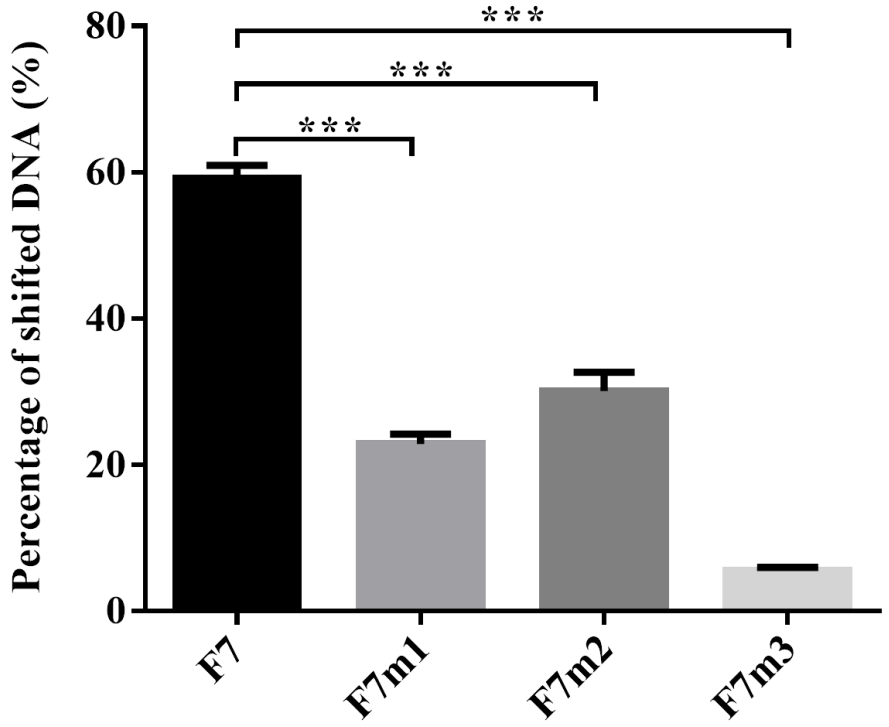

FIG S1 Quantitation of protein-DNA binding in the gel shift assay for F7 and its three mutants. The percentage of shifted DNA was calculated as the ratio amount of shifted DNA/total amount of DNA. The amounts of DNA fragments were determined by measuring the gray values of corresponding bands via ImageJ software. $^{***}P < 0.001$ as determined by Student's *t*-test. Error bars represent standard deviation.

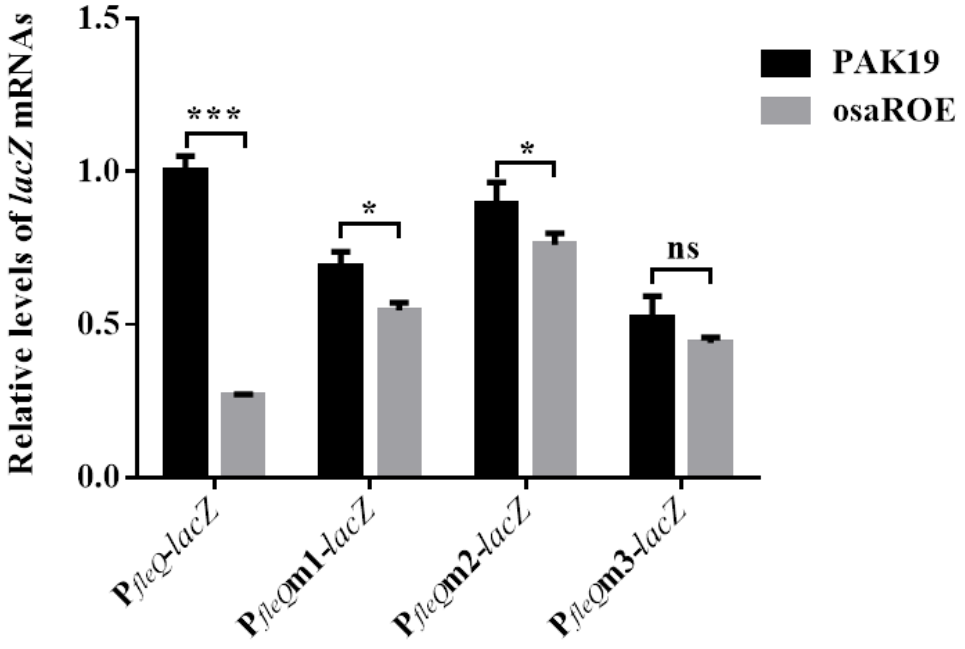

FIG S2 *lacZ* transcription in the reporter strains. mRNA levels were determined by qRT-PCR. ns, not significant, $^{*}P < 0.05$ and $^{***}P < 0.001$ as determined by Student's *t*-test. Error bars represent standard deviation.

