Supplementary Figure Legends

Figure S1. Sequence alignment of the *TGTT1* elements

Sequence identities over 70% were shaded in blue. The TSD site, 5′LTR, PBS, PPT and 3′LTR regions are indicated using red lines and arrows.

Figure S2. Wet laboratory validation of the TGTT and AACA elements.

Each element was randomly selected and analyzed from each family. A schematic view of the LTR-RT, with the location of the region that was amplified (dashed pink boxes), a picture of the PCR amplification of the LTRs using DNA material of the four Rosaceae species (see Table S1), and the alignments of the sequenced PCR products together with the sequences that were mined from the genome sequence are provided. The positions of TSDs, beginnings and ends of LTRs, PBS and PPT are also indicated.

Figure S3. Multiple alignments of PBS sites from TGTT, AACA and normal TGCA elements of the *Ale* lineage.

A 20-bp region of each PBS site was extracted from all of the *TGTT* and *AACA* elements, as were the consensus sequences of the other four *Copia Ale* families from pear [38]. Sequence identities over 70% are shaded in blue.

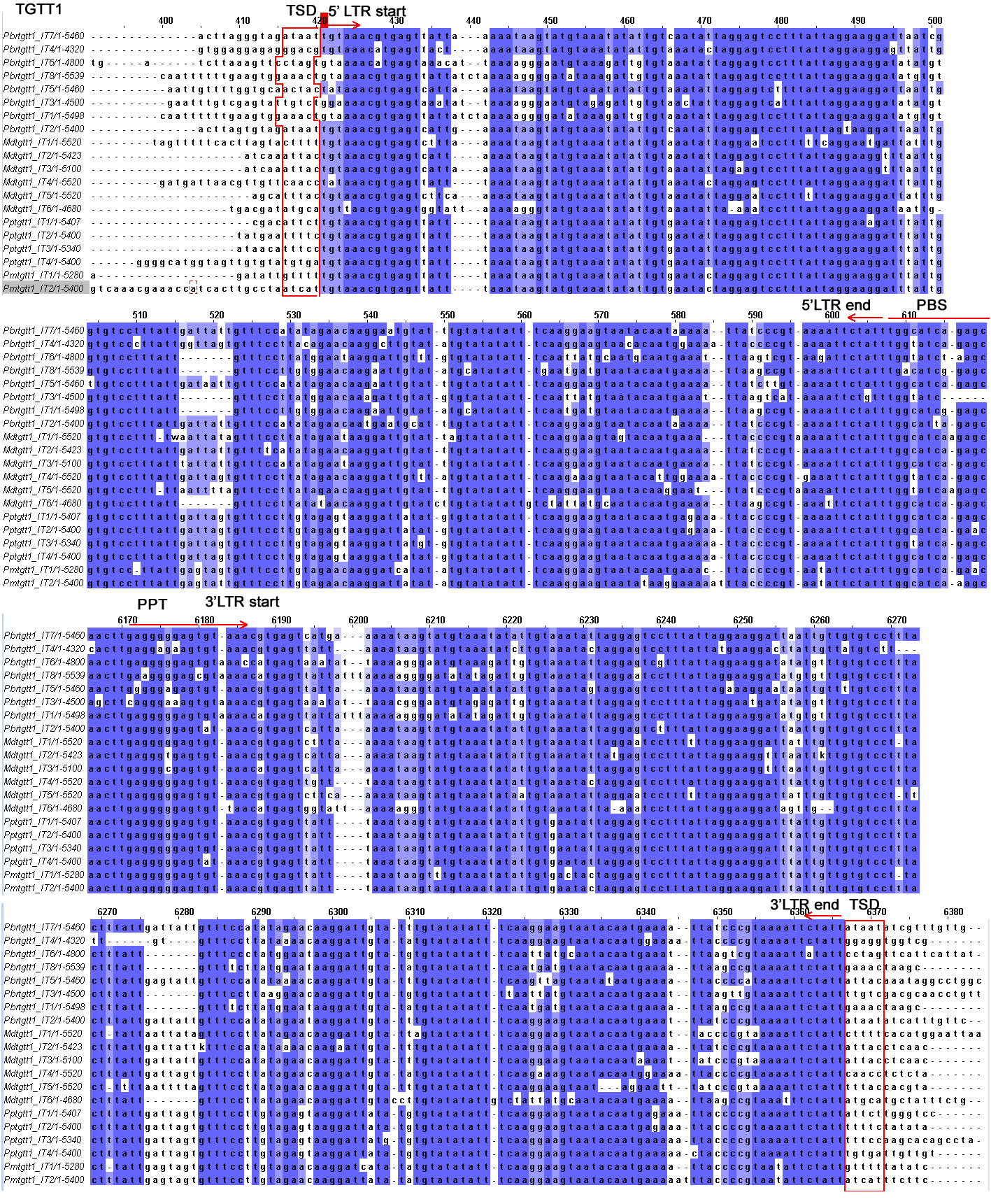
Figure S4. INT phylogenetic relationships among TGTT, AACA and normal TGCA elements.

The INT domains (the integrase core domain, pfam00665) of 67 elements from the six *Copia-like TGTT* and *AACA* families and the consensus sequences of each normal *Copia* TGCA family from pear [38] were used to build the phylogenetic tree. The *TGTT* and *AACA* elements are indicated by various colored branches, and the normal TGCA families are shown in gray. The nucleotide sequence distances are indicated by the scales.

Figure S5. Evidence of transcriptional activity in five *TGTT* and *AACA* elements.

For each element, the whole-nucleotide sequences were used as queries to construct the HISAT alignments using the RNA-seq data from the NCBI species Sequence Read Archive database. Normal short pair reads are shown in the gray bar. Too long paired reads are shown in the purplish red bar. One-sided sequences are indicated by green or blue boxes.

Figure S1.



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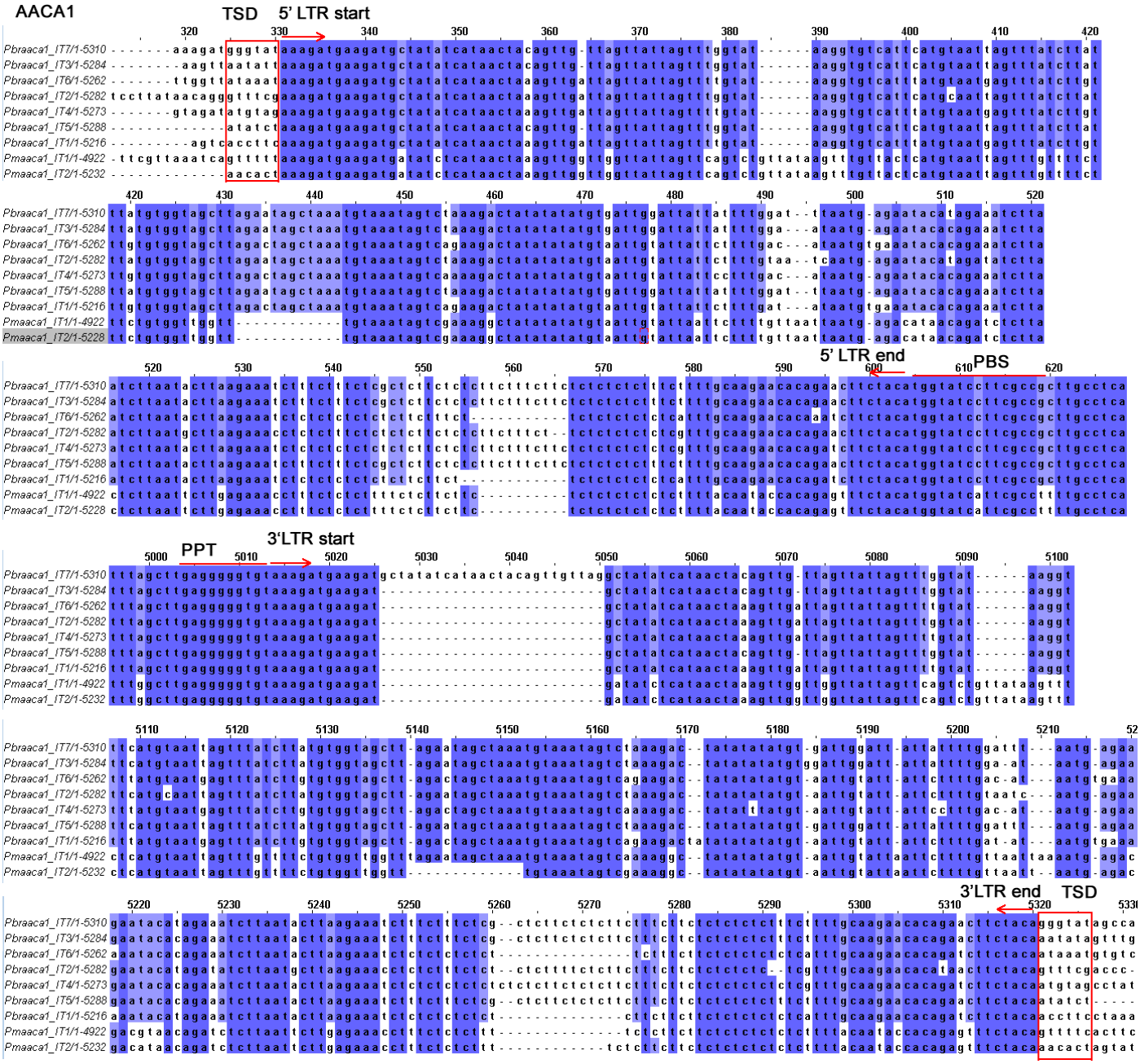

