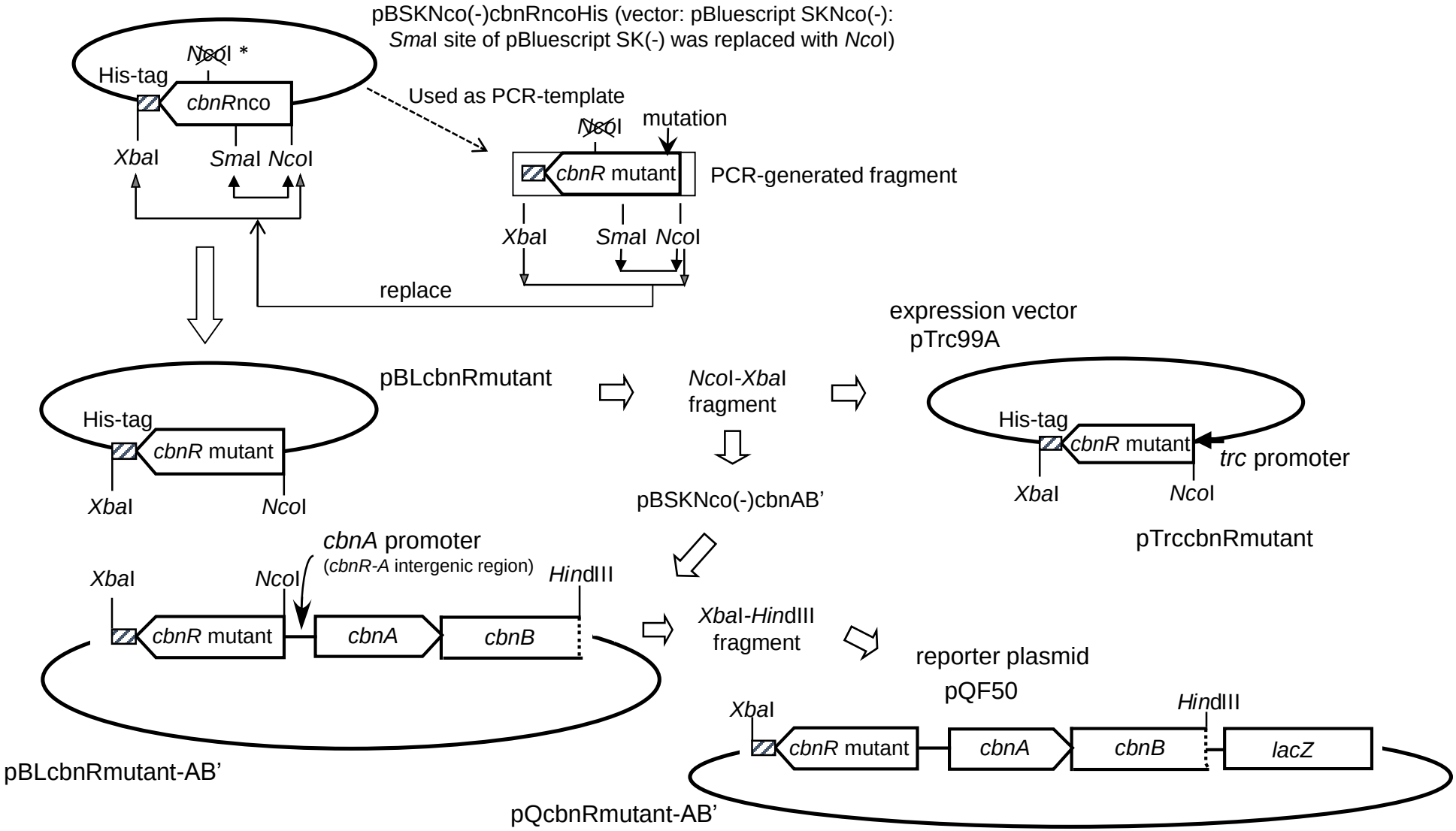
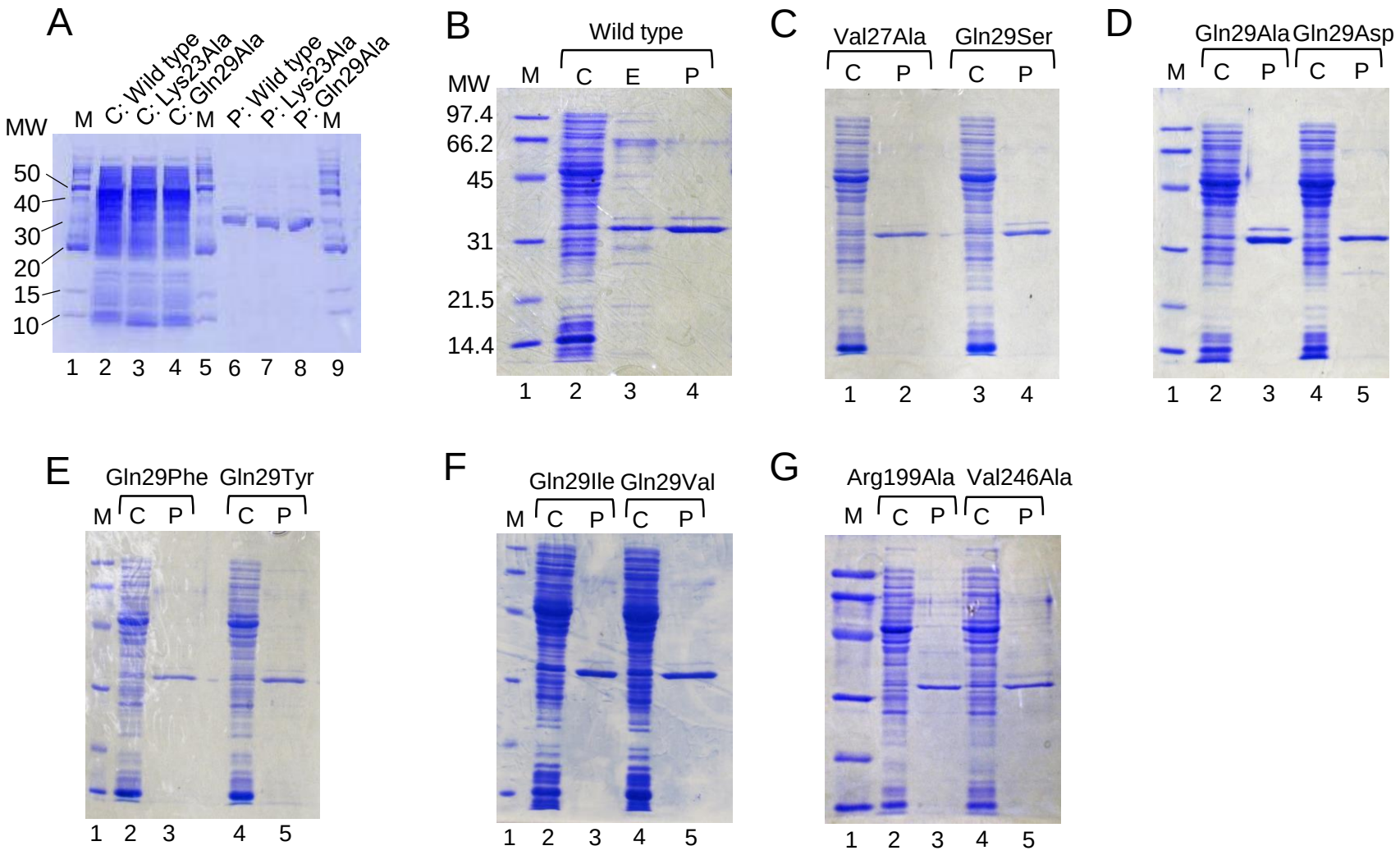
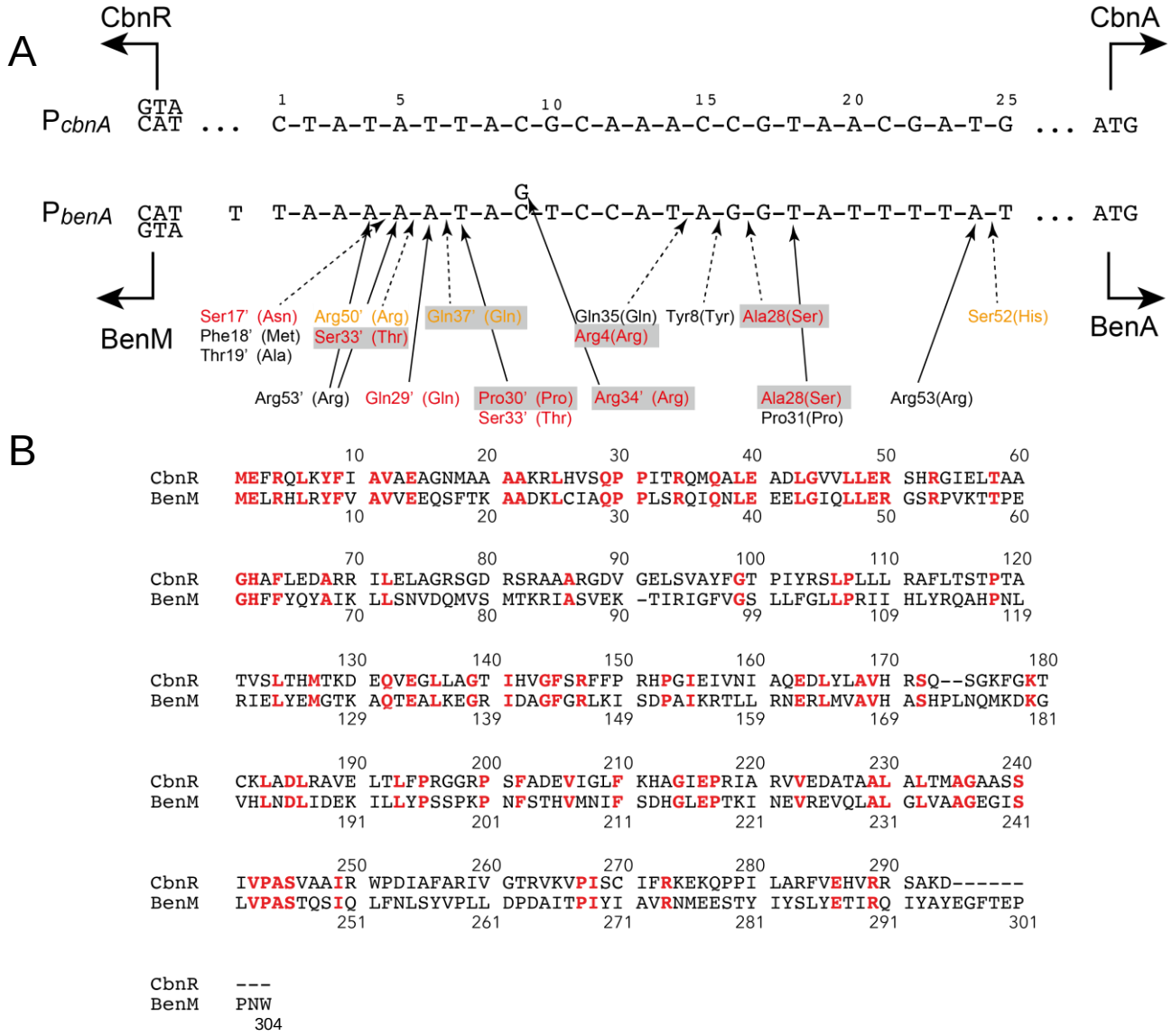


Supplementary Figure 1 Schematic diagram of the plasmid construction in this study.
To generate plasmid pBSKNco(-)cbnRncoHis, a nucleotide sequence of an internal *Nco*I site (CCATGG) in the wild-type *cbnR* gene (marked with * in the figure; positions 698 - 703 from the start codon) was replaced with a sequence, CGATGG, by PCR mutagenesis together with addition of six His codons (His-tag) and a *Xba*I site on the C-terminal and a *Nco*I site overlapping with the start codon on the N-terminal by using the wild-type *cbnR* gene as template. The fragment yielded by PCR as described above was digested with *Xba*I and *Nco*I, and inserted into the *Xba*I and *Nco*I sites of plasmid pBluescript SKNco(-) to yield pBSKNco(-)cbnRncoHis. pBluescript SKNco(-) was made by altering a *Sma*I site in the multicloning site of pBluscript SK(-) to a *Nco*I site.



Supplementary Figure 2 SDS-PAGE analysis of the purified wild-type CbnR and its mutants.
The proteins were partially purified by His Bind Quick 900 Cartridges (panel A) or a Ni-FTA Fast Start Kit (panels B-F). The molecular weight markers used in panel A and panels B-F were BenchMark Protein Ladder (Invitrogen) and SDS-PAGE Molecular Weight Standards, Low Range (BIO-RAD) respectively. MW, M, C and P represent molecular weight, molecular weight marker, crude extract, and purified protein with the method of present study, respectively. CbnR with label E was purified with the elution buffer supplied by the manufacturer.



Supplementary Figure 3 The nucleotide and amino acid sequence alignment tables of promoters and their cognate LTTRs relevant to the present study.

(A) Nucleotide sequence alignment between *cbnA* and *benA* promoters. BenM residues interacting with backbone and base atoms are indicated by dotted and continuous arrows, respectively. Red and orange residues are those showing less than 25% and 50-100% activities when the corresponding residues in CbnR are replaced with alanine (See Fig. 2). Corresponding residues of CbnR are shown in parentheses. (B) Amino acid sequence alignment between CbnR and BenM. Conserved residues are shown in red.