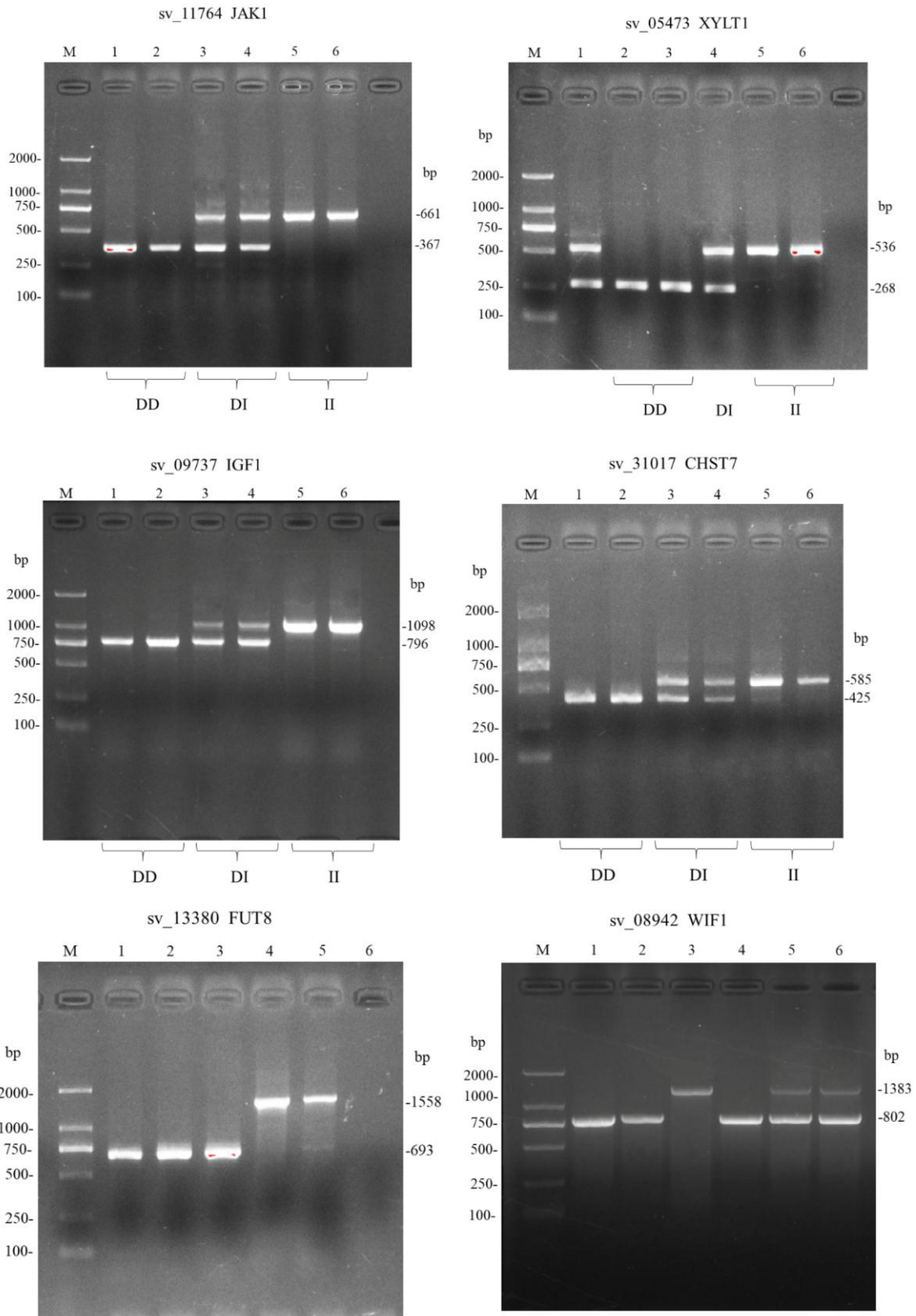
