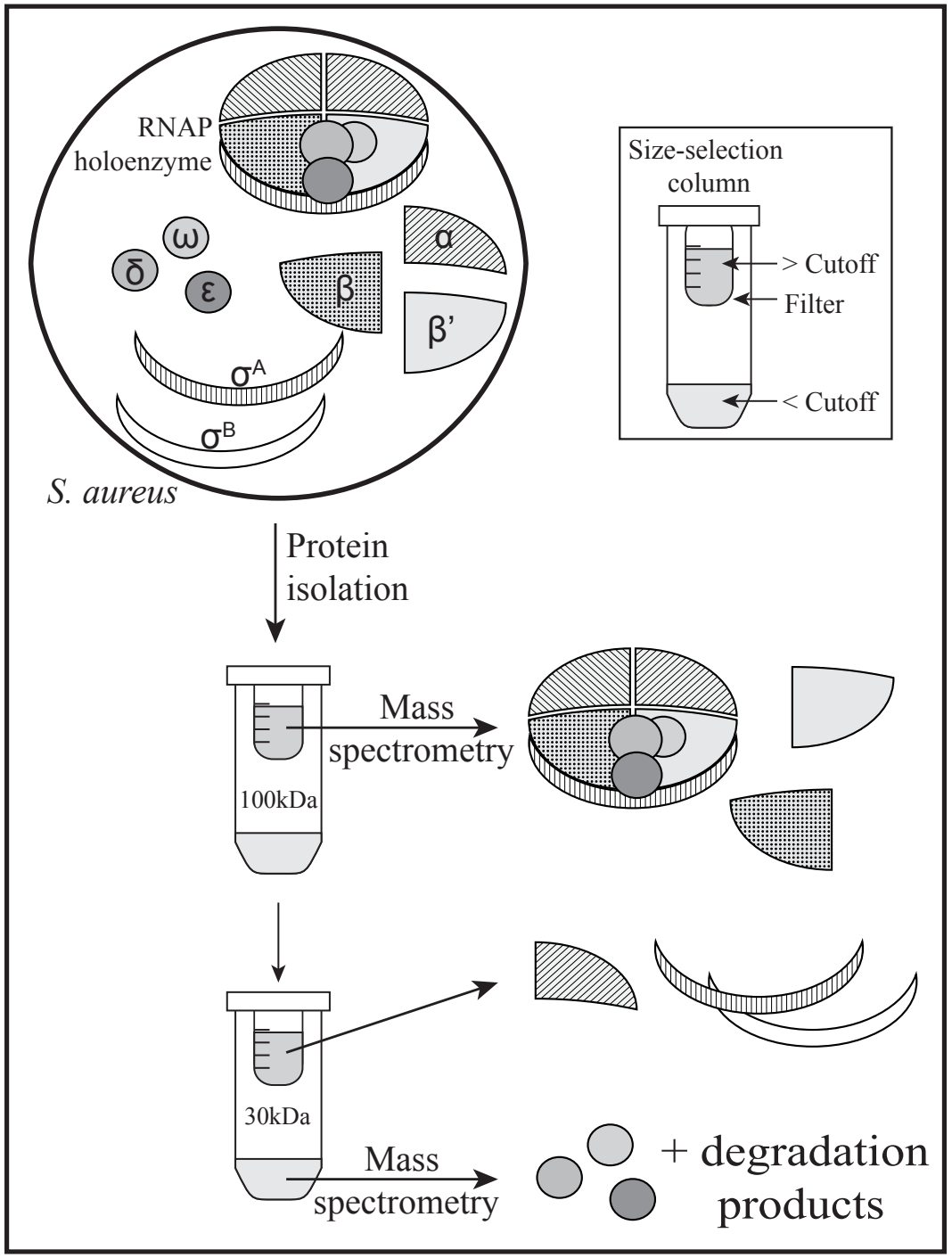
Figure S1: Workflow employed to explore RNAP composition.



