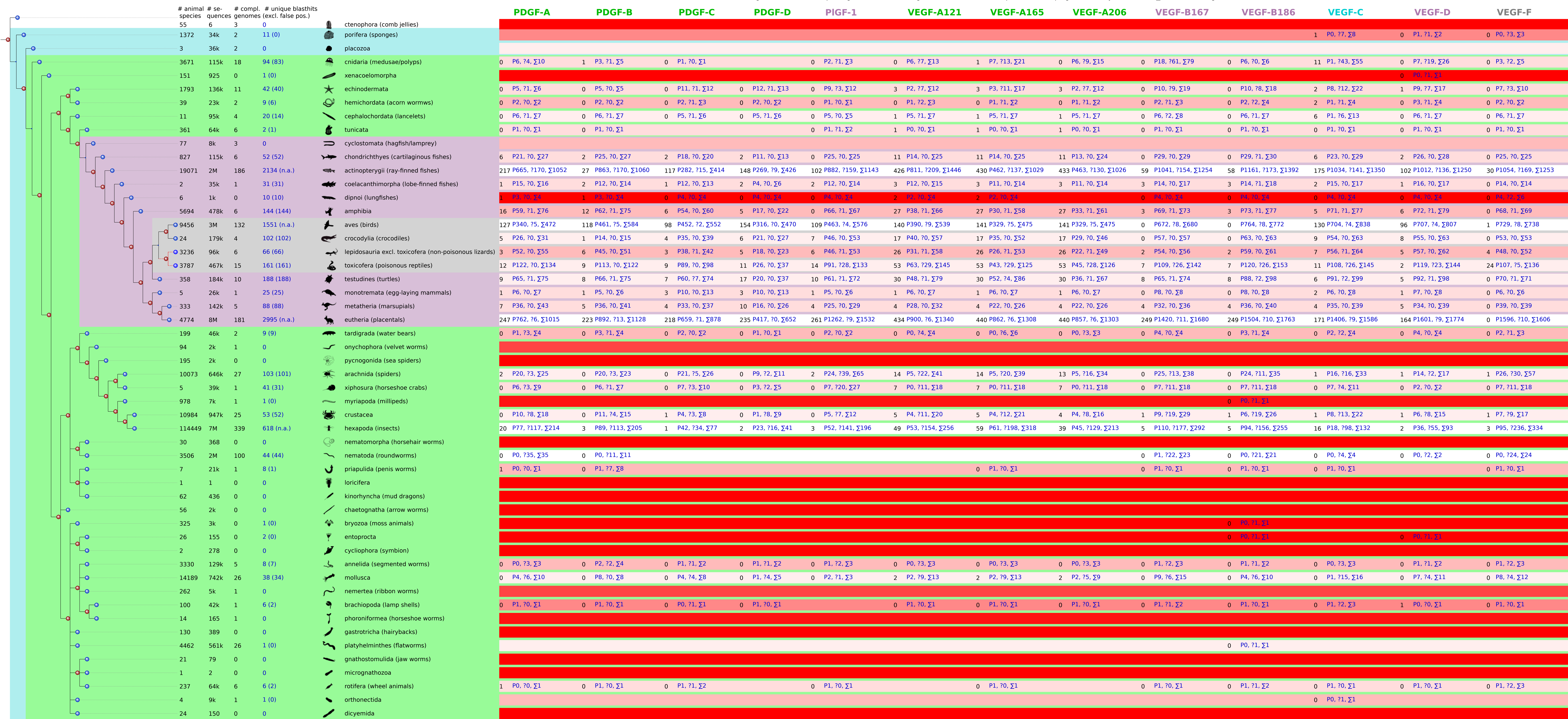


- Analysis performed: 190802_094312
- Analyzed sequences (hits resulting from 676 blast searches, 52 animal groups x 13 query sequences):49992 (out of which unique: 8666, programmatically recognized as VEGF/PDGF family members: 90.5%).
 - Red dotted lines in the tree indicate paraphyletic relationships.
 - The tree background color indicates the presence of the proteins with the corresponding color according to our hypotheses.
 - The red-to-white background of the table indicates a heuristic reliability of the results, where a brighter color indicates a higher reliability. This is calculated using the number of fully sequenced genomes, the number of species in the phylum and the number of protein sequences available for that phylum.
 - The numbers in the table denote the number of: orthologs found (black), P = paralogs found, ? = homologs found, whose relationship could not be programmatically determined, Σ = total homologs found.



Force topology is enabled!
Branch lengths do not represent real values