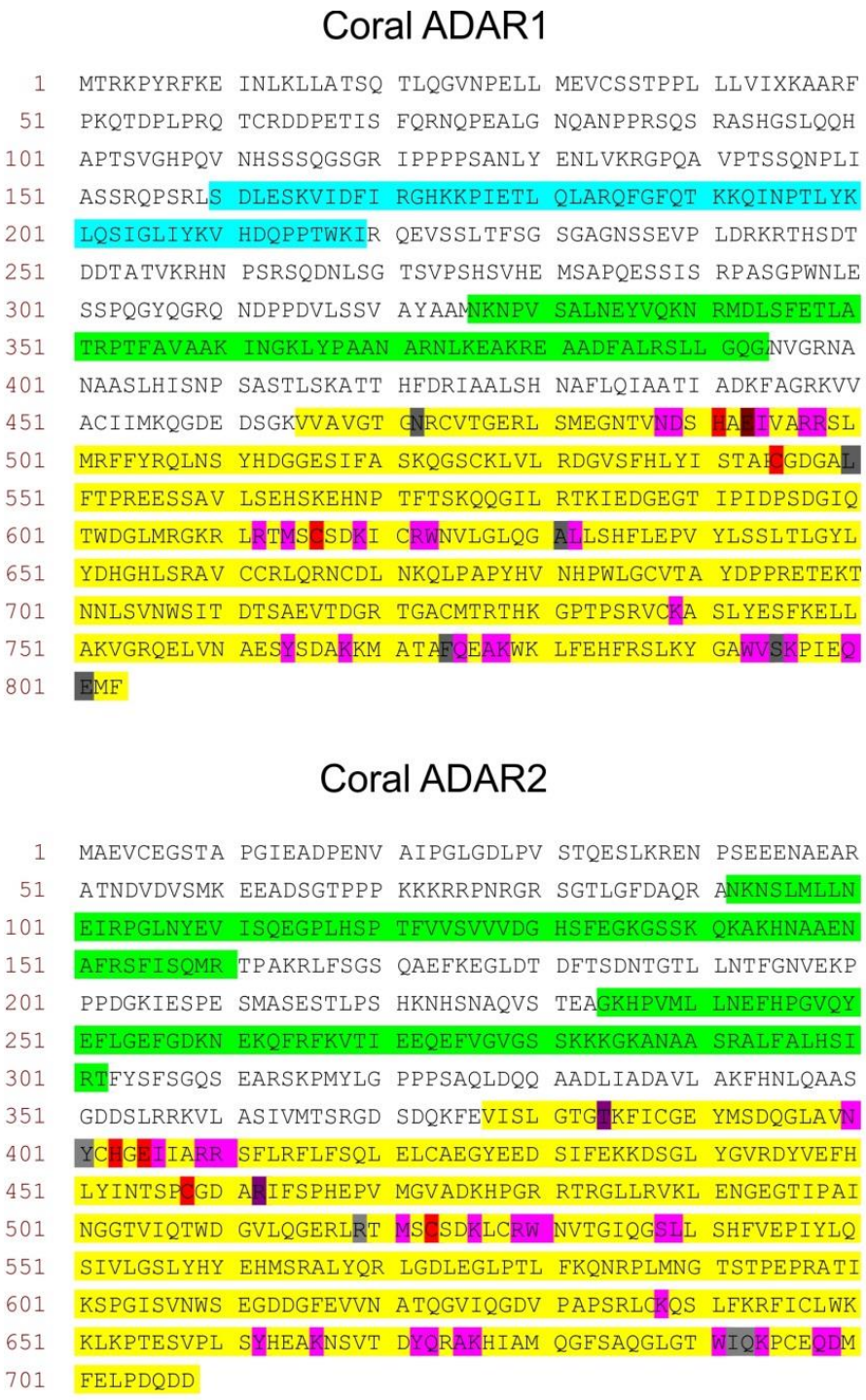
