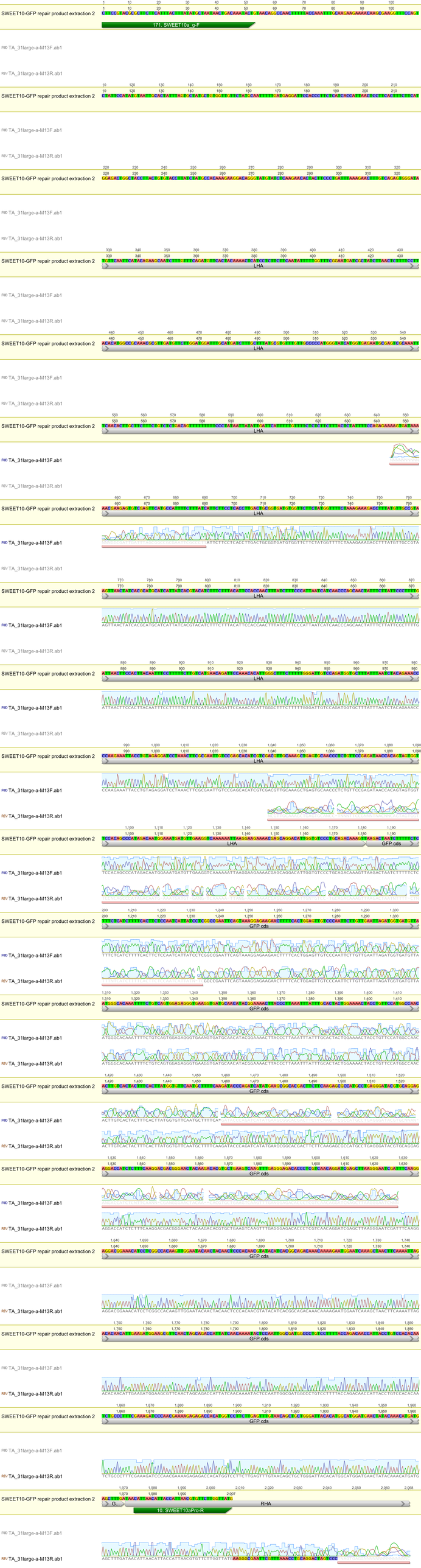
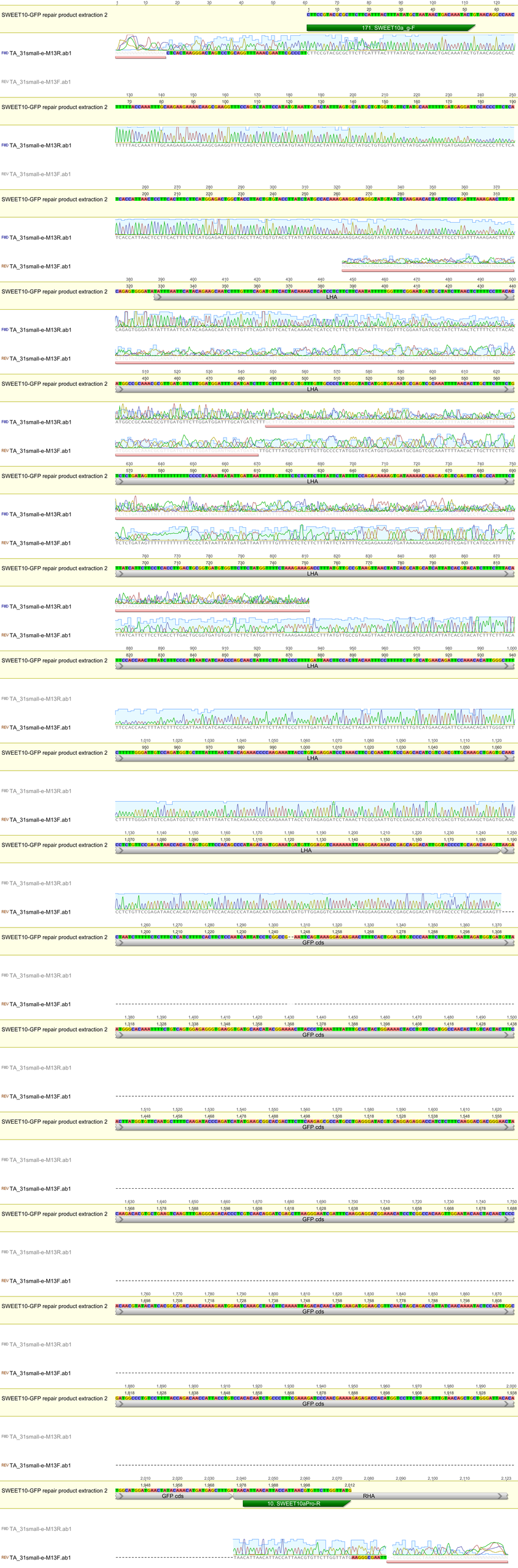