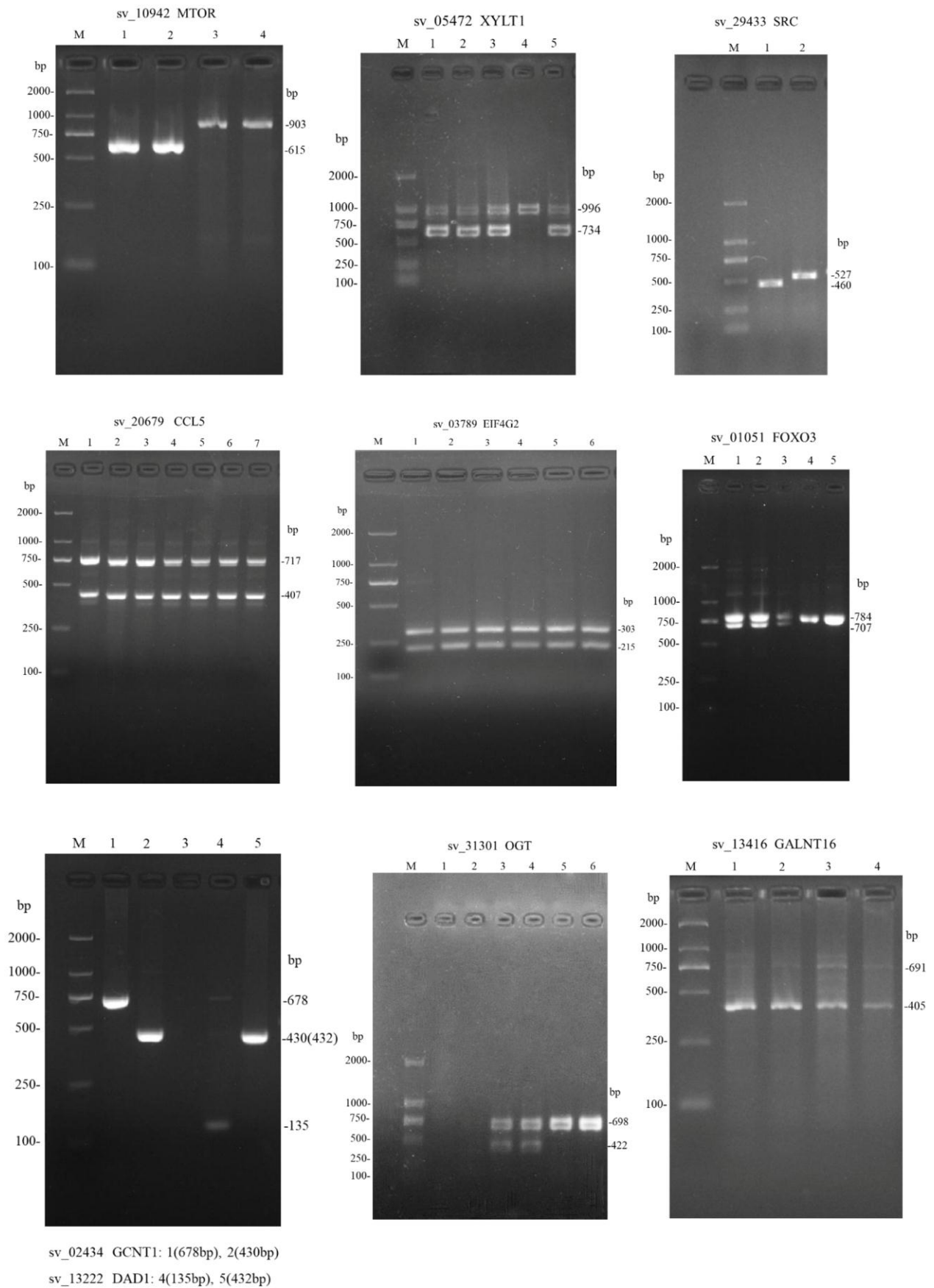


