



**Figure S7. Image of the coverage by sequenced reads around the 12-bp deletion of STRAD $\alpha$ , showing unanimous agreement of the species difference, for *A. palmata* (A) and *A. cervicornis* (B).** Each read is collapsed to a horizontal line of width 1 pt., and if a read ends in the depicted interval, then another read is drawn in the same line, typically after a short gap. Reads from the same sample are drawn with a unique color, nucleotides differing from the *A. digitifera* reference are shown in another color, and a gap in the alignment of the read to the reference is shown in black. One sample in each species has coverage around 150, roughly the same as the total of the 20 low-coverage genomes. In *A. cervicornis*, there is a synonymous C→G substitution to the left of the insertion position, and a T→C substitution to the right, which creates a heterozygous S→P amino acid replacement in the deeply sequenced sample, but not present in most of the low-coverage *A. cervicornis* samples.