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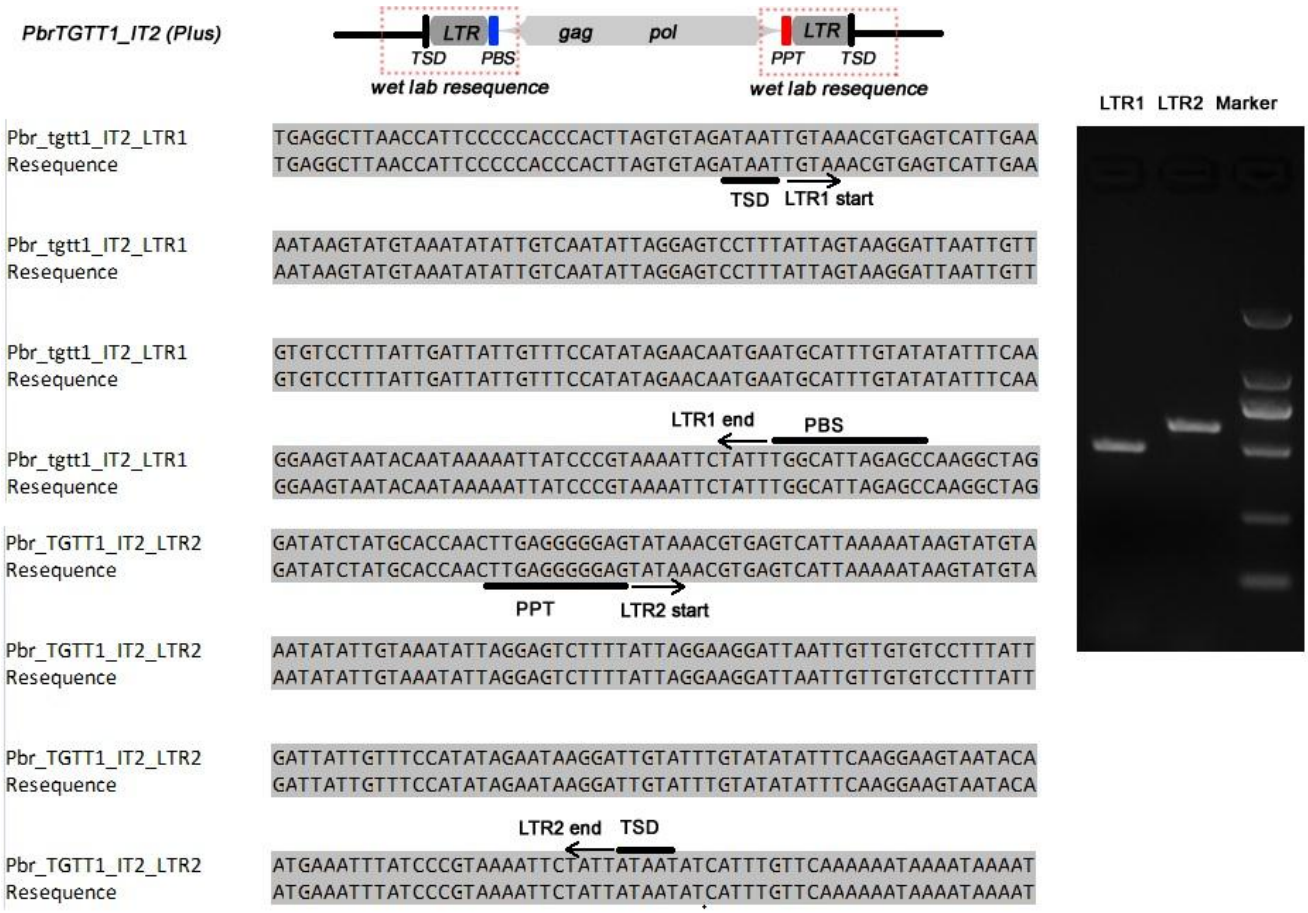
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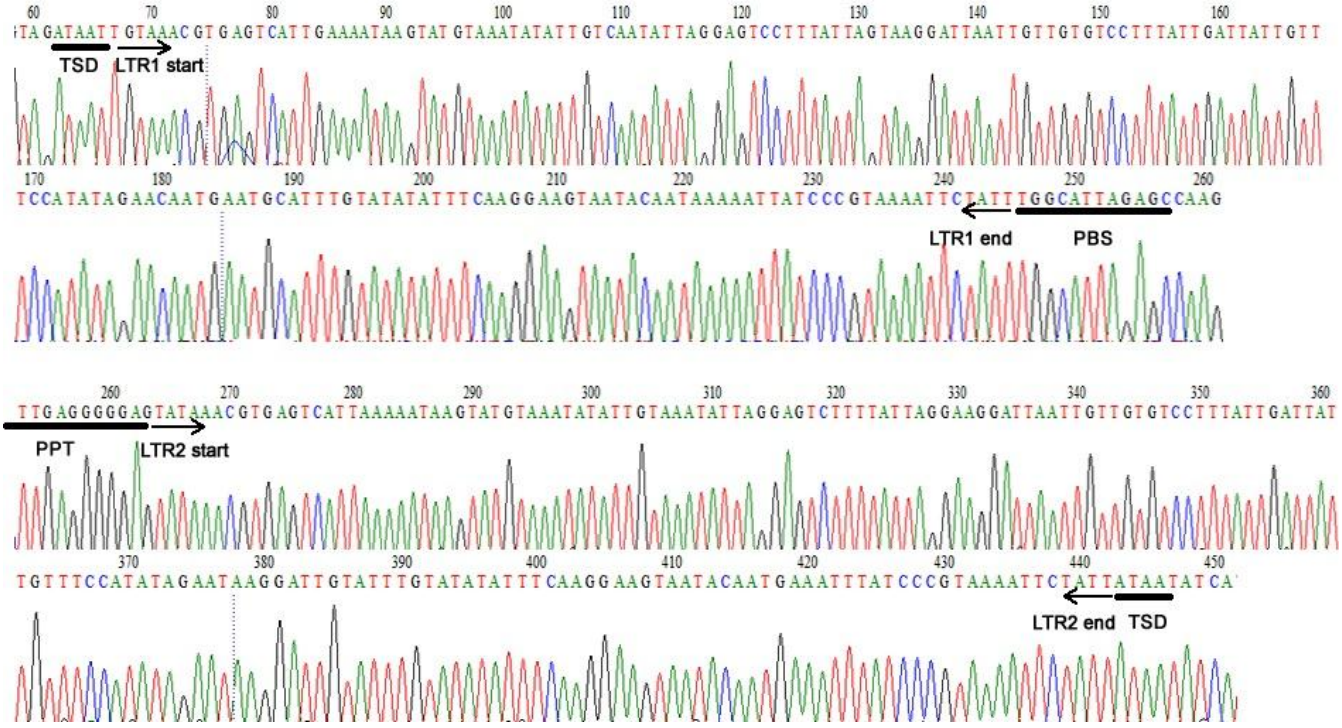
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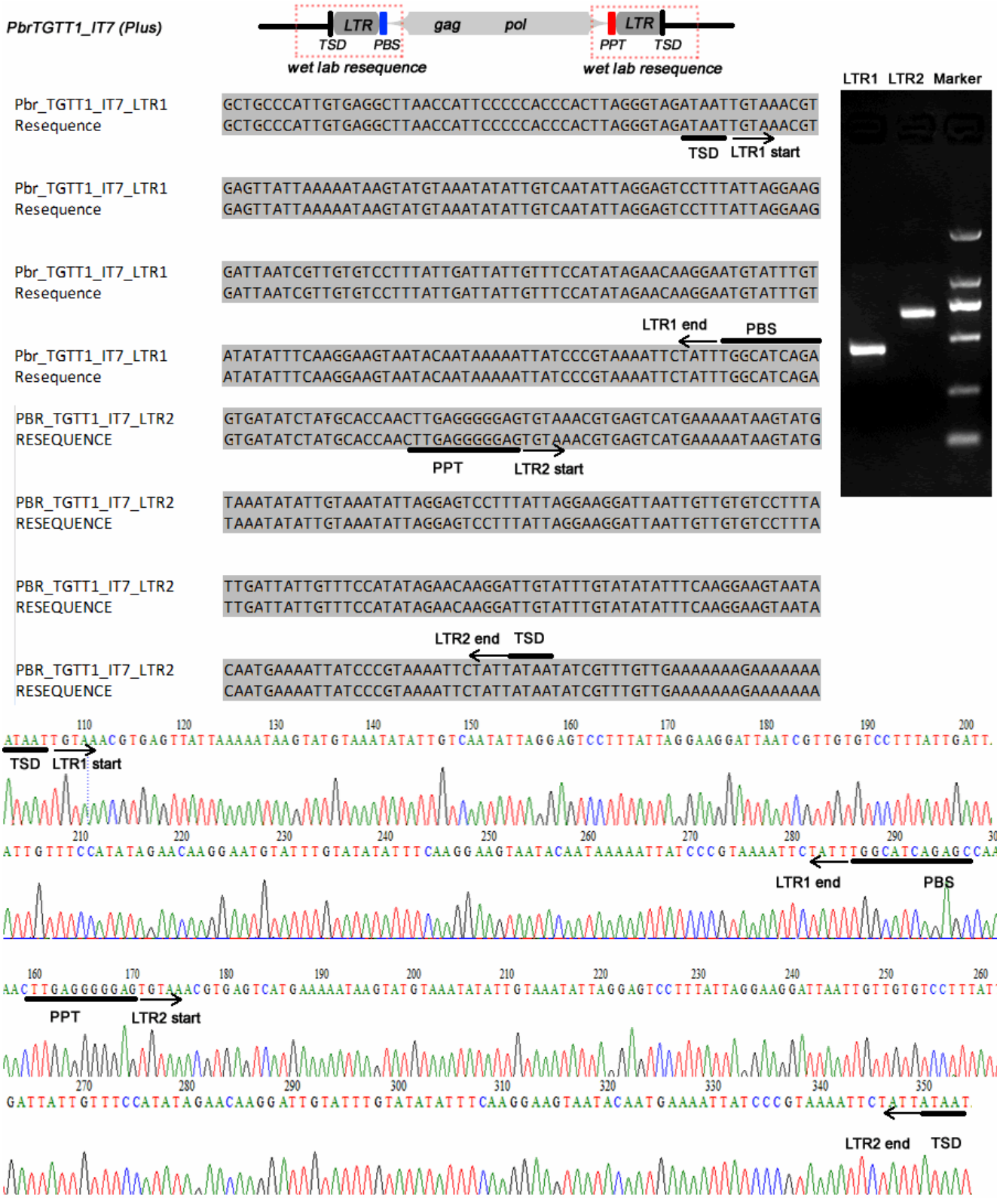
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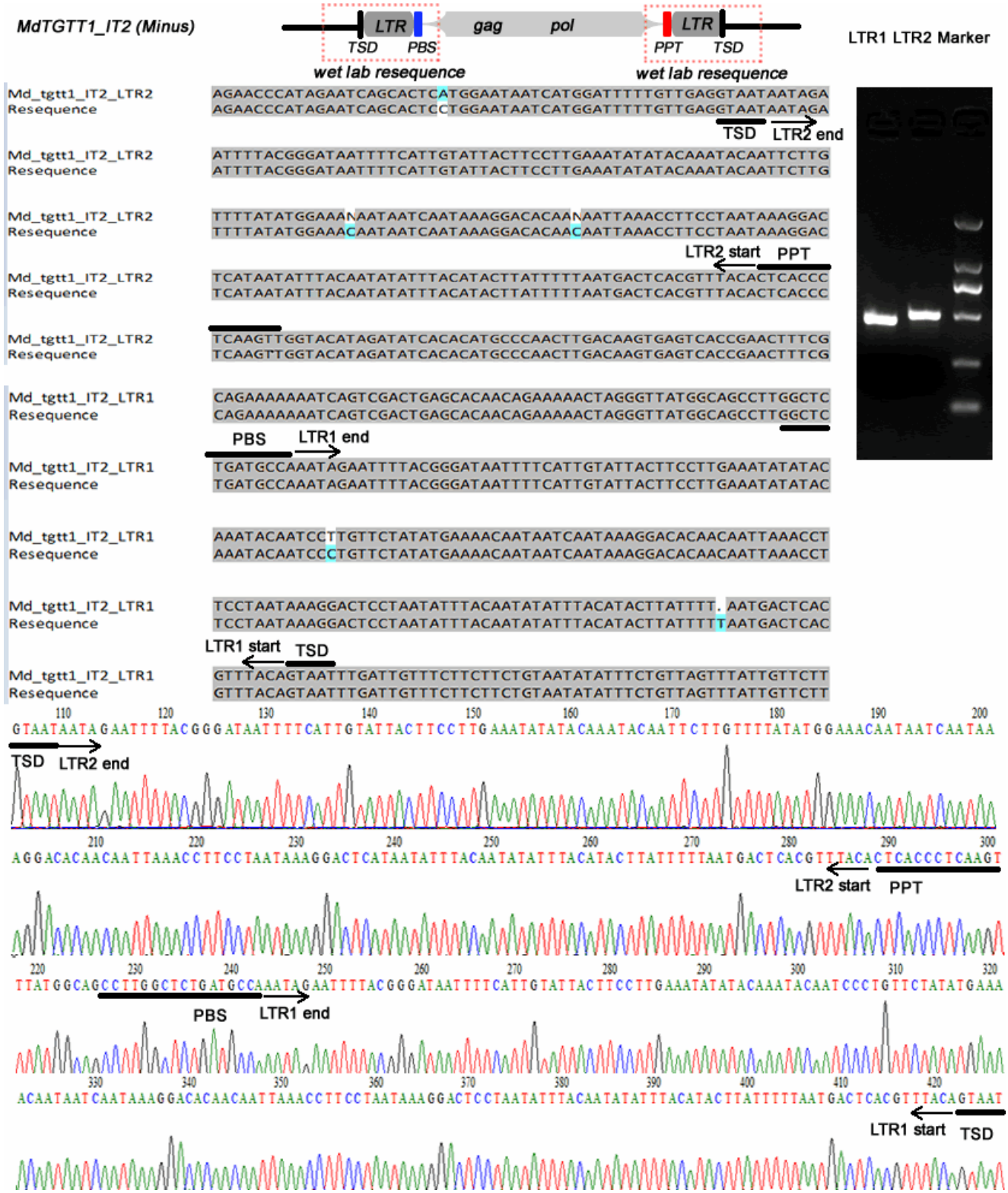
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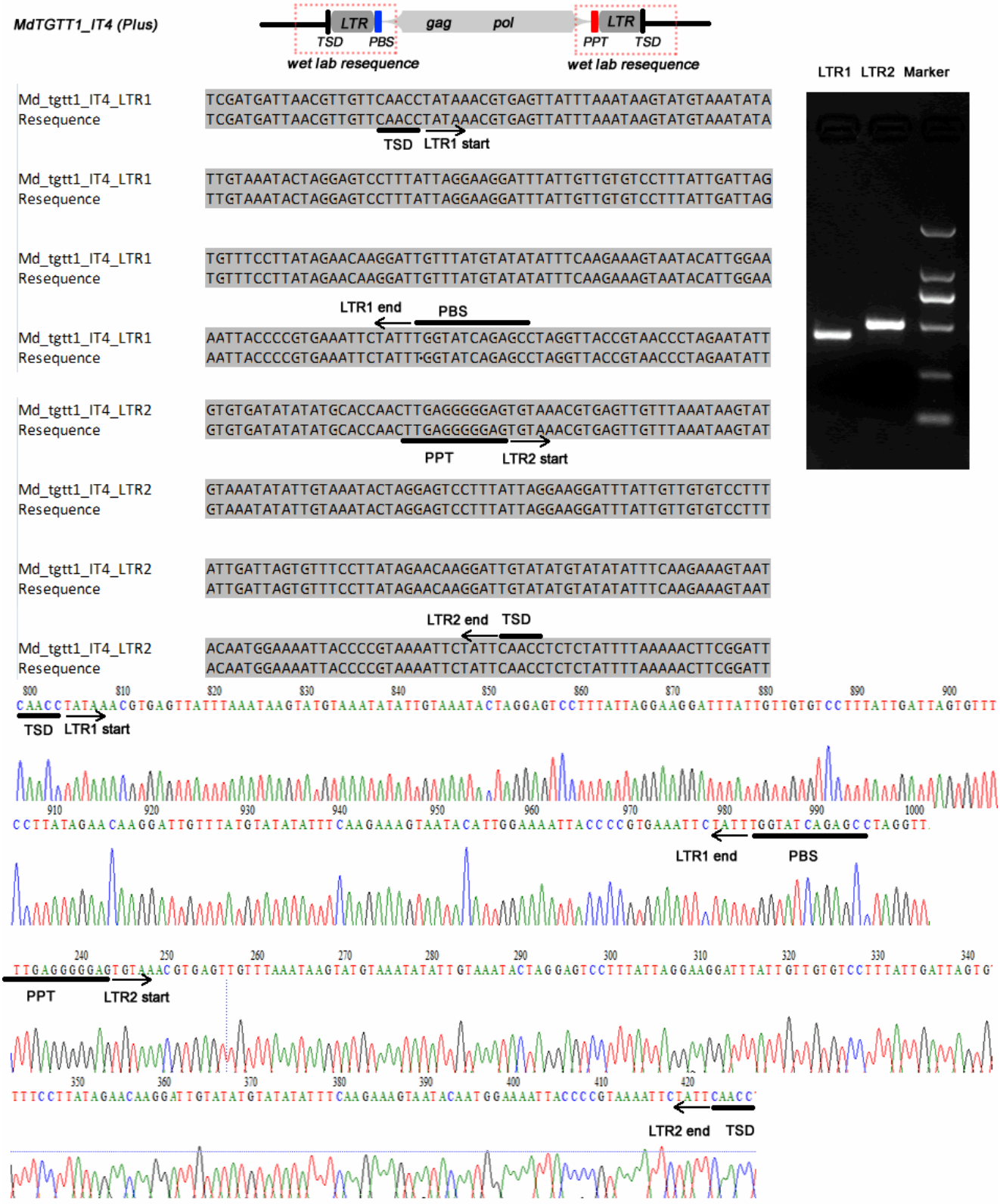
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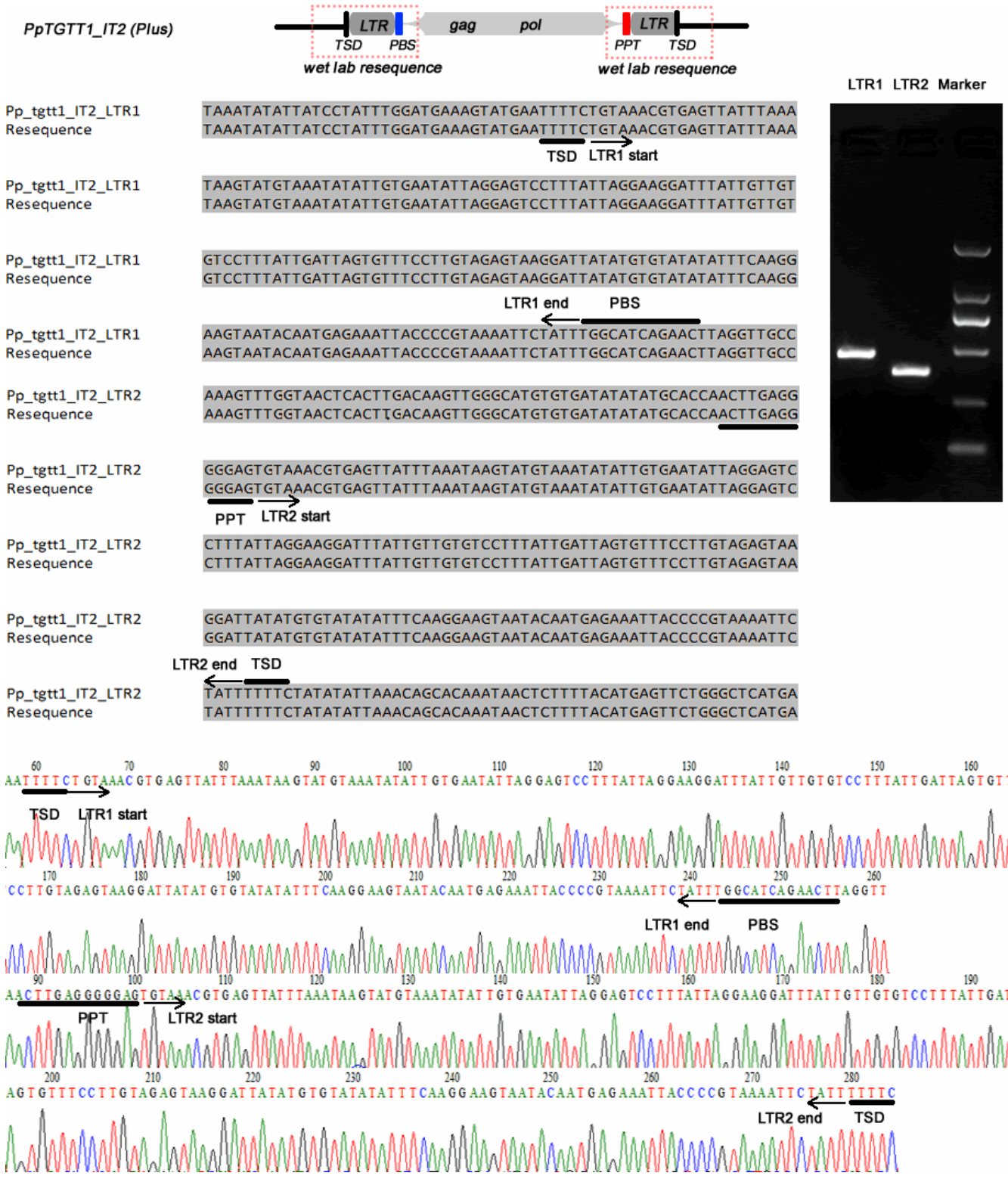
