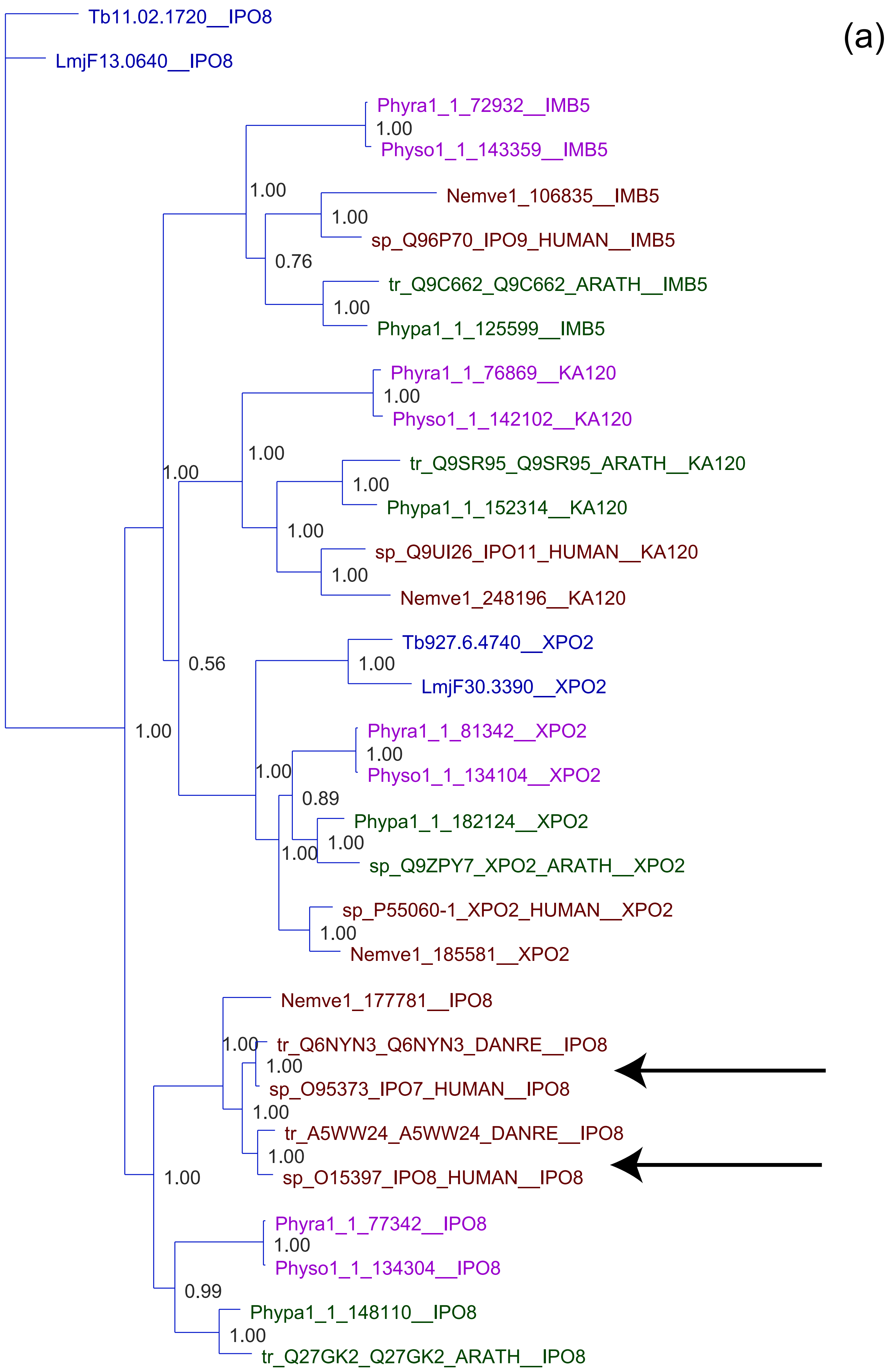
Figure S2

(a-g) MrBayes trees showing lineage-specific events indicated with arrows.
Subfamily names have been added to each taxon label as "__NAME".