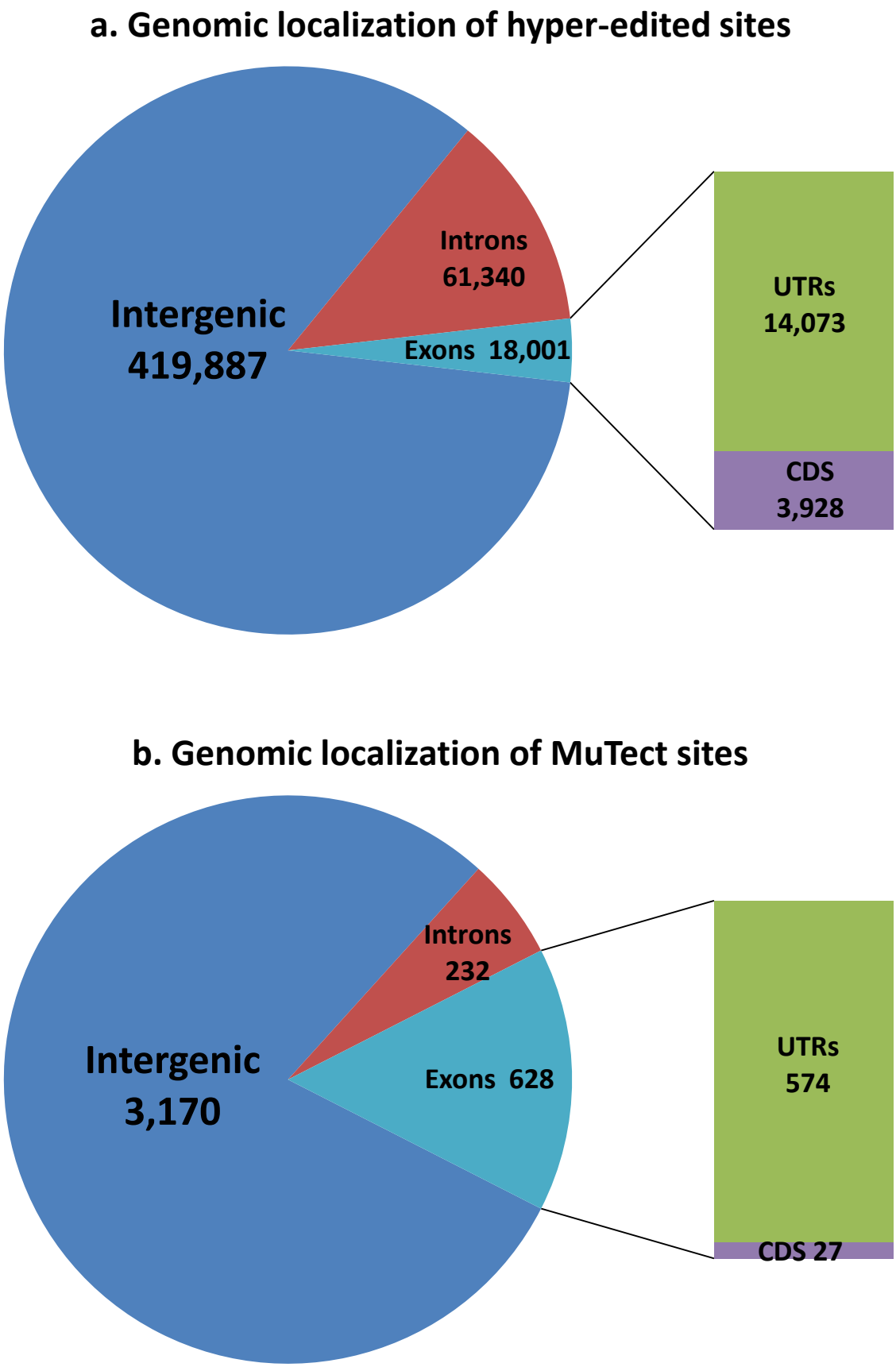
Supplementary Figure 1.



