substantially across the IPs investigated to prevent them from forming phylogenetic clades based on race when considering all the character traits utilized in this study. The one exception was the orcish taxa, who did not form distinct clades except when the designated outgroup was the Protoss (discussed further below). The long branches separating subsets of the orc taxa are likely due to substantial creative shifts that have been made by IP producers in terms of the archetypes and behaviors characterizing their brand of orcs. For example, the orcs of the _Elder Scrolls_ and _Warcraft_ IPs (Orsimer_ES and Orcs_WC, respectively) are much more humanistic than orcs portrayed in other intellectual properties. They have families, form emotionally bound communities, and often fight for causes other than the shear desire to express violence and engage in bloodlust; these departures from the vile and retched orcs of Tolkien and others have resulted in the placement of these taxa as sharing a more recent common ancestor with elves, dwarves and humans than with other orcs. Conversely, the more antagonistic and villainous orc taxa shared more recent common ancestors with the monstrous horrors of the Zerg, Tyranid and Xenomorph outgroups, all three of which are characterized as large, physically powerful and overwhelmingly deadly insectoid creatures who stop at nothing to dispatch their foes.

The exception for orcs not appearing to form distinct clades was when the Protoss where designated as the sole outgroup in an analysis. A bi-pedal, psionically adept alien race from the _Starcraft_ science-fiction universe, the Protoss, despite being the product of a different genre in fiction with many physiological traits that differ substantially from the Tolkien-derived elf variants, share much of their design as a fictional people in terms of behavior and story roles with that of the elves. Their behavioral and archetypal trait states are shared so much so that whenever the Protoss are assigned as the outgroup in an alignment it causes all the elven taxa to shift on the tree topology from a derived monophyletic group to a basal paraphyletic group. This shift additionally alters the placement of the orc taxa in the phylogenies. The orcs and the elves were consistently the most distantly related groups out of the Tolkien four, indicating they shared the least amount of character states overall. As a result, a shift of the elven taxa to a more basal position on the trees when the Protoss were used as the outgroup always shifted the orc taxa to more derived positions. In the trees where this was the case, the orcs would appear to be monophyletic. However, given the degree of similarity between the Protoss and the elves it seems reasonable to determine that the Protoss do not serve well as an outgroup for the set of taxa used in this study. The greater dissimilarity between the Zerg, Tyranids and Xenomorphs relative to the rest of the dataset made these taxa more suitable, hence the tree from Figure 1 is here the preferred representation of the present data in terms of maximum likelihood inference.

The inferred tree topology suggests that elves, dwarves and humans from across seven different fictional universes share more in common with their respective cross-universe variants than they do with each other, but the tree nodes representing these relationships were for the most part poorly supported in the bootstrap analyses. Although the preferred tree topology from the concatenated sequence alignment suggests an interesting conclusion about the general fidelity of content creators to the origins established by Tolkien, the present study was unable

to show strong statistical support for the relationships inferred. An extension of the dataset developed and used here may be necessary to estimate phylogenetic relationships among these fictional races with greater statistical support.

The scope of the present dataset was even more limiting in the case of the assessment of the categorical sequence alignments. Although this study was unable to compare sets of tree topologies generated from each categorical sequence alignment based on different outgroups, the topologies successfully generated from the archetypal traits alignment, when compared to those generated with the concatenated alignment, hint at the idea that IP creators may be more inclined to bend the Tolkien mold in some categorical ways than others. Future phylogenetic studies of the fictional races of Tolkien would likely benefit from an expanded suite of categorical character traits to better assess in what ways IP creators are more or less likely to depart from established source materials.