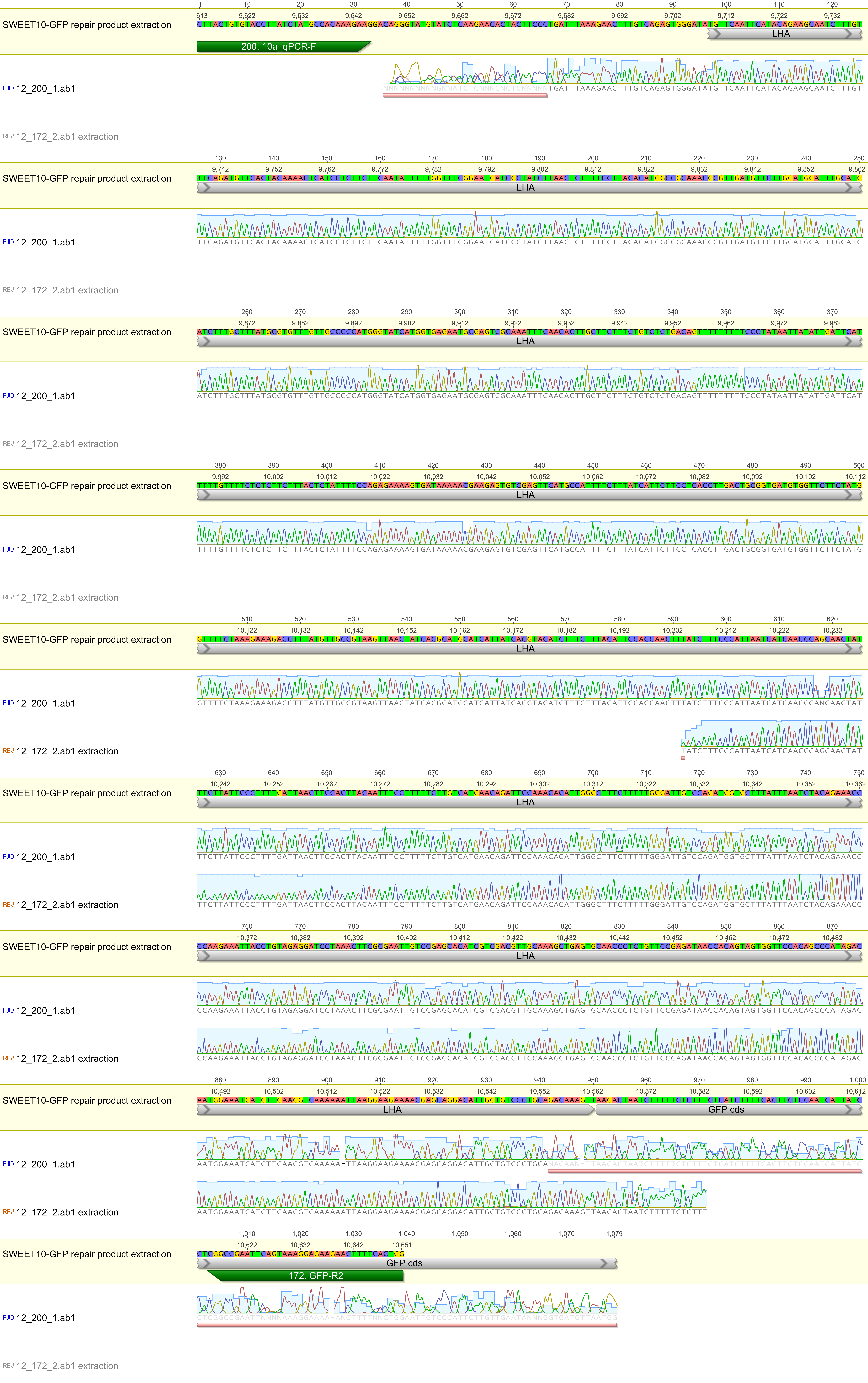
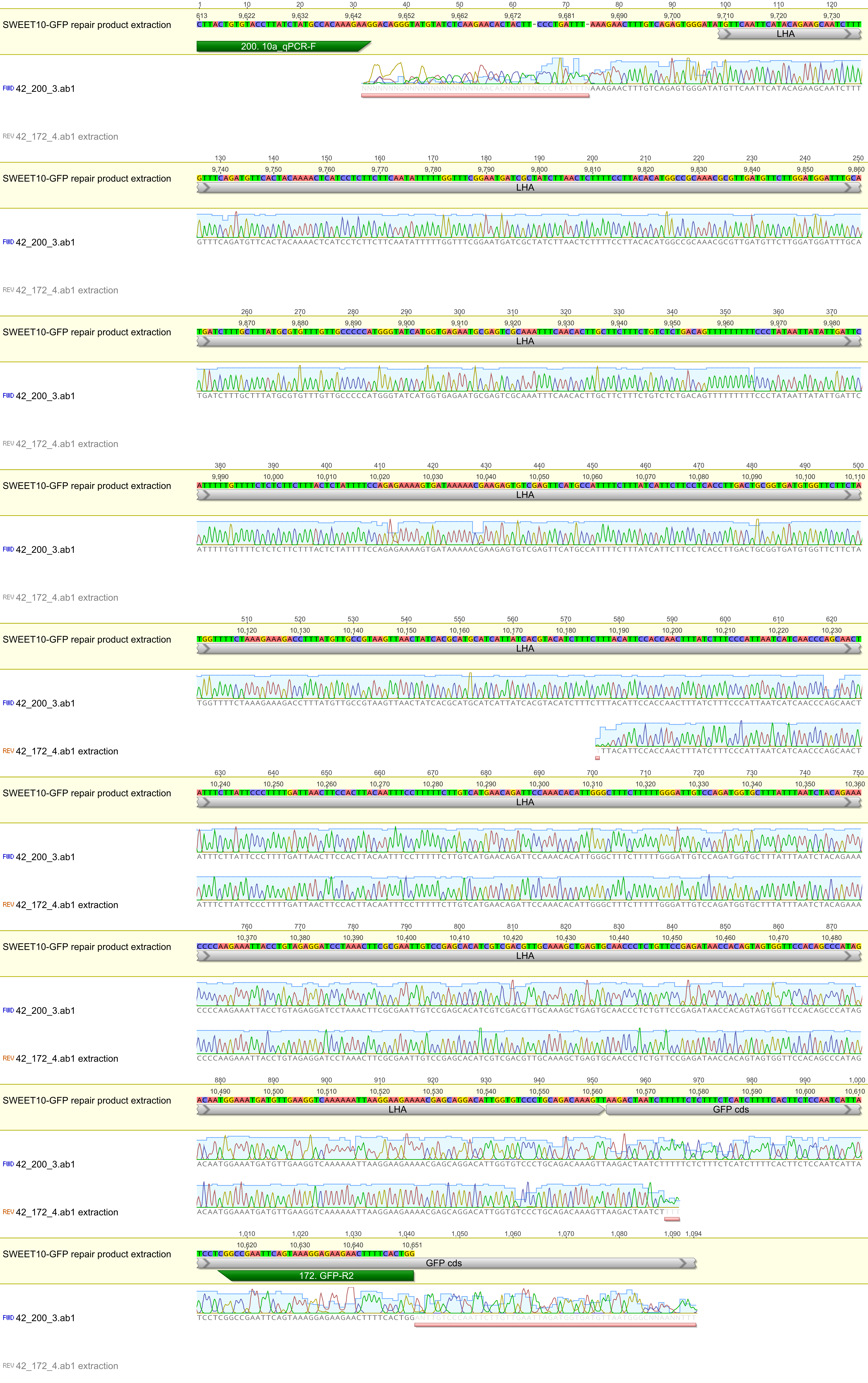