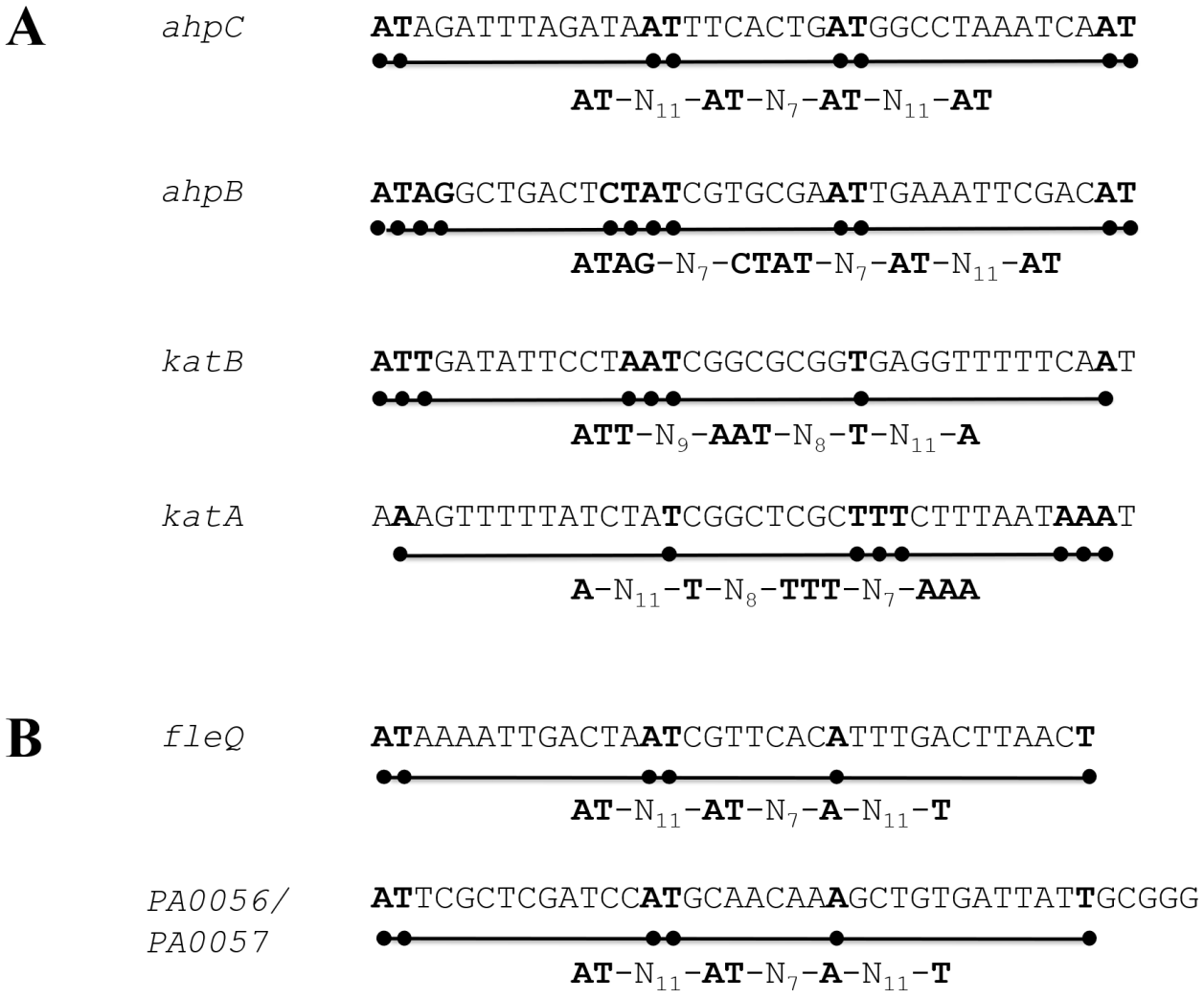

FIG S3 Comparison of OsaR and OxyR binding sites. (A) Features of the OxyR binding sites in antioxidant genes. (B) Features of the OsaR binding site in the *fleQ* promoter and the *PA0056*/*PA0057* promoter. The A-T palindromic base pairs are boldfaced and indicated by dots; the spacer bases are indicated by line segments.

