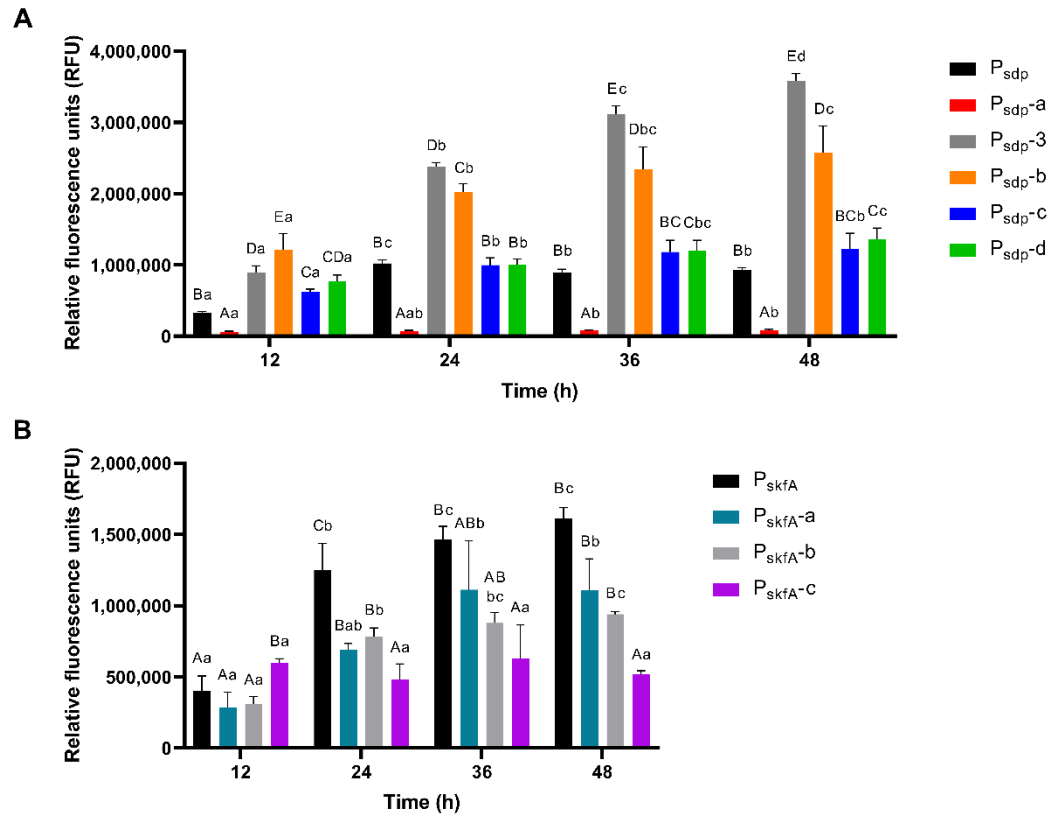
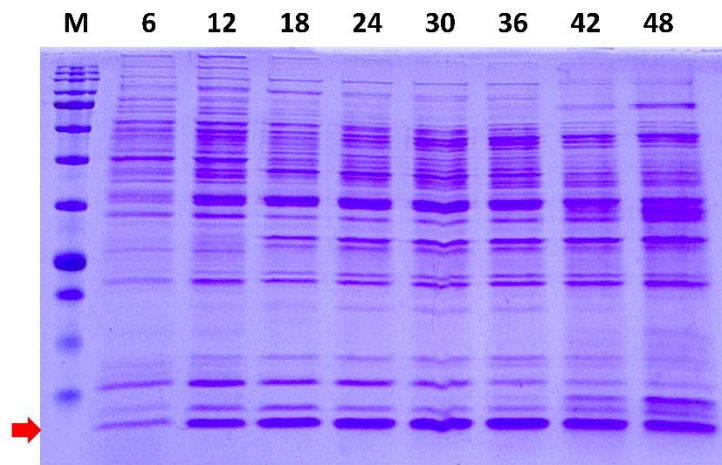


