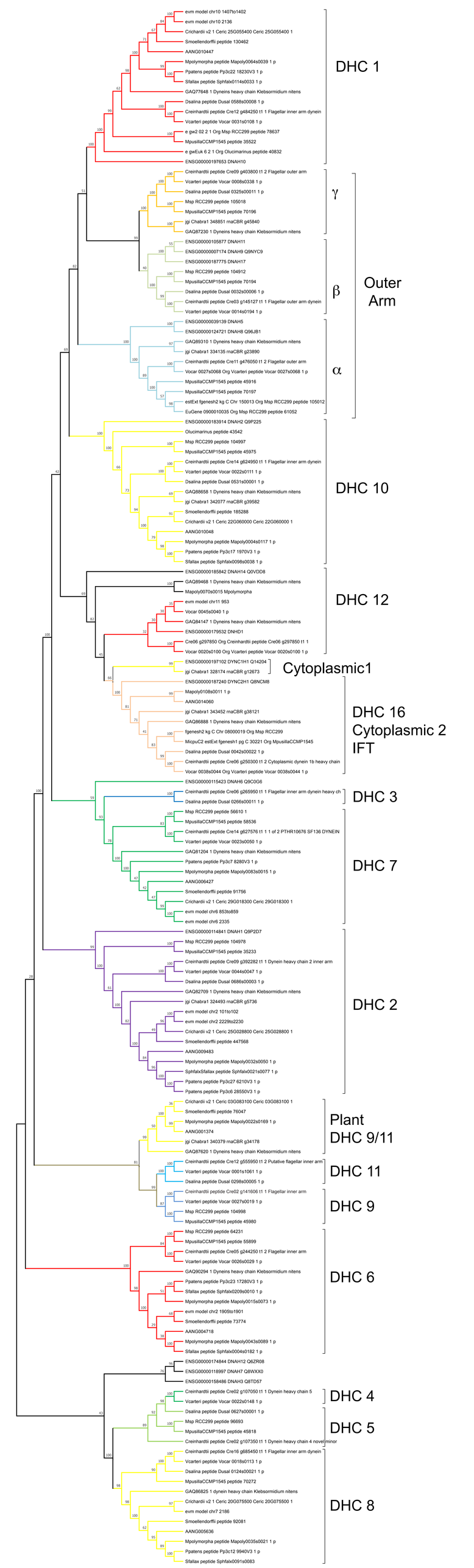
Supplemental Table S1. Dynein sequences used for phylogenetic reconstruction.
Accession numbers were taken from source databases JGI Phytozome V.13 (Chlamydomonas reinhardtii v5.6, Volvox carteri v2.1, Ostreococcus lucimarinus v2.0, Micromonas sp RCC299 v3.0, Dunaliella salina v1.0, Marchantia polymorpha v3.1, Physcomitrium patens v3.3, Sphagnum fallax v1.1, Ceratopteris richardii v2.1, Selaginella moellendorffii v1.0), NCBI genome BLAST (Chara braunii GenBank assembly GCA_003427395.1, Anthoceros angustus GenBank assembly GCA_010909165.1), data deposited by Zang et al. (2019) at doi_10.5061_dryad.msbcc2ftv_v2 (Anthoceros angustus), and Gingko biloba Genome data deposited by Liu et al. (2021).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Sfallax peptide Sphfalx0114s0033 1 p
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Dsalina peptide Dusal 0588s00008 1 p
Creinhardtii peptide Cre12 g484250 t1 1 Flagellar inner arm dynein
Vcarteri peptide Vocar 0031s0108 1 p
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MpusillaCCMP1545 peptide 35522
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Cytoplasmic 2
IFT
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Plant
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DHC 11
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Vcarteri peptide Vocar 0022s0148 1 p
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Dsalina peptide Dusal 0627s00001 1 p
Msp RCC299 peptide 96693
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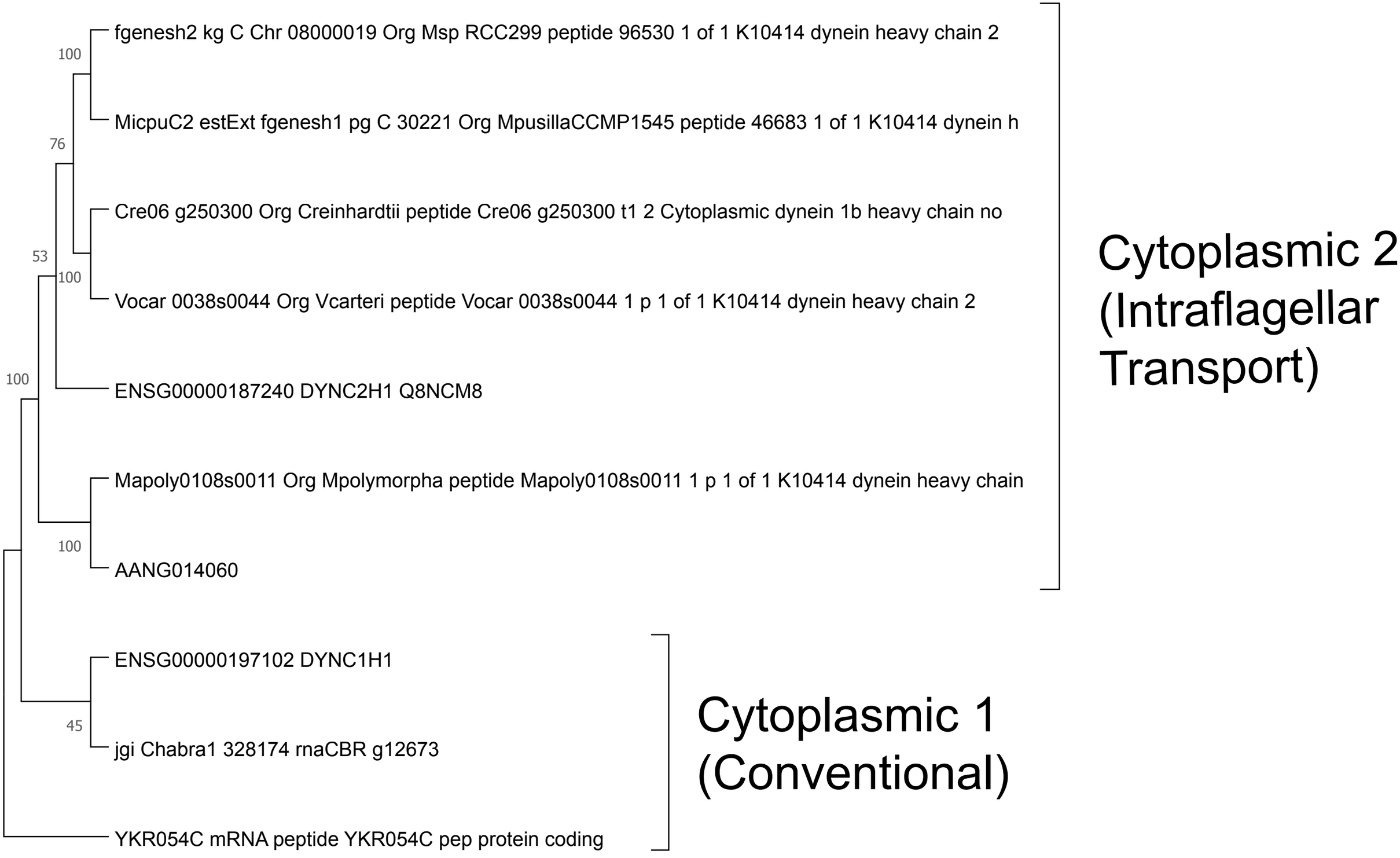
DHC 8

