1 Classification of *Ectocarpus* lncRNAs.

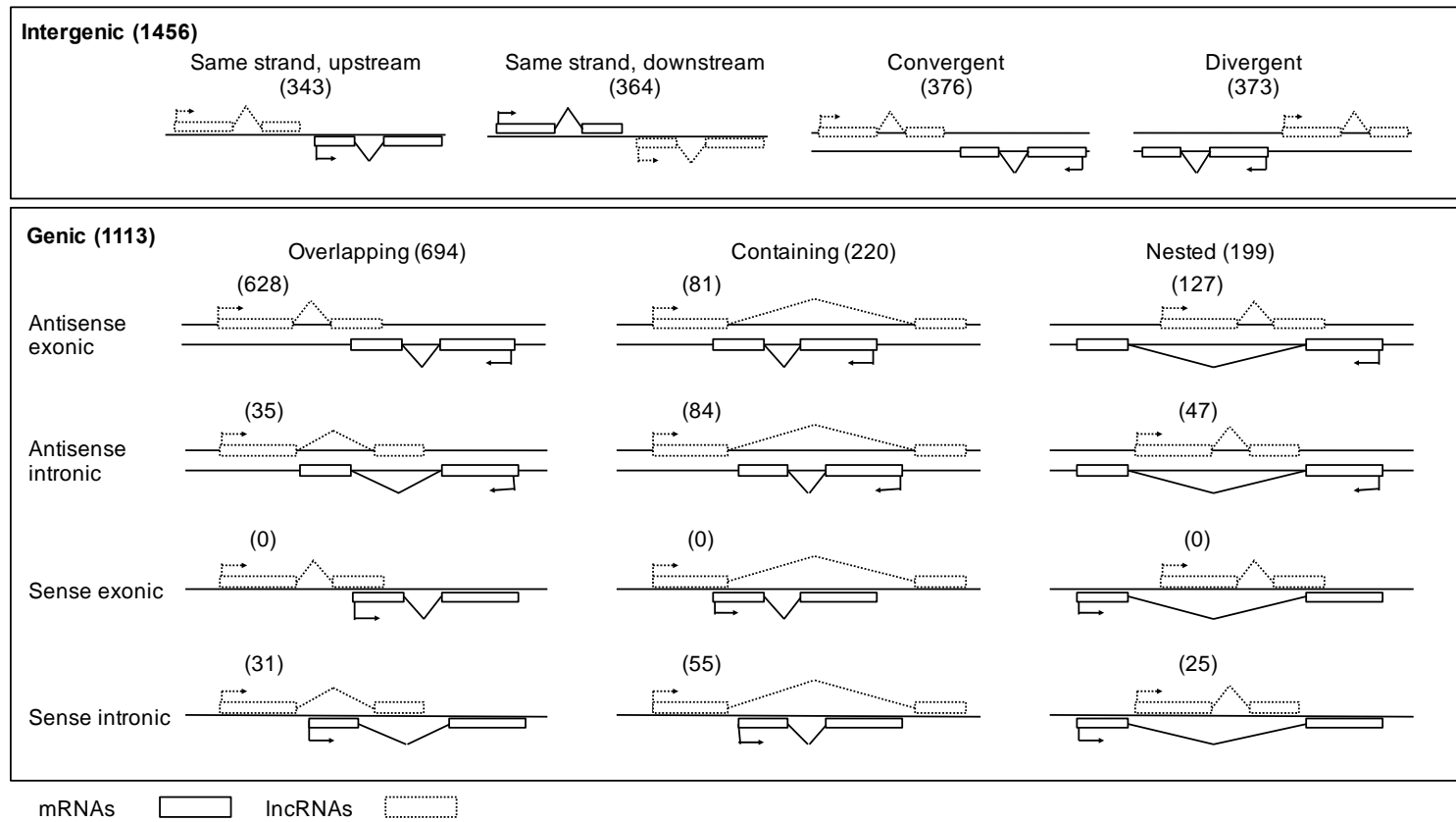


Fig. S2 Classification of *S. japonica* lncRNAs.

