Figure S1. The stem-loop structures of MIR172 loci from *A. thaliana* (At) and *A. arenosa* (Aa) (MIR172a, b, d, and e) were predicted using RNA secondary structure prediction software the Vienna RNA package (http://www.tbi.univie.ac.at/~ivo/RNA/). The miR172 sequence in each locus was indicated by red lines on the structures. For each *AtMIR172*, there are two corresponding *AaMIR172* loci (Aa-1 and Aa-2).
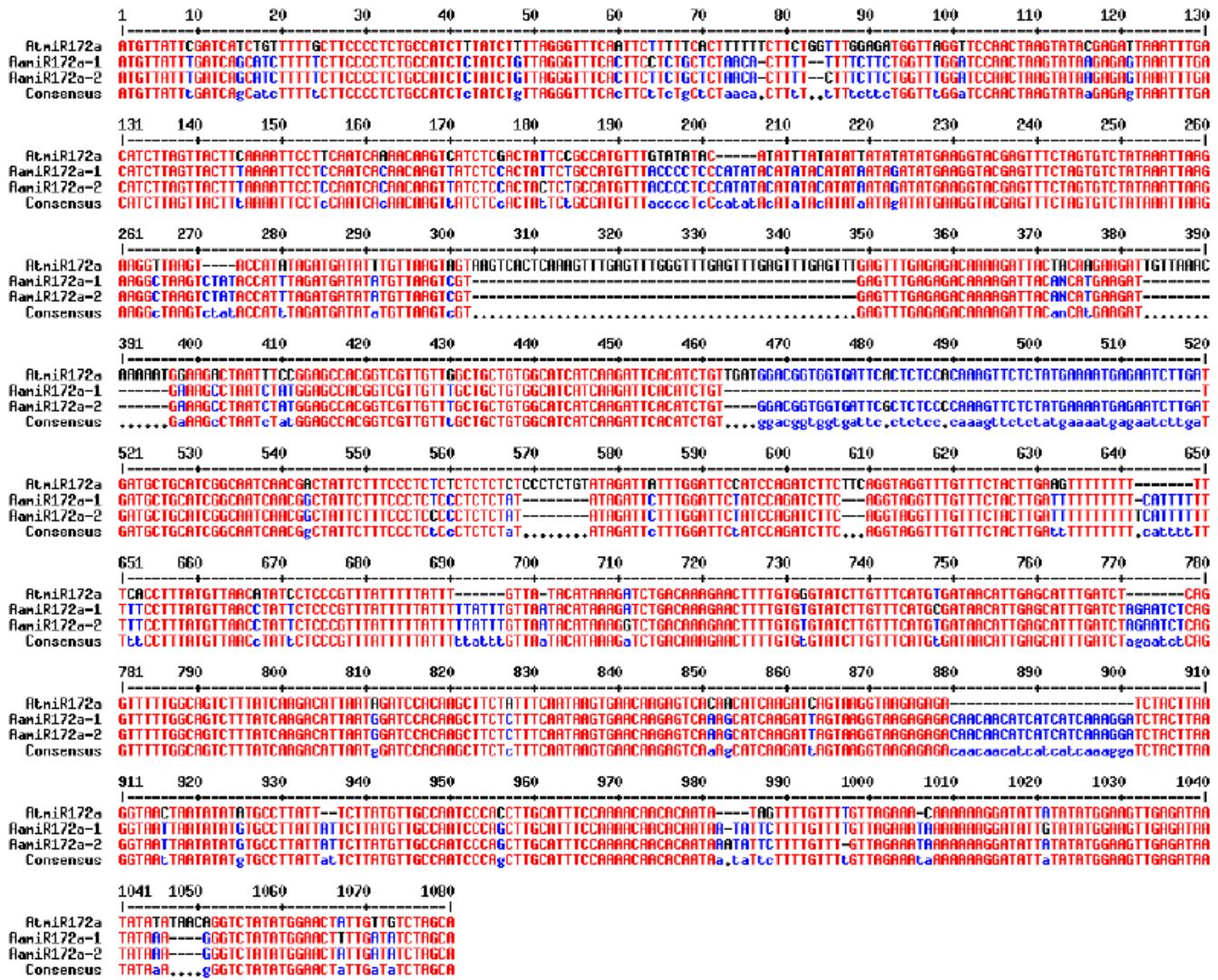
Figure S2. Sequence alignment of *A. arenosa MIR172a* locus with the corresponding *A. thaliana MIR172a*. Multiple sequence alignment performed using MultAlin (http://prodes.toulouse.inra.fr/multalin/).