green = dsRBMs
cyan = Zα domain
Yellow = catalytic domain
Red = Zinc Coordinating residues
Dark Red = glutamate for proton shuttling
Violet = other residues thought to be important for catalysis of adenosine
pink = conserved IP6 coordinating residues

Supplementary figure 1. **The conserved domains of coral ADAR**. Both coral ADAR contain conserved domains: Both contain double stranded RNA binding motifs (dsRBD, in green). While vertebrate ADAR1 contains 3 dsRBDs, coral only contains one. Coral ADAR2 contains 2 dsRBDs similarly to vertebrates. Coral ADAR1 contains a conserved Zα (cyan) domain in its N-terminus compared to vertebrates containing both a Zα and Zβ. Both coral ADARs contain conserved deaminase domains (yellow) with most of the catalytic residues conserved between coral and vertebrate ADAR. These include zinc (red) and IP6 (pink) coordinating residues, glutamate for proton shuttling (dark red) and other residues thought to be important for the catalysis of adenosine (violet).

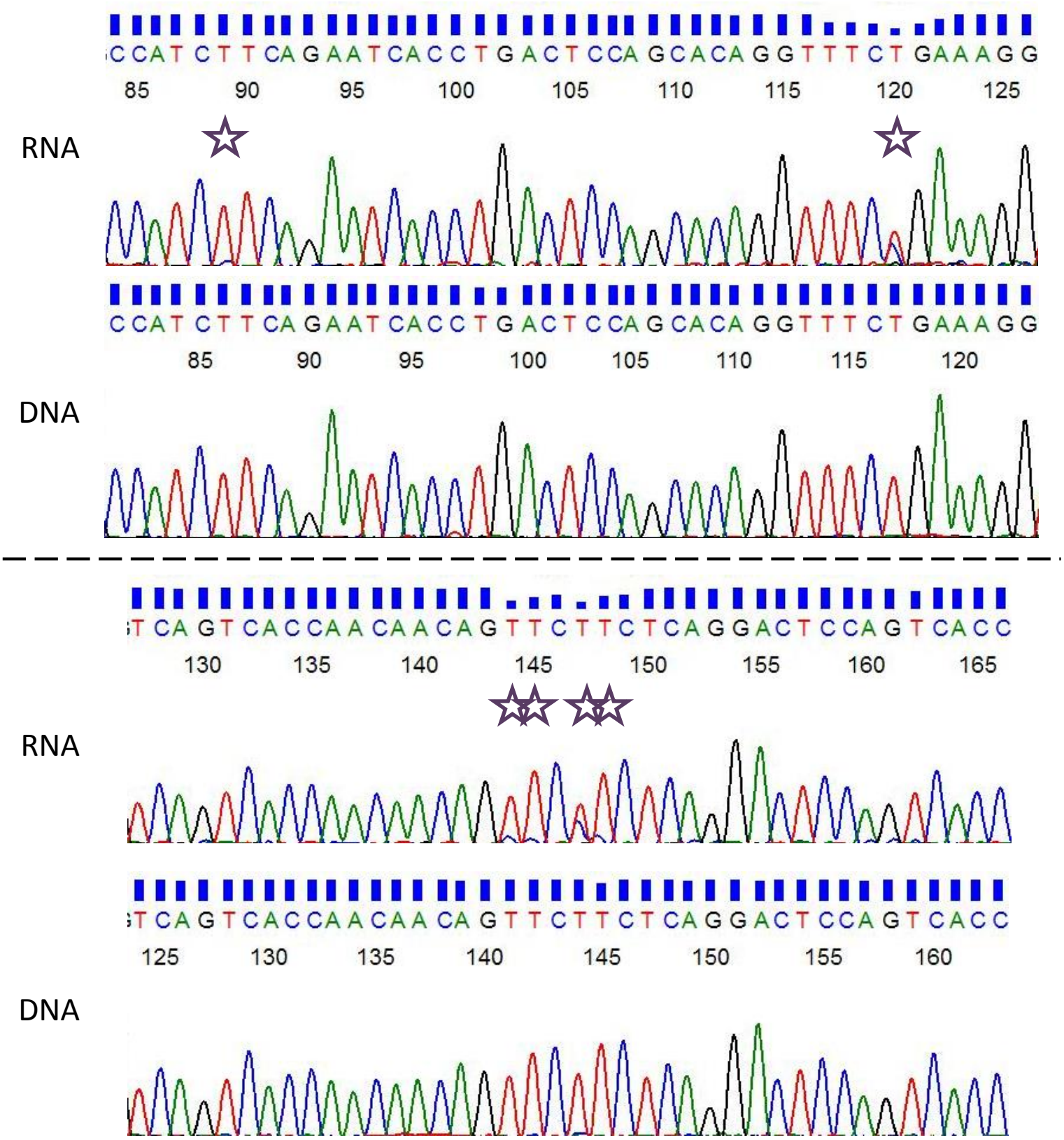
Supplementary Figure 2.



