

## Supplementary Material

Genome-wide survey of the seagrass *Zostera muelleri* suggests modification of the ethylene signalling network

Authors: Agnieszka A Golicz, Martin Schliep, Huey Tyng Lee, Anthony WD Larkum, Rudy Dolferus, Jacqueline Batley, Chon-Kit Kenneth Chan, Gaurav Sablok, Peter J Ralph, David Edwards.

Coding sequence download ftp sites:

*A.thaliana*, *S. lycopersicum*, *O. sativa*, *S. polystachya* – Phytozome v10  
(phytozome.jgi.doe.gov)

*P.dactylifera* - <http://qatar-weill.cornell.edu/research/datepalmGenome/download.html>

*M. acuminata* - <http://banana-genome.cirad.fr/content/download-dh-pahang>

*N. nucifera* - <https://genomevolution.org/CoGe/GenomeInfo.pl?gid=16884>

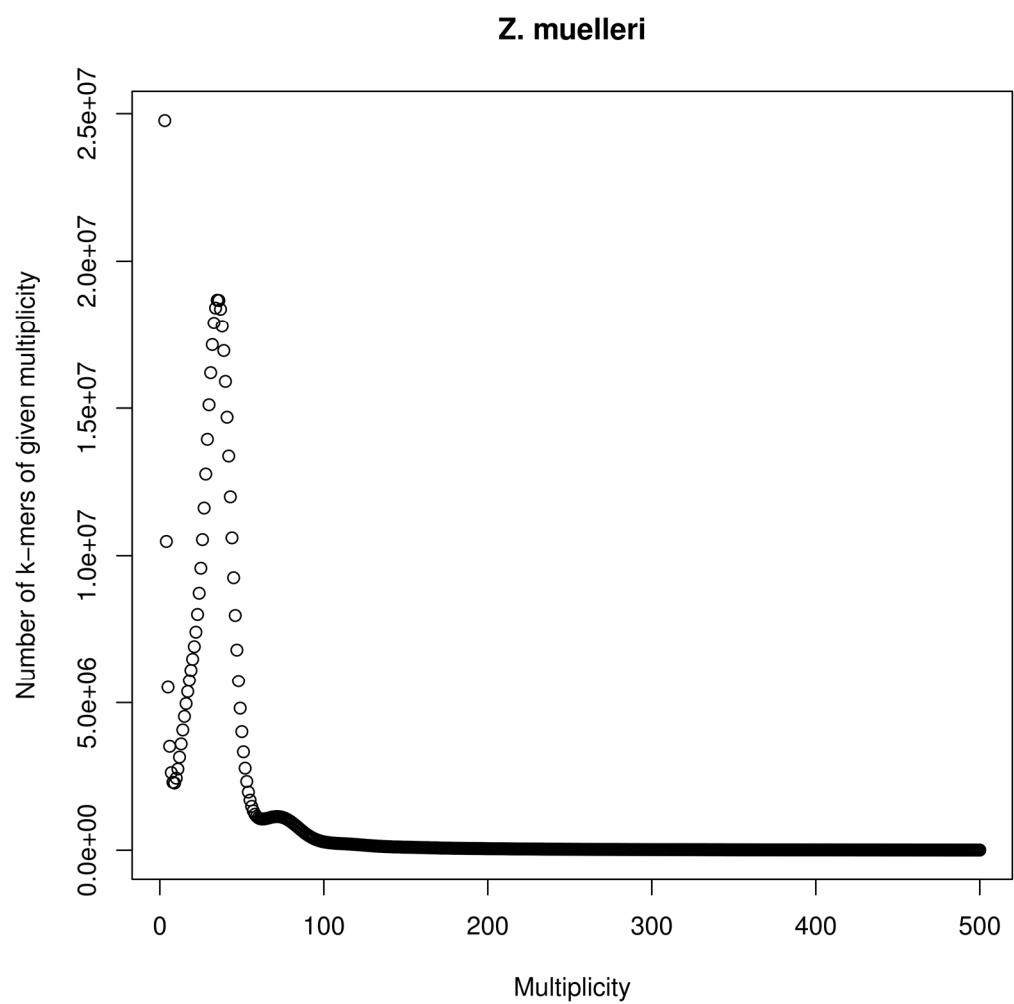


Fig S1. K-mer distribution for *Z. muelleri* genome. K-mers with multiplicity one and two were removed for image clarity.