(h) ClustalW neighbour-joining tree of TNPO3 candidates.

Species	ID key:
HUMAN	*Homo sapiens*
DANRE	*Danio rerio*
Nemve	*Nematostella vectensis*
DICDI	*Dictyostelium discoideum* (strain AX4)
ARATH	*Arabidopsis thaliana* (cultivar Columbia)
Poptr	*Populus trichocarpa*
ORYSJ	*Oryza sativa* (subsp. japonica, cultivar Japonica, strain Nipponbare)
Phypa	*Physcomitrella patens* ssp patens ecotype Gransden 2004
Physo	*Phytophthora sojae*
Phyra	*Phytophthora ramorum*
Lm	*Leishmania major*
Tb	*Trypanosoma brucei*
Tc	*Trypanosoma cruzi*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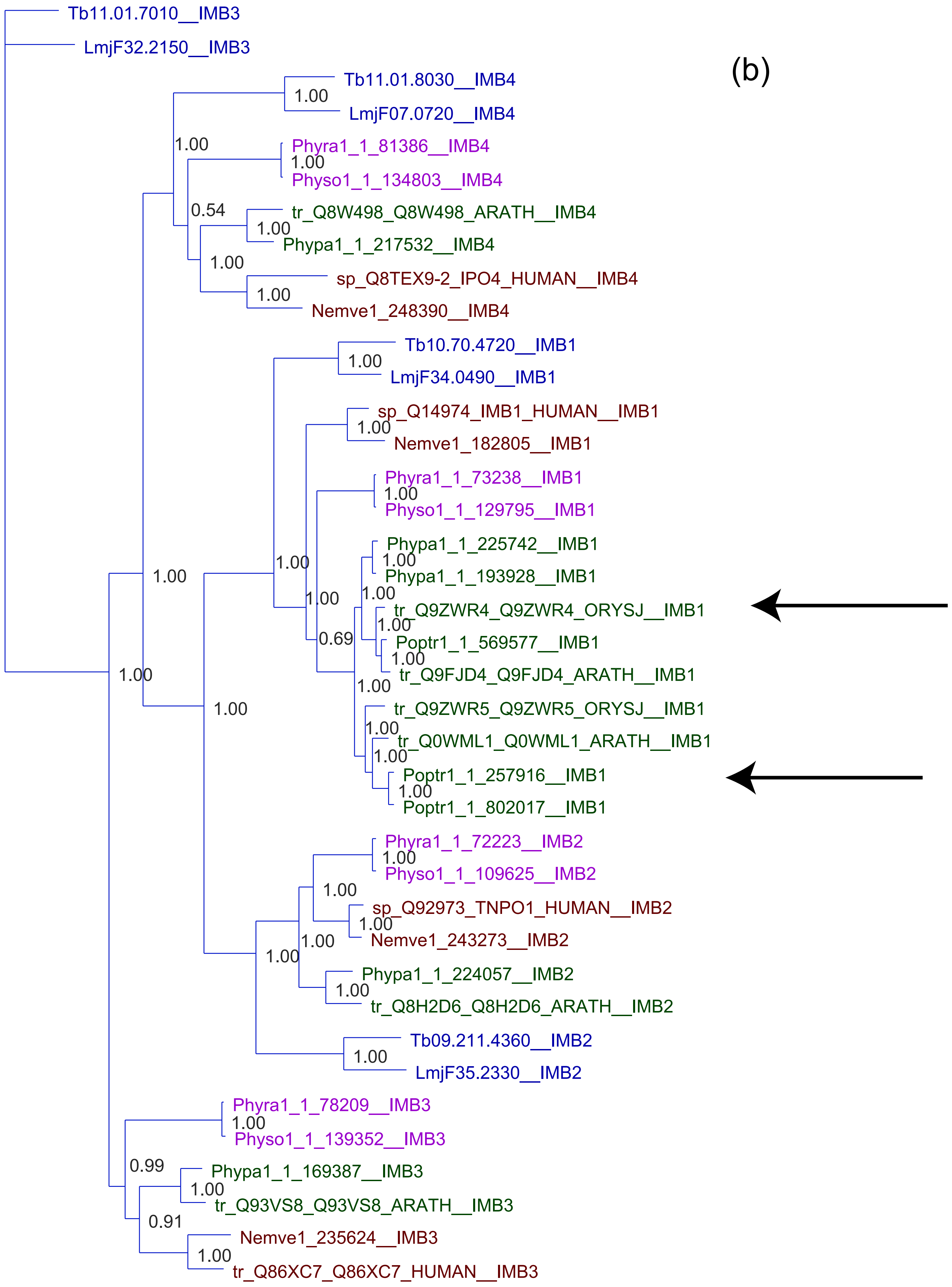
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