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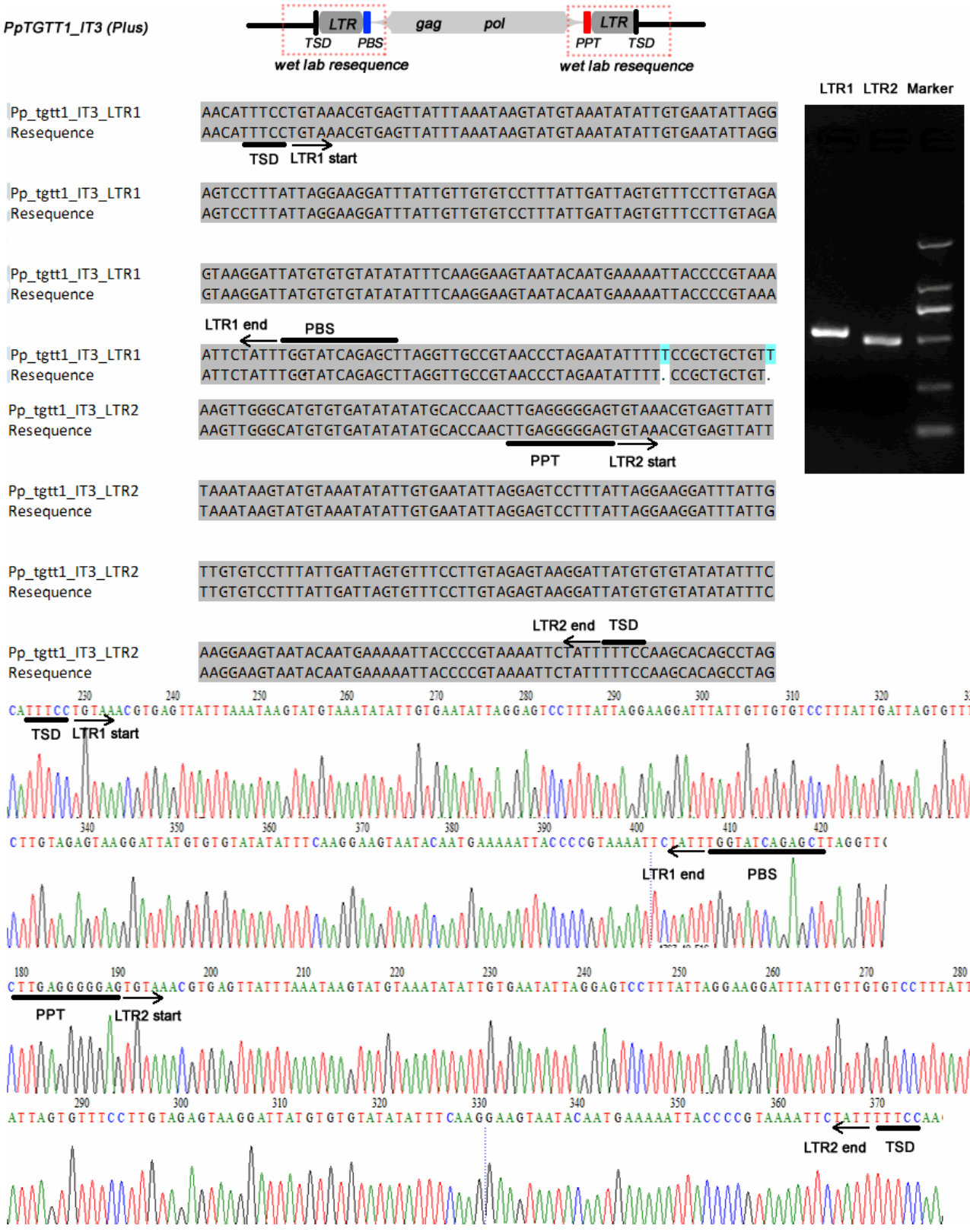
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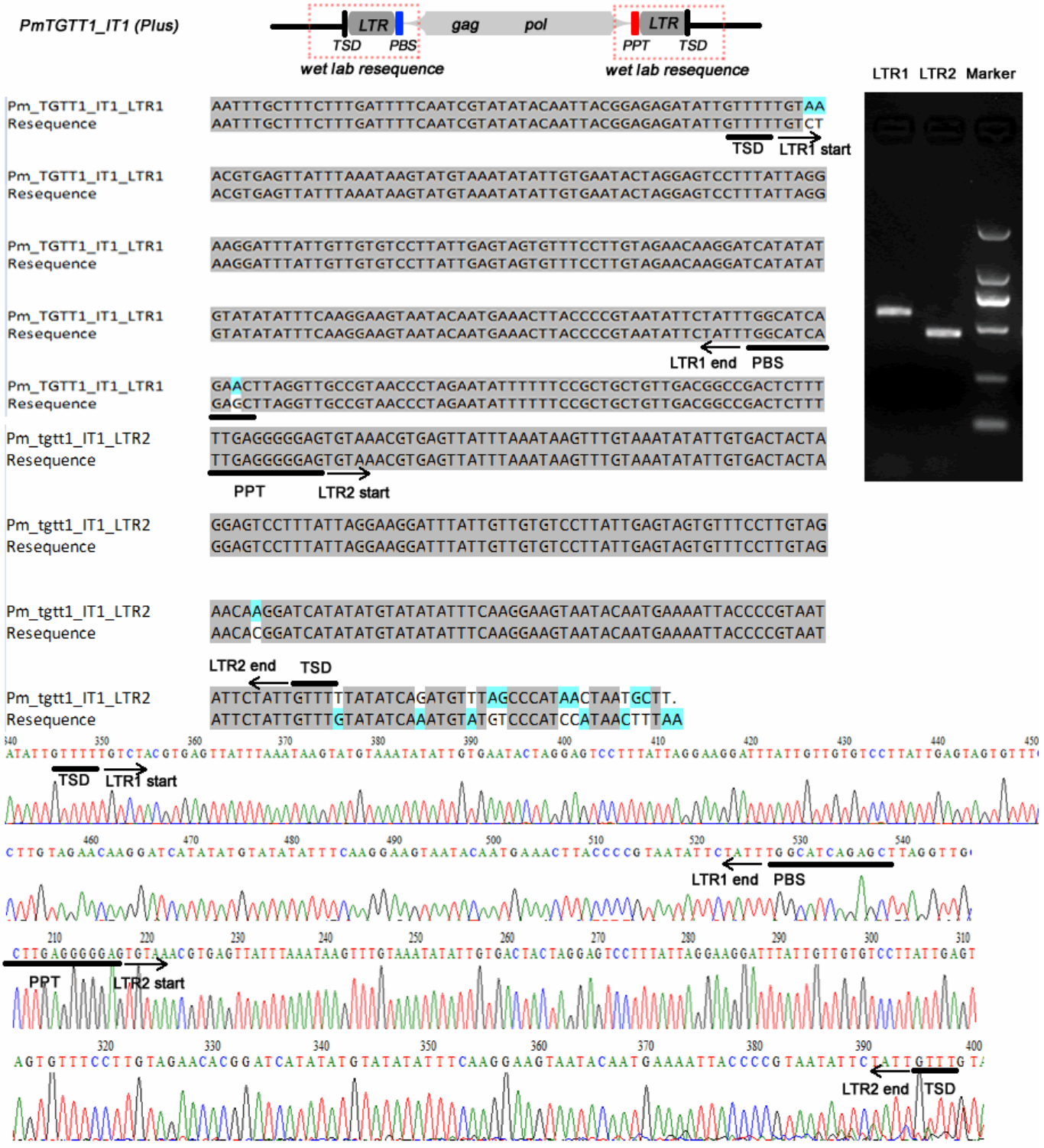
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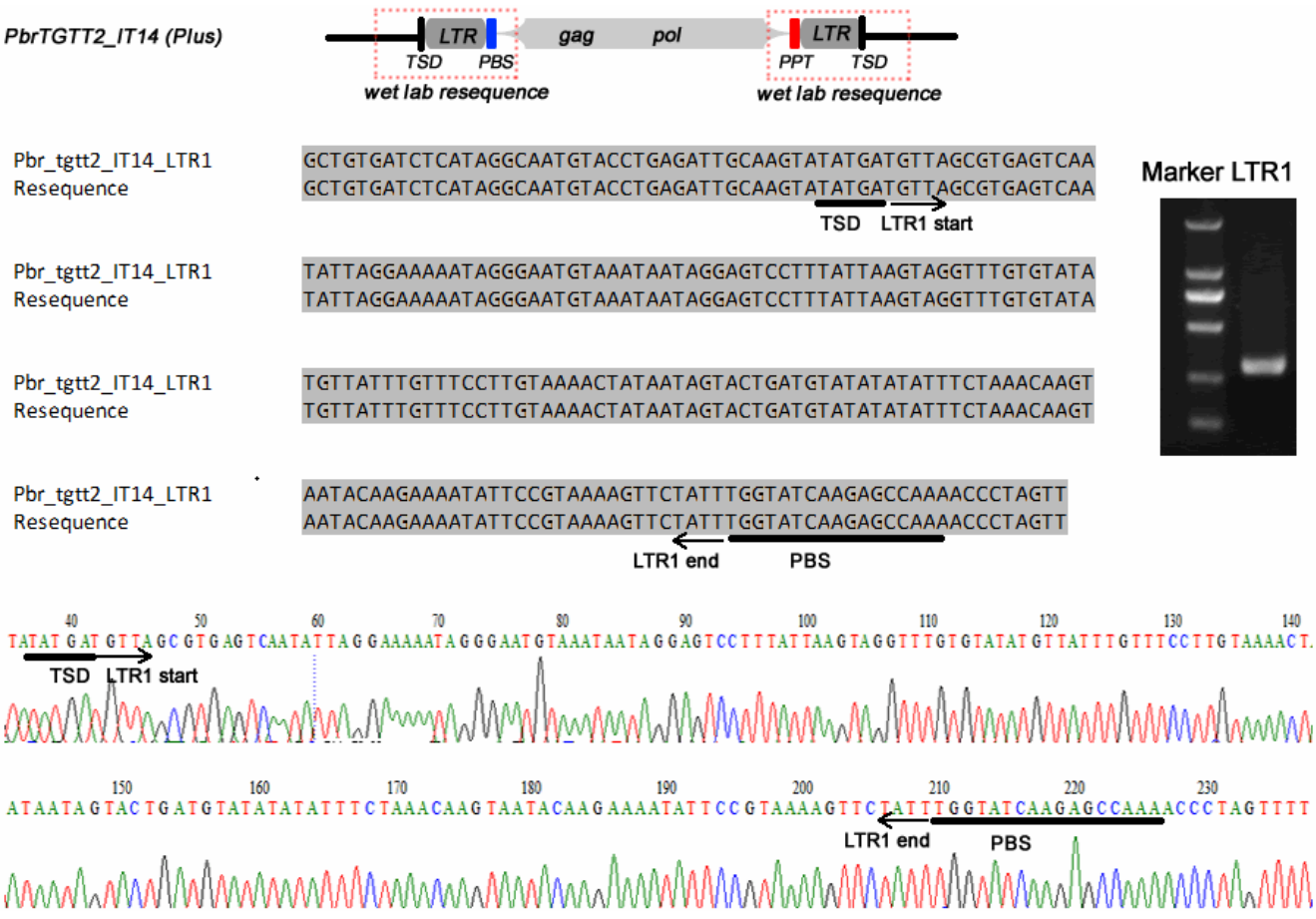
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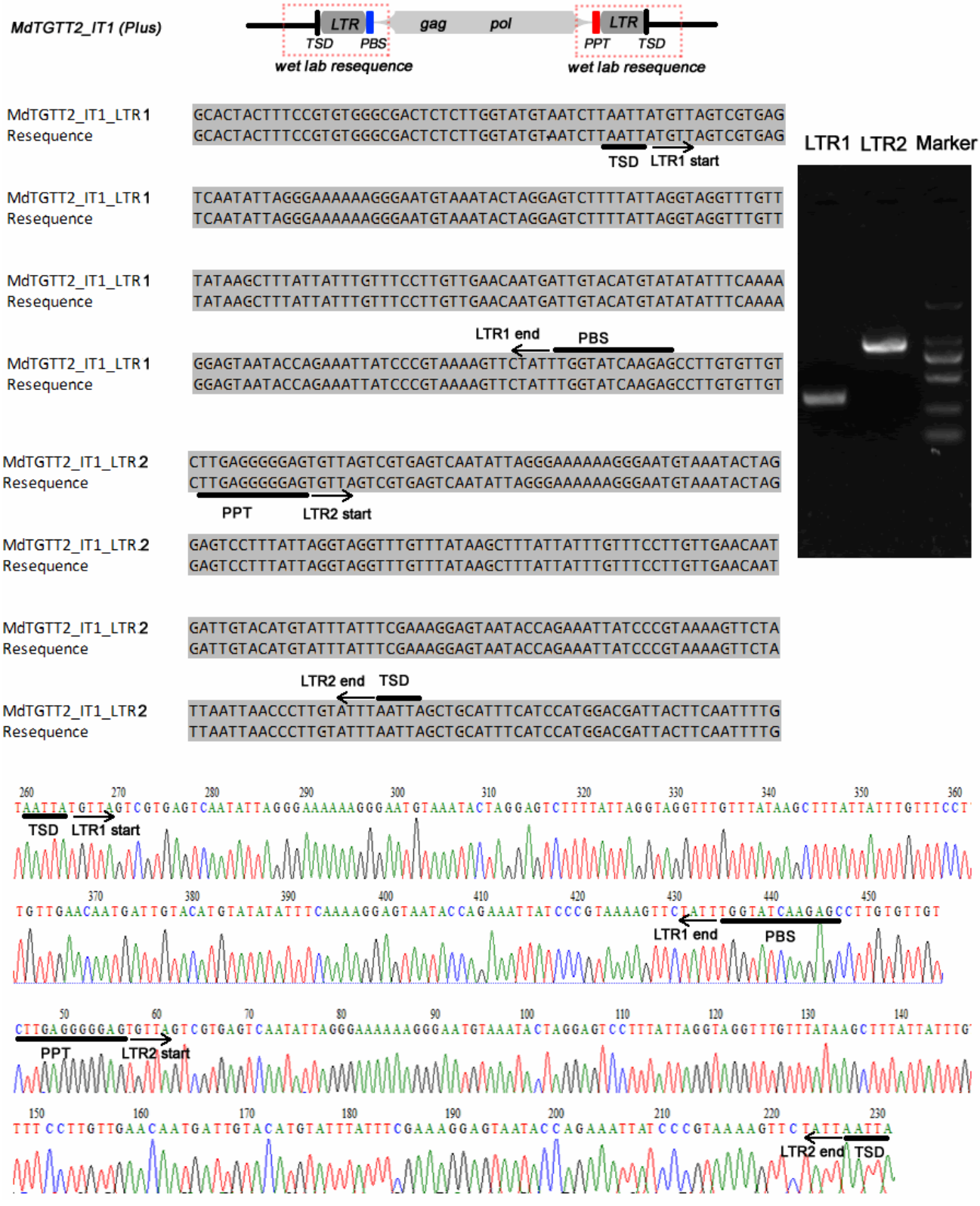
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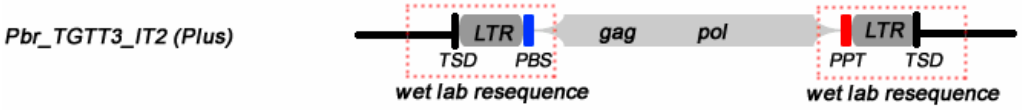
Figure S2.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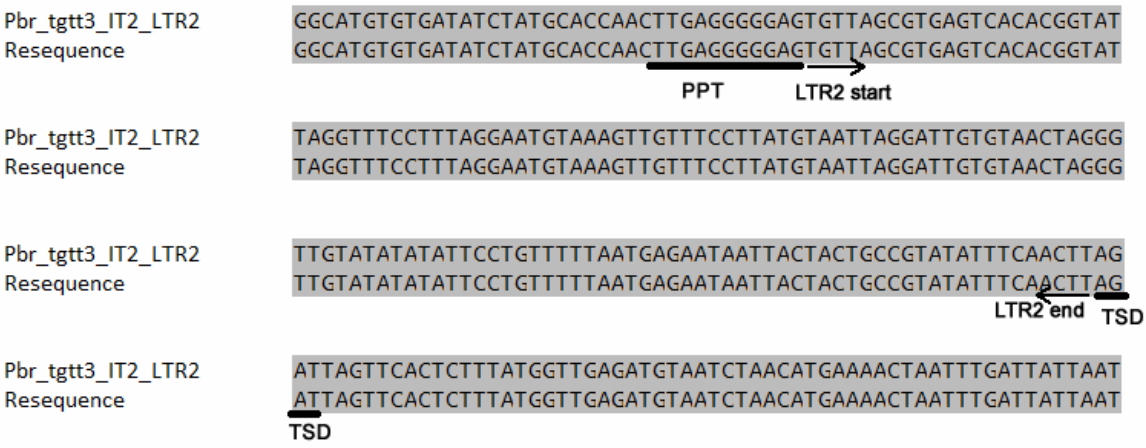
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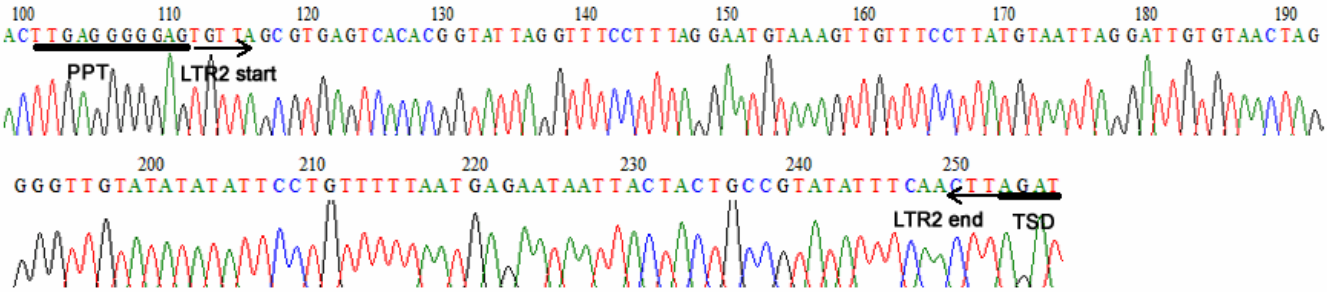