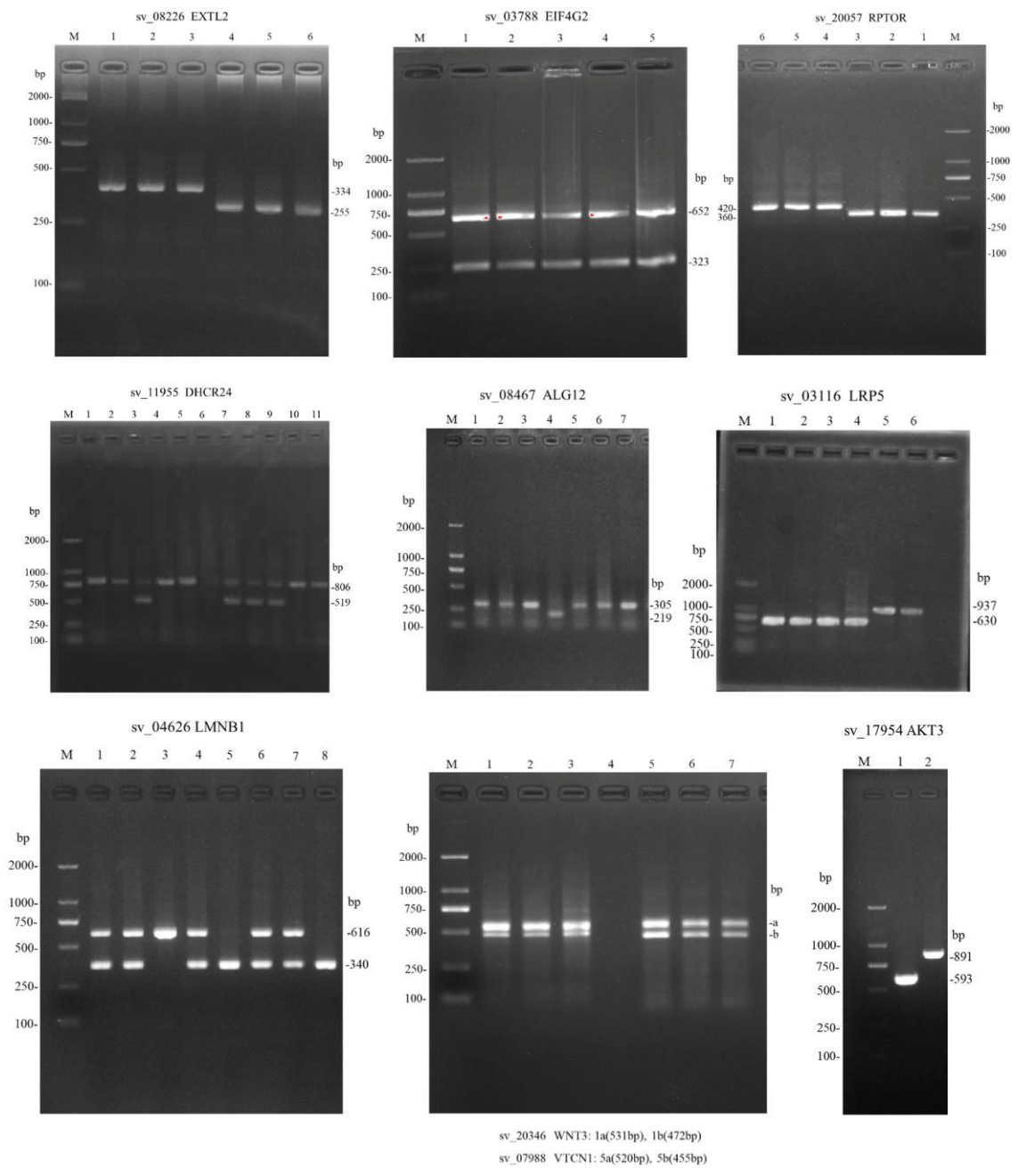
SUPPLEMENTARY FIGURES

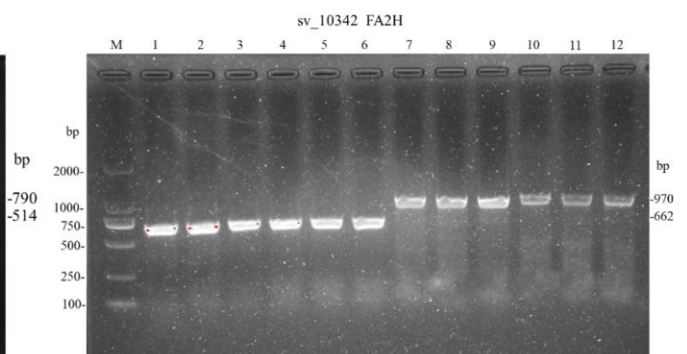
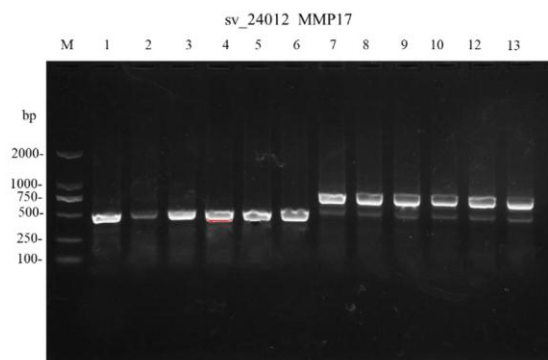
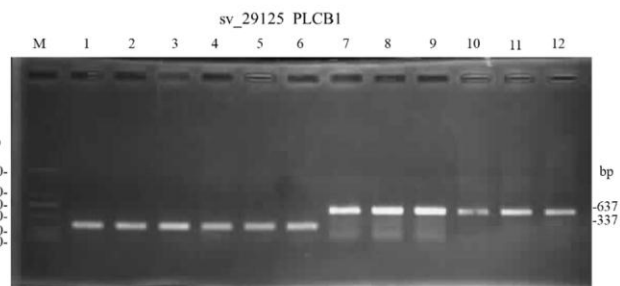
