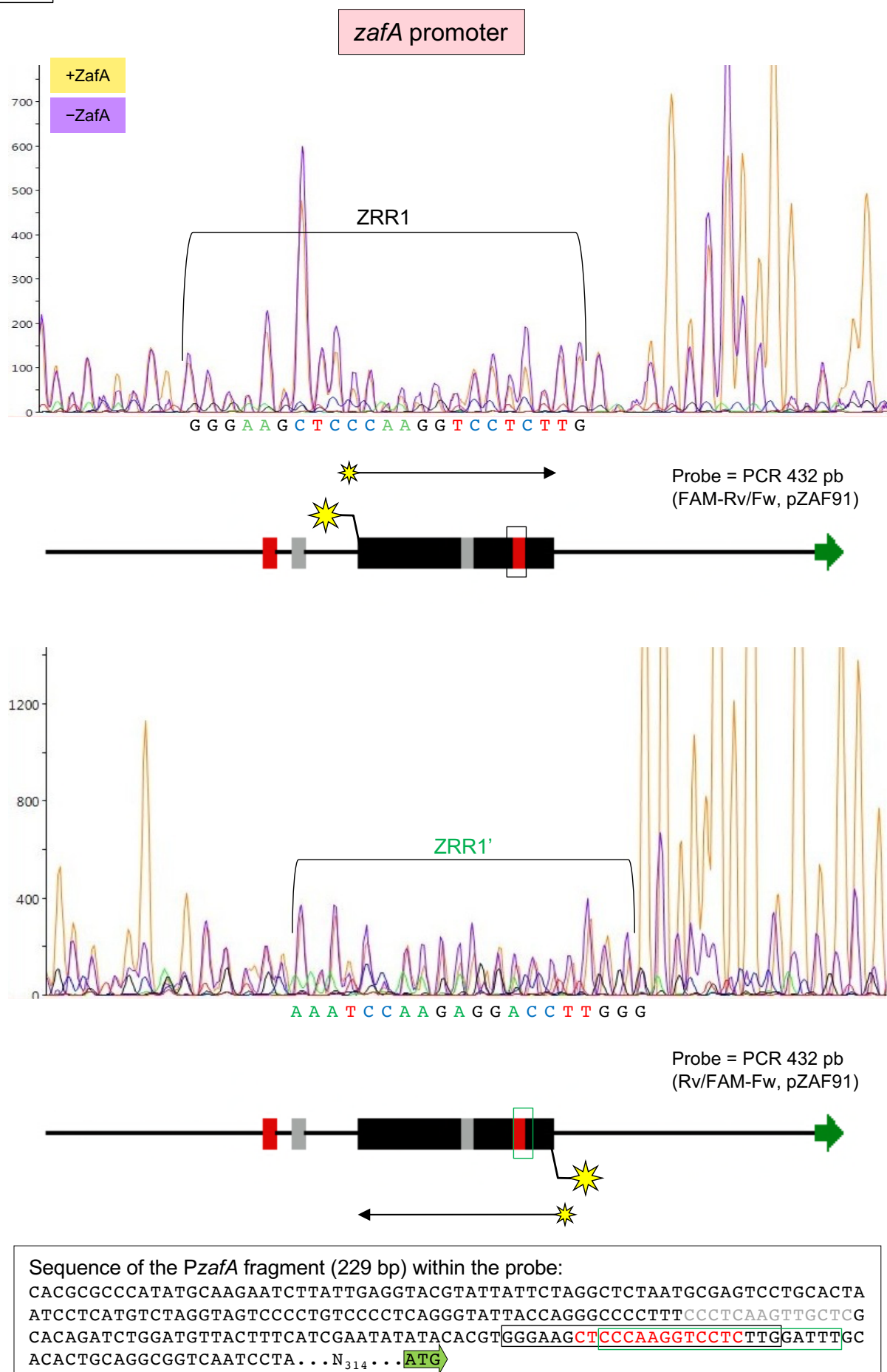
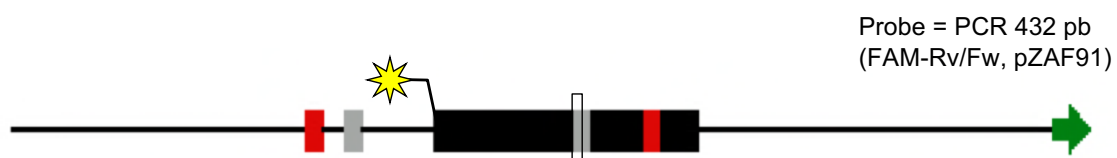
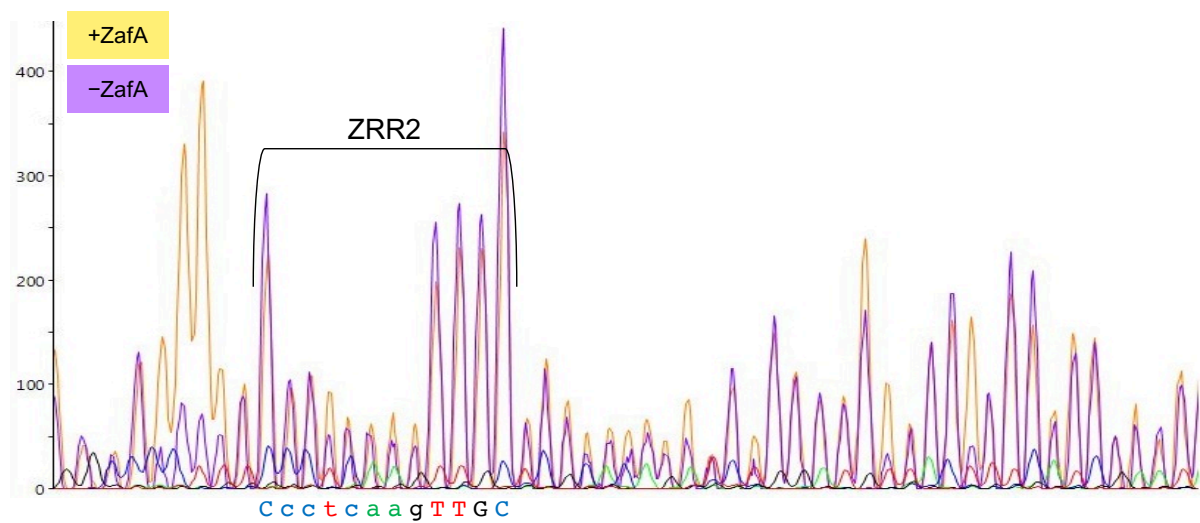


