

Supplementary Table S4. Expression experiments considered in this study.

Condition	Experiment	Original strain	Number of upregulated or essential genes	Reference
Bacteremia	RNA-Seq	ATCC 17978	557	[1]
Bloodstream infection (required)	Tn-insertion	ATCC 17978	59	[2]
BALF	Proteomics	AbH12O-A2	50	[3]
Biofilm vs exponential planktonic cells	RNA-Seq	ATCC 17978	35	[4]
Biofilm vs stationary planktonic cells	RNA-Seq	ATCC 17978	116	[4]
Hydrogen peroxide	RNA-Seq	ATCC 17978	155	[5]
Iron limitation	Microarray	ATCC 17978	463	[6]
Macrophage infection	Proteomics	AbH12O-A2	76	[3]
Mucin 0.5%	RNA-Seq	ATCC 19606	232	[7]
Pneumonia (required)	Tn-insertion	ATCC 17978	157	[8]
Rich medium (required)	Tn-insertion	ATCC 17978	453	[8]
Stationary vs exponential planktonic cells	RNA-Seq	ATCC 17978	130	[4]

References

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3. Mendez *et al.* Quantitative proteomic analysis of host--pathogen interactions: a study of *Acinetobacter baumannii* responses to host airways. *BMC Genomics* (2015) 16:422.

4. Rumbo-Feal *et al.* Whole transcriptome analysis of *Acinetobacter baumannii* assessed by RNA-sequencing reveals different mRNA expression profiles in biofilm compared to planktonic cells. *PLoS One*. (2013) 8:e72968.
5. Juttukonda *et al.* *Acinetobacter baumannii* OxyR Regulates the Transcriptional Response to Hydrogen Peroxide. *Infect Immun*. (2018) 87:e00413-18.
6. Eijkelkamp *et al.* Investigation of the human pathogen *Acinetobacter baumannii* under iron limiting conditions. *BMC Genomics*. (2011) 12:126.
7. Ohneck *et al.* Mucin acts as a nutrient source and a signal for the differential expression of genes coding for cellular processes and virulence factors in *Acinetobacter baumannii*. *PLoS One*. (2018) 13: e0190599.
8. Wang *et al.* Genome-wide identification of *Acinetobacter baumannii* genes necessary for persistence in the lung. *mBio*. (2014) 5:e01163-14.