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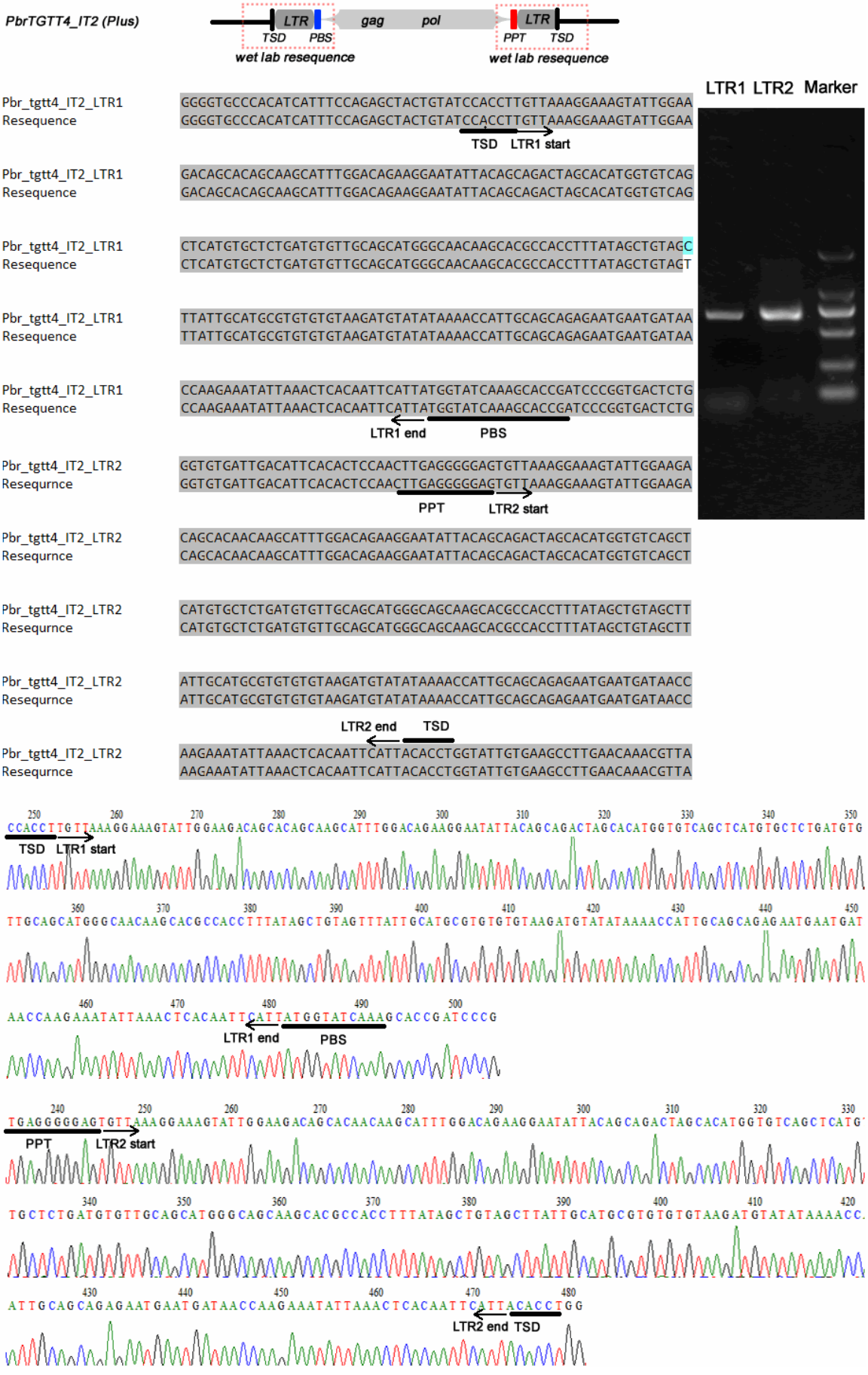
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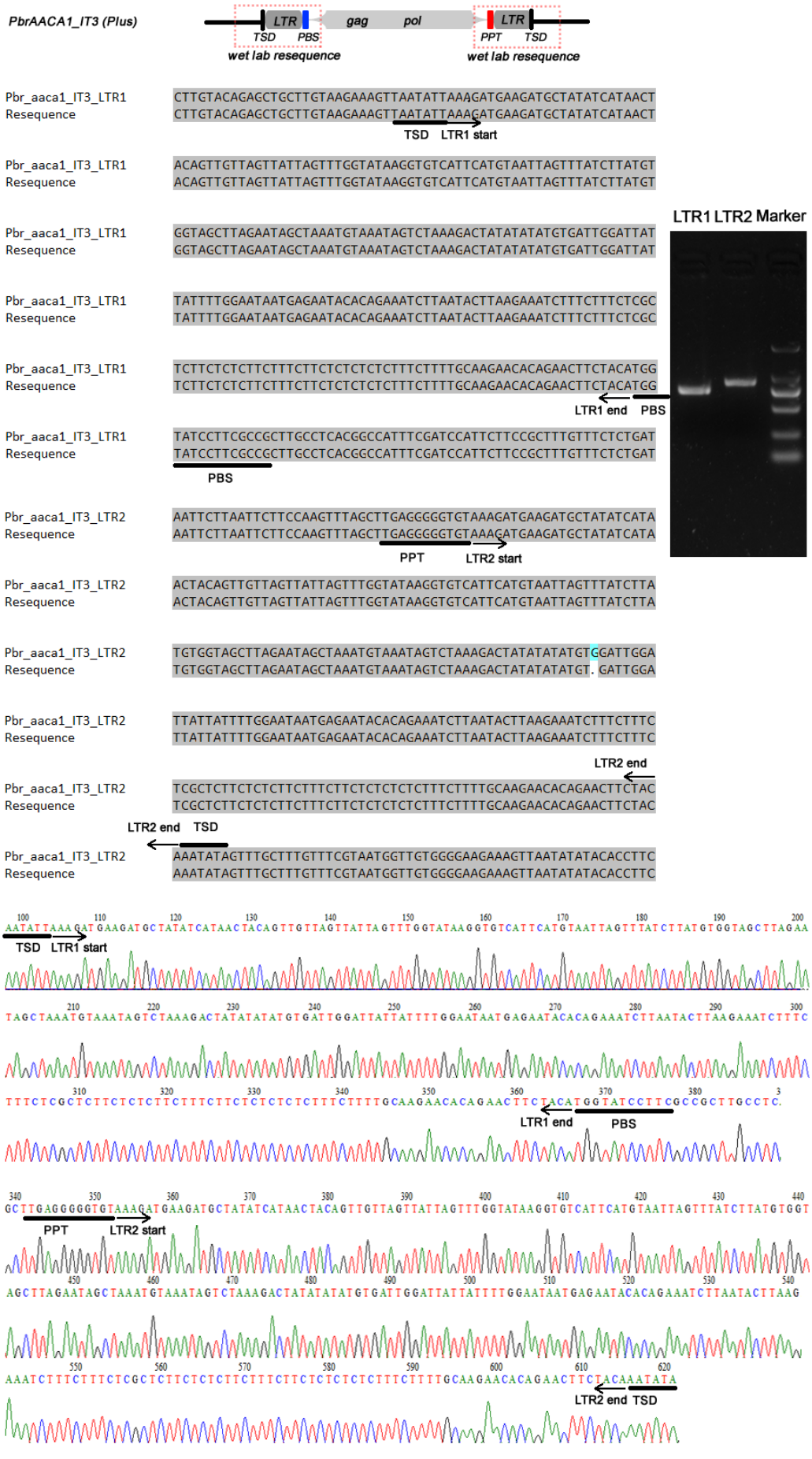
Figure S2.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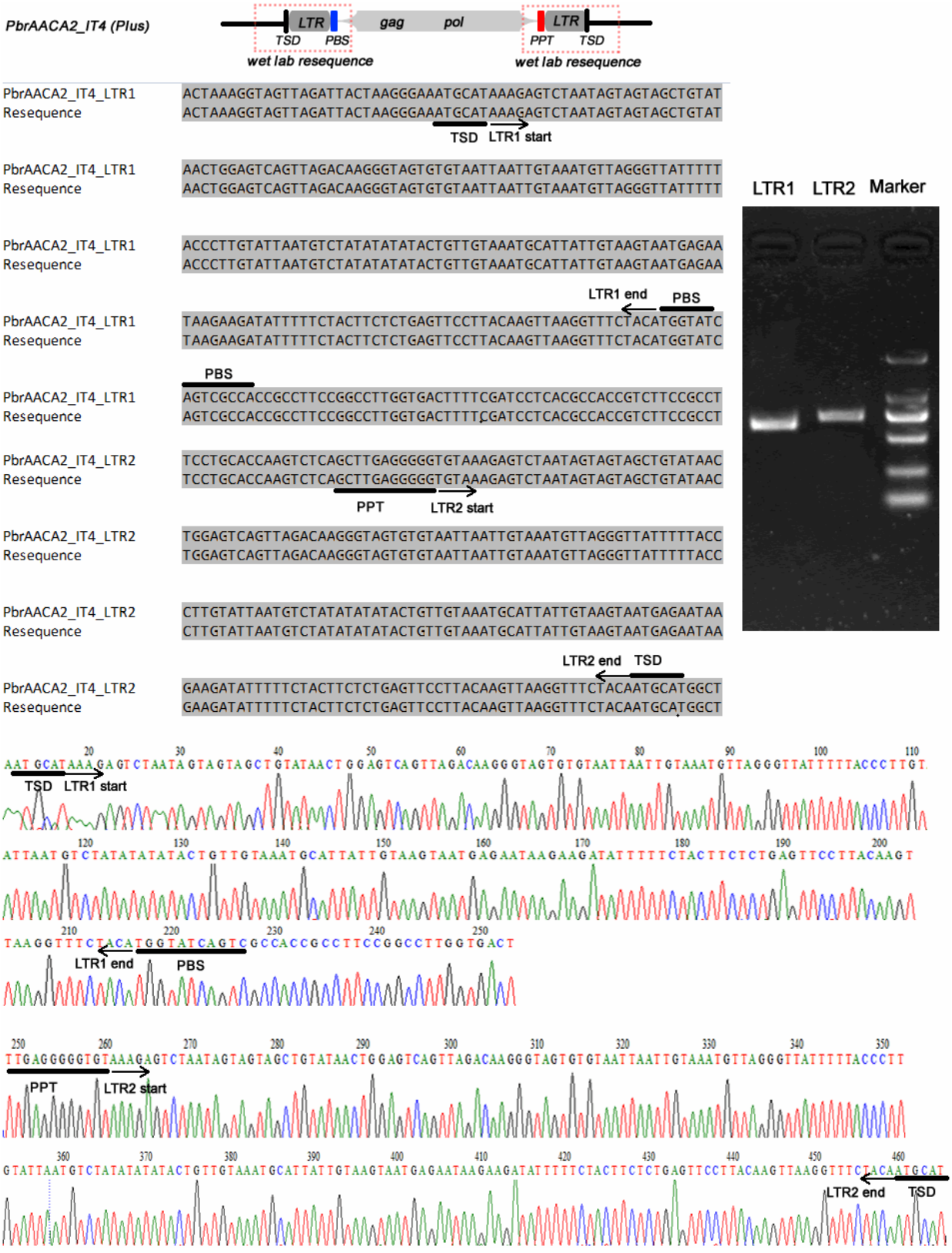
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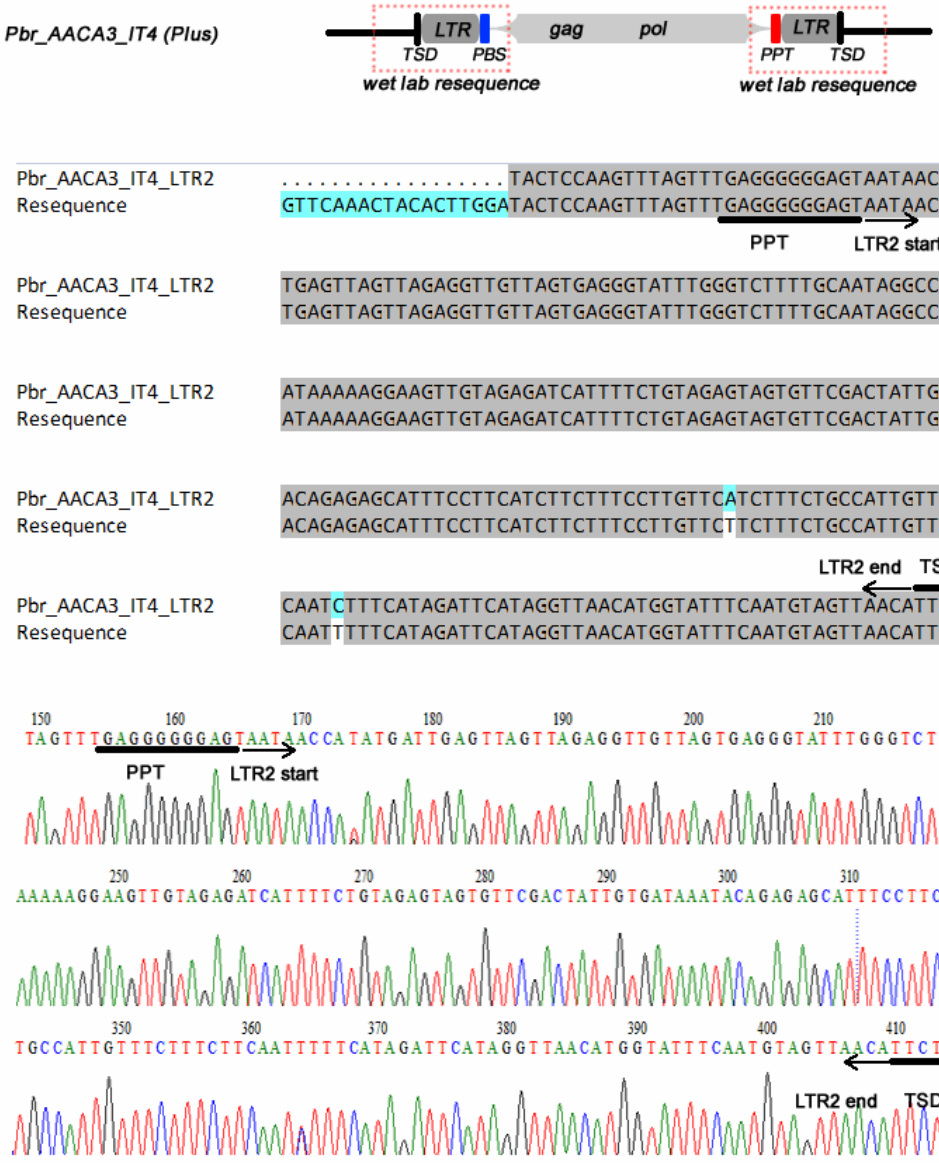
Figure S2.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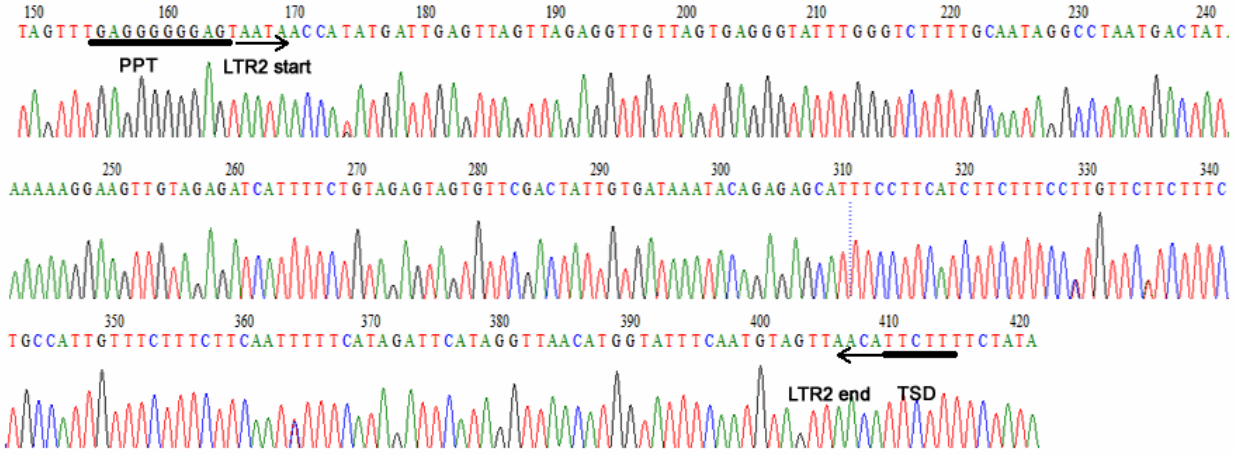
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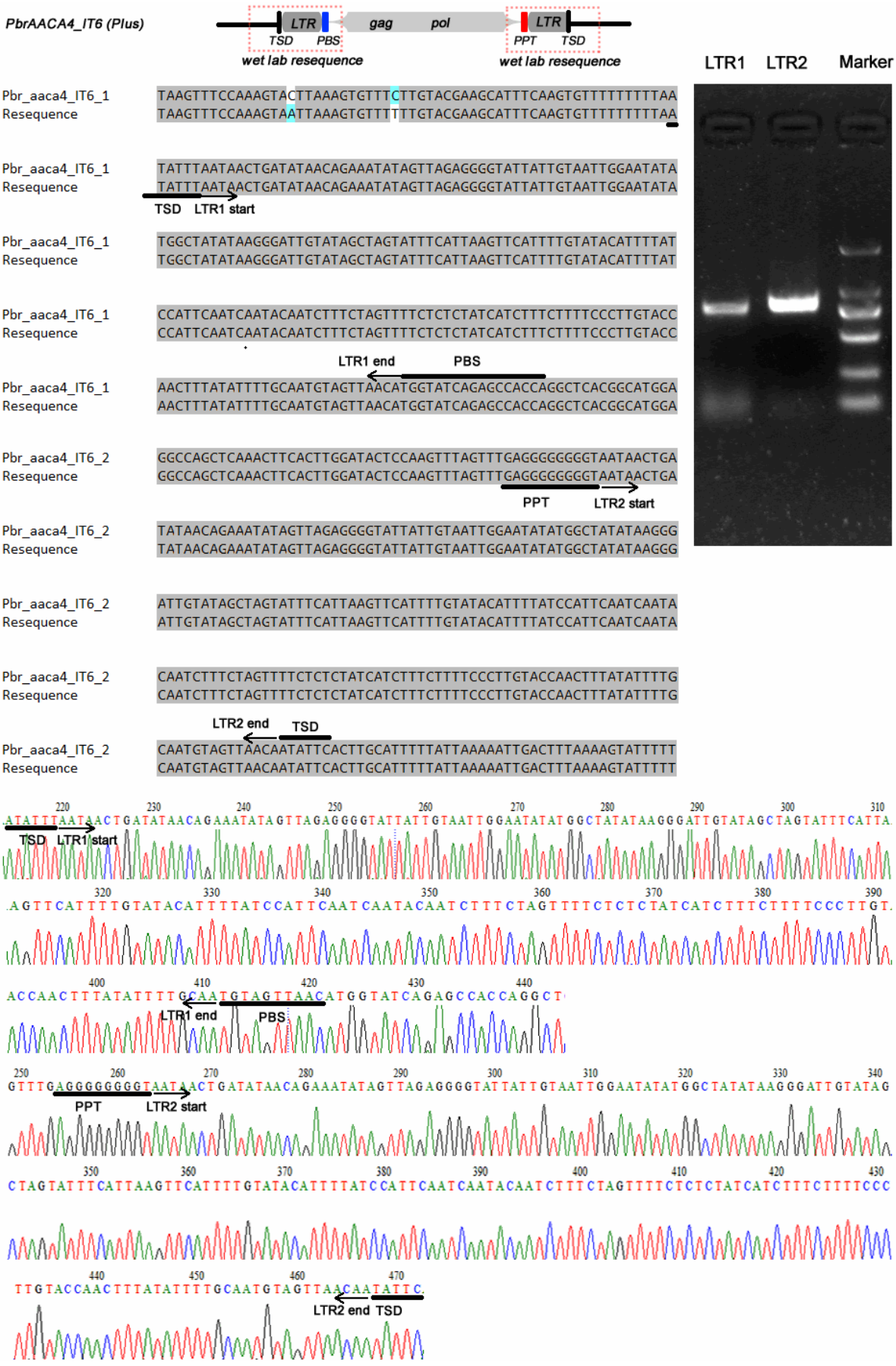