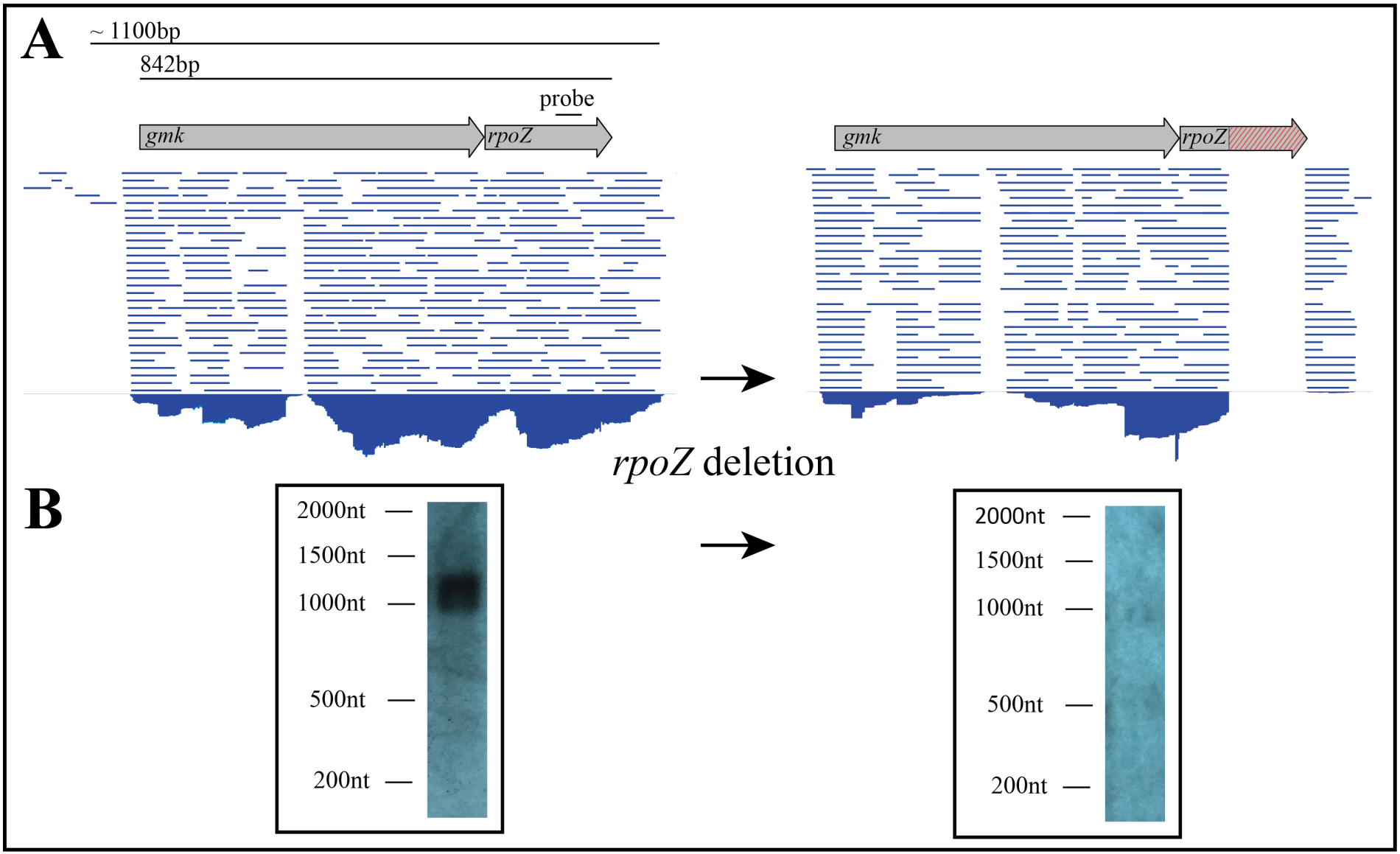


Figure S2: Exploration of the *gmk-rpoZ* operon architecture in *S. aureus*. A) RNA-sequencing analysis, or **B**) Northern blots, of the wild-type and *rpoZ* deletion mutant. The probe used in B is demarcated on the *rpoZ* gene in A. Lines denoting the lengths of 842 bp and ~1100 bp refer to the predicted size of the *gmk-rpoZ* ORF, and the actual length of this transcriptional unit detected by Northern blot, respectively.

