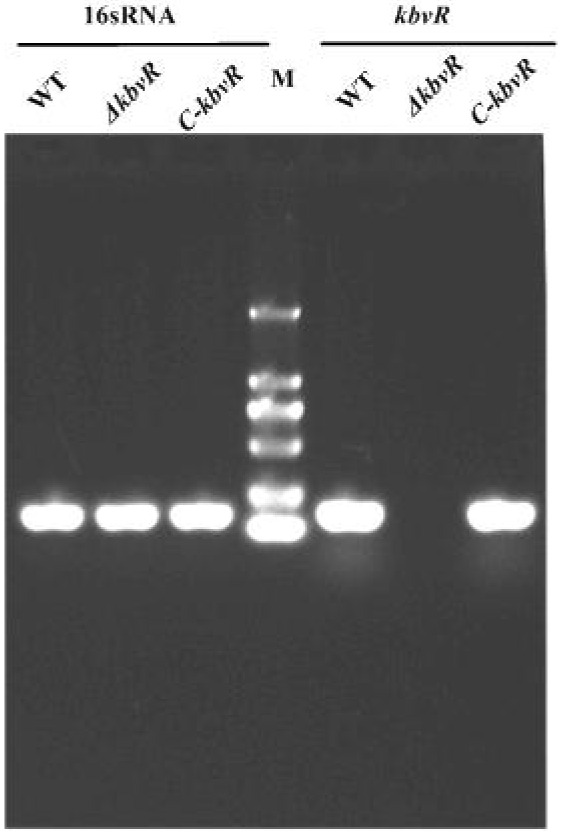
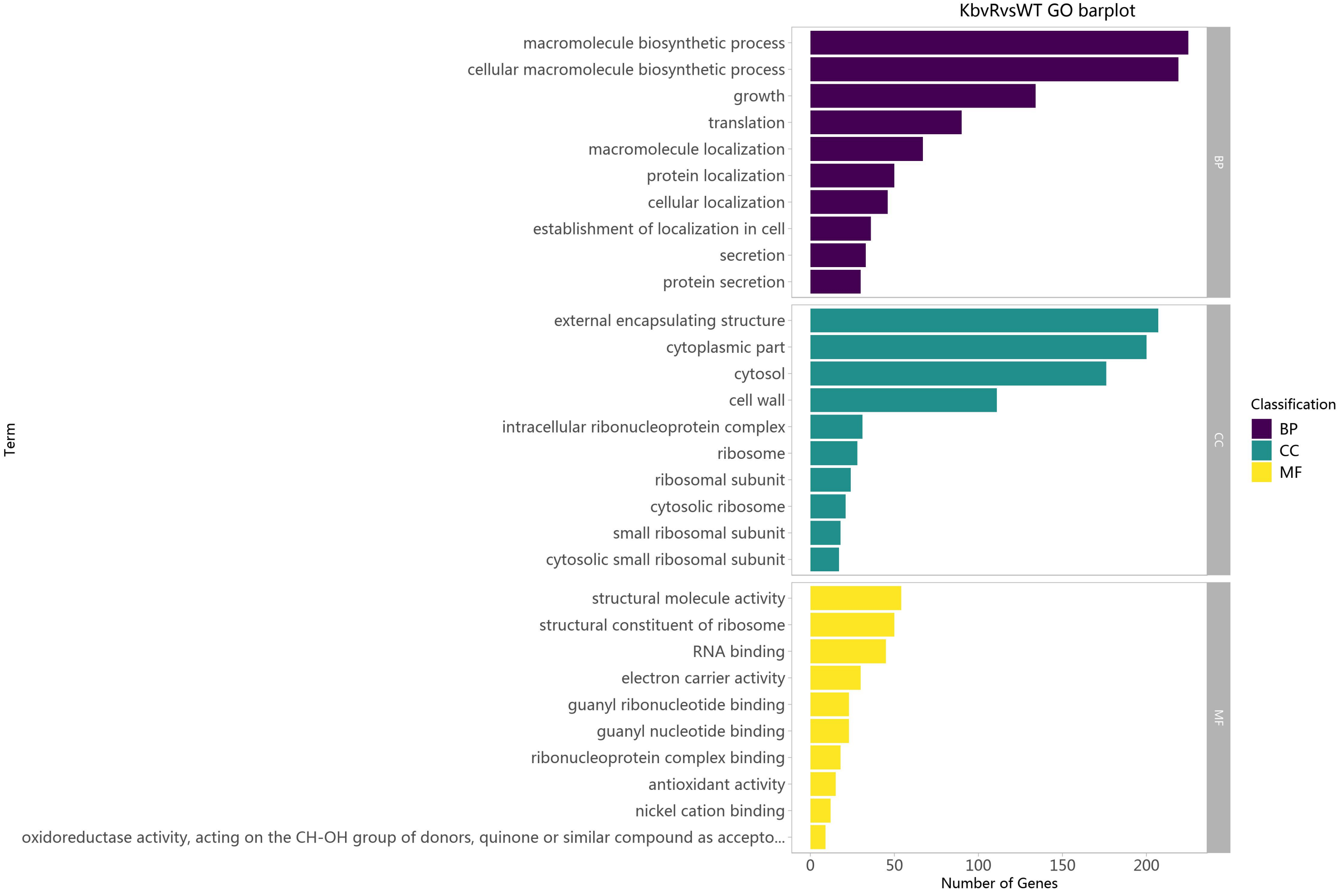
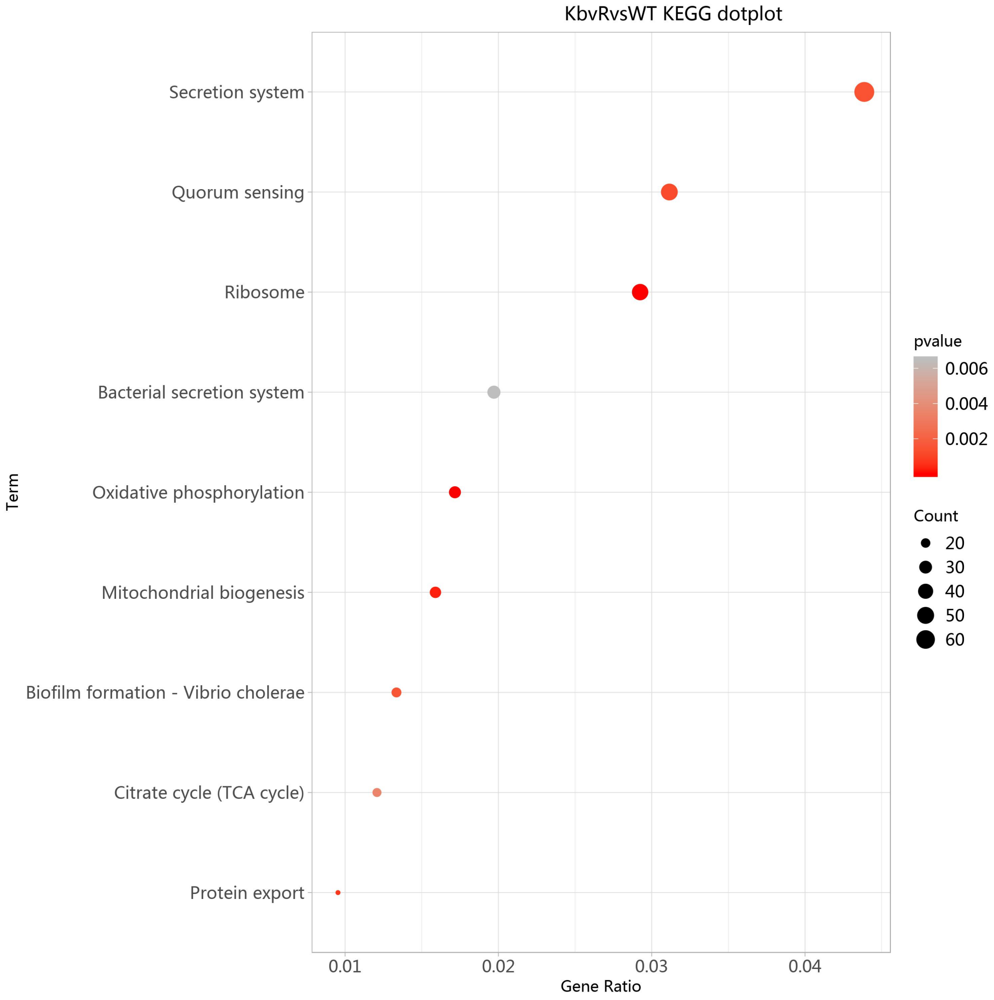
Supplementary Figure S1



