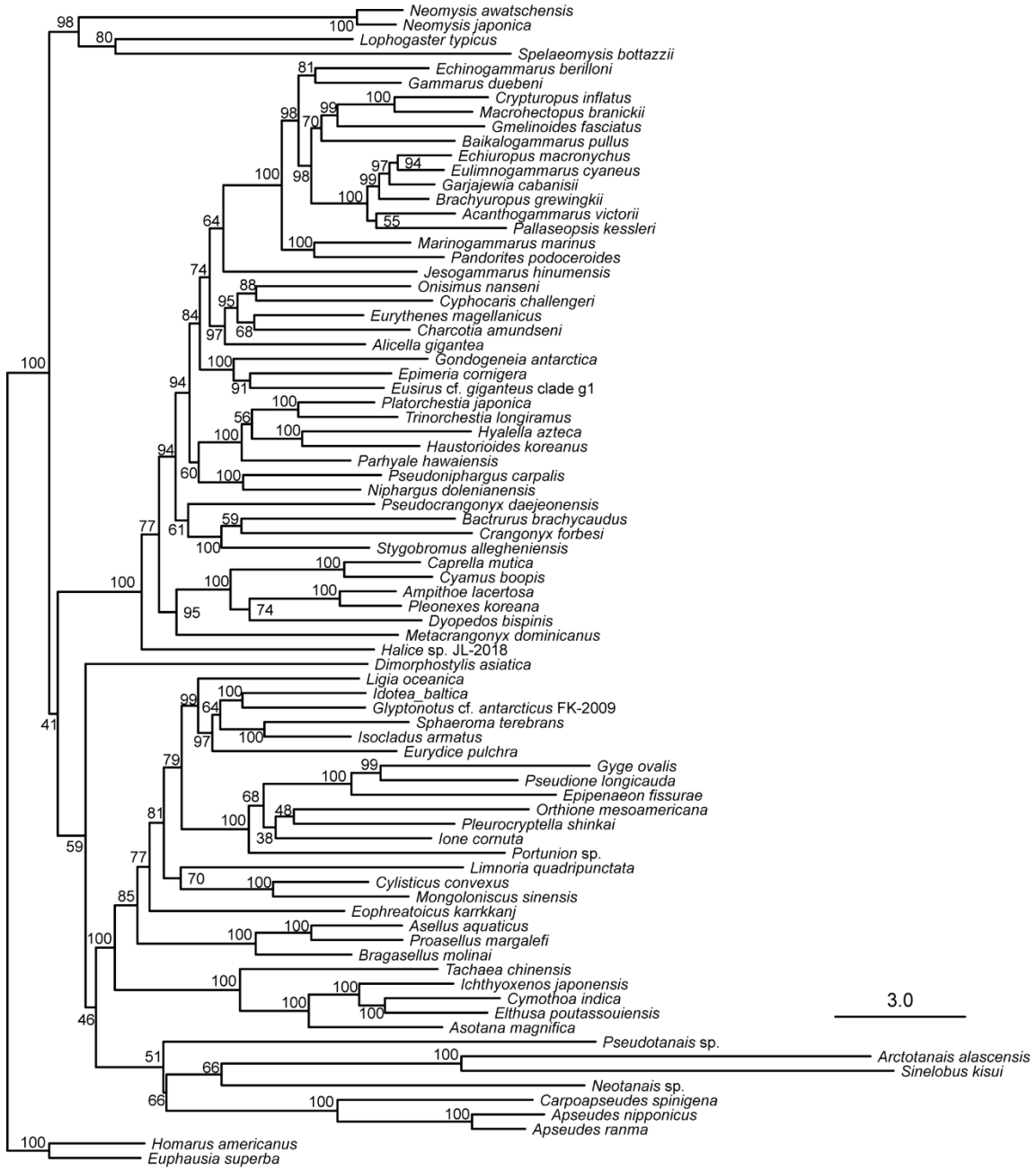
Supplementary File S1 Alignment lengths and optimal substitution models for two rRNA and 13 coding genes (initially partitioned into 41 subsets), Dataset 1. Following page, ML phylogeny from Dataset 1.

Partition Number	Gene / Partition	Length (bp)	Optimal substitution model
1	atp6_pos2 + nad3_pos2	324	GTR+F+I+G4
2	atp6_pos3 + nad2_pos3	545	TN+F+ASC+R4
3	atp8_pos1 + atp8_pos2 + nad6_pos1	180	TVM+F+R5
4	atp8_pos3	46	TPM2u+F+I+R2
5	cox1_pos1	510	GTR+F+I+R5
6	cox1_pos2	510	GTR+F+I+R4
7	cox1_pos3 + cox2_pos3 + cox3_pos3 + cob_pos3 + nad3_pos3	1,471	TIM+F+R5
8	cox2_pos1 + rrnL	815	GTR+F+R6
9	cox2_pos2 + cox3_pos2 + cob_pos2	856	TVM+F+R5
10	cox3_pos1 + cob_pos1 + atp6_pos1 + nad3_pos1	961	GTR+F+R6
11	nad1_pos1	217	TIM+F+I+R5
12	nad1_pos2	216	TIM+F+I+G4
13	nad1_pos3	216	TVM+F+I+R5
14	nad2_pos1	326	TVM+F+R5
15	nad2_pos2	326	GTR+F+R5
16	nad4_pos1 + nad4l_pos1 + nad5_pos1 + nad6_pos2	1,190	GTR+F+R6
17	nad4_pos2 + nad4l_pos2 + nad5_pos2	1,102	GTR+F+R6
18	nad4_pos3	435	HKY+F+R5
19	nad4l_pos3	96	TN+F+ASC+G4
20	nad5_pos3	571	TN+F+ASC+R4
21	nad6_pos3	88	GTR+F+G4
22	rrnS	649	GTR+F+R6



Maximum-likelihood (ML) phylogeny for peracarid crustaceans, based on mitogenome sequences (11,650 characters from 13 protein-coding genes [PCGs] and two rRNA genes; Dataset 1). The dataset was initially partitioned into 41 partitions, representing the three individual codon positions for each of the 13 PCGs and the two separate rRNA genes. These subsets were optimized into a final scheme of 22 partitions. Numbers near nodes are ultrafast bootstrap values (UFBoot).