Figure S2.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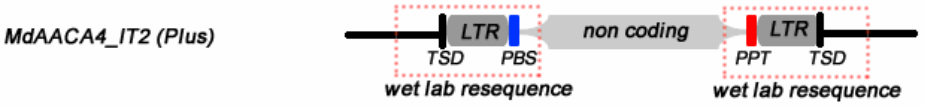
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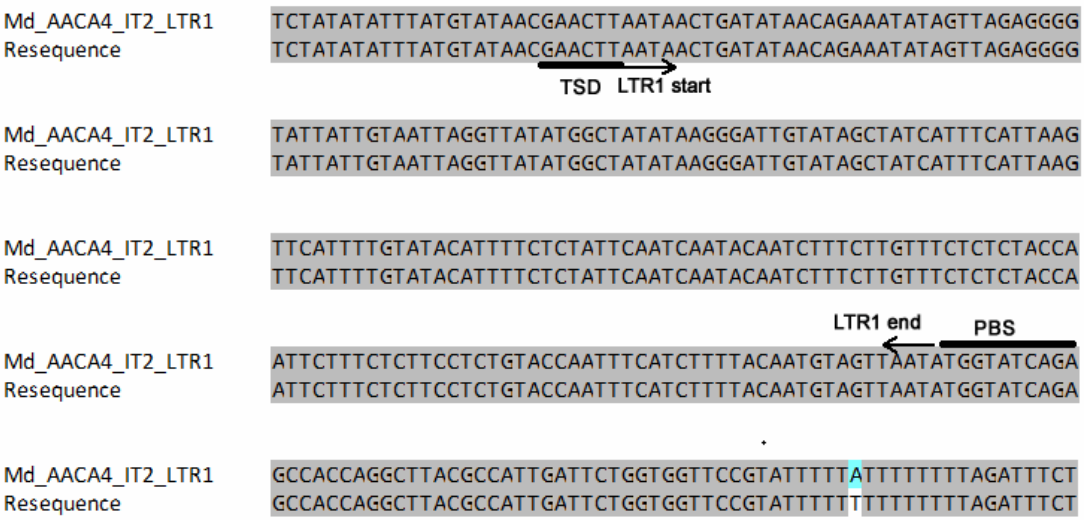
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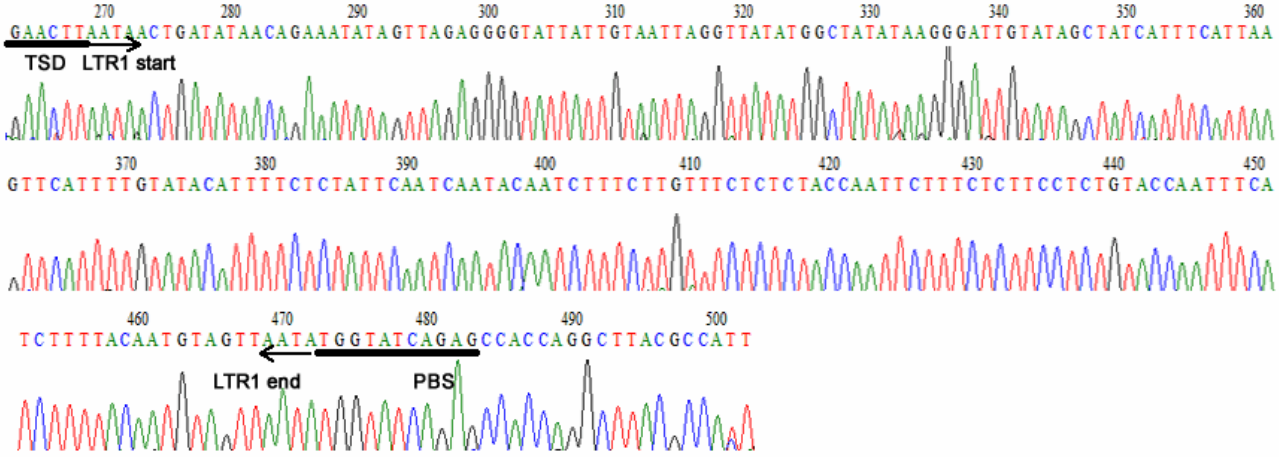
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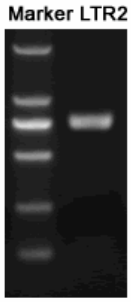
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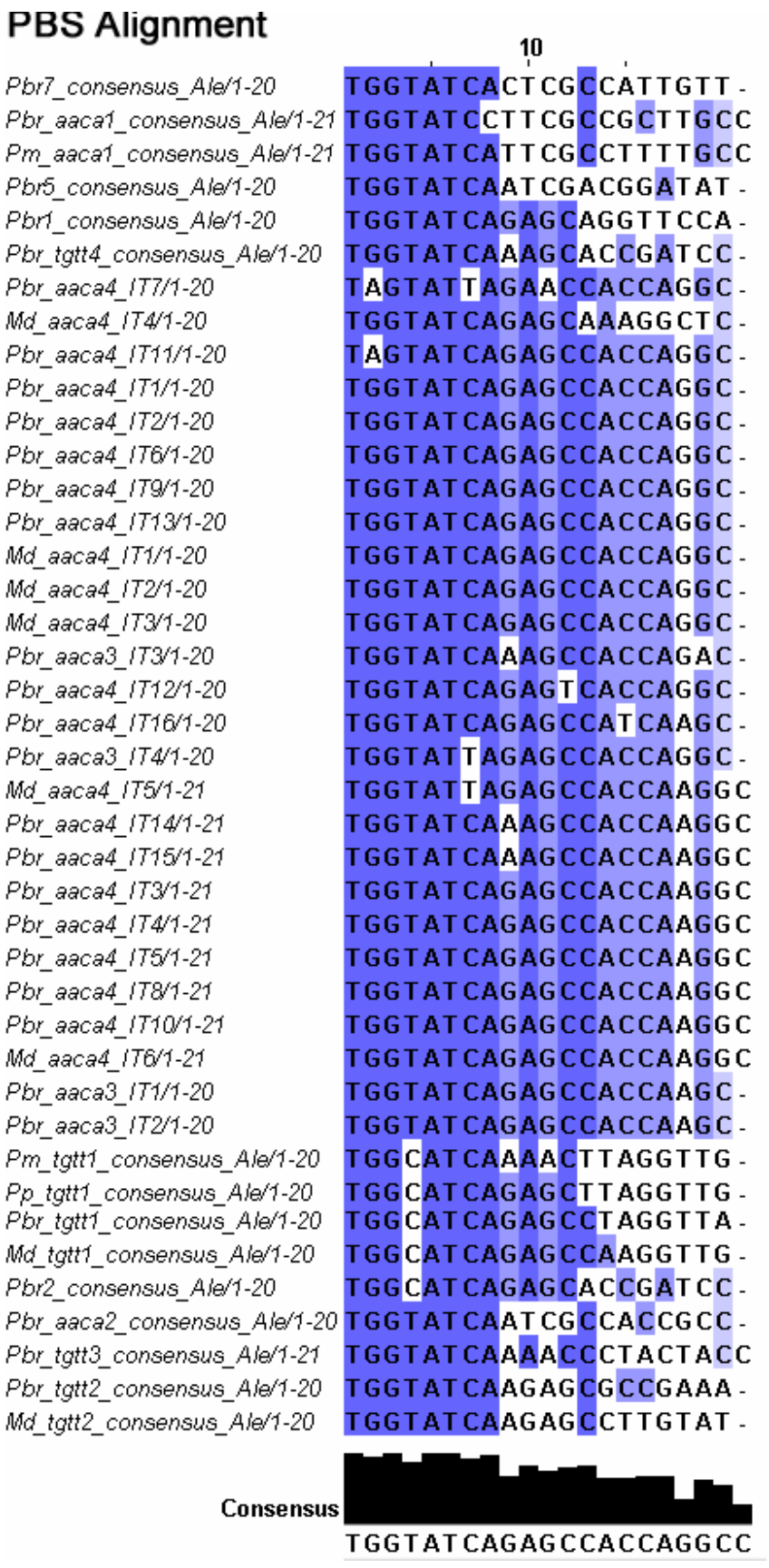
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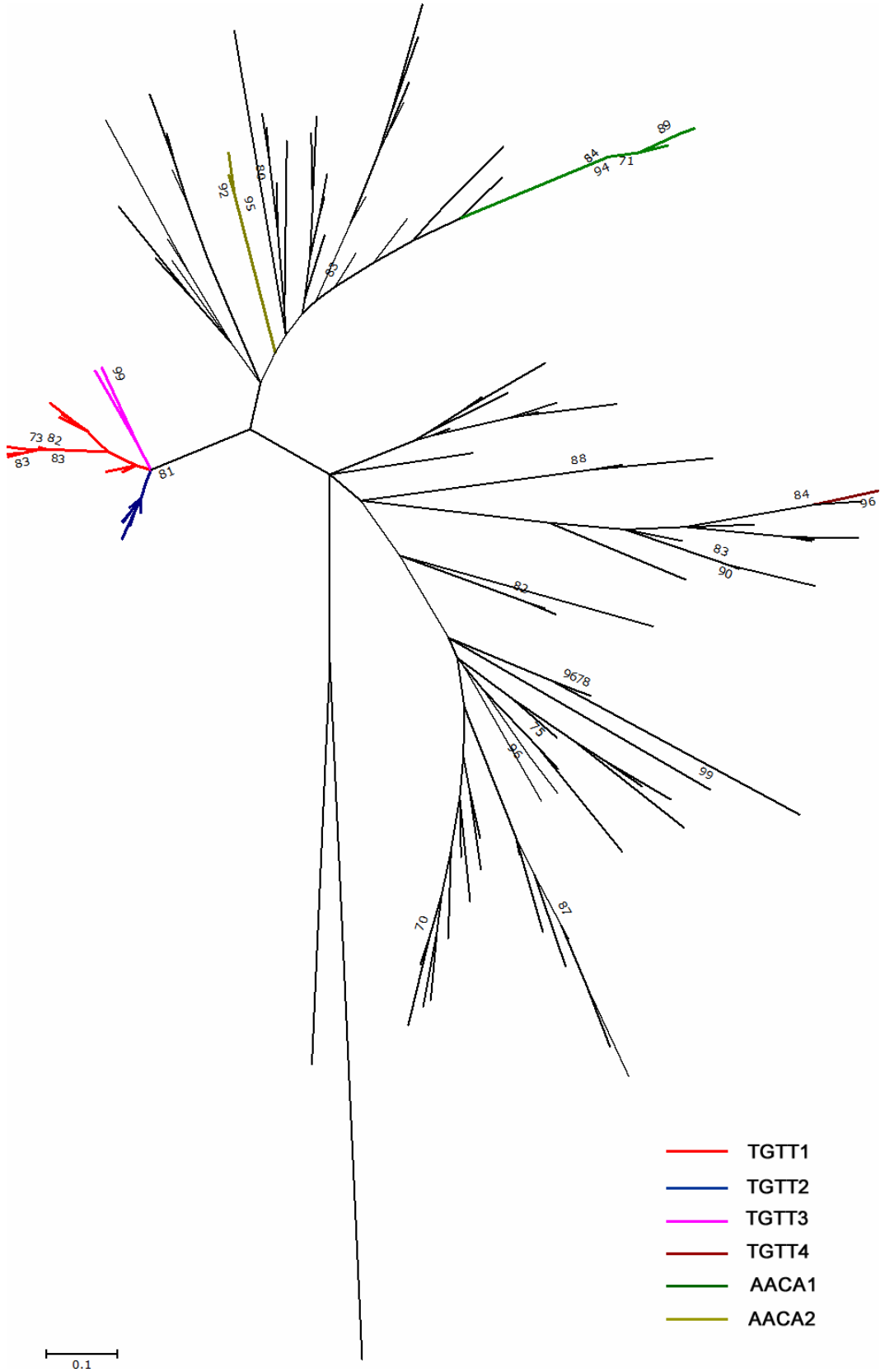
Figure S4.