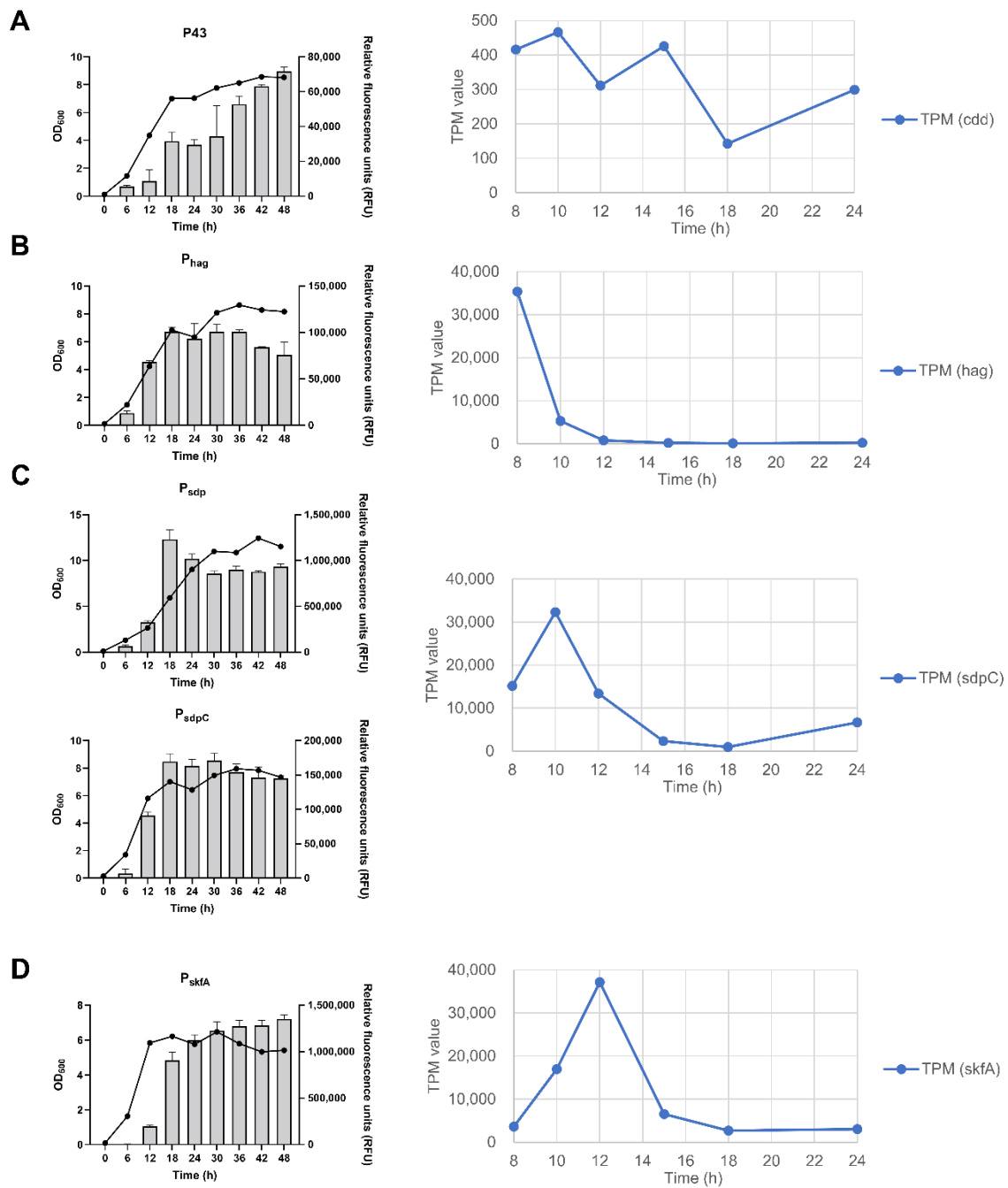
**Figure S1. :** Real-time quantitative reverse transcription PCR validation of genes transcribed by candidate promoters and control gene. The black square represents the TPM value of RNA-seq and the bar represents the fold change of RT-qPCR. RT-qPCR data are presented as the mean  $\pm$  standard deviation ( $n = 3$ ). The relative expression value was normalized to the *rpsJ* gene.