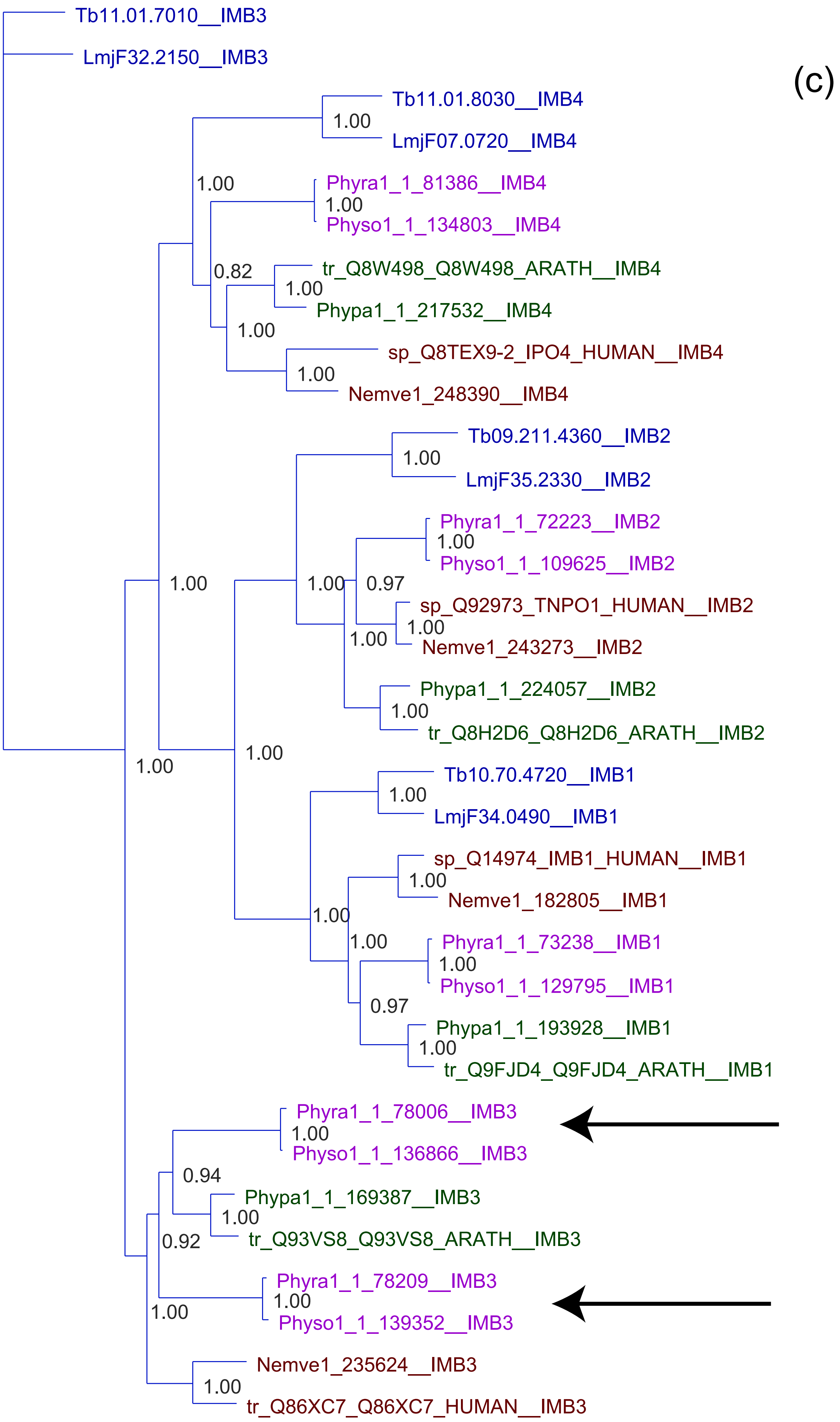
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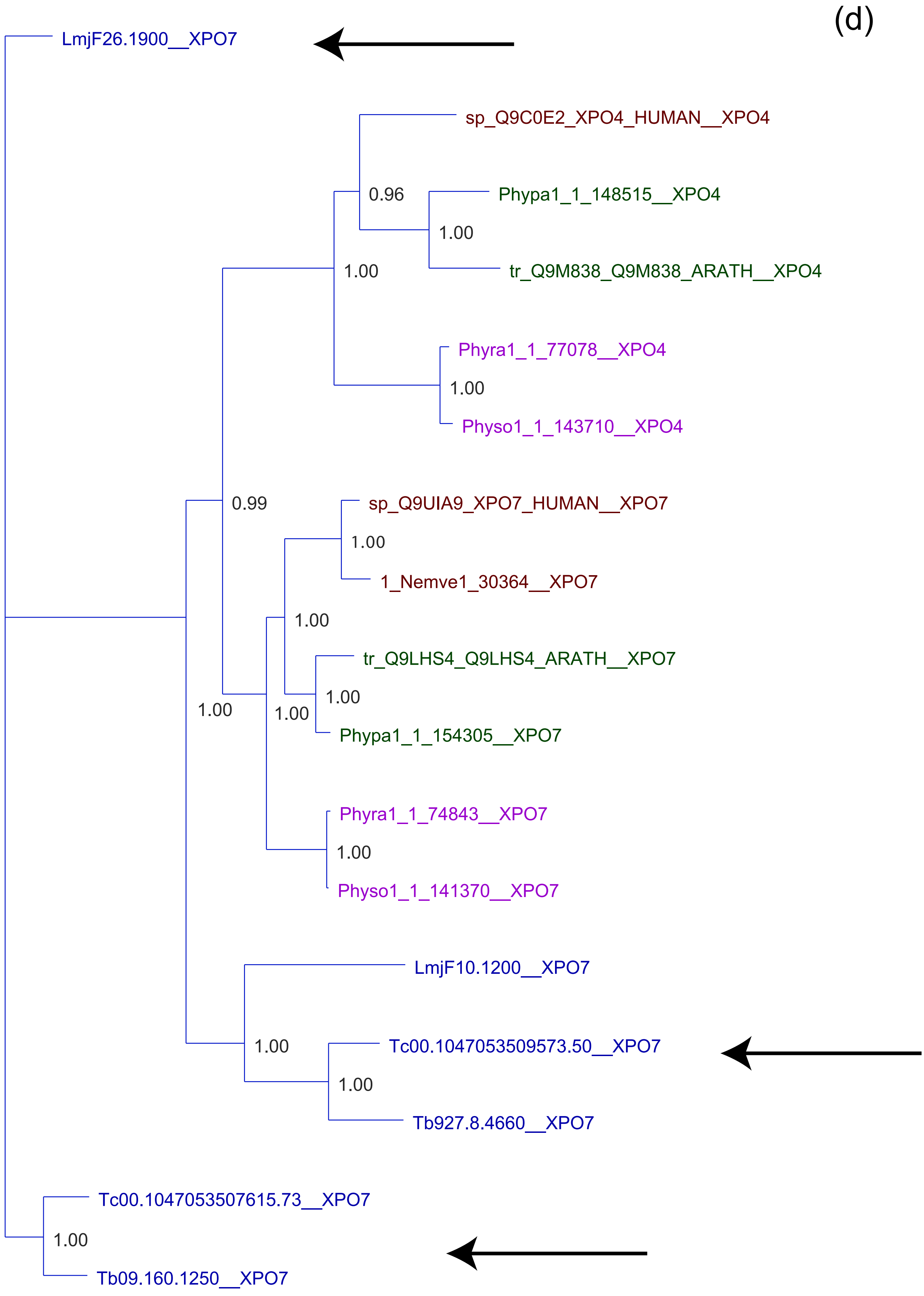
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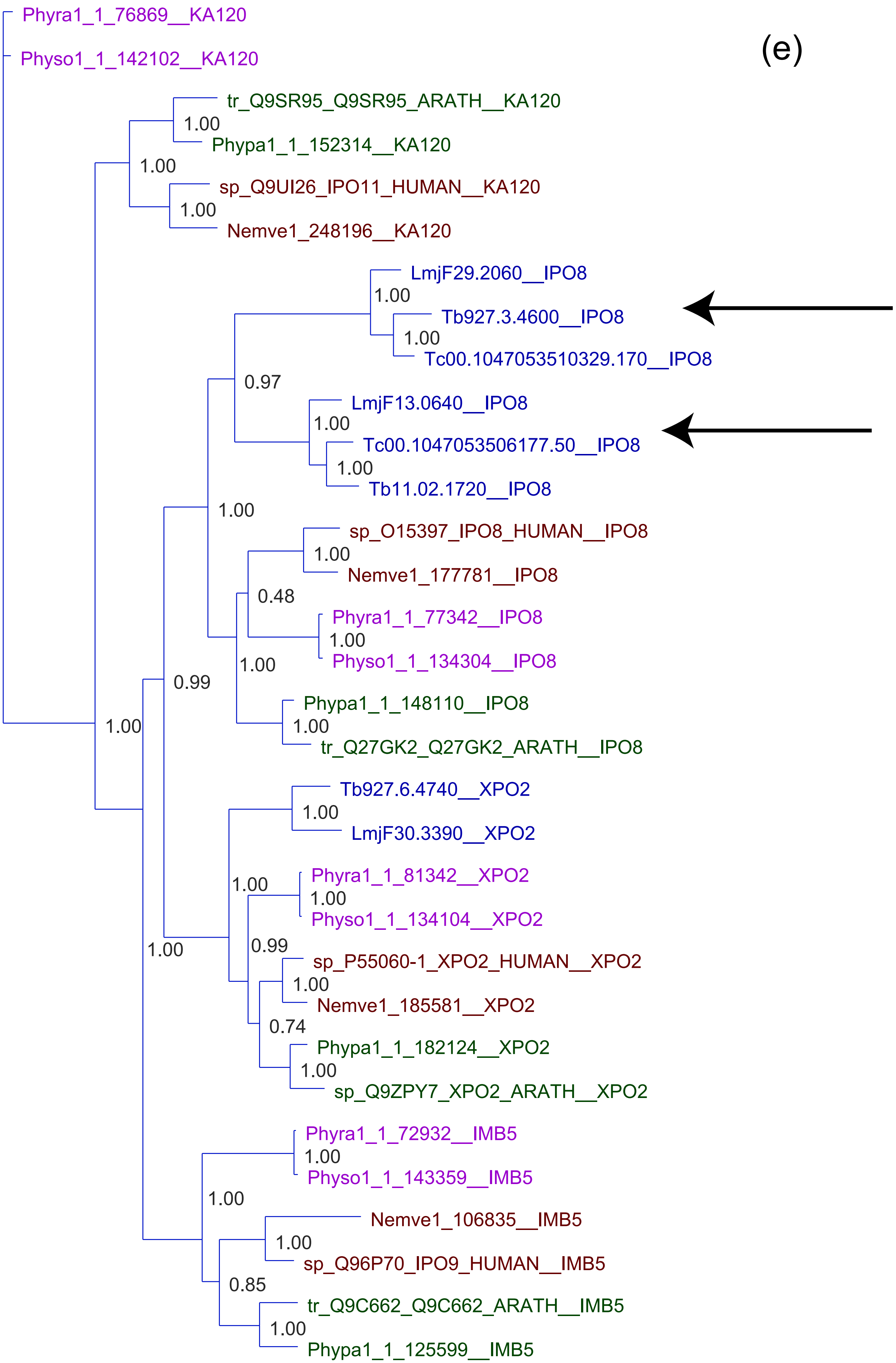