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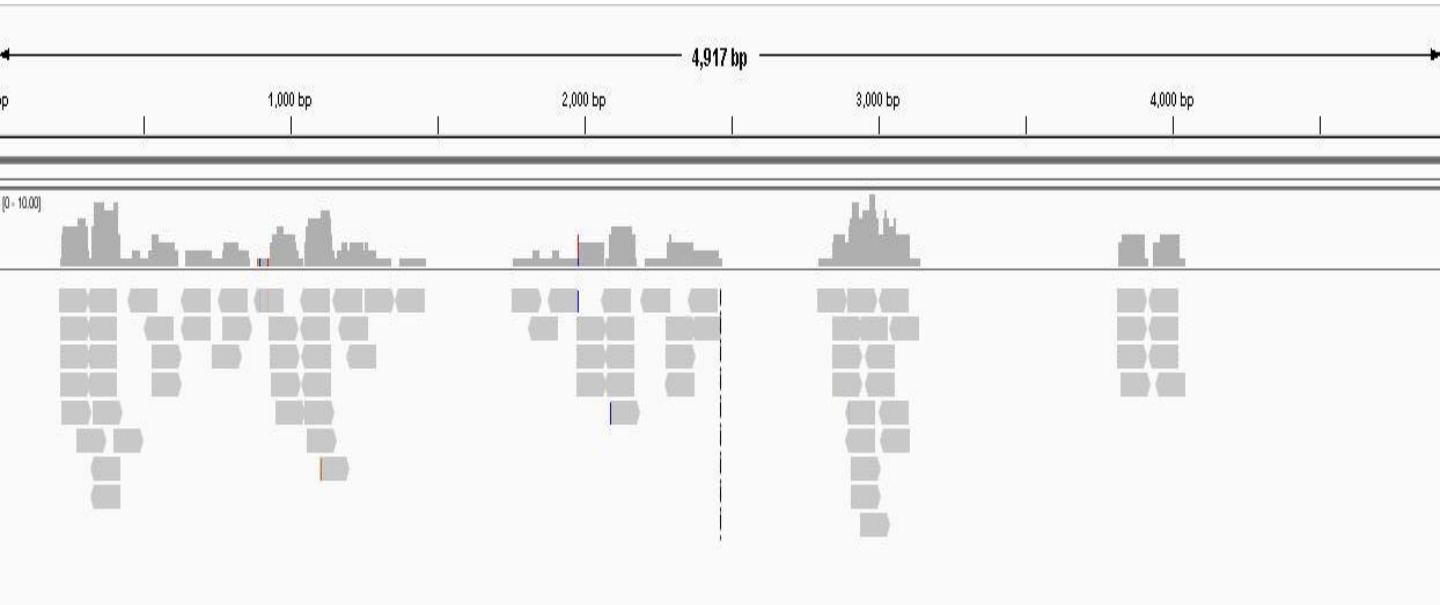
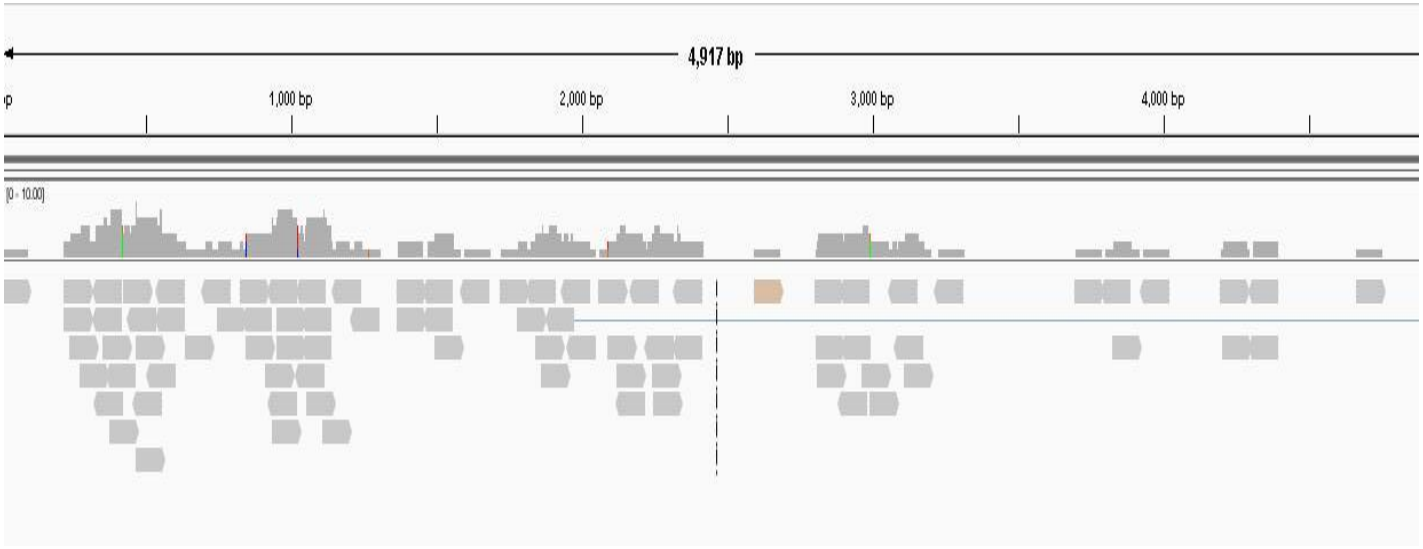
TGTT2
TGTT3
TGTT4
AACA1
AACA2
0.1