**Figure S2. Analysis of ZafA binding to DNA fragments from the promoter regions of genes *zafA*, *zrfA*, *zrfB* and *zrfC* by DNase I footprinting assays.** The purple chromatograms were obtained upon incubating the DNA fragment in the absence of ZafA<sup>ZF3-6</sup>, such that the DNA remained naked and, hence, unprotected from DNase I digestion. The yellow chromatograms were obtained upon incubating the DNA in the presence of ZafA<sup>ZF3-6</sup>. In this case, ZafA bound to DNA prevented its digestion with DNase I resulting in a stretch of relatively low yellow peaks (compared to the high of the control purple peaks) that was typically followed by a hypersensitive region to DNase I digestion, as reflected by a short stretch of high yellow peaks typically observed in most cases at the right of the chromatograms. The protected regions in the chromatograms are delimited by a bracket. Every ZR protected sequence of each gene has been named and numbered properly either in black letters (for sequences in the direct strand) or in green letters followed by a comma (for sequences in the reverse-complementary or antiparallel strand). Below each chromatogram is shown a schematic representation of the whole intergenic region of the corresponding gene with the beginning of its ORF located at the right side (green arrow). The sequence of the DNA fragments used in the assay corresponding to the promoter sequence is indicated in the scheme with a black rectangle and shown at the nucleotide level at the bottom of each set of chromatograms. In these sequences their putative ZR motifs detected in MEME have been highlighted in red or gray. The protected regions are indicated in the schemes with a green rectangle. The yellow stars indicate the end 6-FAM labeled strand detected by the capillary-based automated DNA sequencer.

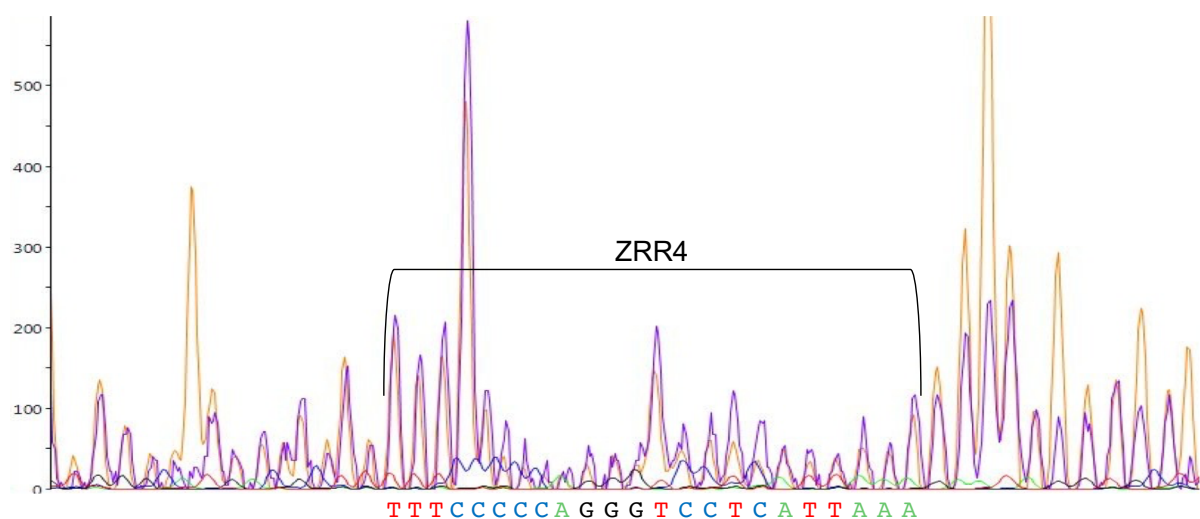
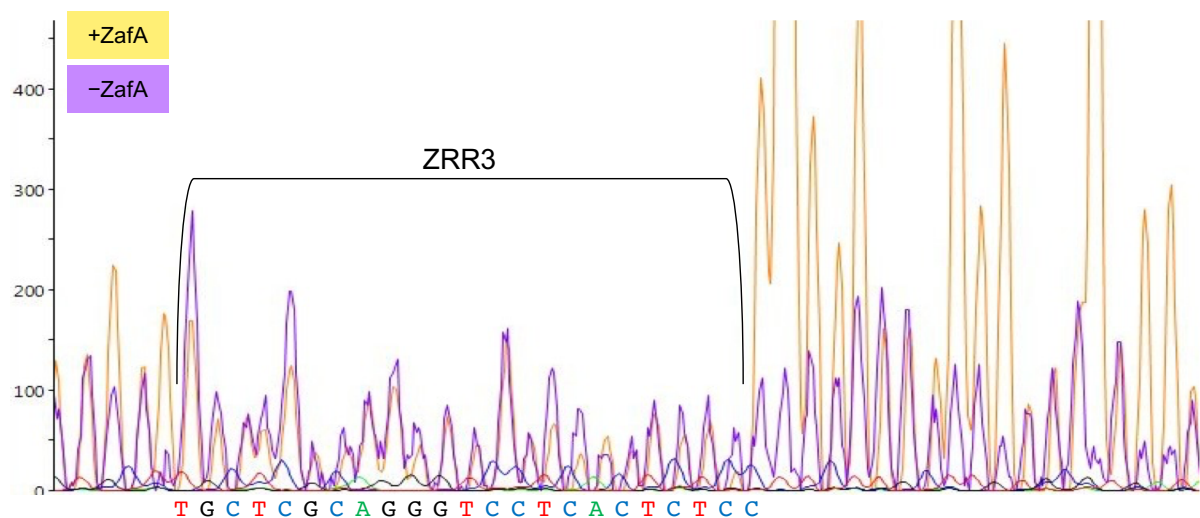
Fig. S2





Sequence of the *PzafA* fragment (229 bp) within the probe:

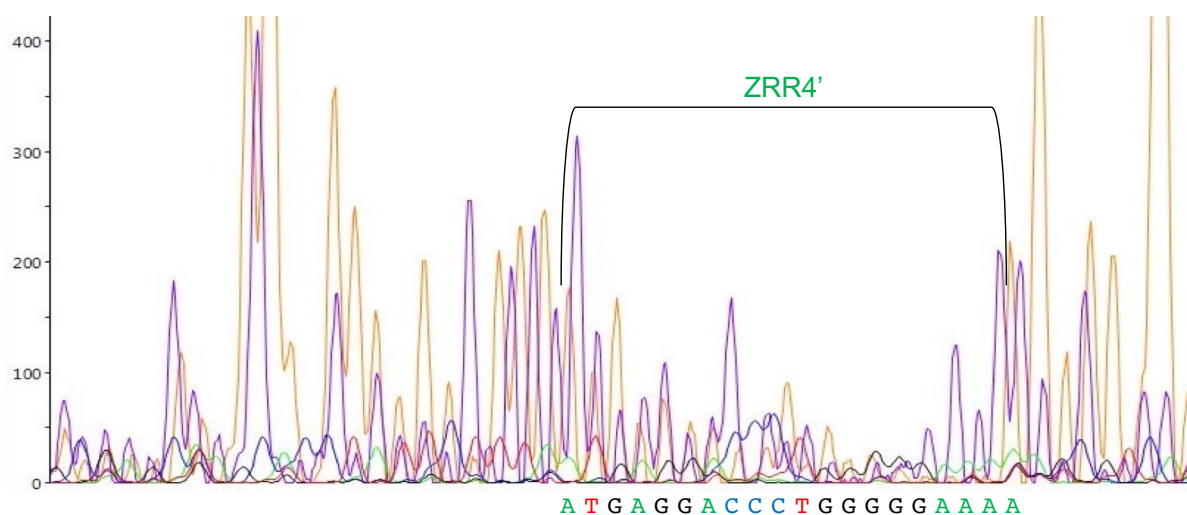
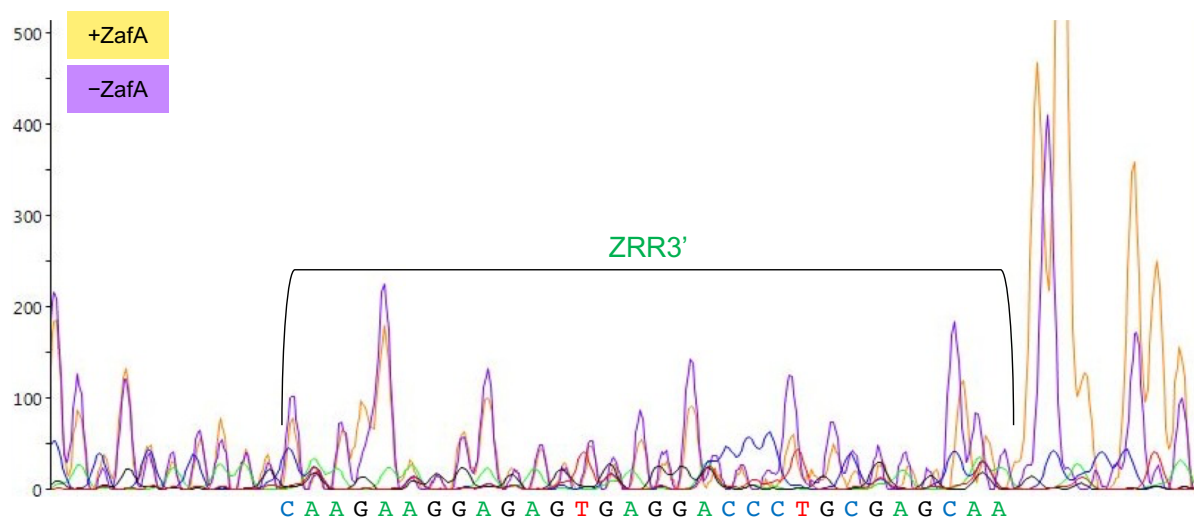
CACGCGCCCATATGCAAGAATCTTATTGAGGTACGTATTATTCTAGGCTCTAATGCGAGTCCTGCACTA  
 ATCCTCATGTCTAGGTAGTCCCCTGTCCCCTCAGGGTATTACCAGGGCCCCTTTCCCTCAAGTTGCTCG  
 CACAGATCTGGATGTTACTTTCATCGAATATATACACGTGGGAAGCTCCCAAGGTCCTCTTGGATTGTC  
 AACTGCAGGCGGTCAATCCTA...N<sub>314</sub>...ATG



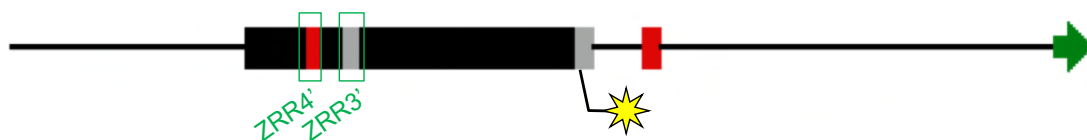
Sequence of the *PzfA* fragment (396 bp) within the probe:

CCTGACAATTCAGGCGATACGATTTCGCCGGCGGGGAGTGGGCATGACGCTTTTTCCTCCAGGGTCCTCA  
TTAAAGAATAGGTGCTTGCTCGCAGGGTCTCTCACTCTCTTCTTGCTTGTGCGTGATAGAATCCGGTCG  
CTGTGCTGGATGGGGCCAGGTAGCACCCACGCGCCCATATGCAAGAATCTTATTGAGGTACGTATTA  
TTCTAGGCTCTAATGCGAGTCCTGCACCTAATCCTCATGTCTAGGTAGTCCCCTGTCCCCTCAGGGTATT  
ACCAGGGCCCCCTTCCCTCAAGTTGCTCGCACAGATCTGGATGTTACTTTTCATCGAATATATACACGTG  
GGAAGCTCCCAAGGTCTCTTGGATTTGCACACTGCAGGCGGTCAATCCTA...N<sub>314</sub>...ATG