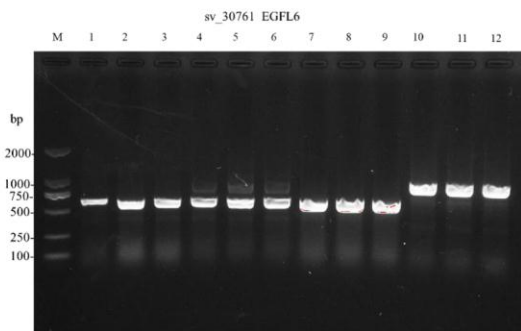
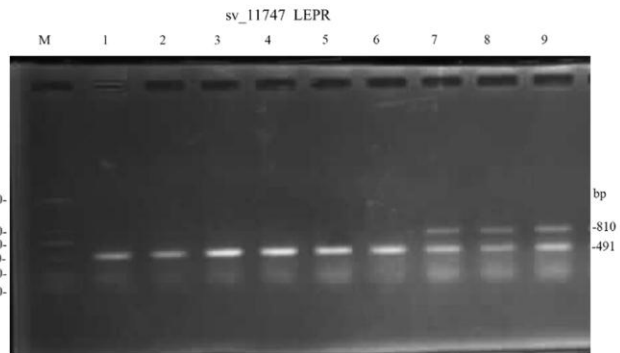
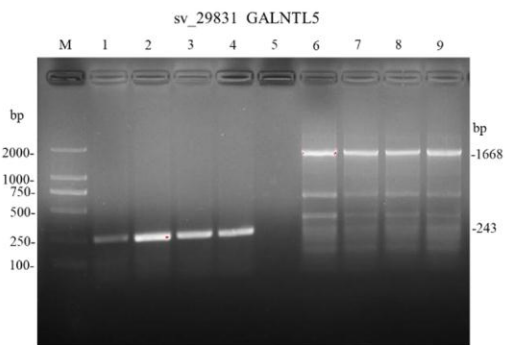
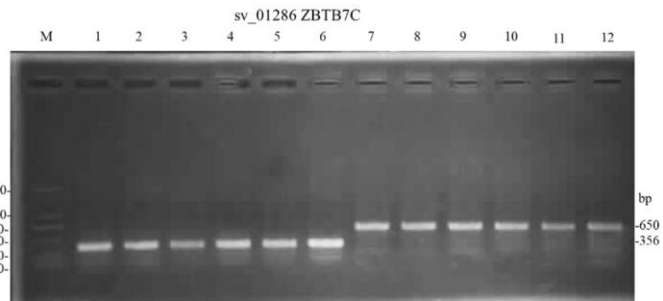
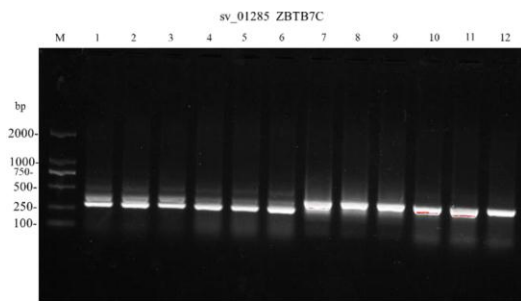