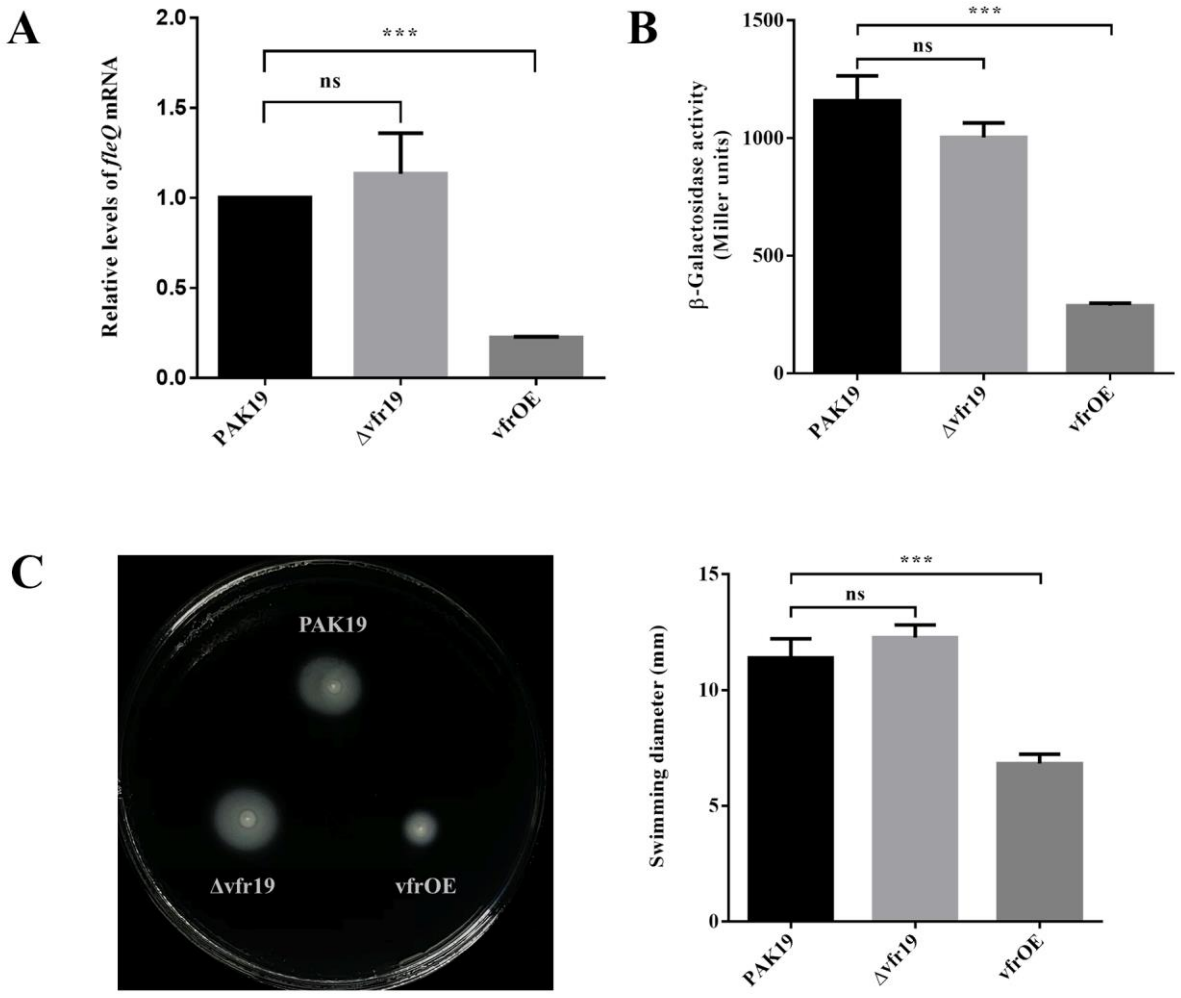

FIG S4 *vfr* overexpression downregulates *fleQ* and swimming motility. (A) The effect of Vfr on the transcriptional level of *fleQ*. The mRNA levels of *fleQ* were determined by qRT-PCR. (B) The effect of Vfr on the promoter activity of *fleQ*. WT strain (PAK19), *vfr* mutant (Δvfr19) and *osaR* overexpressing strain (vfrOE) were transformed with the reporter plasmid P_{fleQ}-*lacZ*, followed by β-galactosidase assays when cultured to an OD_{600} of ~0.6. (C) The effect of Vfr on swimming motility. Motility was detected and quantitated by three independent replicates. ns, not significant, *** $P < 0.001$ as determined by Student's *t*-test. Error bars represent standard deviation.

