

Single-nucleotide polymorphism in the sequence of both adapted strains compared to the original mutant <i>MTLcuaD</i> strain							
Position	Reference base	Observed base	Amino acid change	Effect	Functional class	Localization	Predicted gene product
455589	A	T	NA	Upstream	None	Bw Ccel_R0007 / Ccel_R0008	rRNA-16S / tRNA-Ala
2127097	G	T	NA	Upstream	None	Bw Ccel_1774 / Ccel_R0045	ATP dependant helicase-nuclease subunit A / tRNA-Gln
2127098	C	T	*1249	Synonymous_stop	Silent	Ccel_1774	ATP dependant helicase-nuclease subunit A
2606472	C	G	D380H	Non_synonymous_Coding	Missense	Ccel_2228	Hypothetical protein
2914046	A	C	NA	Upstream	None	Bw Ccel_R0059 / Ccel_R0058	rRNA-16S / rRNA-23S
4055304	A	G	NA	Upstream	None	Bw Ccel_R0088 / Ccel_R0087	rRNA-16S / rRNA-23S
2316753	C	T	G263S	NON_SYNONYMOUS_CODING	MISSENSE	Ccel_1956	cell wall associated hydrolase

Insertions/deletions in the sequence of both adapted strains compared to the original mutant <i>MTLcuaD</i> strain						
Position	Reference base	Observed base	Effect	Functional class	Localization	Gene product
455591	A	Act	Upstream	None	Bw Ccel_R0007 / Ccel_R0008	rRNA-16S / tRNA-Ala
455593	Tgg	T	Upstream	None	Bw Ccel_R0007 / Ccel_R0008	rRNA-16S / tRNA-Ala
2471924	Gga	G	Upstream	None	Bw Ccel_2112 / Ccel_2111	CuaA / CuaB

Additional file 4. Mutations found in the sequence of the adapted *MTLcuaD* mutant strain.

The table reports all single-nucleotide polymorphism (SNP) and insertions/deletions mutations (In/Del) type which were common to two individual *MTLcuaD* mutant strains clones and absent from the *MTLcuaD* mutant strain.(white background), and the mutations that were found only in the mutant strain (grey background). (NA: not applicable ; *: stop codon; Bw: between)