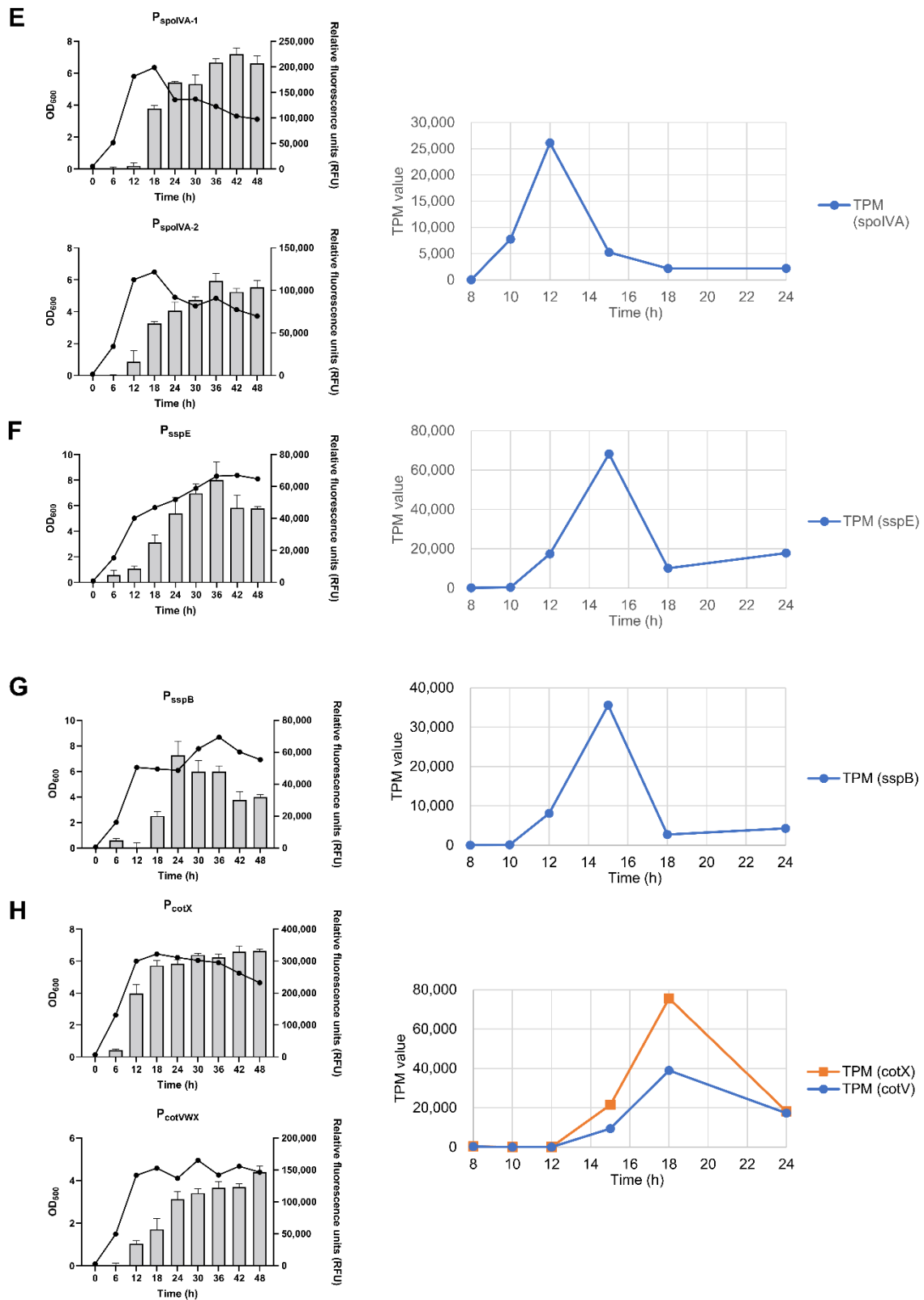
**Figure S2.** Engineering of  $P_{sdp}$  and  $P_{skfA}$  expression cassettes. **A** The eGFP expression level of strains containing  $P_{sdp}$  expression cassette derivatives. **B** The eGFP expression level of strains containing  $P_{skfA}$  expression cassette derivatives. Different lower-case letters denote significant differences between time within each recombinant strain, while different upper-case letters denote significant differences between expression cassettes at each time point ( $P < 0.05$ , ANOVA followed by Duncan's post hoc test).