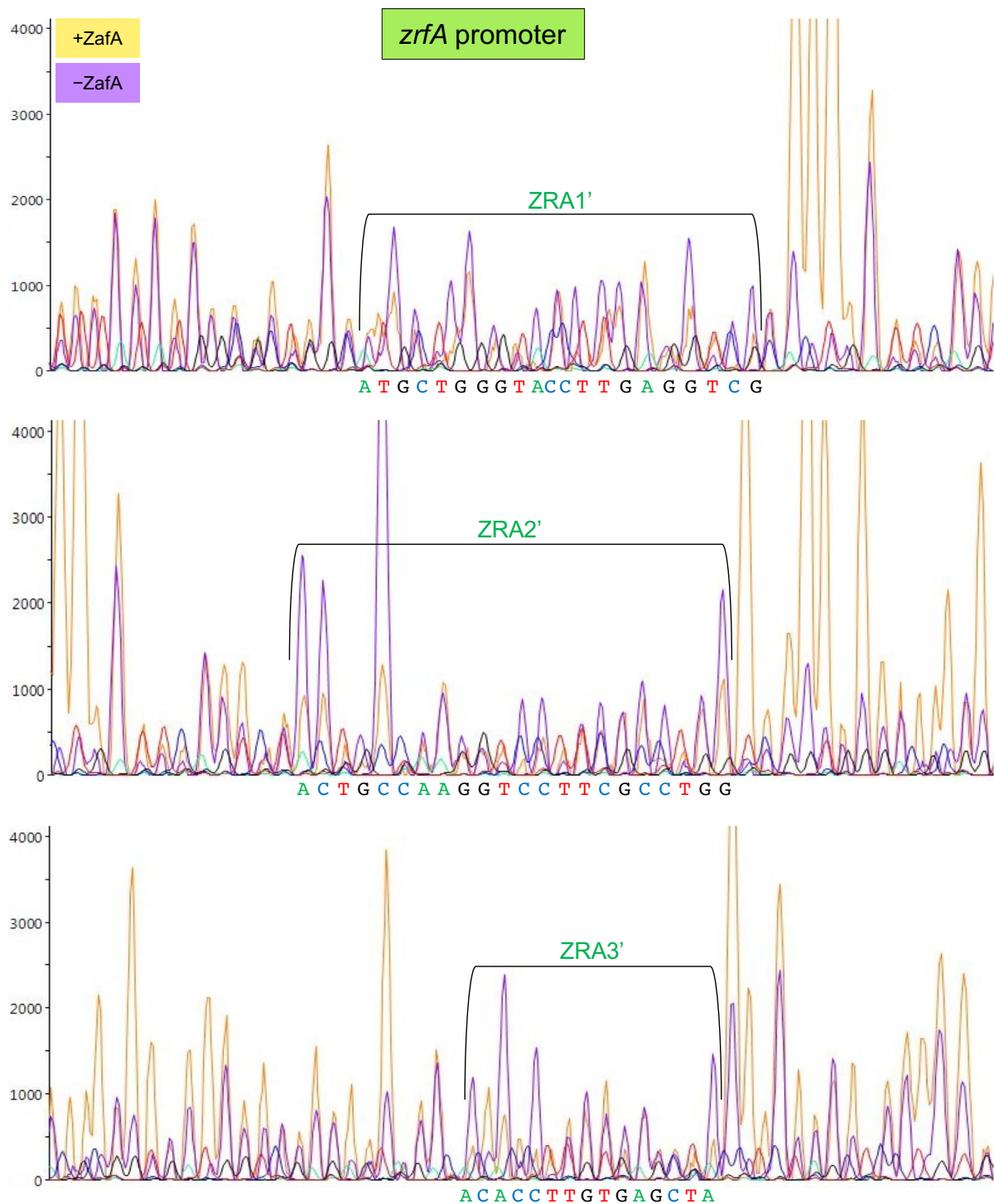


Probe = PCR 435 pb  
(Rv/FAM-JA439, pZAF151)

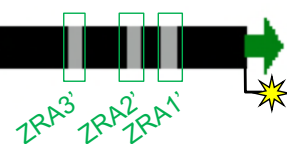


Sequence of the *PzafA* fragment (295 bp) within the probe:

CCTGACAATTCAGGCGATACGATTGCGCGGCGGGGAGTGGGCATGACGCTTTTTCCTCCAGGGTCCTCA  
TTAAAGAATAGGTGCTTGCTCGCAGGGTCCTCACTCTCCTTCTTGCTTGTGCGTGATAGAATCCGGTCG  
CTGTGCTGGATGGGGCCAGGTAGCACCCACGCGCCCATATGCAAGAATCTTATTGAGGTACGTATTA  
TTCTAGGCTCTAATGCGAGTCCTGCACTAATCCTCATGTCTAGGTAGTCCCTGTCCCTCAGGGTATT  
ACCAGGGCCCTTTCCCTC...N<sub>415</sub>...ATG



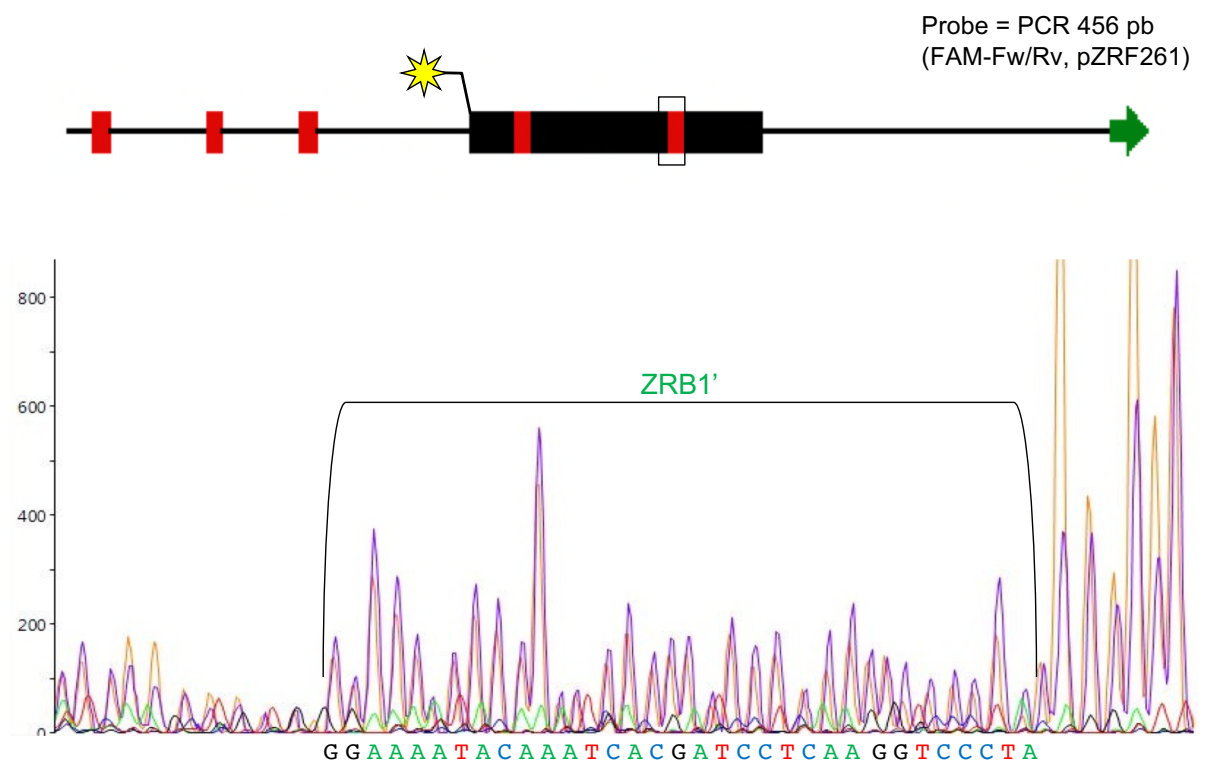
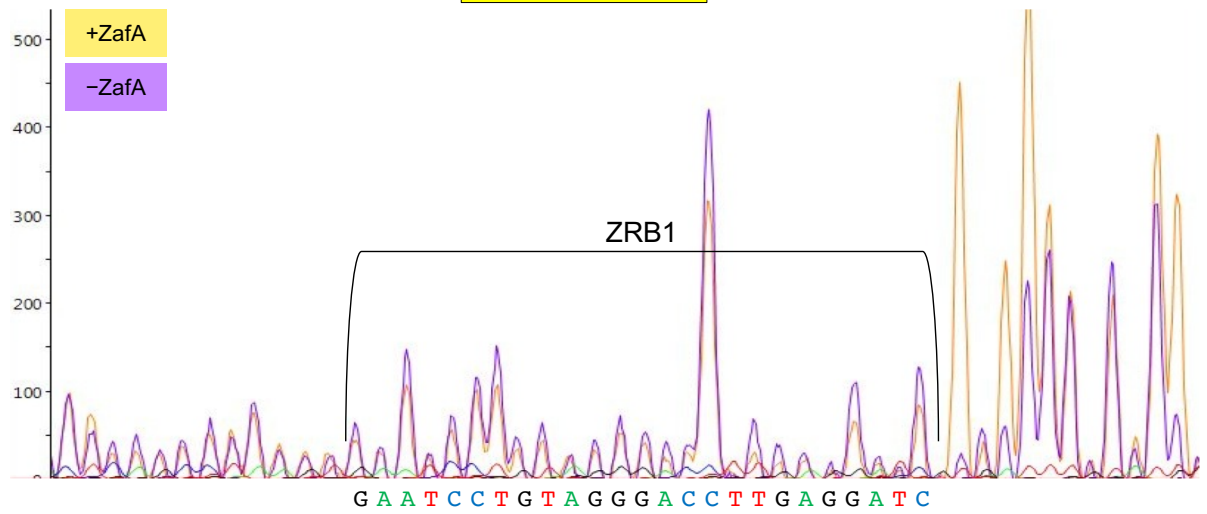
Probe = PCR 350 pb  
(JA378/FAM-Rv, pZRF10)