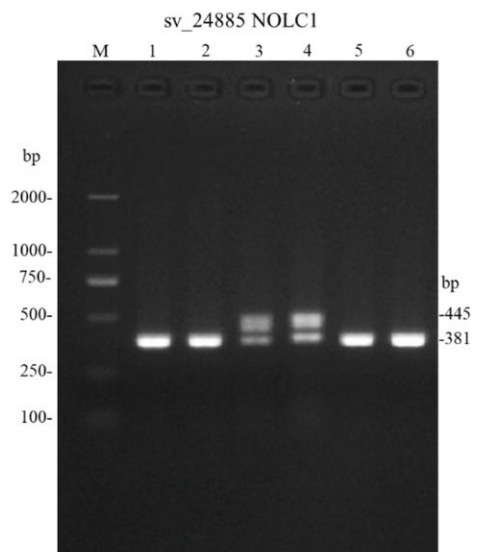
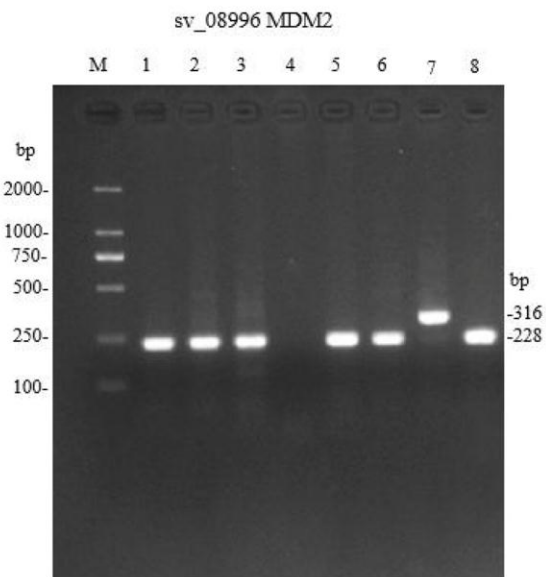
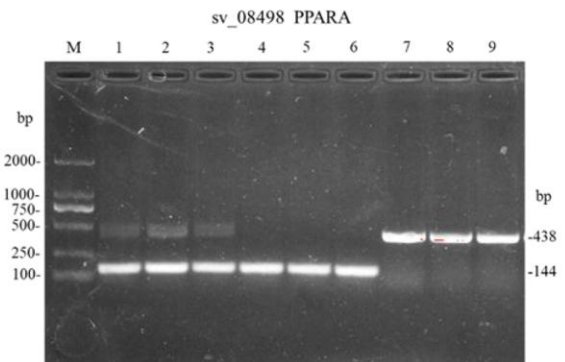
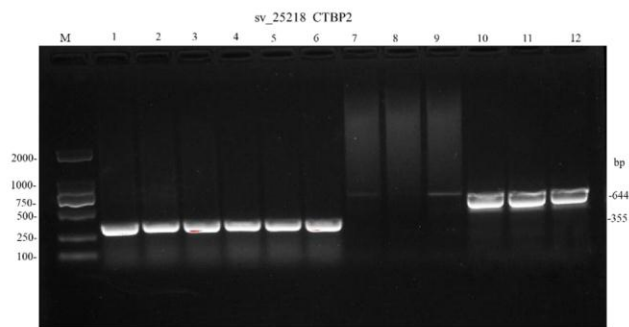
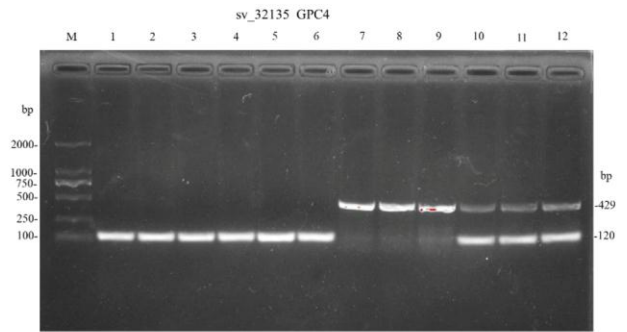
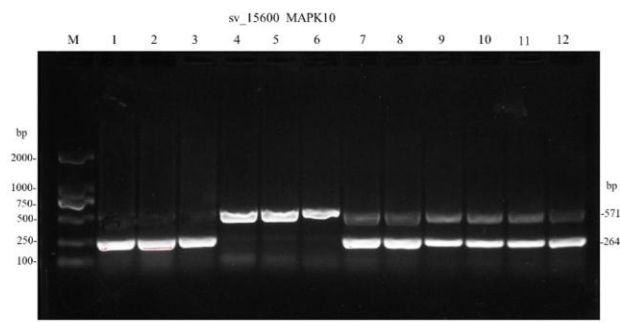