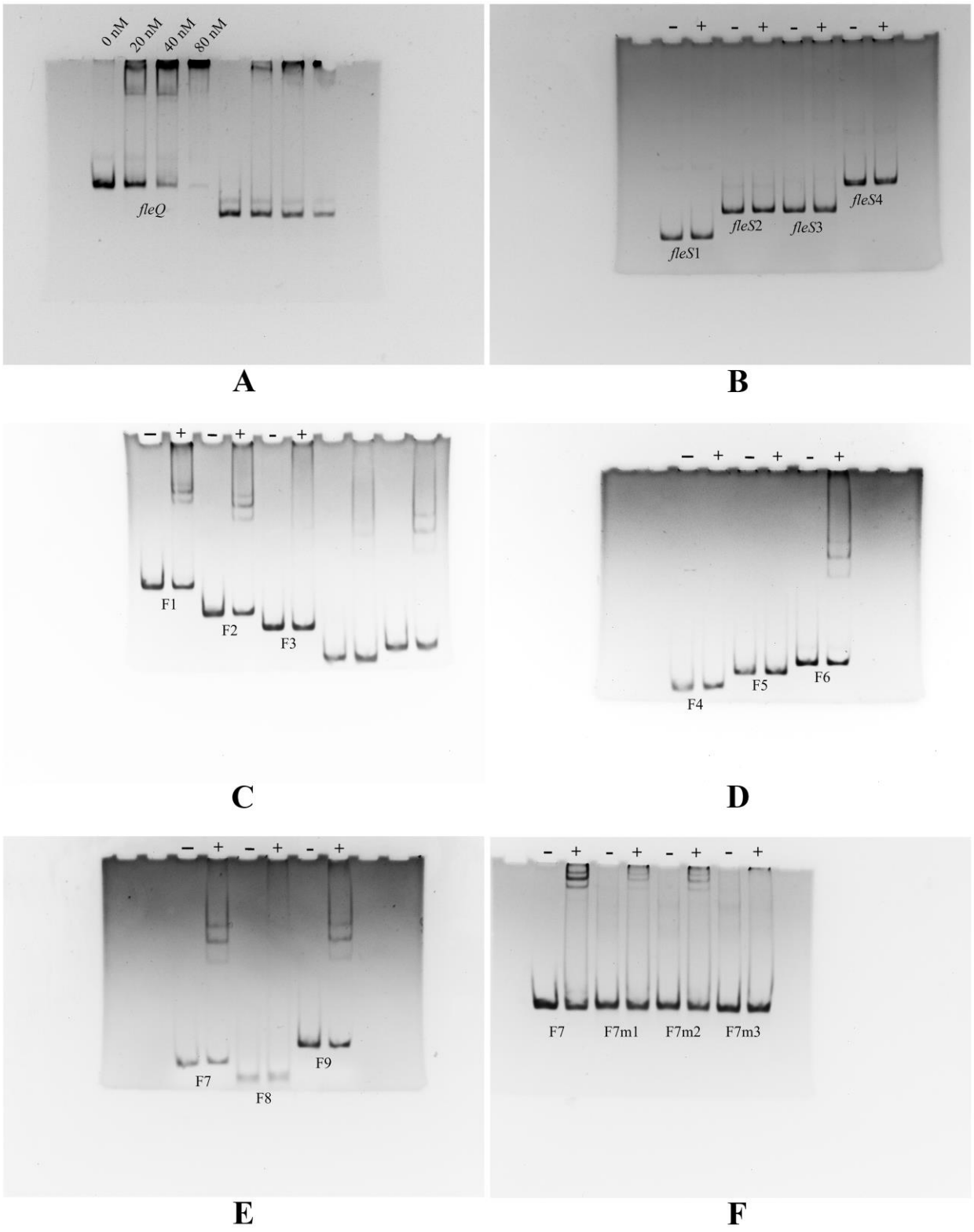

FIG S5 Row figures of the gels presented in this study. A-B, C-E, F corresponds to Fig. 1B, Fig. 3B, Fig. 4B, respectively.