**S1 File.** Alignment and phylogenetic analysis of Myo-inositol-1-phosphate synthase (INO1) predicted proteins from stramenopiles.

1. Alignment in nexus format of 38 INO1 amino acid sequences obtained after BLASTP analysis (NCBI nr) of 2 INO1 predicted proteins identified in the *S. latissima* transcriptome (SL\_25748.1\_384\_1991\_- and SL\_25960.2\_333\_2118\_-). The alignment was performed using Muscle[1] and curated with Gblocks[2] and low stringency parameters to remove gaps and poorly-aligned regions, resulting in 486 amino acid characters.

#NEXUS

BEGIN DATA;

 DIMENSIONS NTAX=38 NCHAR=486;

 FORMAT DATATYPE=PROTEIN

 GAP=-

 ;

MATRIX

[1] 'SL\_25748.1\_384\_1991\_-'

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VLGGWDICSDNLADAMGKASVLDFDLQQKLKPMMVDMVPLPSIYFPDFIAANQSERADNV

LKGSKQEQMDQIRKDIREFKEKNKLDKVVVLWTANTERFSALEAGINDTKDNILASITRG

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MVDFLVSAGIKPTSIVSYNHLGNNDGRNLSAPQQFRSKEISKSNVVDDMVASNRLLYKAG

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ENHMLL

[2] 'SL\_25960.2\_333\_2118\_-'

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GGVIANREGISWNTKAGVRNPNYFGSITQASTINVGS-TGGKDVFVPFSSVLPMVNPNDL

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ENFMAL

[3] SJ17716

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[4] CBN77493.1

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[5] XP\_002292968.1

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[6] EJK66432.1

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[7] GAX27321.1

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[8] GAX27432.1

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[9] OEU16376.1

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[10] XP\_002179168.1

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NNHMTL

[11] XP\_012896216.1

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[12] XP\_012898387.1

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[13] GAX94616.1

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[14] XP\_008890663.1

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[15] XP\_024579037.1

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[16] KUF98217.1

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[17] OWZ08203.1

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[18] KUF75721.1

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[19] POM76882.1

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[20] XP\_002908320.1

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[21] RAW35630.1

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[22] XP\_009523578.1

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[23] XP\_009821348.1

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[24] RHY94259.1

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[25] RLN67203.1

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[26] RLN20242.1

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ESHMLL

[27] CCA14059.1

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[28] XP\_008862724.1

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EHPDHCVVIKYVPFVGDSKRAMDEYTSKIFMNGTNTIAMHNTCEDSLLATPLILDLVIIC

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ENYIQL

[29] CCI44519.1

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VIGGWDISCLNLAEAMKRAQVLEYDLQRQLIPHMEKIEPLPSIYYPDFIAANQSDRANNV

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ENHMLL

[30] OQR85630.1

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[31] XP\_012201001.1

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ENYMQL

[32] XP\_008605672.1

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[33] OQS05457.1

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[34] RLN68240.1

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ENHMLL

[35] RLN58161.1

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ENHMLL

[36] POM73461.1

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ESHMLL

[37] GBG32238.1

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LTGSKQEQLEQIKADIEAFKKDNDLDKVIVLWSANTERFSEIQEGVNDSMSNLMQAIEED

EEEISPSTLFAVAAIETGSAYINGSPQNTFVPGVIELAQERNVYIGGDDFKSGQTKFKSA

LVDFLVSAGIAPRSIVSYNHLGNNDGKNLSAPKQFRSKEISKSNVVDDMVQSNGILYKPG

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ESHMSL

[38] EWM29092.1

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DNNMLL

;

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BEGIN NOTES;

 TEXT TAXON=1 TEXT='contig SL\_25748.1\_384\_1991\_- [Saccharina latissima]

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 TEXT TAXON=2 TEXT='contig SL\_25960.2\_333\_2118\_- [Saccharina latissima]

';

 TEXT TAXON=3 TEXT='scaffold6694|size3610:531-3396(-) [Saccharina japonica]

';

 TEXT TAXON=4 TEXT='Inositol-3-phosphate synthase [Ectocarpus siliculosus]

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 TEXT TAXON=5 TEXT='myo-inositol-1-phosphate synthase-like protein, partial [Thalassiosira pseudonana CCMP1335]

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 TEXT TAXON=6 TEXT='hypothetical protein THAOC\_12648 [Thalassiosira oceanica]

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 TEXT TAXON=7 TEXT='myo-inositol-1-phosphate synthase [Fistulifera solaris]

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 TEXT TAXON=10 TEXT='predicted protein [Phaeodactylum tricornutum CCAP 1055/1]

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 TEXT TAXON=12 TEXT='uncharacterized protein [Blastocystis hominis]

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 TEXT TAXON=14 TEXT='hypothetical protein PPTG\_00853 [Phytophthora parasitica INRA-310]

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 TEXT TAXON=15 TEXT='inositol-3-phosphate synthase [Plasmopara halstedii]

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 TEXT TAXON=16 TEXT='40S ribosomal protein S11 [Phytophthora nicotianae]

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 TEXT TAXON=19 TEXT='Inositol-3-phosphate synthase [Phytophthora palmivora var. palmivora]

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 TEXT TAXON=20 TEXT='inositol-3-phosphate synthase, putative [Phytophthora infestans T30-4]

';

 TEXT TAXON=21 TEXT='Inositol-3-phosphate synthase [Phytophthora cactorum]

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 TEXT TAXON=22 TEXT='hypothetical protein PHYSODRAFT\_350632 [Phytophthora sojae]

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 TEXT TAXON=31 TEXT='inositol-3-phosphate synthase [Saprolegnia parasitica CBS 223.65]

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';

 TEXT TAXON=33 TEXT='inositol-3-phosphate synthase [Thraustotheca clavata]

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 TEXT TAXON=34 TEXT='hypothetical protein BBJ28\_00011071, partial [Nothophytophthora sp. Chile5]

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';

 TEXT TAXON=37 TEXT='Inositol-3-phosphate synthase [Hondaea fermentalgiana]

';

 TEXT TAXON=38 TEXT='inositol-3-phosphate synthase [Nannochloropsis gaditana]

';

END;

1. ML phylogenetic tree of stramenopile INO1 protein sequences. The tree was built using PhyML[3] (LG model; aLRT branch support; model-given amino-acid frequencies; optimized across-site rate variation; best of NNI and SPR tree search). *S. latissima* INO1 contigs are well-supported within the Phaeophyceae (brown algal) clade. The non sex-biased copy SL\_25748.1 is sister to the *S. japonica* INO1. The female-biased copy SL\_25960.2 is more divergent. It should be noted that following Lipinska et al. (2017)[4], the *S. japonica* genome sequence derives from a male gametophyte strain.



References

[1]. Edgar RC. MUSCLE: multiple sequence alignment with high accuracy and high throughput. Nucleic Acids Res. 2004 Mar 19;32(5):1792–7.

[2]. Castresana J. Selection of conserved blocks from multiple alignments for their use in phylogenetic analysis. Mol Biol Evol. 2000 Apr;17(4):540–52.

[3]. Guindon S, Dufayard J-F, Lefort V, Anisimova M, Hordijk W, Gascuel O. New algorithms and methods to estimate maximum-likelihood phylogenies: assessing the performance of PhyML 3.0. Syst Biol. 2010 May;59(3):307–21.

[4]. Lipinska AP, Toda NRT, Heesch S, Peters AF, Cock JM, Coelho SM. Multiple gene movements into and out of haploid sex chromosomes. Genome Biol. 2017 Dec 8;18(1):104.