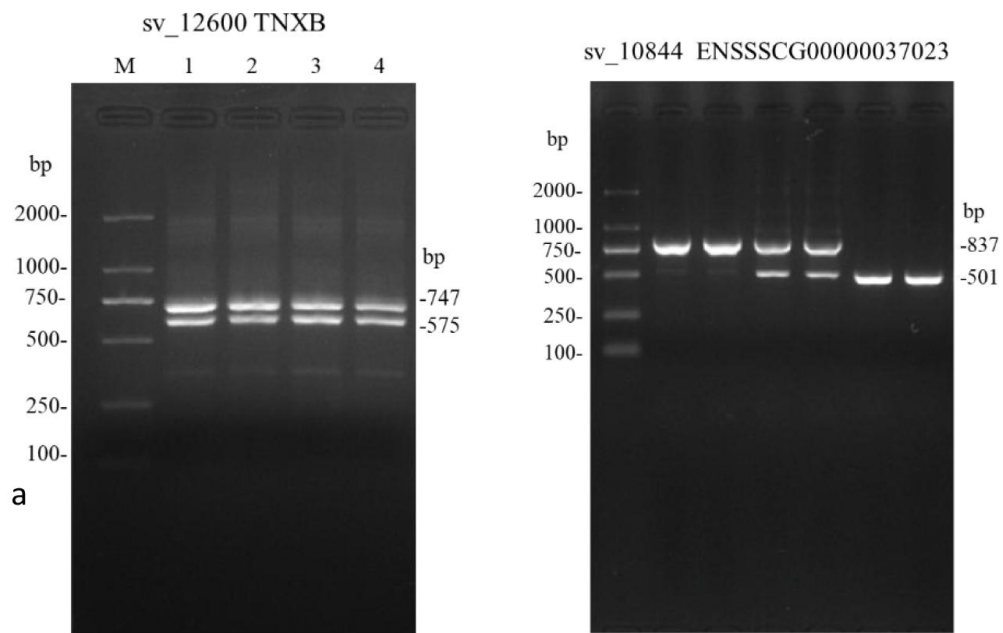
sv_02434 GCNT1: 1(678bp), 2(430bp)