Sequence of the PzrfA fragment (217 bp) within the probe:

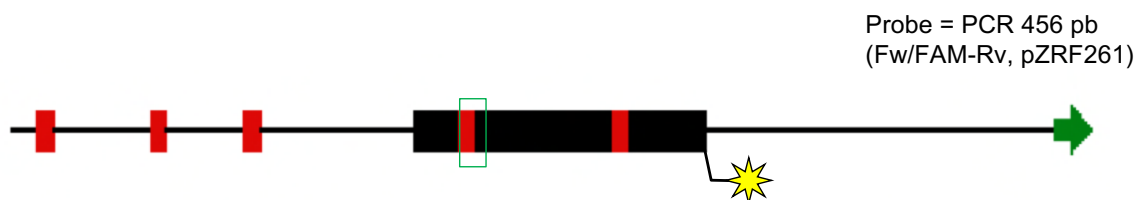
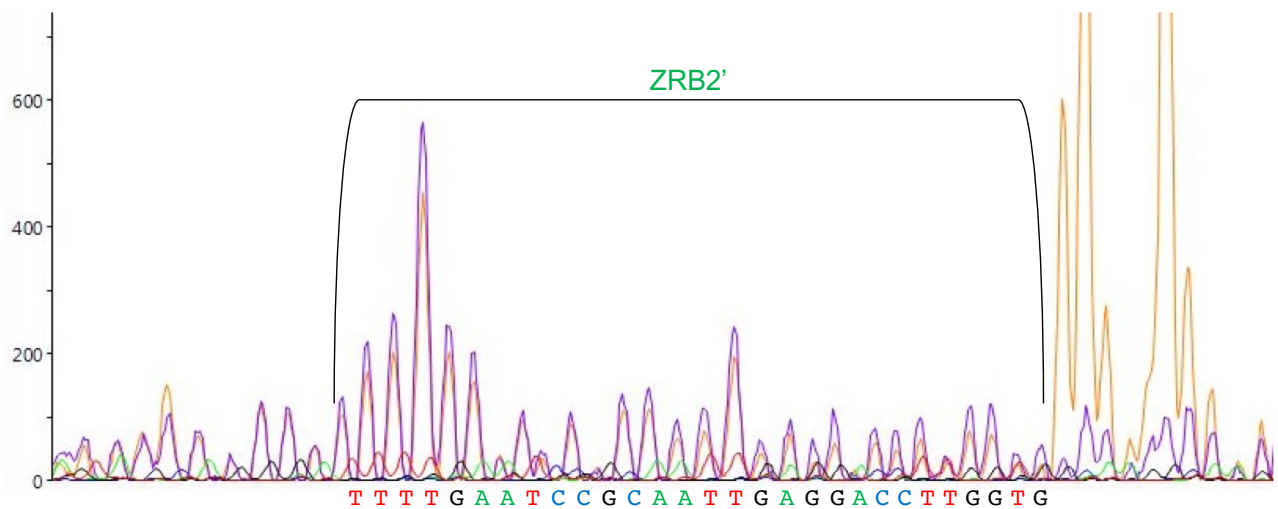
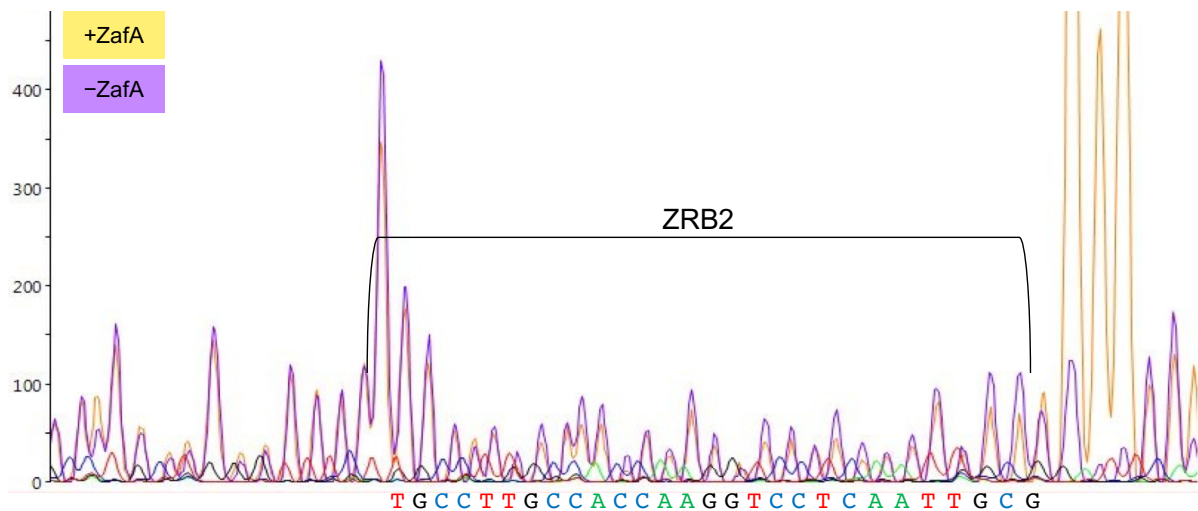
ACAGGCTAACGCTTGTGATGACACTTTTCTTTCTCGTCTTGCCACAGGAGCTAGAGG TAGCTCACAAG  
GTGTGTCTACTCTCGACCATCACC GCGTCCCACCGA CCAGGCGAAGGACCTTGGCAGT AGACTGAATCA  
GTGCGACCTCAAGGTACCCAGCA TGCCAGCGCCATATAAAGGAAACAGTGTCTAGCACTTCGATGCGGA  
TGATGCAACC ATG

