Supplementary Figure 1) Additional differentially expressed genes from Figure 1. Median and interquartile ranges from pooled analysis between clinical and laboratory isolate transcriptomes. Significant differences determined by Wilcoxon rank-sum test with Benjamini-Hochberg correction (** p-value ≤ 0.001).

Supplementary Figure 2 | Differential expression of valine biosynthesis and degradation pathways. Fold change differential expression analysis across all analyzed transcriptomes in pathways associated with both
KEGG Valine (A) Biosynthesis or (B) Degradation. Red represents areas of the pathway that are more highly transcribed in clinical isolates, and green represents areas that are more highly transcribed in laboratory strains.

Supplementary Table 1 | K. pneumoniae transcriptomic dataset metadata
Supplementary Table 2 | Differential expression analysis summary statistics
Supplementary Table 3 | Complete gene and reaction essentiality results
Supplementary Table 4 | Valine-associated reaction net import flux quantification
Supplementary Table 5 | Flux analysis summary table
Supplementary Table 6 | RNA-Seq mapping summary table