Supplementary figure 2. **Distribution of edited sites in coral transcriptome. a)** Hyper-edited sites. A total of 499,228 unique sites were found using the hyper-editing pipeline. Of these, 79,341 sites were found in genes. 61,340 sites were intronic and 18,001 sites were found in exonic regions, with 14,073 being in UTRs and 3,928 in coding regions. **b)** Editing sites found by MuTect. Of the A-to-G mismatches, roughly 20% were found in gene regions with only 27 out of the 628 being in coding regions.

Supplementary Figure 3

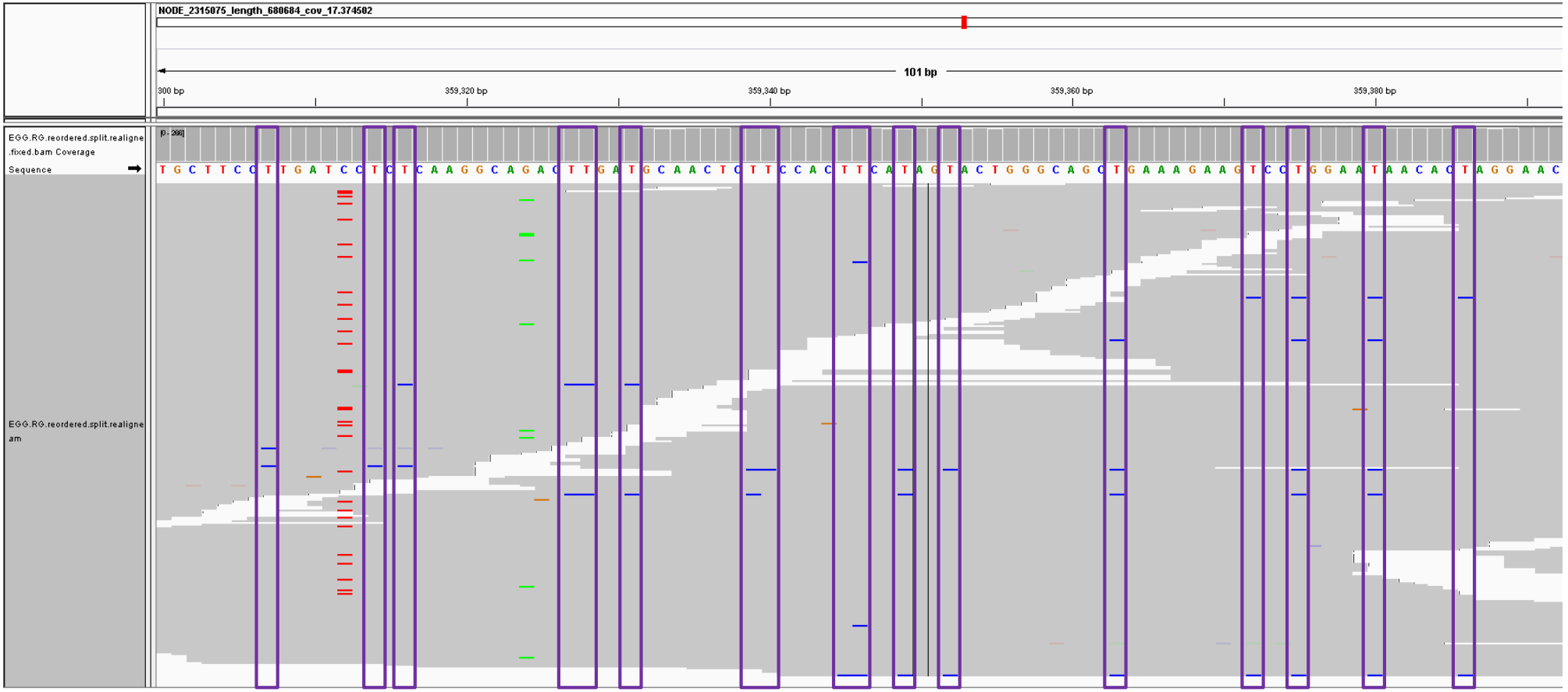
> ***Acropora millepora*** **NODE_1899612_length_377773_cov_21.822311: 204470-204770 (+)**