SWEET10-GFP repair product extraction 2
171. SWEET10a_g-F
FWD TA_31large-a-M13F.ab1
REV TA_31large-a-M13R.ab1
LHA
GFP cds
RHA
10. SWEET10aPro-R


SWEET10-GFP repair product extraction 2
171. SWEET10a_g-F
FWD TA_31small-e-M13R.ab1
REV TA_31small-e-M13F.ab1
LHA
GFP cds
RHA
10. SWEET10aPro-R


SWEET10-GFP repair product extraction
200. 10a_qPCR-F
LHA
FWD 12_200_1.ab1
REV 12_172_2.ab1 extraction
GFP cds
172. GFP-R2



SWEET10-GFP repair product extraction
200. 10a_qPCR-F
LHA
GFP cds
172. GFP-R2
FWD 42_200_3.ab1
REV 42_172_4.ab1 extraction

Figure S2. Sanger sequencing of successful knock-in lines. (Supports Figure 2)

Sanger sequencing of successful knock-in lines 31 (the focus of this manuscript), 12 and 42. Shown: raw sequencing data aligned to cultivar TME 419 (WT) reference sequence expected following scarless integration of GFP. The data are wrapped in multiple rows within a single page per sequencing product to aid in viewing. Page 1: sequencing data (base call and quality graphs) for line 31 from the upper (larger) band shown in the gel in Figure 2D (primers 171 and 10, Table S1). Page 2: data from the lower (smaller) band. Heterozygous SNPs are highlighted with colored backgrounds. These PCR products were sequenced using clone-seq with standard M13 sequencing primers. The products that were sequenced for lines 12 (page 3) and 42 (page 4) were generated using primers 171 and 164 (Table S1). Sequencing of these lines was performed directly on the PCR product using primers 200 and 172 (Table S1). Each page shows the sequencing data aligned to the expected product of HDR (highlighted in yellow). The LHA, GFP, and RHA sequence of the repair template are labeled in grey. Consensus sequence is given above the yellow-highlighted reference and sequencing data below. The names of the sequencing runs, which include the line number and either “large” or “small” for the bands sequenced from line 31 or the primer number used for lines 12 and 42, are to the left. Trimmed areas of poor sequence quality are indicated with a pink bar. Relevant primer sequences are shown in green. Analysis was performed using the algorithm built in to Geneious® version 9.1.8.