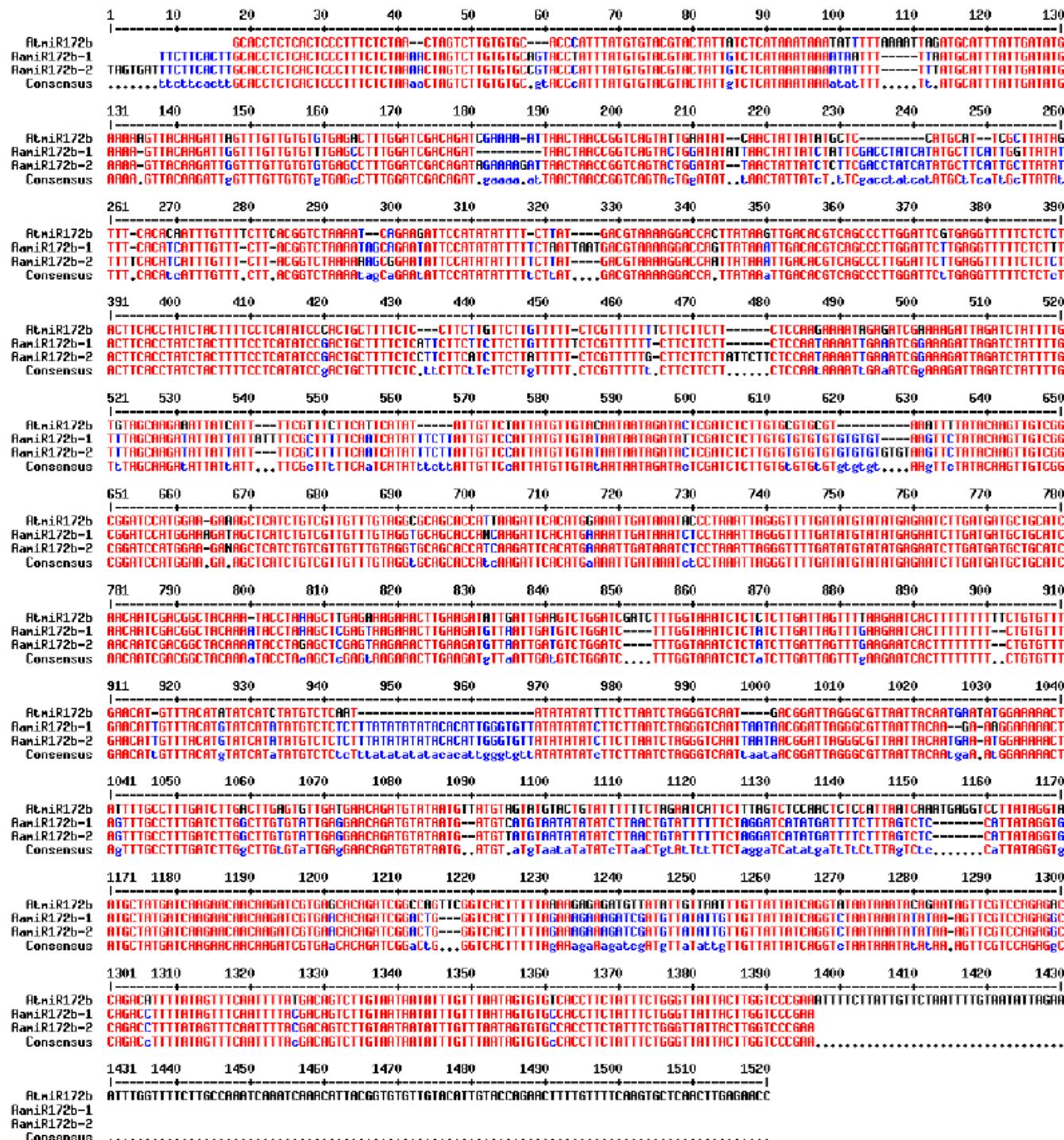
Figure S3. Sequence alignment of *A. arenosa MIR172b* locus with the corresponding *A. thaliana MIR172b*. Multiple sequence alignment performed using MultAlin (http://prodes.toulouse.inra.fr/multalin/).