Supplementary figure 3. **Sanger sequencing chromatograms of edited region.** A chromatogram of *Acropora millepora*, NODE_1899612_length_377773_cov_21.822311: 204470-204770 (+), in the antisense of the predicted 3' UTR of Calcium-binding protein NCSA gene (Swiss-Prot accession number of the ortholog protein Q75K28; NCBI transcript accession number JR986886.1, GI:37908921). Chromatograms of genomic DNA are presented along with those of the corresponding cDNA (RNA) of. Bases are colored as: A- green, C- blue, G- black, T- red. Editing sites are usually evident as nucleotides having an A in the DNA and a G (or a mixed A/G signal) in the RNA, at the presented region the editing was occurred on the antisense strand, thus appears as a T in the DNA and a C (or T/C) in the RNA. The 7 validated editing sites are marked with purple stars.

Supplementary Figure 4.

a.

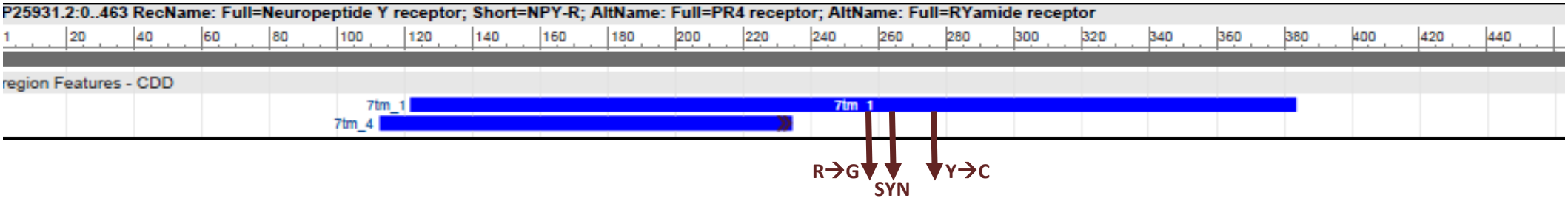


Supplementary Figure 4.

b.

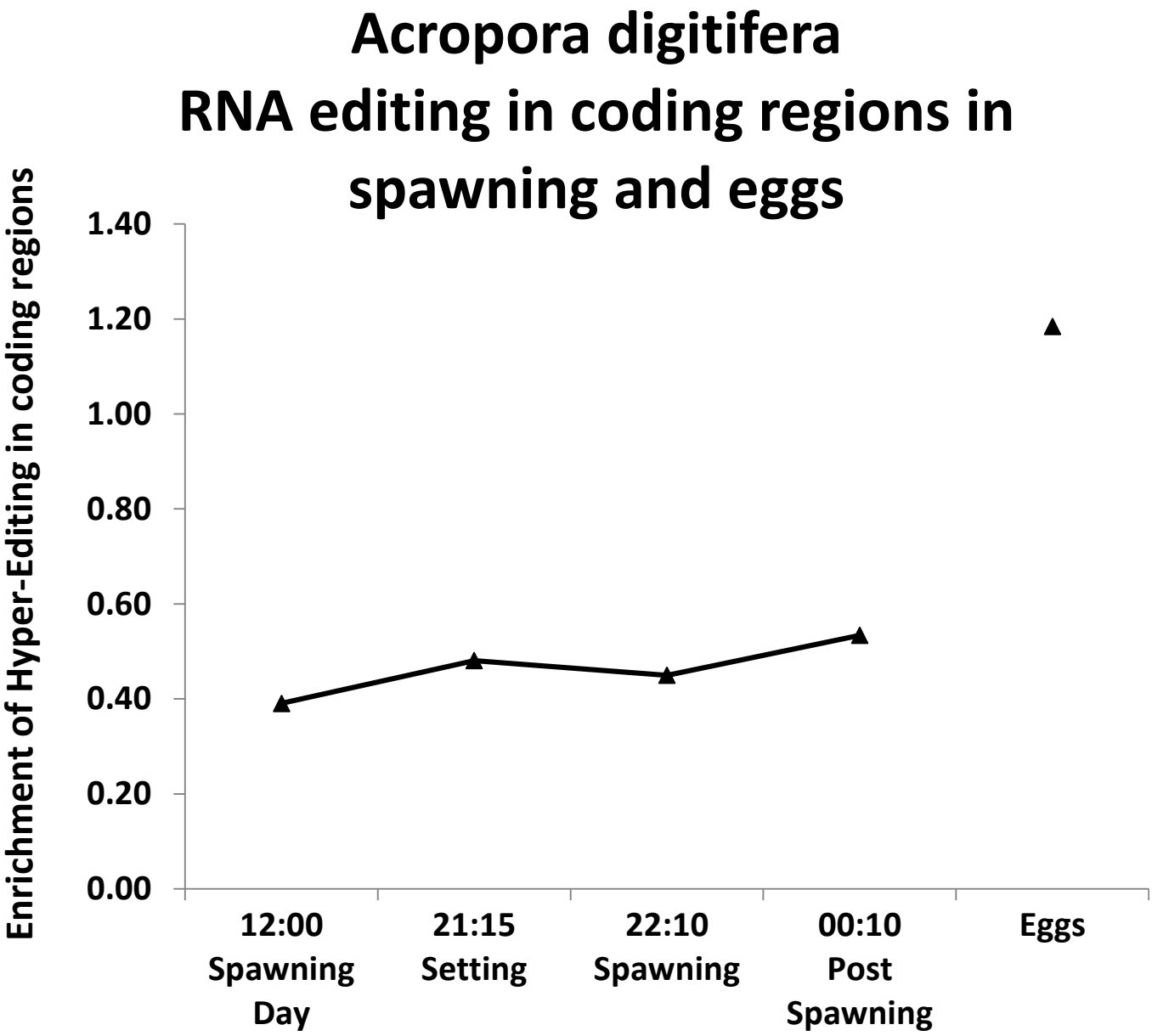
Supplementary figure 4. **Editing in coding regions of *Acropora millepora* egg sample.** Two examples of the reads composition in coding regions of **a)** RPGP1 (Rap1 GTPase- activating protein) and **b)** ADDA (Alpha- adducin) genes as seen in IGV (Thorvaldsdottir, Robinson, and Mesirov 2013). Detected editing sites are highlighted with purple square. Coding editing sites (mostly) cause nonsynonymous recoding of the protein sequences resulting in distinct protein variants that may function differently.