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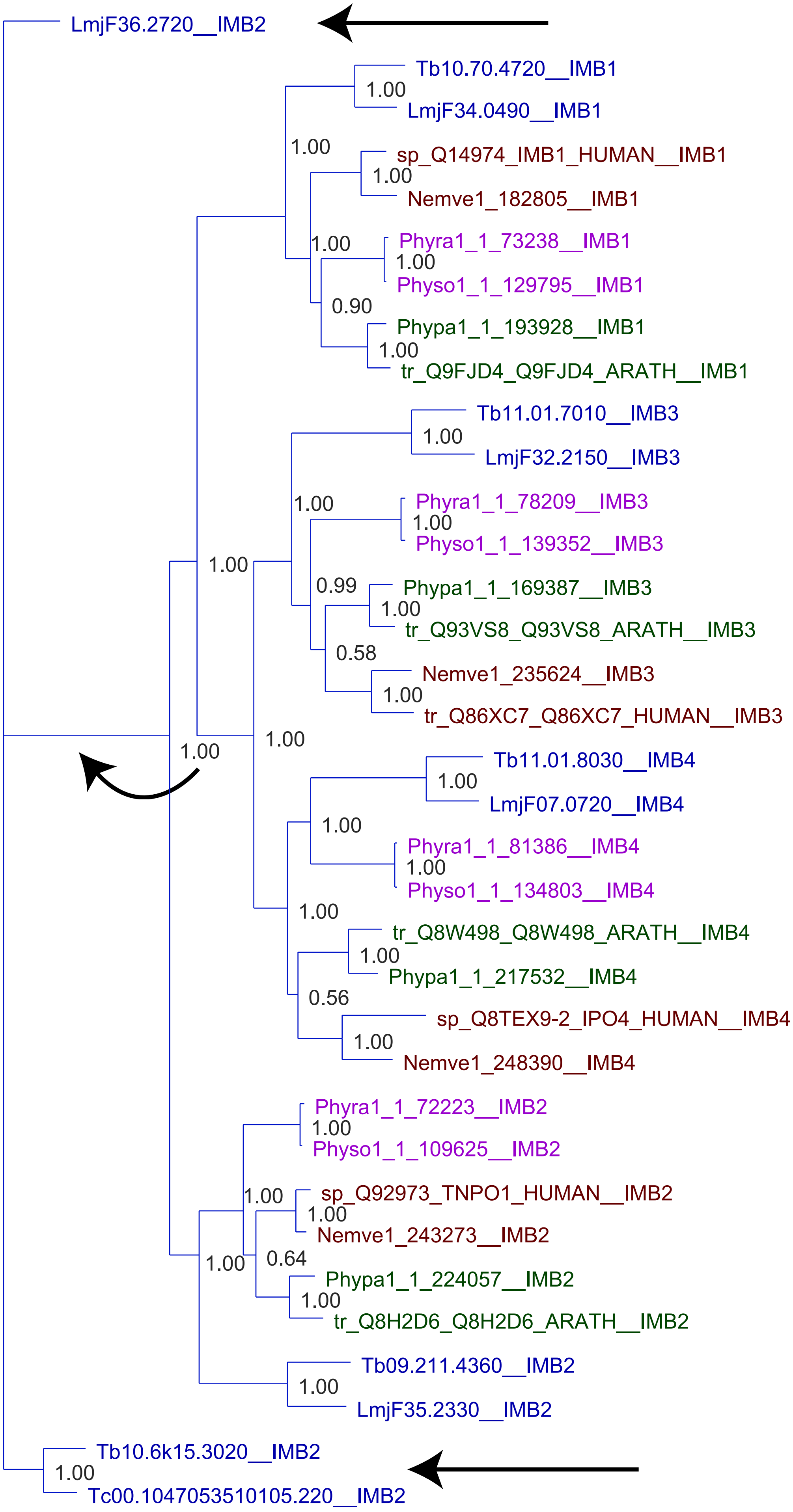
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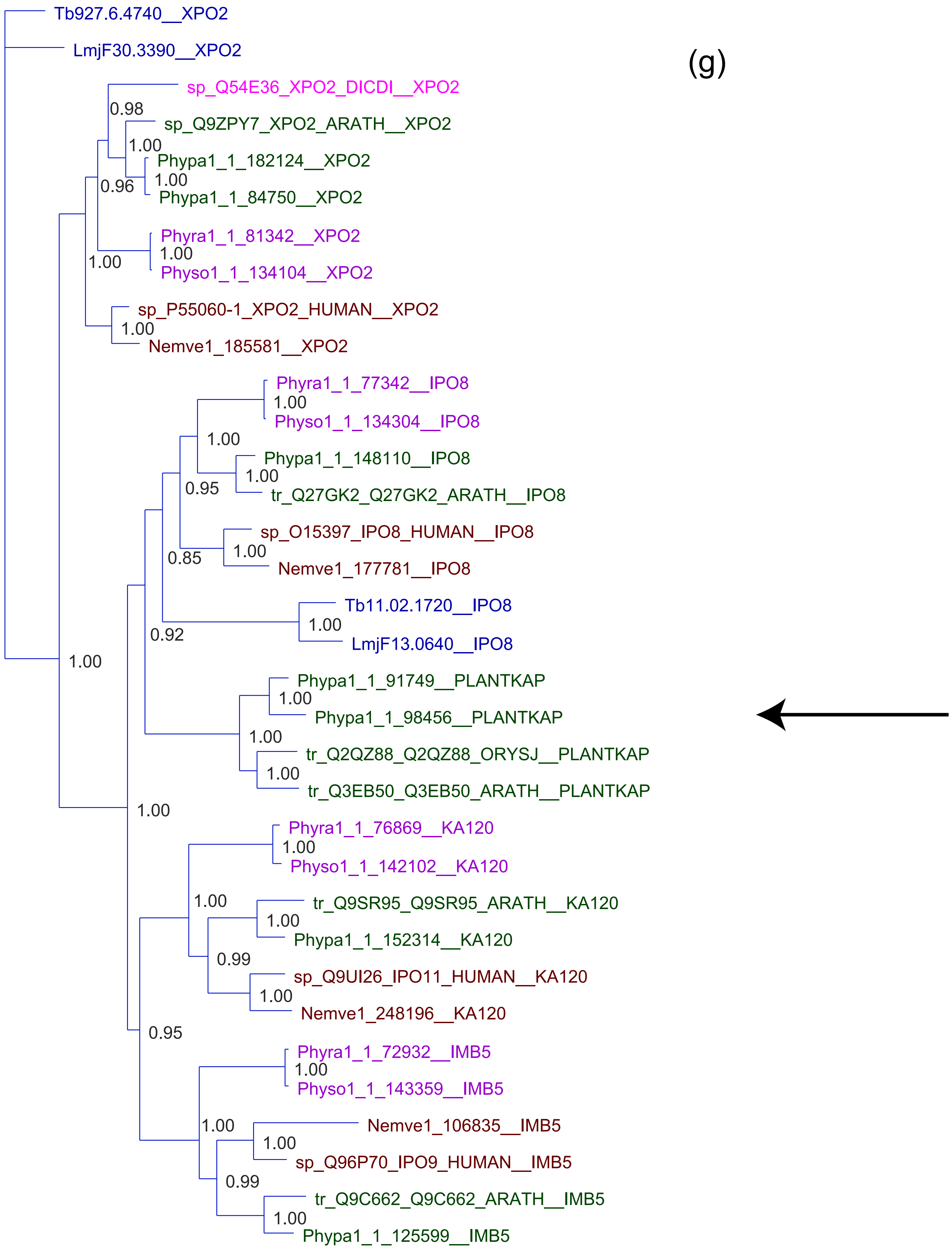