### Z. marina

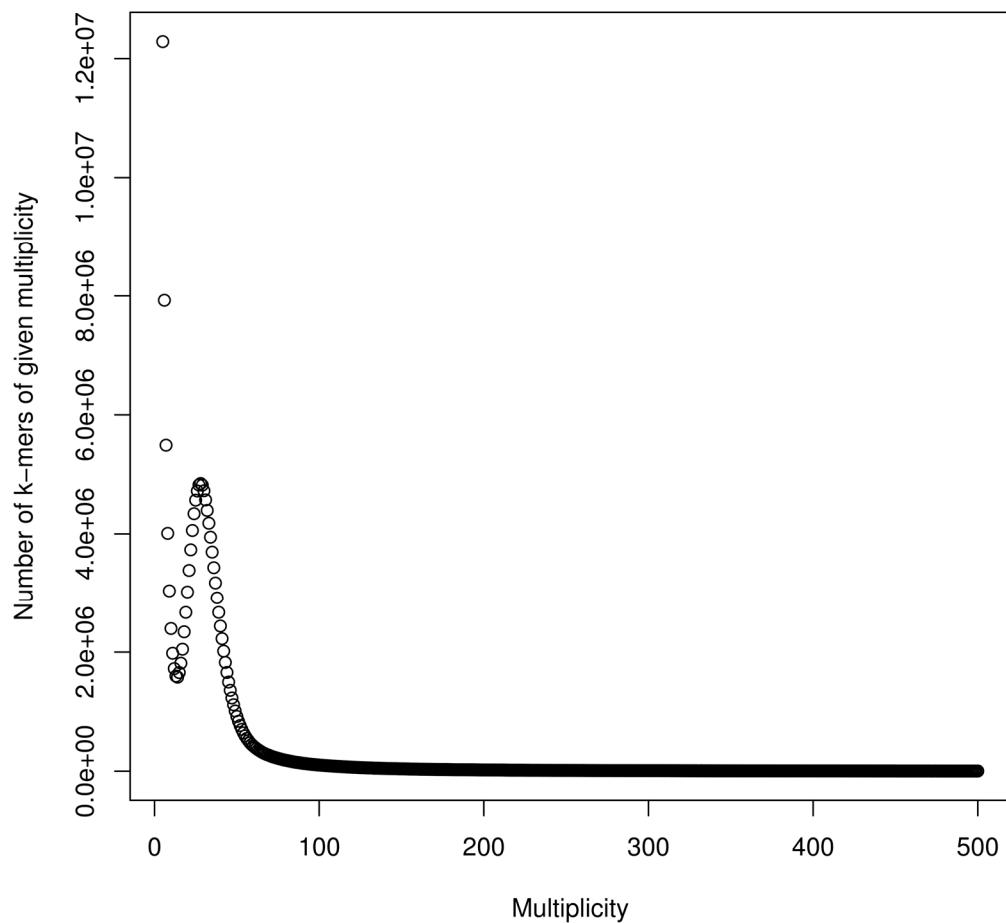


Fig S2. K-mer distribution for *Z. marina* genome. K-mers with multiplicity one to four were removed for image clarity.

Fig S3. EIL1 multiple sequence alignment. Multiple sequence alignment between *Z. marina* EIL1, *Z. noltii* EIL 1 and EIN3/EIL1 putative orthologs found in OGCs (atha – *A. thaliana*, slyc – *S. lycopersicum*, osat – *O. sativa*, pdact – *P. dactylifera*, macu – *M. acuminata*, spol – *S. polyantha*, zaet – *Z. aethiopica*, aand - *A. andraeanum*, Zoma – *Z. marina*, Znoltii – *Z. noltii*).