

Table S1. Results of reciprocal BLASTp search identifying putative homologues in *Hyphochytrium catenoides* genome of Meiosis functioning gene families (1).

Meiosis specific genes	Seed sequence (<i>Homo sapiens</i> [Hs] or <i>Saccharomyces cerevisiae</i> [Sc])	Hit in <i>Hyphochytrium catenoides</i>	Reciprocal hit	Transcriptome
SPO11	AAD52562.1 (<i>Hs</i>)	Hypho2016_00006629	Yes	Yes
HOP1	NP_012193 (<i>Sc</i> , weak hit for <i>Hs</i>)	Hypho2016_00001841	Weak	Yes (for weak hit)
HOP2	AHZ60122 (<i>Sc</i> , weak hit for <i>Hs</i>)	Hypho2016_00004240	Yes	Yes
MND1	NP_011332.2 (<i>Sc</i>)	Hypho2016_00011726	Yes	Yes
DMC1	NP_011106.1 (<i>Sc</i>)	Hypho2016_00007211	Yes	Yes
MSH4	NP_116652.1 (<i>Sc</i>)	Hypho2016_00003686	Yes (possible paralog)	Yes
MSH5	AAA67649.1 (<i>Sc</i>)	Hypho2016_00005653	Yes	Yes

1. Ramesh MA, Malik SB, Logsdon JM, Jr. A phylogenomic inventory of meiotic genes; evidence for sex in *Giardia* and an early eukaryotic origin of meiosis. *Curr Biol.* 2005;15:185-91.