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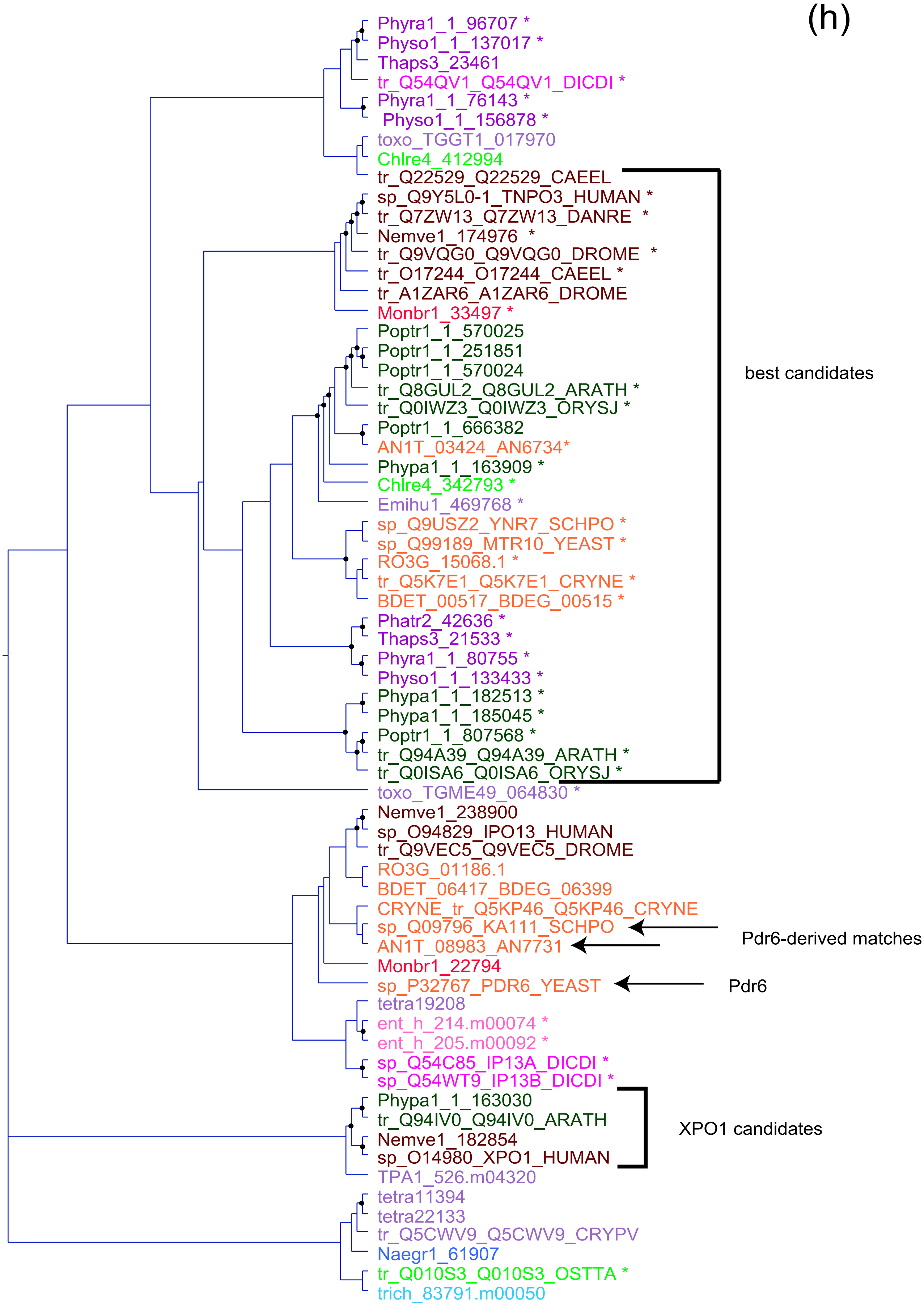

ClustalW-generated NJ cladogram of all TNPO3 subfamily candidates and a small number of XPO1 subfamily candidates. The cluster of best TNPO3 candidates, the XPO1 clade, and matches detected by Pdr6 are all indicated. All TNPO3 candidates that verified as subfamily members by phylogeny are marked with an asterisk. Nodes with bootstrap support greater than 90% are marked with a dot.