Supplementary Figure S2



Supplementary Figure S3



Supplementary Table S1   Bacterial strains and plasmids used in this study

Strains and plasmids	Description
Strains	
K. pneumoniae	
NTUH K-2044 (WT)	Wild-type strain; Ap^r
ΔKbvR	Deletion of *KbvR* from WT; Ap^r
C-KbvR	Complemented *KbvR* mutant; Ap^r ; Km^r
NTUH K-2044 (WT)-GFP	Wild-type strain with pLac-EGFP
ΔKbvR-GFP	Deletion of *KbvR* strain with pLac-EGFP
E. coli DH5α	F- φ 80 lac Z Δ M15 Δ (lac ZYA-arg F)U169 endA1 rec A1 hsd R17(rk-,mk-) sup E44 λ - thi -1 gyr A96 rel A1 pho A
Plasmids	
pKO$_3$-Km	pKO3-derived plasmid, with an insertion of Km resistance cassette from pUC4K into *AccI* site
pGEM-T-easy-km	pGEM-T easy with an insert of Km cassette from pUC4K into NdeI site for trans complementation

Supplementary Table S2 Primers used in this study

Target gene	Primer sequences (forward/reverse, 5'-3')	Purpose
		Construction of mutant
KbvR	GTATGCGGCCGCGTGGCGAGAGCGAAAGC/GTGAATGAATCGTTTTGGGAATAACTTCCCTGTGGGCATT	Amplification of the 640 bp DNA fragment upstream of the 612 bp target deletion region
KbvR	AATGCCCACAGGGAAGTTATTCCCAAAACGATTCATTCAC/GTATGCGGCCGCTTCAACCAACCGTGATGTCC	Amplification of the 584 bp DNA fragment downstream of the 612 bp target deletion region
		Construction of complemented mutant
KbvR	GAGT CCATGGAAAACGAGCCAGAGGTAG/GAGT GTCGACATCAGGGTGGTTAGCATAG	Amplification of 1693bp fragment including the *KbvR* coding region with its promoter-proximal region (889 bp upstream the coding sequence) and transcriptional terminator
		Detection by RT-PCR
KbvR	GGACAATGAACACGCTACCG/CGCCGCAGACGATTGAAC	Amplification of a 165 bp intragenic region of *KbvR*

magA	CGAAAGTGAACGAATTGATGCT/GTTTCTGCTGCAGATTCGAAGA	Amplification of a 121bp intragenic region of *magA*
16S rRNA gene	ATGACCAGCCACACTGGAAC/CTTCCTCCCCGCTGAAAGTG	Amplification of a 151 bp intragenic region of the 16sRNA gene