

The authors show strong evidence of recent adaptive introgression from *C. robusta* into *C. intestinalis* (absent in *C. roulei*) on chromosome 5, against a background of low genomewide admixture. This case study of adaptive introgression is particularly interesting given the relatively high divergence between these sea squirt species and their human-mediated secondary contact. The evidence for long introgressed haplotypes surrounding a “missing data region” where *C. robusta* has excess copy number is particularly striking, and the authors have identified a promising candidate gene in this region for future work. The authors use small but strategic geographic samples and whole genome sequencing phased by trios to reach their conclusions. Congratulations on a fine paper! I have only a few suggestions for a stronger manuscript:

The SweepFinder results for *C. robusta* (line 273) combined with the star-like phylogeny including some *C. intestinalis* haplotypes are key pieces of evidence that this locus was selected in *C. robusta* and then subsequently introgressed into *C. intestinalis*. Consider making these a combined main figure. The neighbor-joining tree could be presented as a simplified version of S8 (e.g. labeling the tips only by species/color not individual sample IDs). I could not find the SweepFinder results for *C. robusta* showing positive selection on chr 5, which should at least go into the supplement.

Please give the datasets more informative names, e.g. ‘phased SNP set’ for Dataset #1, ‘all parental SNPs’ for Dataset #2, and ‘ancestry informative SNPs’ for Dataset #3. You can still keep the numbers that correspond to the reference table at the end of the supplement; it’s just hard to keep track of in the main text when the datasets are only labeled by number.

Please acknowledge the uncertainty around your 75 years estimate for the date of introgression (methods ~line 230). While a point estimate is useful, there are still many unknowns. Rapid rises in frequency due to selection can create longer tracts than neutral models. Additionally, the r used is an unpublished estimate of the average recombination rate genomewide. Local recombination could be much lower around the hotspot.

Figure 1: Please provide separate legend entries to distinguish intraspecific and interspecific lab hybrids visually and specify the cross. The legend should clearly indicate the number of individuals analyzed (not the number sampled). The figure description says ‘the F1s were considered as supplementary individuals in the PCA’ but the methods describe a regular PCA analysis with all 45 individuals treated the same. Please clarify.

Figure 2: It’s hard to see the red arrows and how many there are. It could be more effective to color the portion of each bar in the histogram that corresponds to tracts on chr 5.

Figure 4E: If space allows, would be clearer to label '8% SNPs iHS outliers'.

Figure 5: Really nice figure!