Phylogenomic resolution of major tunicate relationships

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INTRODUCTION
Tunicata is a diverse clade of approximately 3,000 described species of marine, filter-feeding chordates. Tunicates are of great interest because 1) they are the closest living relatives of vertebrates, 2) there are numerous invasive species with economic consequences, and 3) some are edible. Despite their diversity and importance, relationships among major lineages of Tunicata are not completely resolved.

Traditional tunicate taxonomy is based on suites of gross morphological and life history characters (Table 1). Three classes are generally recognized: Ascidiae (sea squirts), Thaliacea (pelagic salps, doliolids, and pyrosomes), and Appendicularia (larvaceans).

Despite recent studies (e.g., Swalla et al., 2000; Turon and López-Legentil, 2004; Tsagkogeorga et al., 2009; & Govindarajan et al., 2011) that have greatly advanced understanding of relationships within clades, many questions about tunicate higher-level phylogeny remain unanswered. Here, we supplemented data with transcriptomes that span the diversity of Tunicata and re-evaluated the higher-level evolutionary history using a phylogenomic approach.

METHODS
We sampled all tunicate orders (with the exception of Doliolida, which was previously shown to be nested within the otherwise well-sampled taxon Tunicata) for genome or transcriptome data. We sampled all tunicate orders (with the exception of Doliolida, which was previously shown to be nested within the otherwise well-sampled taxon Tunicata) for genome or transcriptome data. We sampled all tunicate orders (with the exception of Doliolida, which was previously shown to be nested within the otherwise well-sampled taxon Tunicata) for genome or transcriptome data.

RESULTS & DISCUSSION
We analyzed datasets of up to 798 genes sampled from 28 taxa (matrix occupancy = 77.43%; Figure 1). All analyses recovered Olfactores (Tunicata + Vertebrata) as monophyletic within deuterostomes. Syst. Biol. 49, 52–64. Turon and López-Legentil, 2004; & Govindarajan et al., 2011) that have greatly advanced understanding of relationships within clades, many questions about tunicate higher-level phylogeny remain unanswered. Here, we supplemented data with transcriptomes that span the diversity of Tunicata and re-evaluated the higher-level evolutionary history using a phylogenomic approach.

In most analyses, phlebobranch tunicates were recovered paraphyletic with respect to Aplousobranchia. Support for this varied but was strong in some cases. However, when only the 50 best genes based on compositional heterogeneity were analysed, Phlebobranchia and Aplousobranchia were recovered reciprocally monophyletic with strong support, consistent with traditional hypotheses. Although internode certainty values for the complete dataset were generally low, the node nesting Aplousobranchia within Phlebobranchia was sister to a clade in which Thaliacea was sister to Phlebobranchia plus Aplousobranchia.

CONCLUSIONS
Phylogenomic analysis of tunicate transcriptomes enables the inference of the deep evolutionary history of Tunicata. The biodiversity of Tunicata is likely to be far greater than currently recognized.

REFERENCES