Figure S5.

PbrAACA1_IT3



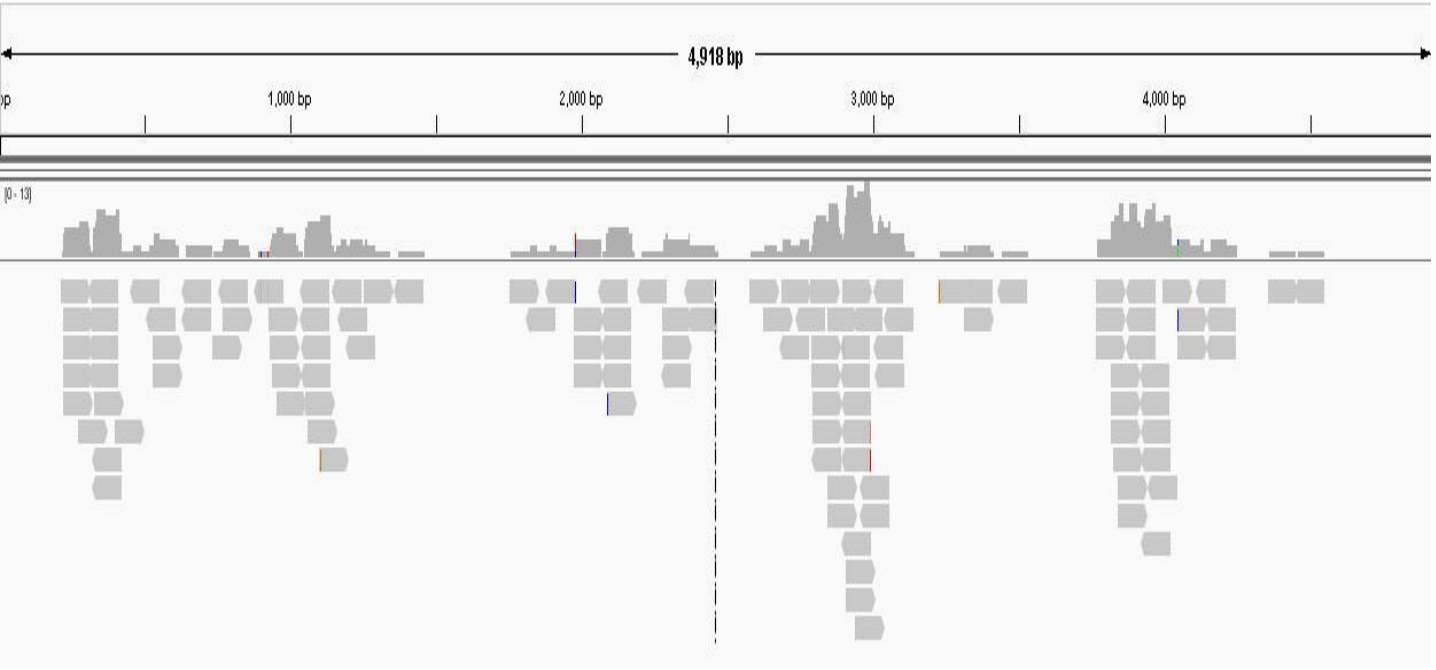
NCBI SRA database: SRX147917



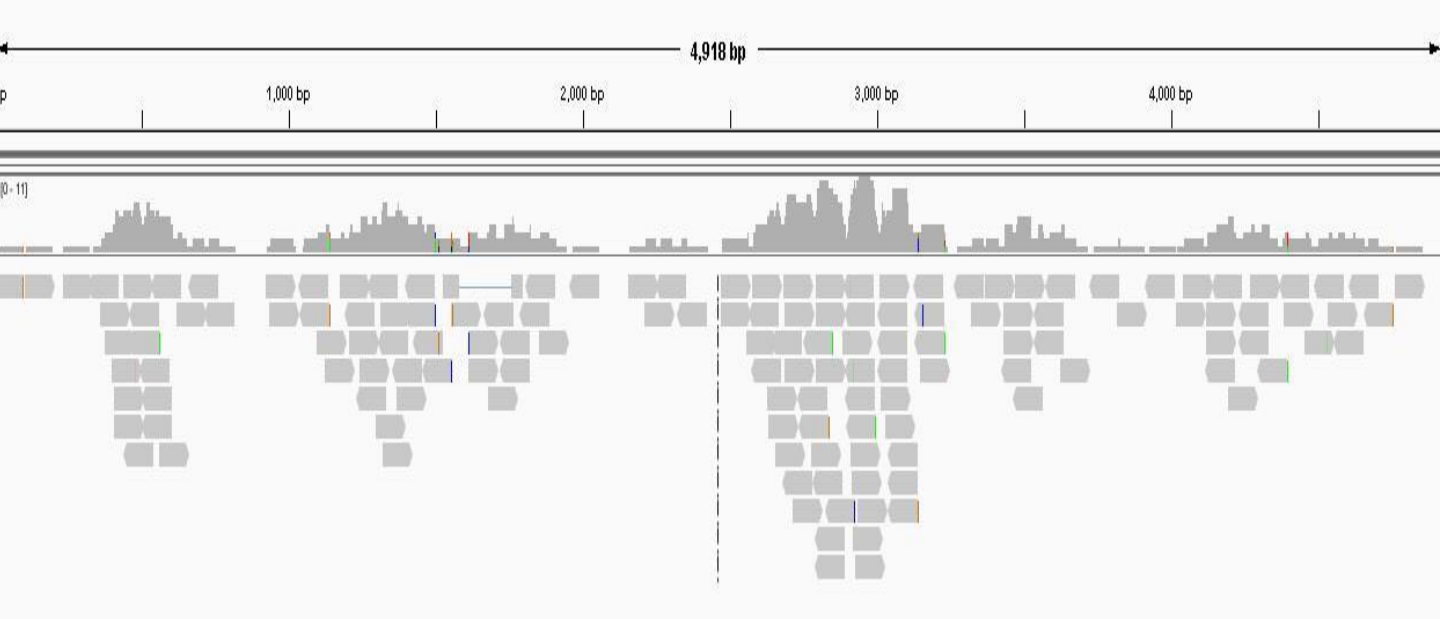
NCBI SRA database: SRX298075

Figure S5.

PbrAACA1_IT5



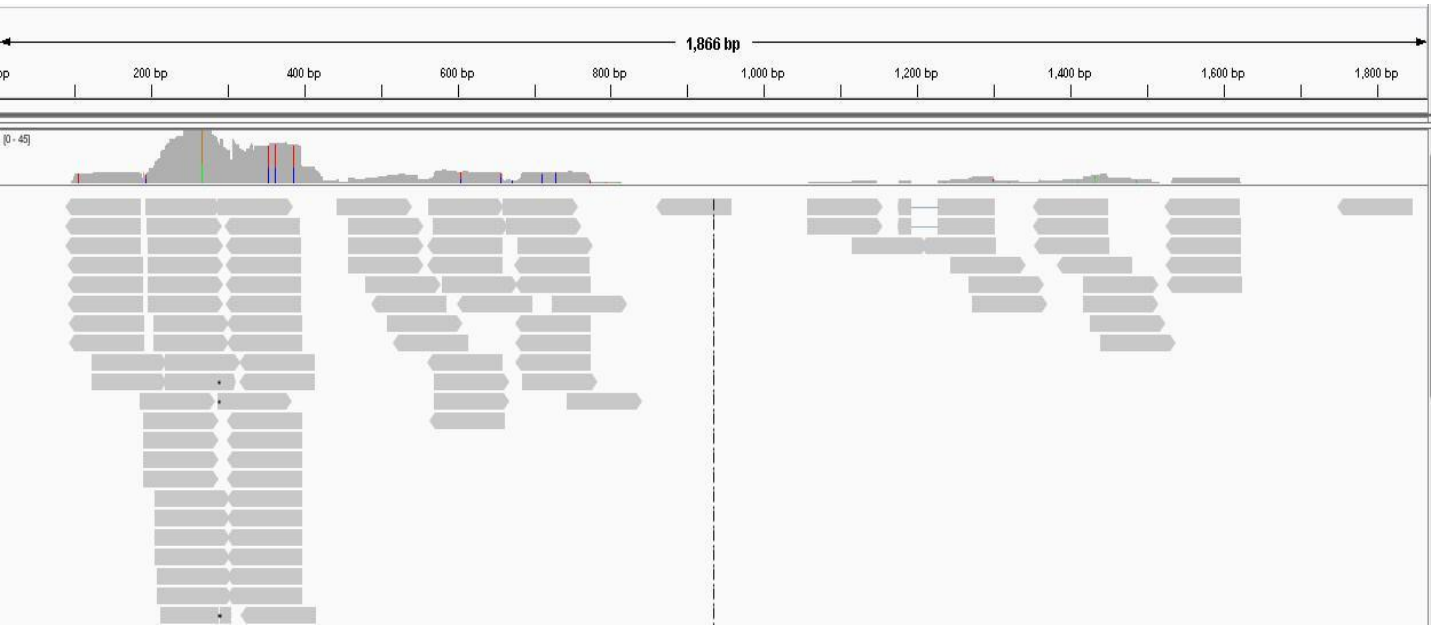
NCBI SRA database: SRX147917



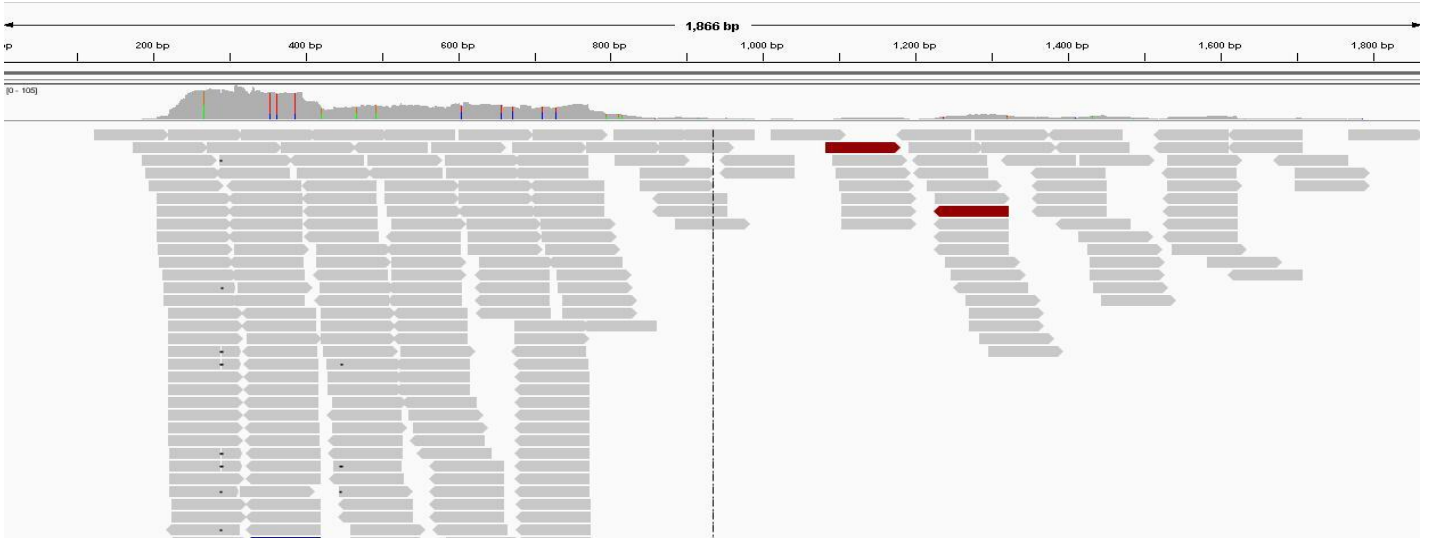
NCBI SRA database: SRX298075

Figure S5.

PbrAACA3_IT4



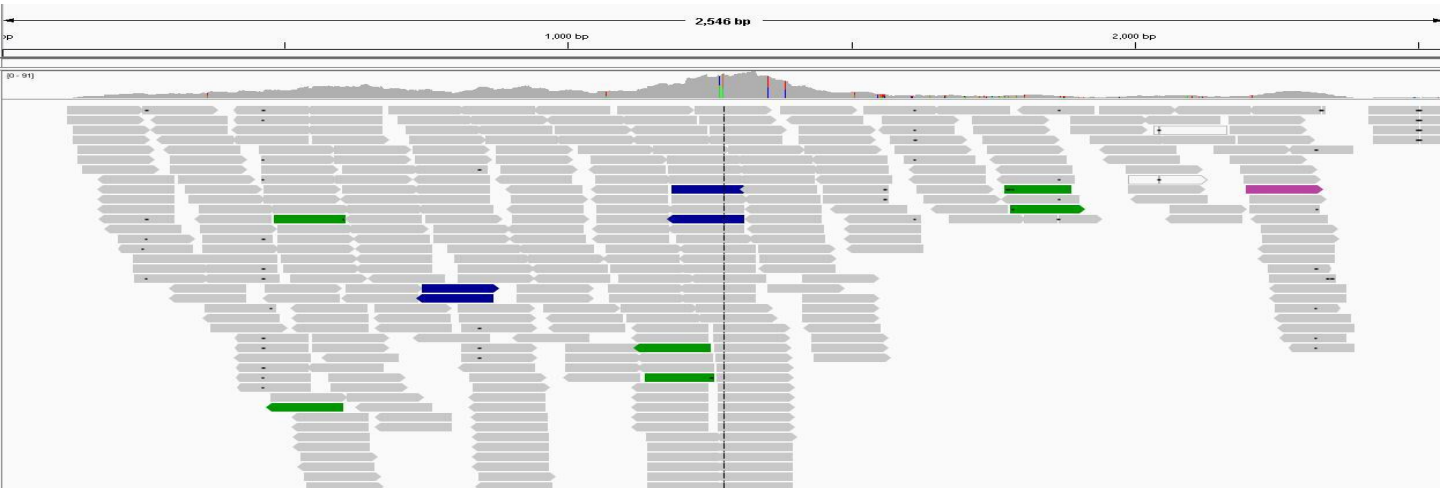
NCBI SRA database: SRX147917



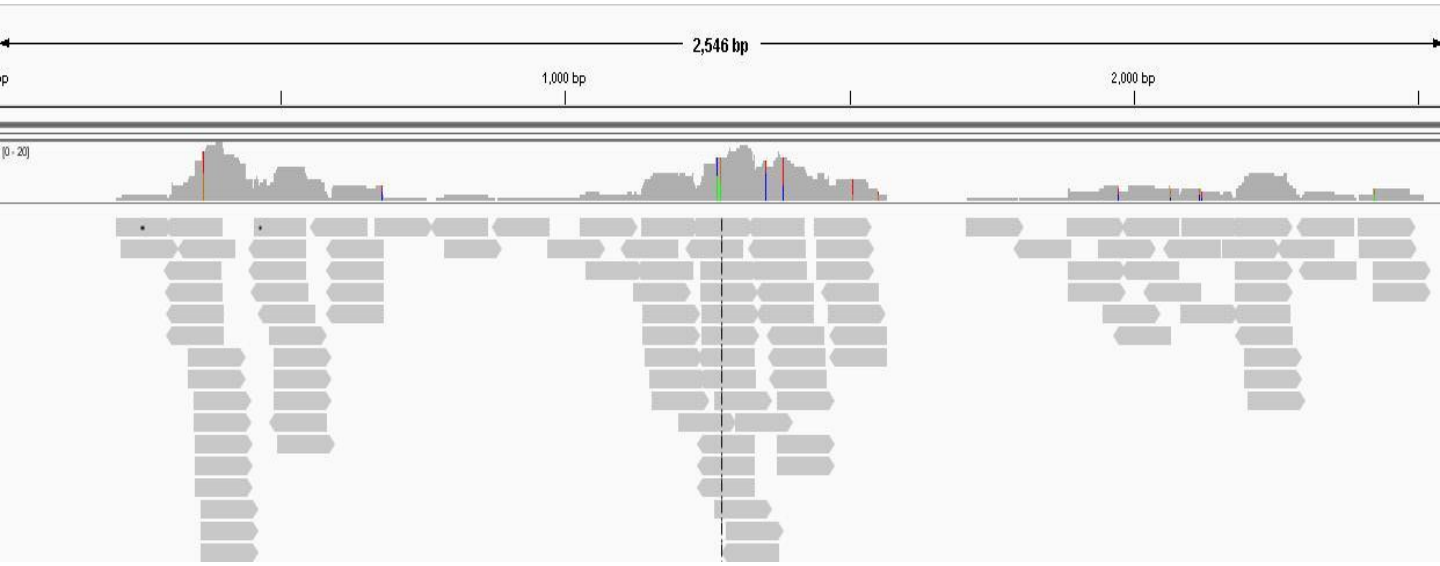
NCBI SRA database: : SRX298075

Figure S5.