# *zrfB* promoter



Sequence of the *PzrfB* fragment (256 bp) within the probe:

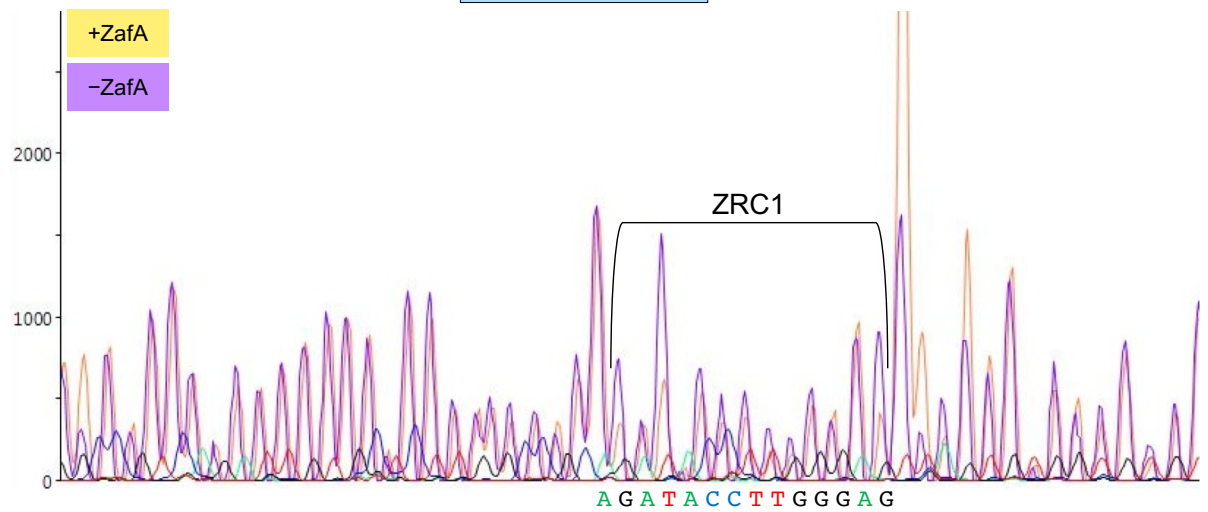
TCGGACATAACGAACGACTCATTGGGGATCGCAGAATACCTGCTTGCCTGCTGGGTTTCTTGCCTTGCC  
ACCAAGGTCCTCAATTGCGGATTCAAAATCCCTGCTACTGCGTTAACTGCGAGCGATCACACGACAGTC  
AAGCCTCTGACCTCGTTCTTATCACAGGCTTAGAAGTCTTAGTACTCAGCCTAAGTGAATCCTGTAGGG  
ACCTTGAGGATCGTGATTGTATTTTCCACAGCTTGATCCAAGGGAGT...N<sub>306</sub>...ATC



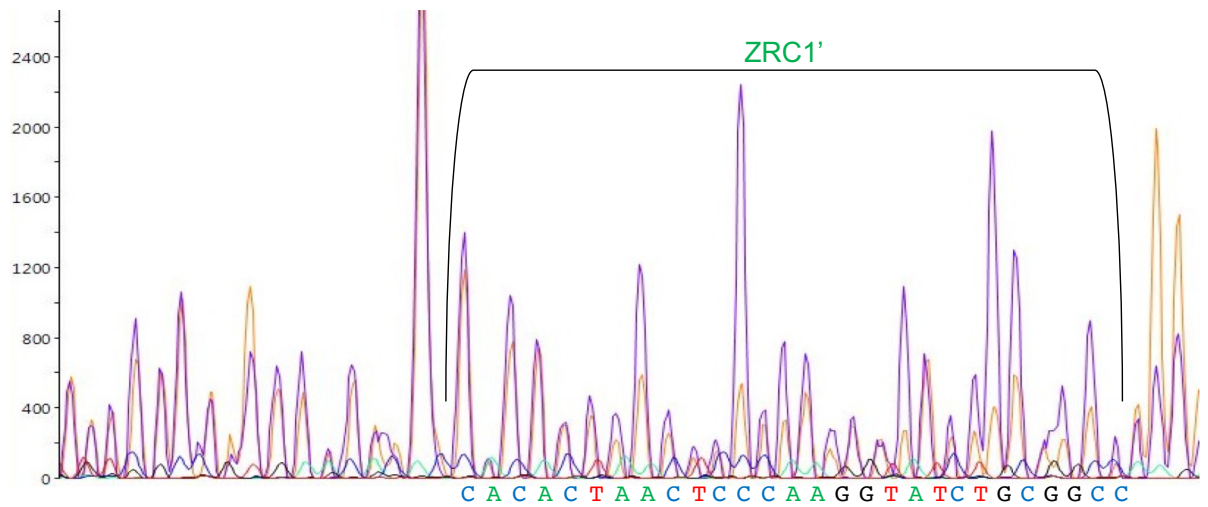
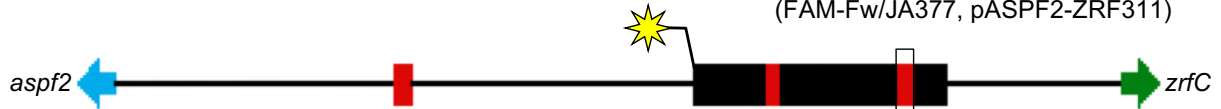
Sequence of the *PzrfB* fragment (256 bp) within the probe:

TCGGACATAACGAACGACTCATTGGGGATCGCAGAATACCTGCTTGCCTGCTGGGTTTCTTGCCTTGCC  
 ACCAAGGTCCTCAATTGCGGATTCAAAATCCCTGCTACTGCGTTAACTGCGAGCGATCACACGACAGTC  
 AAGCCTCTGACCTCGTTCTTATCACAGGCTTAGAAGTCTTAGTACTCAGCCTAAGTGAATCCTGTAGGG  
 ACCTTGAGGATCGTGATTGTATTTTCCACAGCTTGATCCAAGGGAGT...N<sub>306</sub>...ATC