sv_13222 DAD1: 4(135bp), 5(432bp)









Supplementary Figure 1. Representative gel images for the confirmation of SVs. Note: About 38 SVs really exist in genome. Most genes detected three genotypes, namely normal genotype (II), heterozygous genotype (DI), mutant genotype (DD). See diagram SV_11764.

MDM2

Aberrant transcripts (395 bp)

Sbjct 33174918 TCAGACAAGCAAATAGCCCTCTTTCATAGAAAGACTGAGCACTTTATAGTCAGATGCCTC 33174977
Sbjct 33174978 AGCACTGGGCCCTGAGGGTAGCCAGGTAAGTCTGCGAGAGTCCTTTAGGTACTGTCTCTC 33175037
Sbjct 33175038 AGTTTGCATAGCCTTGTTGTTCTCATGGATACAAACCCTGTCTCTTTCAAGCTAGATG 33175097
Sbjct 33175098 TTTTGTAGGCTTGTCTCTTAGGTGCAGGCTCTAAAAGTTGGGGTGCCAGATGTGGGATTC 33175157
Sbjct 33175158 AAACATTTTCTTCTCAGGGA 33175177
AGCTAGATGTTTTGTAGGCTTGTCTCTTAGGTGCAGGCTCTAAAAGTTGGGGTGCCAGATG
TGGGATTCAAACATTTTCTTCTCAGGGA
Sbjct 33175178 GCAGCTTGGAGTTGTGTGTTCTCCTTATTGATTGTGGGTTGCTATACCA 33175224

NOLC1

pre-mRNA (389 bp)

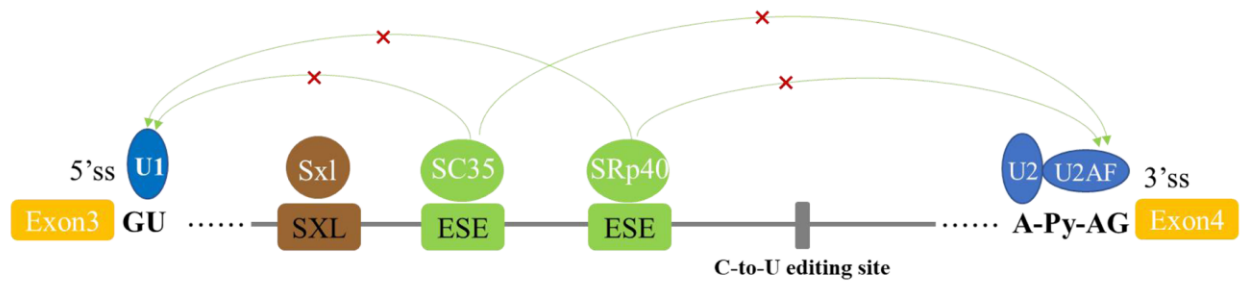
Sbjct 113163333 TACCAAAGCCGCTACTAAAGCAGCTCCAGCAAAGAAGGCAGCAGAGAGCTCTTCAGATA 113163392
Sbjct 113163393 GCTCAGGTAAGGCATATGGAGGCCTTTGGGGCAGTGGGAGCTCCAGGGACTCCCCAGAGT 113163452
Sbjct 113163453 CTAGTTTGGGAGCCACTGATTCTATTCTTGTCTGTAGACTCTGACAGTTCTGAGGATG 113163512
Sbjct 113163513 AAGCTCCTCCAAGCCAGCCAGTGCCACCAAGAATTCAAGTAAGCCAGCTGCCACTCCCA 113163572
Sbjct 113163573 AGCAGTCTATAG 113163584
CTAAGCCAGCCAGTGCCACCAAGAATTCAAGTAAGCCAGCTGCCACTCCCAAGCAGTCTATAG
Sbjct 113163585 CTAAGCCAGCCACAAGTTCCAAGCAGCCTGTAGGCAGTGCCAGAAGCCTCTGACCAGAA 113163644
Sbjct 113163645 AGGCTGATAGCAGCTCCAGTGAGGAGGAGAGCAGTTCTAGTGAGGACGAGAAGATGAAGA 113163704
Sbjct 113163705 AGACTGTAGCAACGCCT 113163721

