S2 Table: Genotypes of bioreactor-adapted TGC resistant (BTR) clonal strains isolated from the end of adaptation

Run	**Strain**[a]	**MIC_{TGC} (µg/mL)**	**Deletions in 5'UTR of *tetM***	**New Tn916 Insertion Sites**[b]	**Clones**[c]
N/A	S613	0.125	None	None	N/A
1	BTR87a	2.0	Δ87-bp, 51-bp upstream *tetM*	*yycI*	2
1	BTR87b	2.0	Δ87-bp, 51-bp upstream *tetM*	Intergenic site J	1
1	BTR22	2.0	Δ22-bp, 231-bp upstream *tetM*	None	3
1	BTR37	1.0	Δ37-bp, 98-bp upstream *tetM*	*yycI*, Sulfatase, Intergenic sites C, D, H, and I	2
1	BTR0	0.5	None	None	1
2	BTR125a	2.0	Δ125-bp, 36-bp upstream *tetM*	O-antigen ligase[d]	1
2	BTR125b	2.0	Δ125-bp, 36-bp upstream *tetM*	None	3
2	BTR0	0.5	None	None	1

[a] All BTR strains have the $\text{S10}^{\text{R53Q-}\Delta\text{54-58KTHK}}$ allele.

[b] All strains retained the ancestral insertion of Tn916. Strains with multiple copies of Tn916 retained the wildtype sequence at the ancestral site.

[c] Number of clones sequenced with the corresponding genotype.

[d] This copy of Tn916 has an insertion of the IS204 transposon downstream of *tetM*.