PbrAACA4_IT11



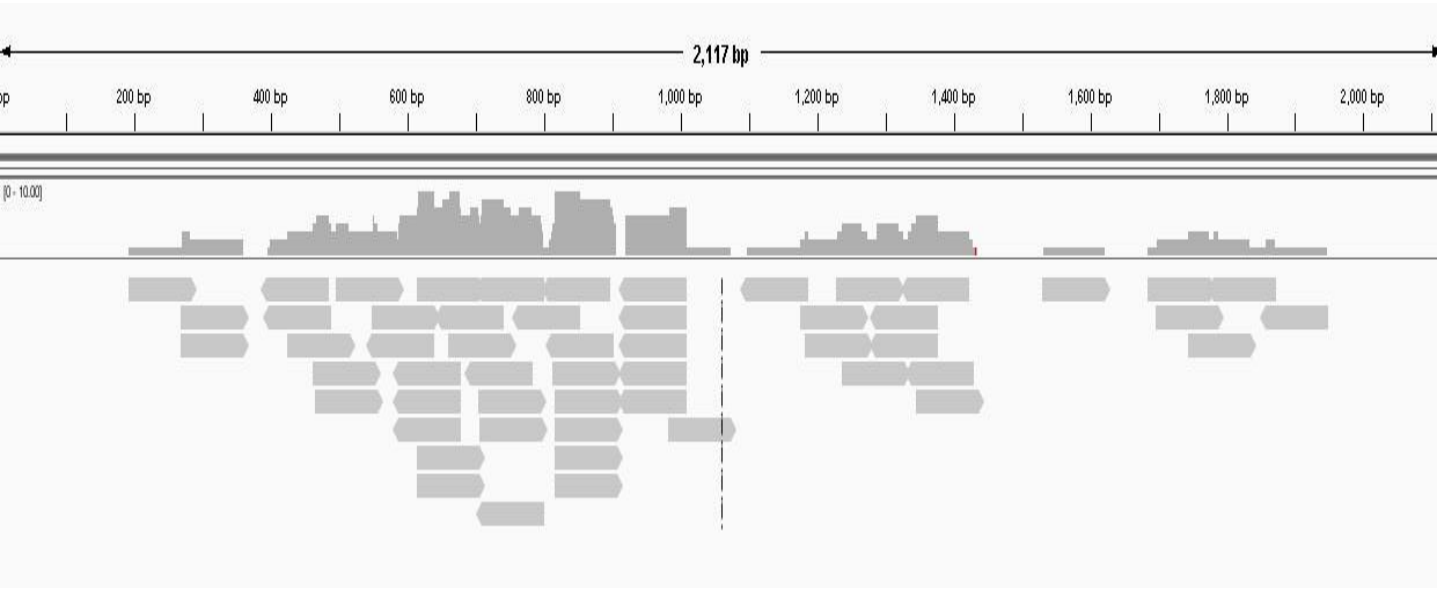
NCBI SRA database: SRX147917



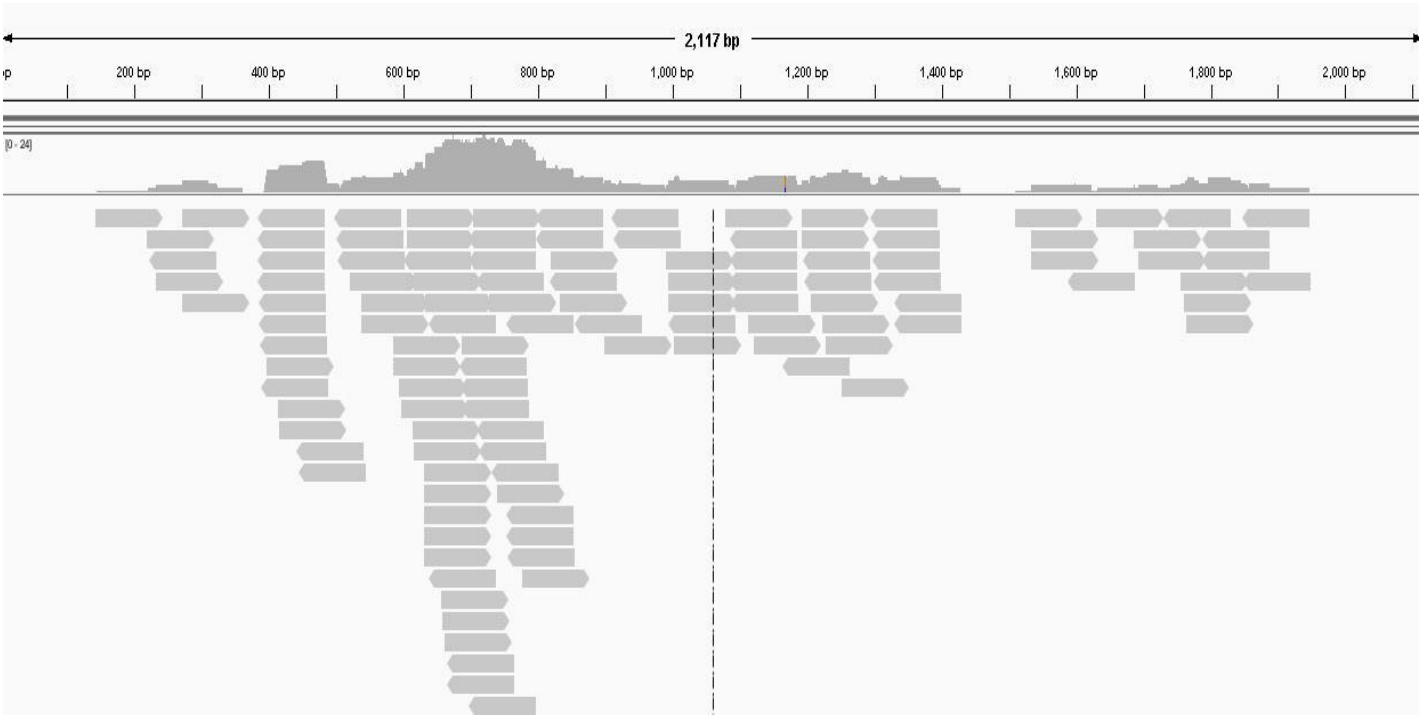
NCBI SRA database: SRX298075

Figure S5.

PbrAACA4_IT14



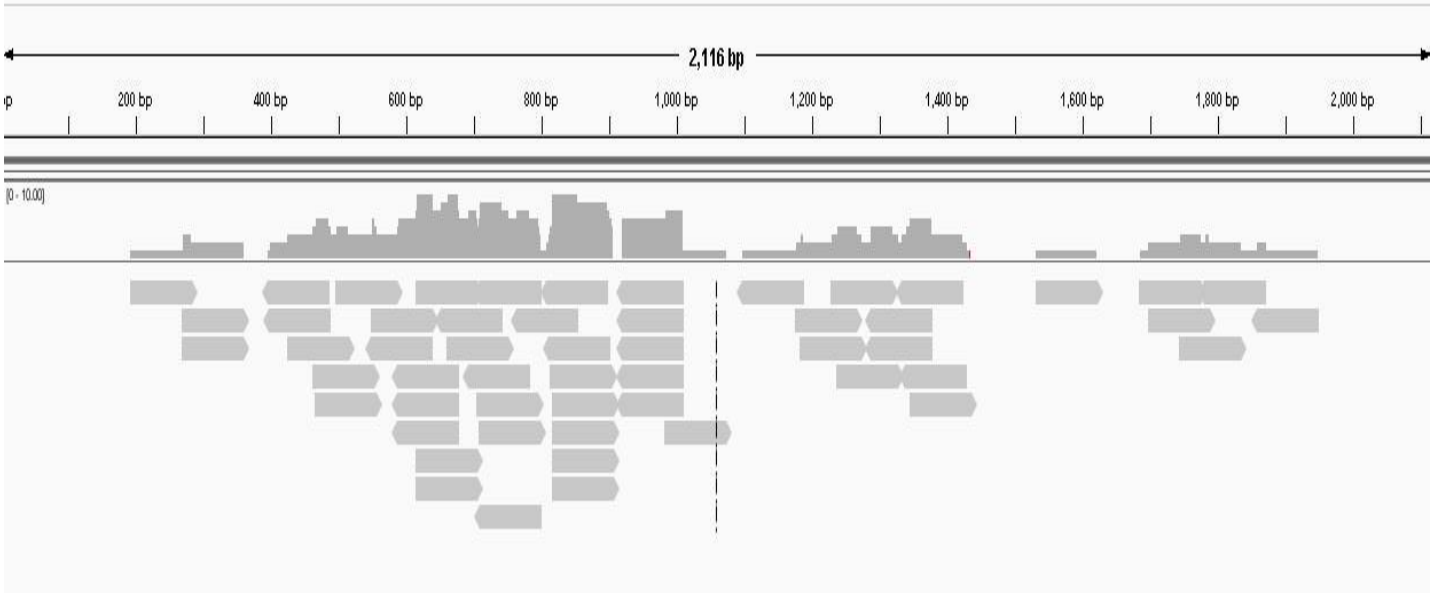
NCBI SRA database: SRX147917



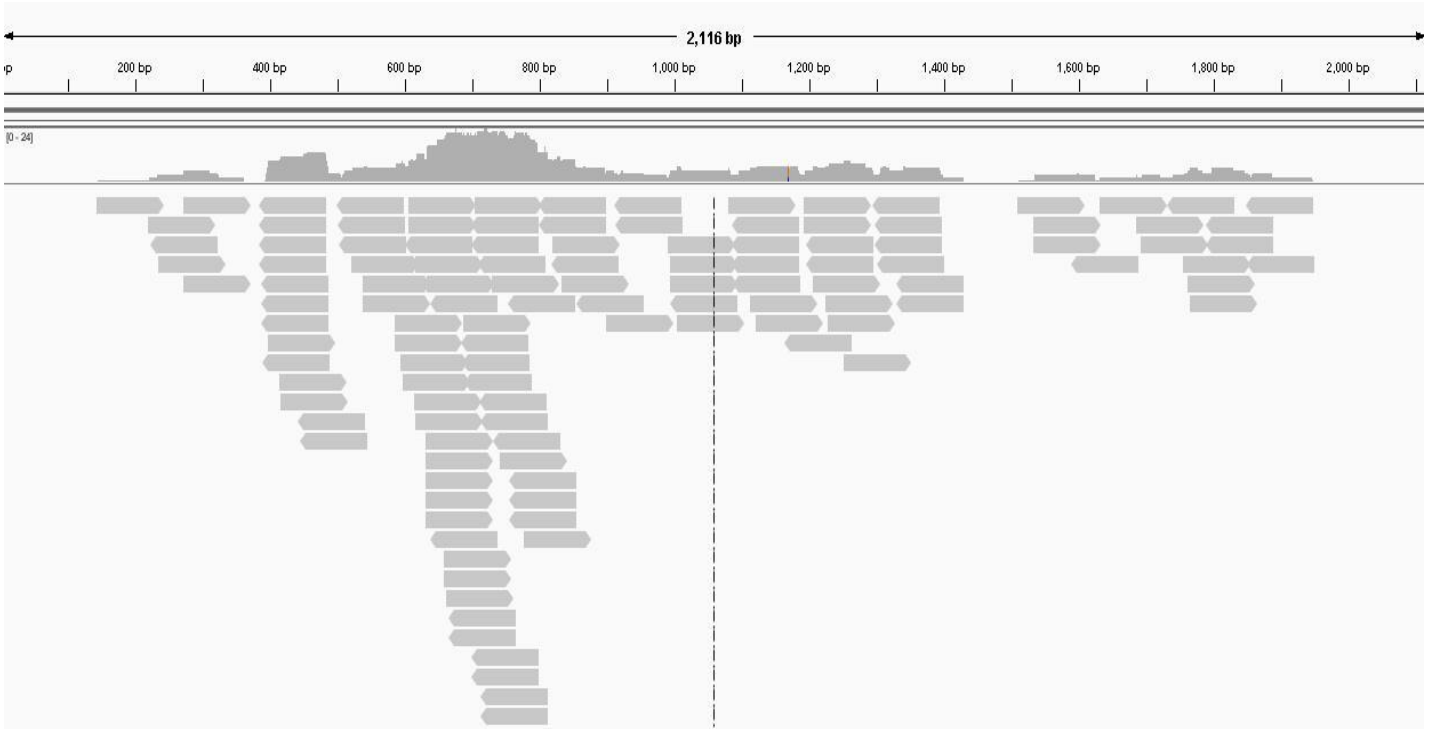
NCBI SRA database: SRX298075

Figure S5.

PbrAACA4_IT15



NCBI SRA database: SRX147917



NCBI SRA database: SRX298075