Supplemental Figure S1. Topology of linear maximum parsimony tree of Viridiplantae and Human DHC's.

Amino acid sequences of 169 plant and algal DHC's were sorted into classes by maximum parsimony analysis of their evolutionary history. The bootstrap consensus tree topology shown is inferred from 500 replicates. The percentage of replicate trees is shown at each node above the branches. Colored clades presented here match those of Figure 2 in the paper. This supplement presents the same data as Figure 2, but arranges clades in a linear rectangular tree for easy reading of accession numbers for all aligned protein sequences (matching those in Supplemental Table S1).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100
Vocar 0038s0044 Org Vcarteri peptide Vocar 0038s0044 1 p 1 of 1 K10414 dynein heavy chain 2
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45
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YKR054C mRNA peptide YKR054C pep protein coding
Cytoplasmic 2 (Intraflagellar Transport)
Cytoplasmic 1 (Conventional)

Supplemental Figure S2. Maximum likelihood tree of cytoplasmic DHC's.

Maximum likelihood analysis was done with MEGA X, using the Whelan and Goldman model for 10 plant, algal, human, and yeast cytoplasmic DHC sequences. The bootstrap consensus tree topology presented here was inferred from 500 replicates, with bootstrap percentages shown on each node. Gamma distribution was used to model the evolutionary rate differences among sites. All positions with less than 50% site coverage were eliminated.

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