



Figure S2. (A) Top-hit species distribution of the final transcriptome of *H. cruentum* showing abundance of top hits to sequences of Bryophyta, Lycophyta, and Pinophyta. (B) Transcript size distribution showing high proportion of small transcripts in the final transcriptome assembly. (C) GO-category distribution of *H. cruentum* transcripts among level 2 GO categories: Cellular component (CC), biological process (BP) and molecular function (MF). Values indicated on X axis are not in the same scale.