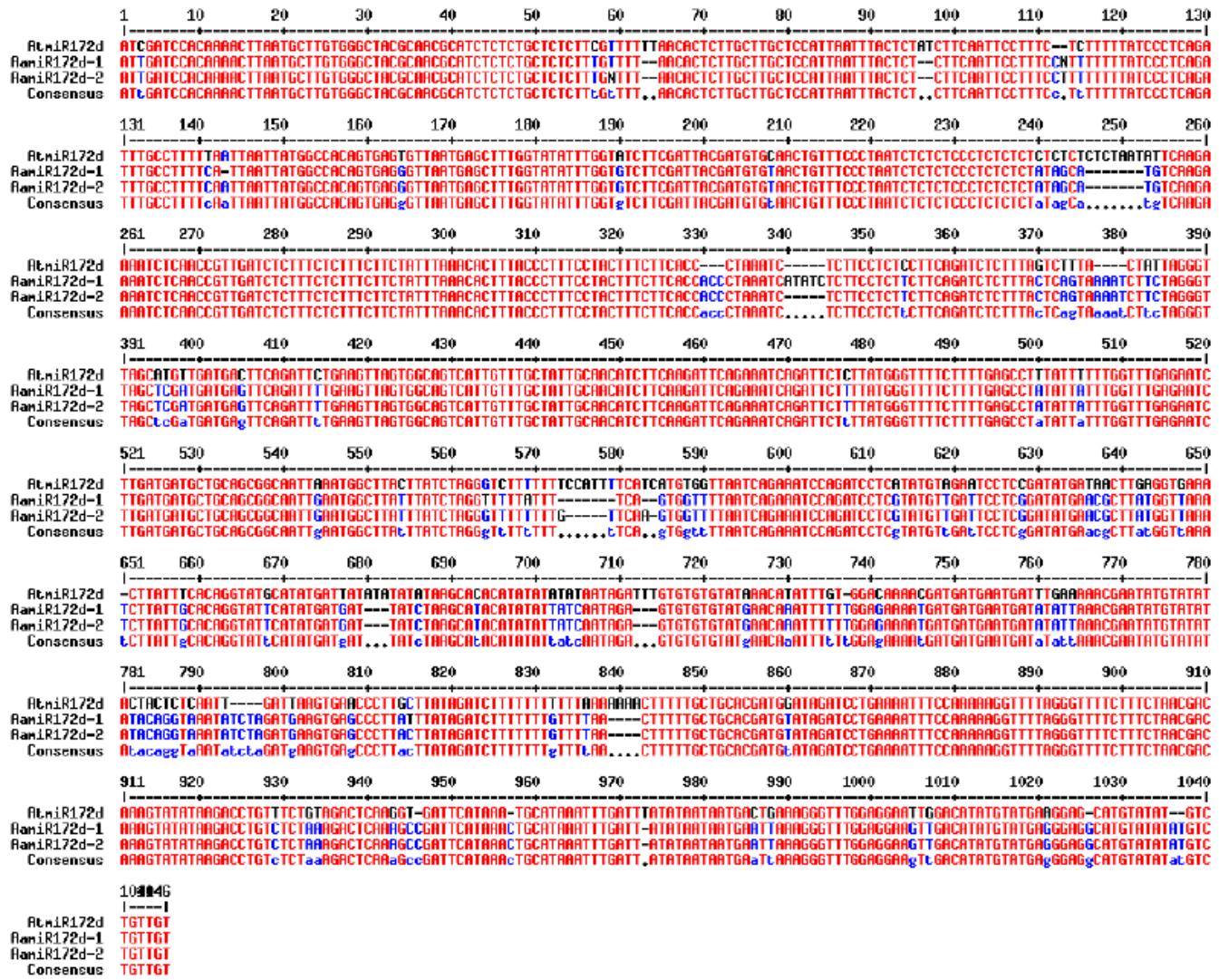
Figure S4. Sequence alignment of *A. arenosa MIR172d* locus with the corresponding *A. thaliana MIR172d*. Multiple sequence alignment performed using MultAlin (http://prodes.toulouse.inra.fr/multalin/).
