

Supplementary Material 1:

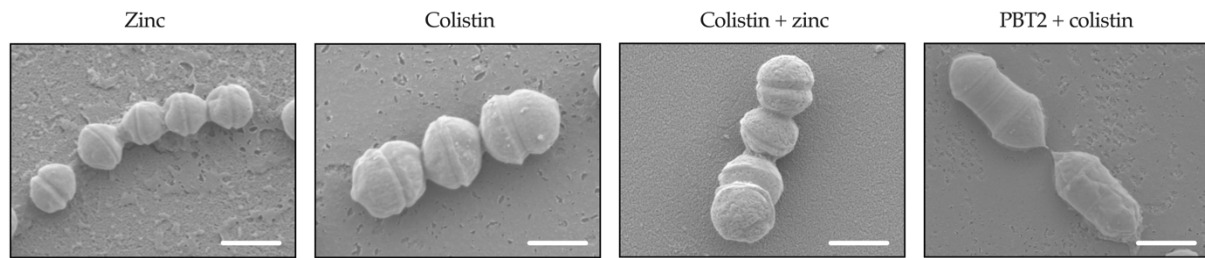


Figure S1. Scanning electron microscopy images of GAS strain 5448 grown in THY media, or in THY media supplemented with combinations of PBT2 (7 μ M), zinc (50 μ M), and colistin (2 μ g/mL) for 24 h at 37°C. White scale bars = 1 μ m. Arrows indicate membrane indentations and membrane ruffling.

Supplementary Material 2:

Table S1. GAS 5448. Mutant chromosomal differences as identified by Illumina whole genome sequencing.

Locus_tag	Gene; Product	Position	Mutation
SP5448_08615	<i>pabB</i> ; aminodeoxychorismate synthase component I	205,511	(TGGCTG) _{1→2}
SP5448_08450	<i>pnp</i> ; polyribonucleotide nucleotidyltransferase	247,553	+GCG
SP5448_07680	<i>mtsR</i> ; metal dependant transcriptional regulator	390,289	Δ 1 bp
SP5448_06655	<i>atpA</i> ; F0F1 ATP synthase subunit alpha	596,049	C→G
SP5448_06005	<i>parC</i> ; DNA topoisomerase IV subunit A	734,072	(TCCTTC) _{1→2}
SP5448_09200	<i>cadX</i> ; Cd ²⁺ Zn ²⁺ -sensing metalloregulatory transcriptional regulator	1,777,811	(T) _{7→6}

Supplementary Material 3:

Table S2. Primers used in this study.

GAS 5448		
Deletion mutation and reverse complementation constructs		
Primer	Sequence 5'→3'	
mntEKO-F1	CCCGGCTCGAGAAACCAATGAACCCGTGGAG	
mntEKO-R1	CAAAGTTGGCGTATAACATATGCAATCGGATCCTGTGTCA	
mntEKO-F2	TGATATTCTCATTTTAGCCATTGCAATCGGATCCTGTGTCA	
mntEKO-R2	CGCGCGAAGCTTTTTACAGCCAACAGACCGTG	
kan-F	ATGGCTAAAATGAGAATATCA	
kan-R	CTAAAACAATTCATCCAGTAA	
Quantitative real-time PCR		
Gene	Primer direction	Sequence 5'→3'
<i>czcD</i>	Fwd	ACCATCCATCGACCAAACAT
<i>czcD</i>	Rev	ATTGCACTTTGCACCATGAA
<i>mntE</i>	Fwd	CCATGATTCCCGAAGAAGAG
<i>mntE</i>	Rev	CATTGCGATCAATCAGTTGG
<i>mtsA</i>	Fwd	CAAACAATTGATTGCAAAGGATCC
<i>mtsA</i>	Rev	GTCTAGTTTTTCCAATTTAGCCACA
<i>gyrA</i>	Fwd	GAAGTGATCCCTGGACCTGA
<i>gyrA</i>	Rev	CCCGACCTGTTTGAGTTGTT