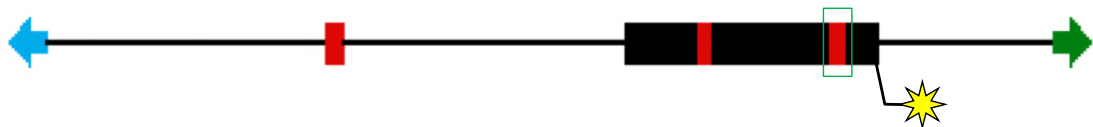
### *zrfC* promoter



Probe = PCR 322 pb  
(FAM-Fw/JA377, pASPF2-ZRF311)



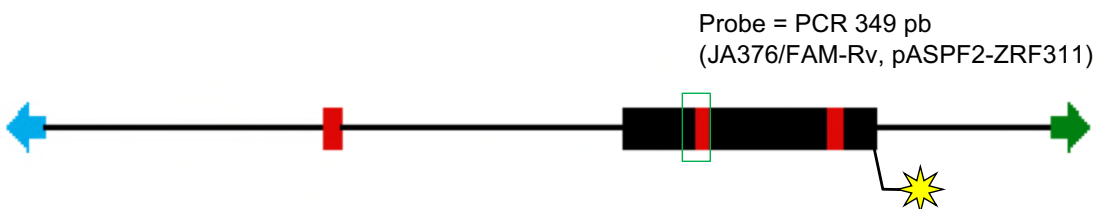
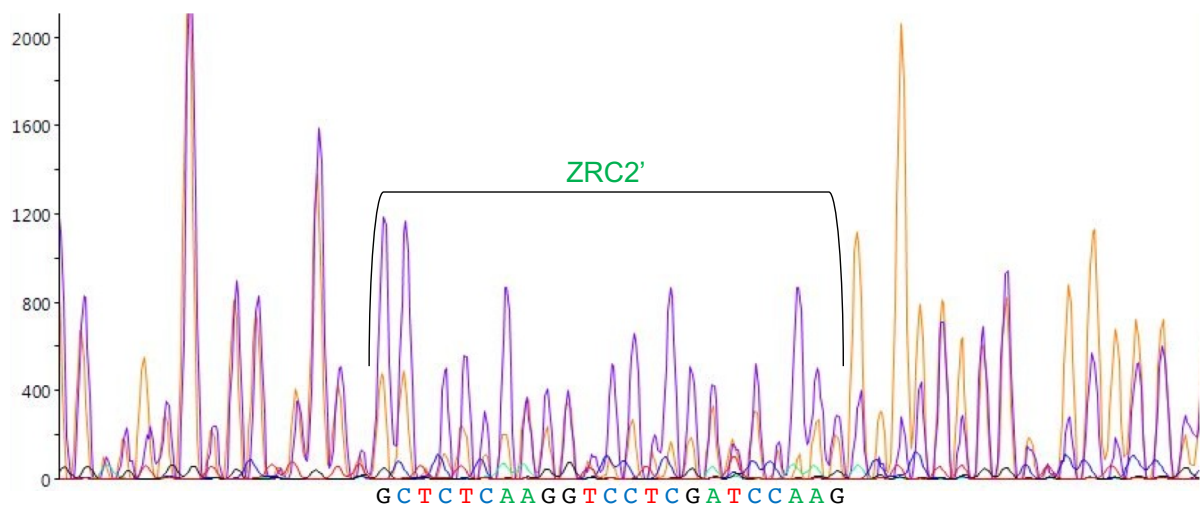
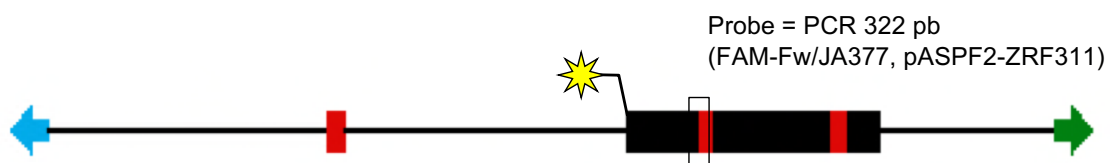
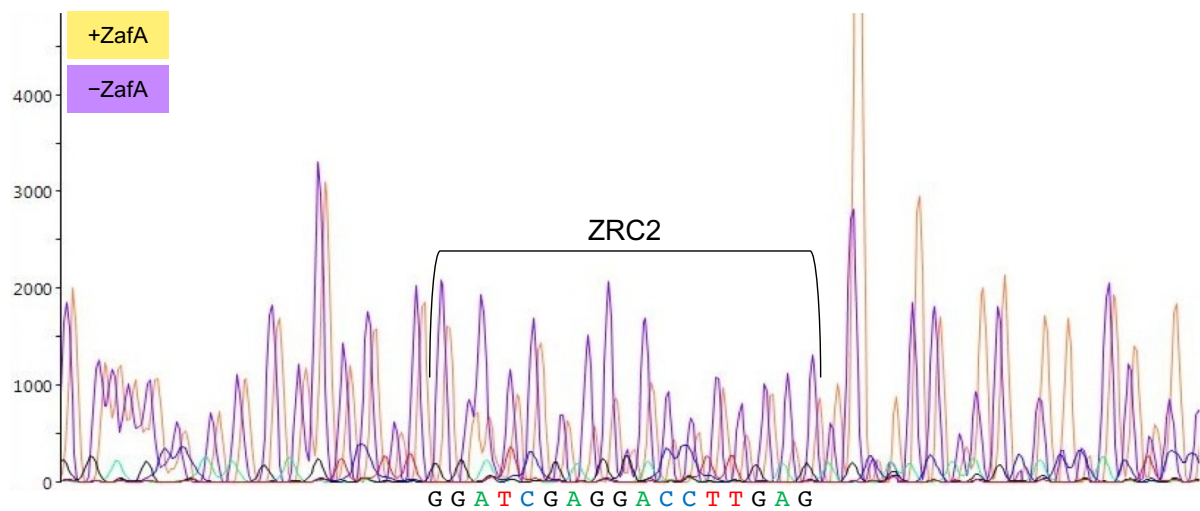
Probe = PCR 349 pb  
(JA376/FAM-Rv, pASPF2-ZRF311)



Sequence of the *PzrfC* fragment (215 bp) within the probe:

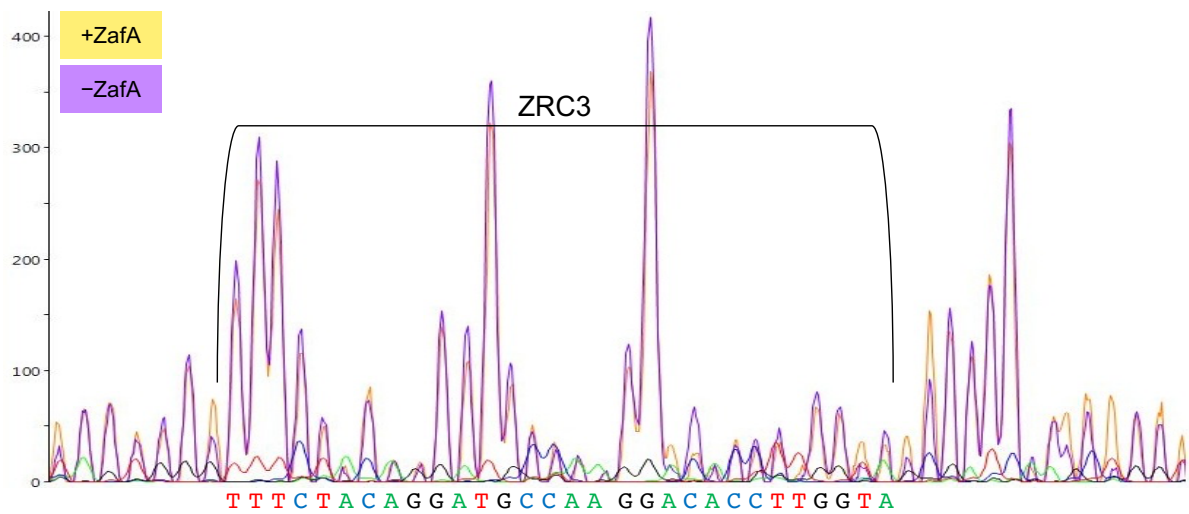
CAATGCATGGAGGCAGCCCGCGCCAAGATCCTGGCGGAGGAGCCAAGAGTCTTGGATC**GAGGACCTTGA**  
**GAG**CAACAAGCACCACCTCCCAGATCATTTTGCTCCGGGAATATAGCCGCTTCTCGCCGAATGGACGGAG  
 TTTTGCTGCTTGCCCGTCAGATTGTGCTCTTGGCCGC**AGATACCTTGGGAG**TTAGTGTGGTGTGTTTCAC  
 GGCGAAAG...N<sub>156</sub>...**ATG**



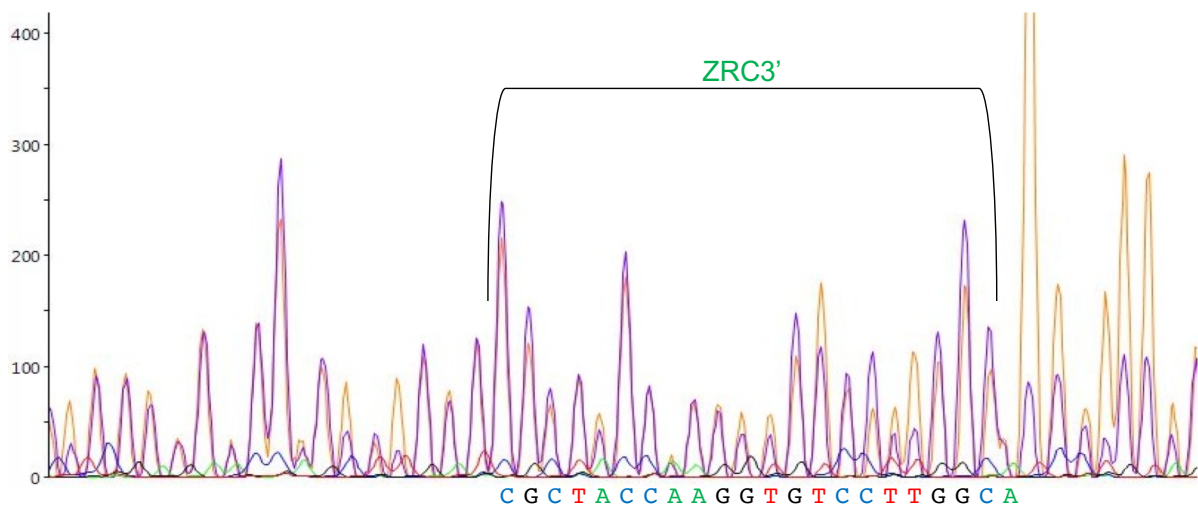
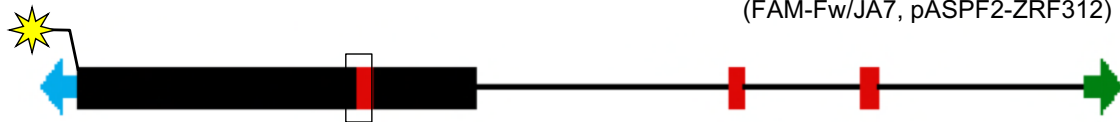


Sequence of the *PzrfC* fragment (215 bp) within the probe:

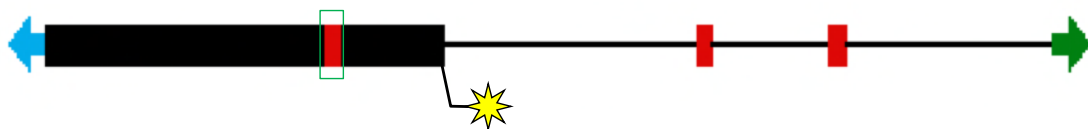
CAATGCATGGAGGCAGCCCGCGCCAAGATCCTGGCGGAGGAGCCAAGAGTCTTGGATCGAGGACCTTGA  
GAGCAACAAGCACCACCTCCCATCATTGCTCCGGGAATATAGCCGCTTCTCGCCGAATGGACGGAG  
 TTTTGCTGCTTGCCGTCAGATTGTGCTCTTGCCGCAGATACCTTGGGAGTTAGTGTGGTGTGTTTAC  
 GGCGAAAG...N<sub>156</sub>...ATG



Probe = PCR 393 pb  
(FAM-Fw/JA7, pASP2-ZRF312)



Probe = PCR 504 pb  
(JA194/FAM-Rv, pASP2-ZRF312)



Sequence of the *PzrfC* fragment (349 bp) within the probe:

CATTTGTGAGTACATTTTCTTTTTTCAAGGTTGGATGGTGCGTGACTCTTGCATTGTAGCCAGAGGTAG  
 AACATCCTTATATACCTCGAGGATGGCCTCCTTTTCGCGGTGCCAGAGAGGTACTCATTGTTGGATTG  
 GCCATCAGGGTAGACACGCCACCGGCCACCCCAACAGTAGGTCACGGCCGCAAGCCATCAAGATGCAT  
 GGTTTCGTTTGTTCGTATTCTAGTGGGTTTCTACAGGATGCCAAGGACACCTTGGTAGCGGATCAAGCTGG  
 TTCTCGAGTCGATGATTCCGAAAGCTATGATCTCCGAGCTTCTGTTCAGCCCTATATGATCCTGTCCGT  
 ACGTGAT...N<sub>535</sub>...ATG