Supplementary Figure 5.



Supplementary figure 5. **Editing sites detected at *Acropora millepora* egg Neuropeptide Y receptor active site.** Example of putative alterations in a protein active site caused by RNA editing. The change of these AA in the functional 7 transmembrane domaincould affect the folding and function of the protein, creating different active protein variants.

Supplementary Figure 6.



Supplementary figure 6. ***Acropora digitifera*: Comparison of enrichment of editing in coding regions of eggs and spawning adults.** *Acropora digitifera* eggs also showed enrichment of editing sites in the coding region similarly to the *Acropora millepora*. This result strengthens the proposed mechanism of utilizing editing to provide a beneficial mutation for selected gametes without relying on somatic changes in the egg genome.

Supplementary Table 1.

Primers used for PCR sequencing for sanger sequencing validation of editing in selected genes.

Forward Primer					Product Size (bp)	Reverse Primer				
Name	Sequence	Length	Tm (C)	GC Con. (%)		Name	Sequence	Length	Tm (C)	GC Con. (%)
4-F	GCTCAAACAGGTCATGTCCT	20	57.8	50	527	4-R	TGCGTTGACATACGTTGCTG	20	59.5	50
6-F	AAATGGTTTGAGCTCAGGGA	20	57	45	299	6-R	TGCATTTTTGGGCATGAAAGTCT	23	59.9	39.1
8-F	CGGGTACGTGCCGTGTAG	18	60.2	66.7	271	8-R	TAAAAGGCAAGTGTCAGGGC	20	58.4	50
14-F	TGGCTTACTTGTTTTCTAAGAGCA	24	58.6	37.5	233	14-R	TGTCCTATTTCCATCGTATTTGCT	24	58.3	37.5
15-F	TAGTTCCAGCCCTTGTGCTT	20	59.9	50	244	15-R	AATGCGTCCAGCTACCCTTA	20	59.7	50
18-F	GTGCCAATAACCCCAAAATG	20	60.1	45	614	18-R	AGTGCCACTAACACCCCAAA	20	60.4	50

Supplementary Tables 2-5.

https://goo.gl/gP19O5