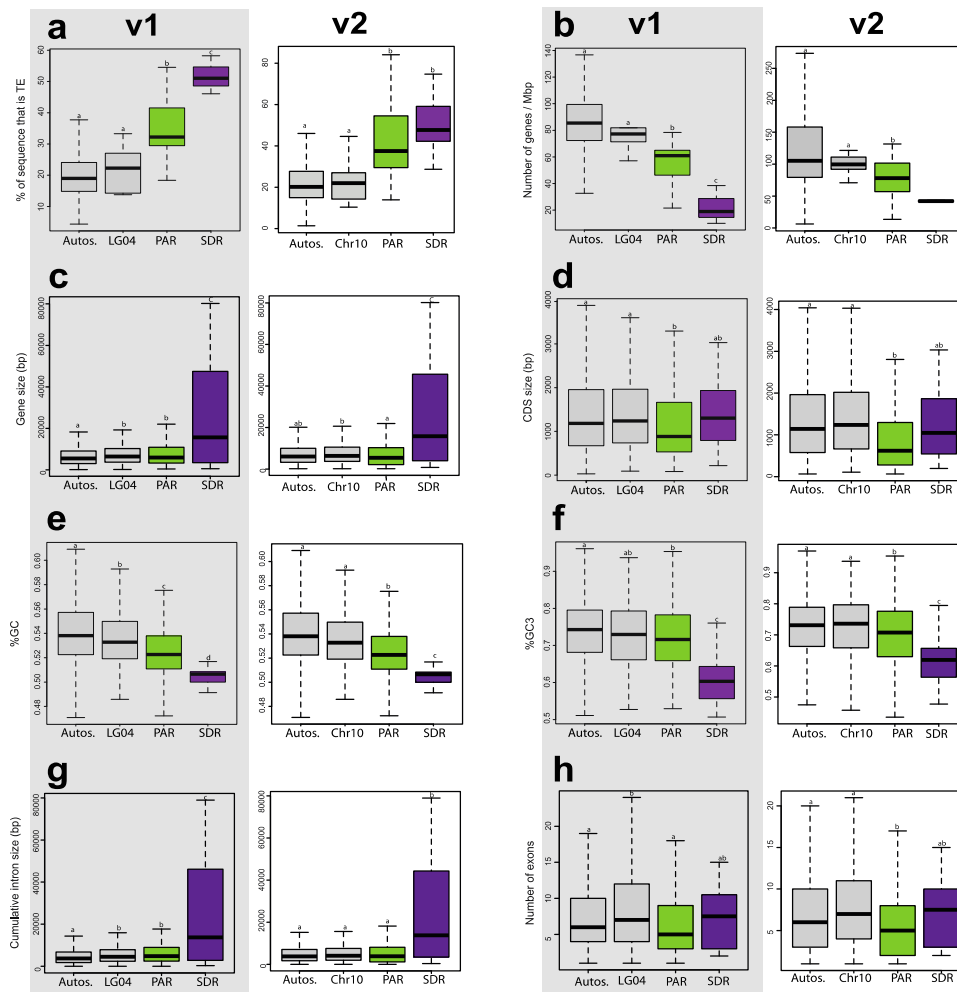


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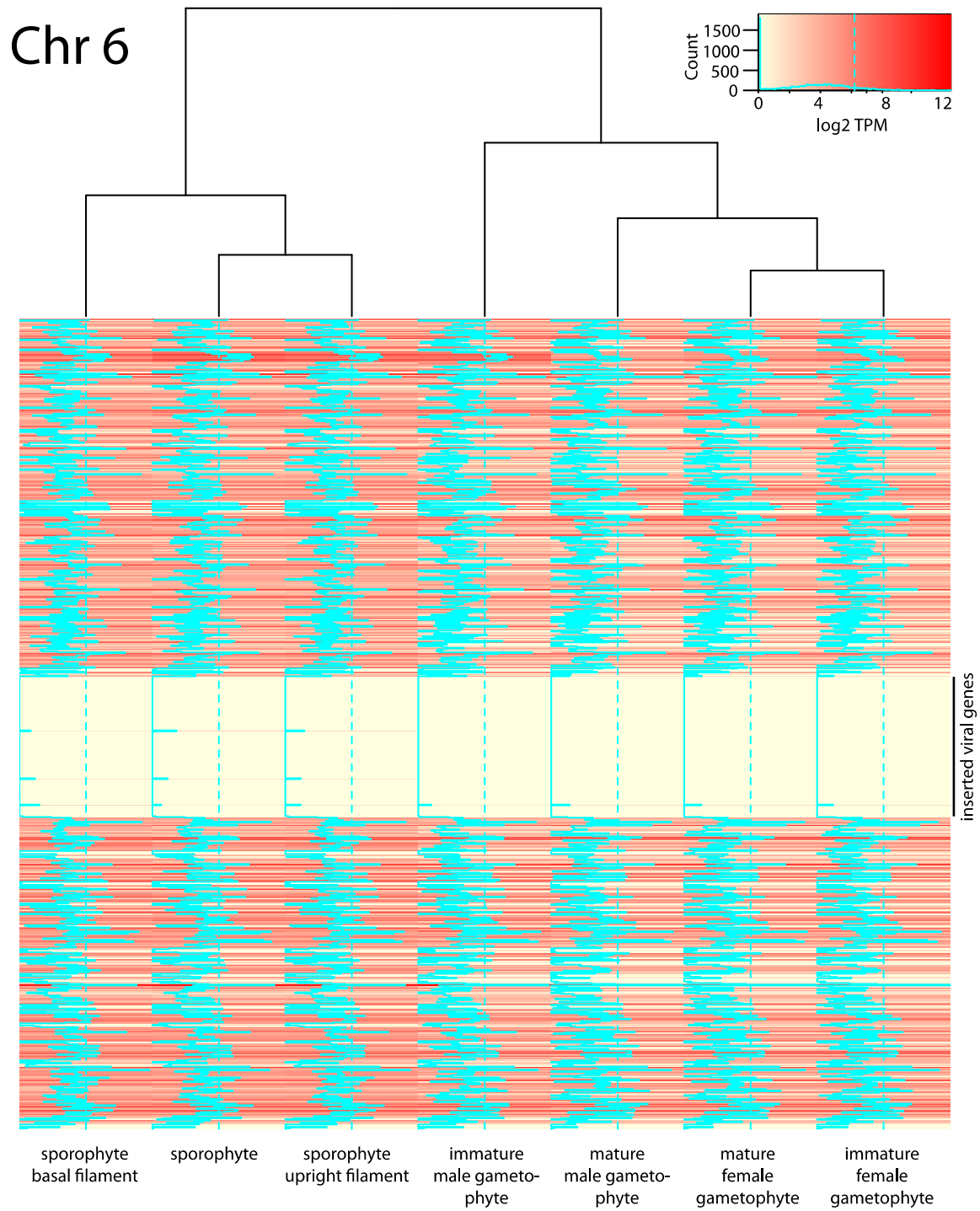


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