**Supplementary Table 3**

Plasmid construction details.

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | Size (kb) of DNA fragments after amplificationa | Protein size (aa) | Vector name/  Resistance to | Restriction sites added to amplified DNAb | Changes needed in amplified DNA sequencesc | | | | Experiment |
| Start codon | | Stop codon | |
| From | To | From | To |
| WhiB1 | 249 | 82 | pKT25 (T25)/  Kanamycin  (KanR) | XbaI (TCTAGA) and KpnI (GGTACC) | ATG | - | TGA | - | Protein expression for Bacterial two hybrid system |
| WhiB2 | 267 | 82 | pKT25/  Kanamycin  (KanR) | XbaI (TCTAGA) and KpnI (GGTACC) | GTG | ATG | TGA | - |
| WhiB3 | 300 | 99 | pKT25/  Kanamycin  (KanR) | XbaI (TCTAGA) and KpnI (GGTACC) | ATG | - | TGA | - |
| WhiB7 | 291 | 97 | pKT25/  Kanamycin  (KanR) | XbaI (TCTAGA) and KpnI (GGTACC) | ATG | - | TGA | - |
| SigmaA-CTD  (σA–CTD ) | 243 | 81 | pUT18 (T18)/ Ampicillin (AmpR) | HindIII (AAGCTT) and KpnI (GGTACC) | ATG | - | TGA | CGG  (stop codon removed) |
| SigmaB (σB) | 786 | 261 | pUT18/  Ampicillin (AmpR) | HindIII (AAGCTT) and KpnI (GGTACC) | ATG | - | TGA | CGG  (stop codon removed) |
| SigmaH  (σH) | 663 | 220 | pUT18/  Ampicillin (AmpR) | HindIII (AAGCTT) and KpnI (GGTACC) | ATG | - | TGA | CGG  (stop codon removed) |
| SigmaJ  (σJ) | 951 | 316 | pUT18/  Ampicillin (AmpR) | HindIII (AAGCTT) and KpnI (GGTACC) | ATG | - | TGA | CGG  (stop codon removed) |
| WhiB1 | 249 | 82 | PMyNT/  Hygromycin (Hygro-BR) | NcoI (CCATGG) and HindIII (AAGCTT) | ATG | - | TGA | - | Protein overproduction for biochemical characterization |
| WhiB2 | 267 | 88 | pMyNT/  Hygromycin (Hygro-BR) | NcoI (CCATGG) and HindIII (AAGCTT) | GTG | ATG | TGA | - |

aThe oligonucleotide primers used to amplify the indicated coding regions are provided in online supplementary Table 1.

bThe restriction sites were incorporated into the amplified DNA fragments to facilitate ligation into the indicated vectors (online supplementary Fig. 1).

cChanges to nucleotide sequences of the wild type open reading frame necessary to facilitate ligation into the indicated vectors and remove stop codons to create hybrid genes coding for σ-T18 fusion proteins.