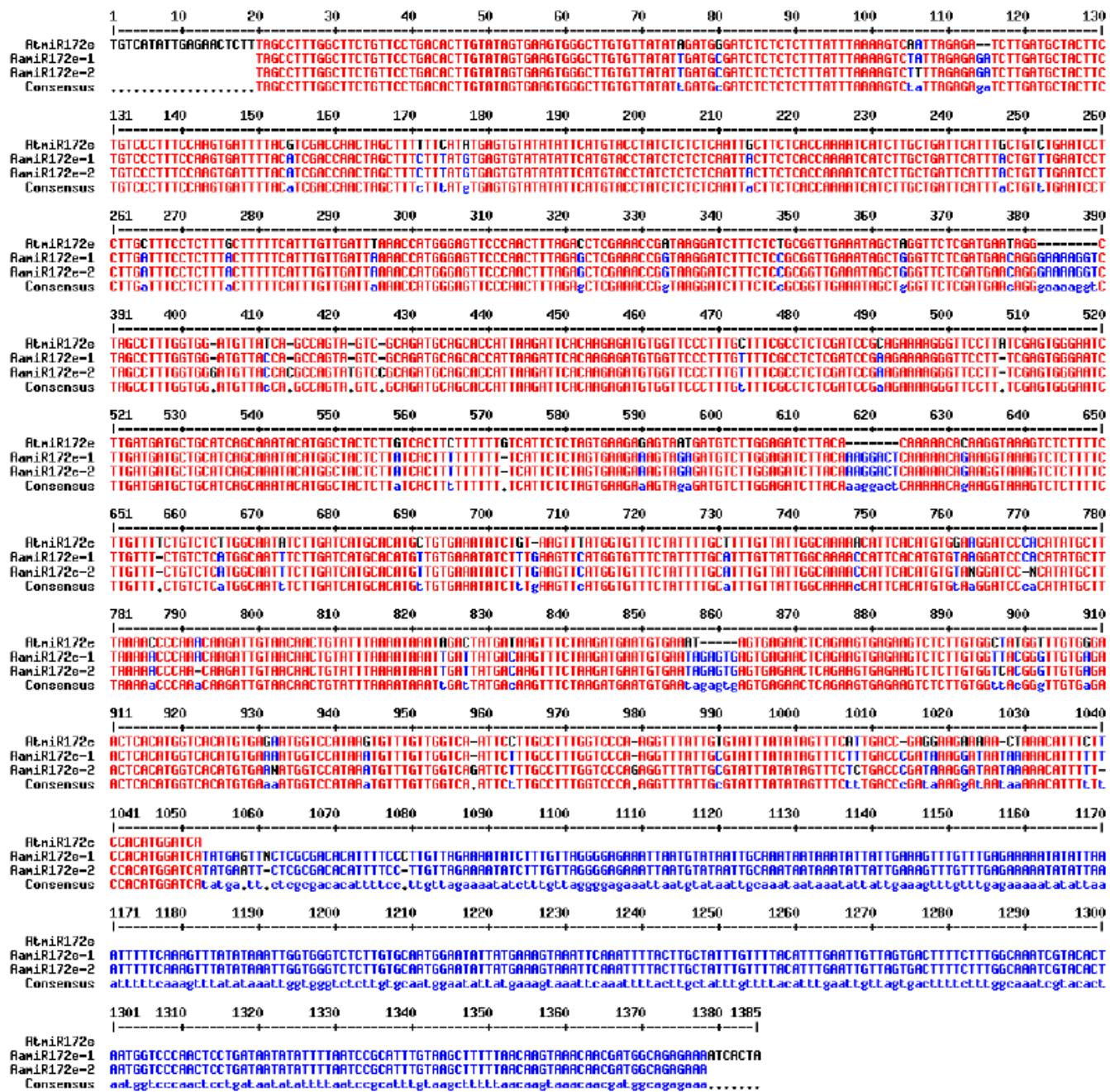
Figure S5. Sequence alignment of *A. arenosa MIR172e* locus with the corresponding *A. thaliana MIR172e*. Multiple sequence alignment performed using MultAlin (http://prodes.toulouse.inra.fr/multalin/).