Aberrant transcripts (296 bp)

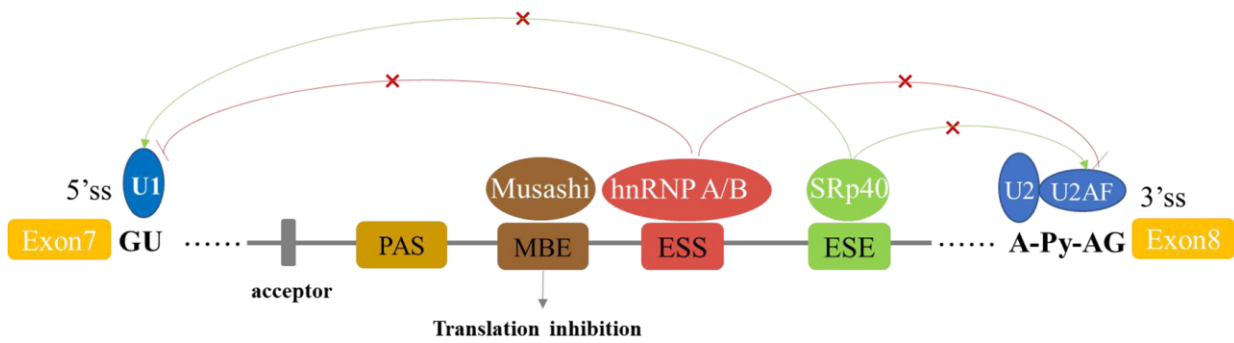
Sbjct 113163333 TACCAAAGCCGCTACTAAAGCAGCTCCAGCAAAGAAGGCAGCAGAGAGCTCTTCAGATA 113163392
Sbjct 113163393 GCTCAG 113163398
Sbjct 113163492 ACTCTGACAGTTCTGAGGATGAAGCTCTGCCAAGCCAGCCAGTGCCACCAAGAATTCAA 113163551
Sbjct 113163552 GTAAGCCAGCTGCCACTCCCAAGCAGTCTATAGCTAAGCCAGCCACAAGTTCCAAGCAGC 113163611
Sbjct 113163612 CTGTAGGCAGTGCCAGAAGCCTCTGACCAGAAAGGCTGATAGCAGCTCCAGTGAGGAGG 113163671
Sbjct 113163672 AGAGCAGTTCTAGTGAGGACGAGAAGATGAAGAAGACTGTAGCAACGCCT 113163721

Supplementary Figure 2. The abnormal transcript information of *MDM2* and *NOLC1* gene. Note: Blue letters represent exons, black letters represent introns. And the red shading and yellow filled sequences denote insertion site and variant fragment, severally.

XYLT1 sv_05472



FUT8 sv_13380



Supplementary Figure 3. Splice sites, regulatory elements and splicing alterations caused by mutations. Note: Intron mutations lead to the loss of splicing elements and may lose the enhancement or inhibition of splicing.