Untargeted metabolomics analysis reveals key pathways responsible for the synergistic killing of colistin and doripenem combination against *Acinetobacter baumannii* 

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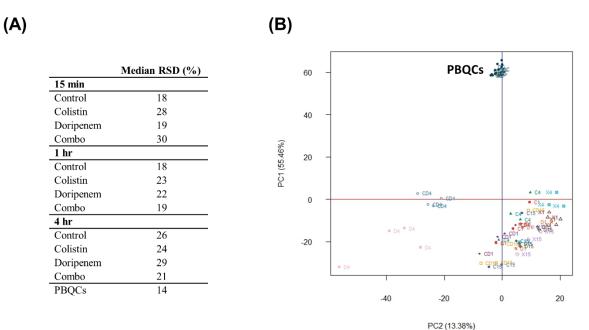
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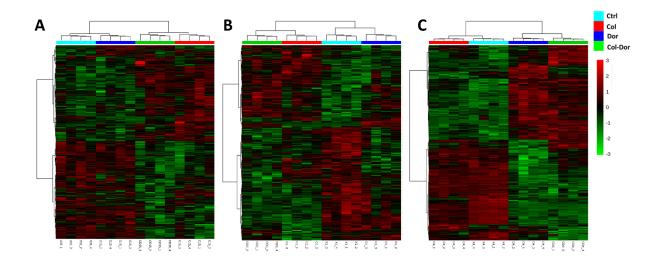
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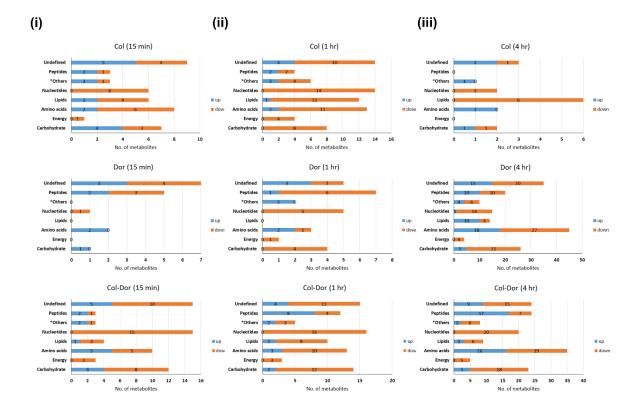
## **Supplementary Information**



Supplementary Figure S1. (A) Data precision of individual samples represented as the median relative standard deviation (RSD) for all metabolites based on all replicates (n=4) of each group (n=11 for technical replicates of PBQCs). (B) PCA score plot of all metabolites of A. baumannii ATCC 19606 treated with colistin and doripenem alone and in combination. Eleven PBQCs were analyzed throughout the LC-MS batch. Each dataset represents four biological replicates of antibiotic-treated and untreated control samples of all the time points. Pooled biological quality controls = PBQCs.



Supplementary Figure S2. Monotherapy and combination of colistin and doripenem induce global metabolic changes. Heatmap profiles with hierarchical clustering of top 600 significantly changed metabolites after treatment with single and combination of colistin and doripenem at (A) 15 min, (B) 1 hr, and (C) 4 hr. Light blue = untreated control (Ctrl); Red = Colistin (Col); Blue = Doripenem (Dor); Green = colistin and doripenem combination (ColDor).  $p \le 0.05$ , FDR  $\le 0.1$ .



Supplementary Figure S3. Summary number of metabolites changes classified according to different metabolite classes after antibiotic treatment at (i) 15 min, (ii) 1 hr, and (iii) 4 hr. Changes  $\geq 1.5$ -log<sub>2</sub>-fold,  $p \leq 0.05$ , FDR  $\leq 0.1$  (one-way ANOVA for multiple comparison).