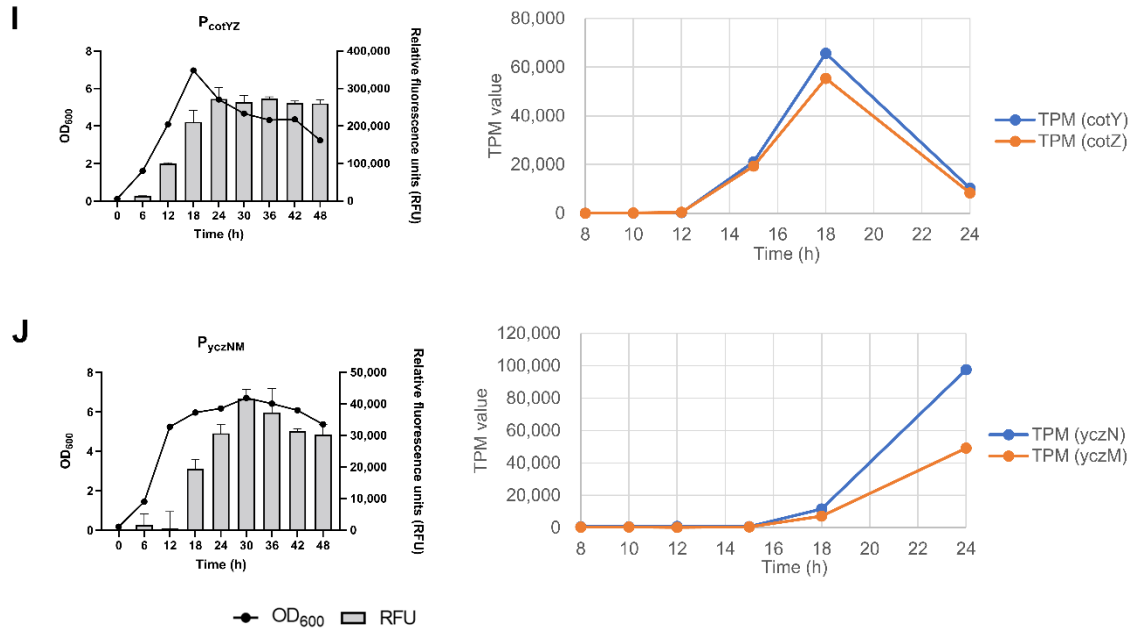
**Figure S3.** Time-course expression of His-hEGF driven by  $P_{sdp-4}$ . lane M, Protein molecular maker; The His-tagged hEGF bands were indicated by red arrows.



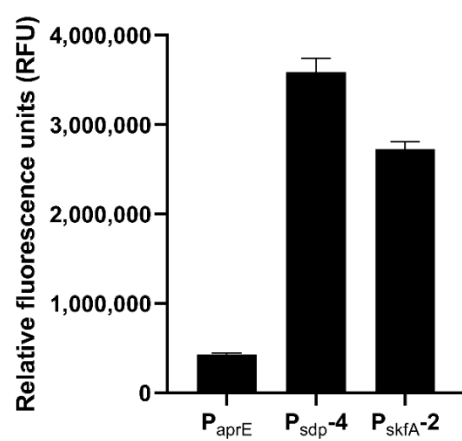
**Figure S4. Cont.**



**Figure S4. Cont.**



**Figure S4.** Expression patterns of eGFP and TPM value. The left panels are the eGFP expression patterns driven by **A** P<sub>43</sub> **B** P<sub>hag</sub> **C** P<sub>sdp</sub> and P<sub>sdpC</sub> **D** P<sub>skfA</sub> **E** P<sub>spoIVA-1</sub> and P<sub>spoIVA-2</sub> **F** P<sub>sspB</sub> **G** P<sub>sspE</sub> **H** P<sub>cotX</sub> and P<sub>cotVWX</sub> **I** P<sub>cotYZ</sub> and **J** P<sub>yczM</sub> and the right panel are the TPM value of their gene.



**Figure S5.** Maximum fluorescence intensities of P<sub>aprE</sub>, P<sub>sdp-4</sub>, and P<sub>skfA-2</sub>.