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

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| --- | --- | --- | --- | --- |
| **Meiosis specific genes** | **Seed sequence (*Homo sapiens* [*Hs*]or *Saccharomyces cerevisiae* [*Sc*])** | **Hit in *Hyphochytrium catenoides*** | **Reciprocal hit** | **Transcriptome** |
| SPO11 | AAD52562.1 (*Hs*) | Hypho2016\_00006629 | Yes | Yes |
| HOP1 | NP\_012193  (*Sc*, weak hit for *Hs*) | Hypho2016\_00001841 | Weak | Yes (for weak hit) |
| HOP2 | AHZ60122 (*Sc*, weak hit for *Hs*) | Hypho2016\_00004240 | Yes | Yes |
| MND1 | NP\_011332.2 (*Sc*) | Hypho2016\_00011726 | Yes | Yes |
| DMC1 | NP\_011106.1 (*Sc*) | Hypho2016\_00007211 | Yes | Yes |
| MSH4 | NP\_116652.1 (*Sc*) | Hypho2016\_00003686 | Yes (possible paralog) | Yes |
| MSH5 | AAA67649.1 (*Sc*) | 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.