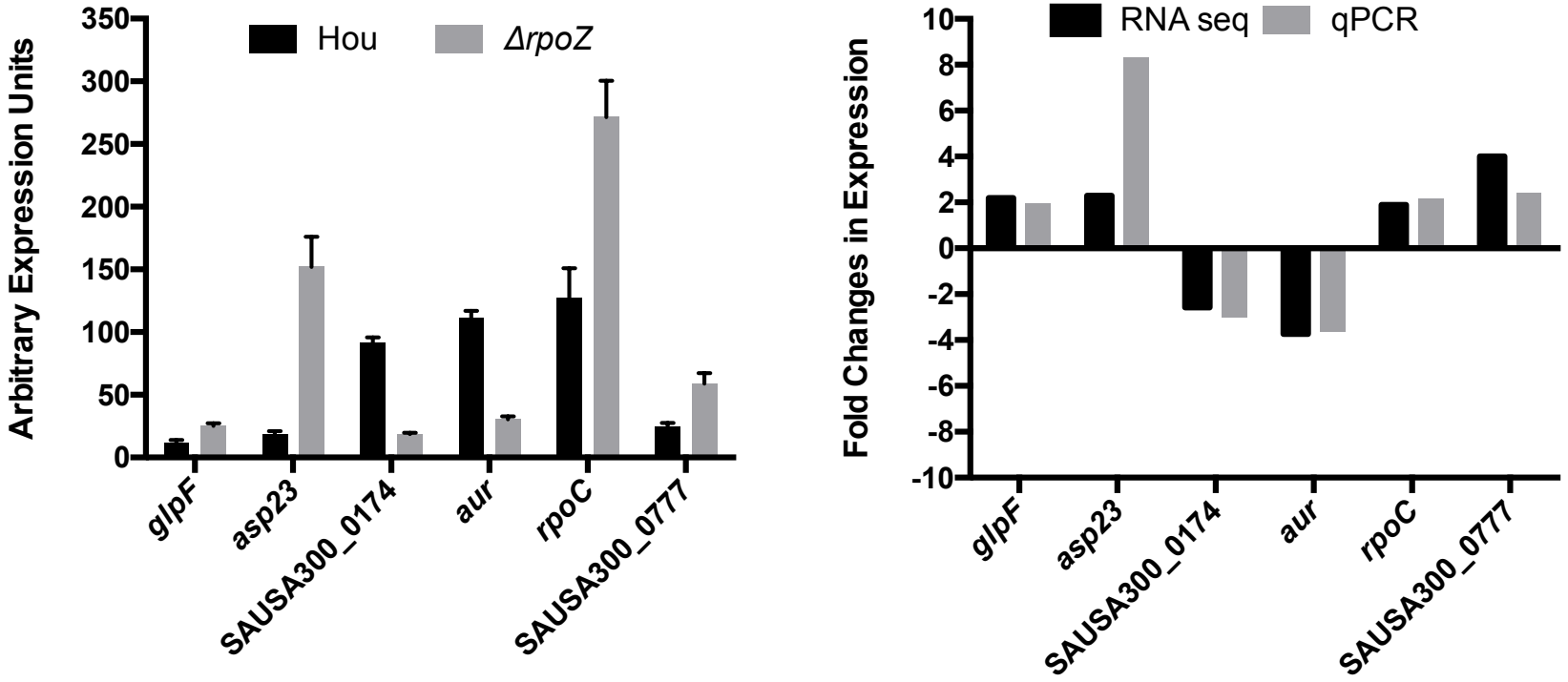


Figure S3: Validation of transcriptional changes from RNA-sequencing experiments using RT-qPCR. A) RNA-sequencing data was confirmed using RT-qPCR analysis for representative genes. Error bars are shown ±SEM. **B)** Fold-changes for RT-qPCR and RNA-sequencing were subsequently compared.

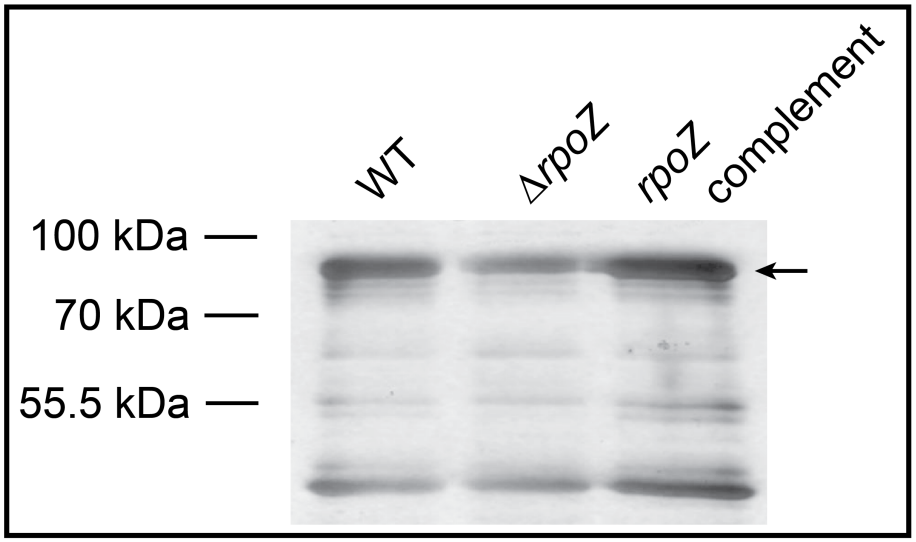


Figure S4: ω affects the abundance *S. aureus* lipases. Secretomes of the *S. aureus* wild-type, Δ*rpoZ* mutant and complemented strains after 24 h of growth were assessed via SDS-PAGE. A black arrow denotes the protein band found to have decreased abundance, which was identified as two different lipases by mass-spectrometric analysis.