Appendix Table. Deleted coding sequences in RD8 (Mexican strains) of *Mycobacterium ulcerans**

Deleted coding sequences	Functional classification	Description
MUL_2863	Cell wall/cell processes	Conserved mce associated membrane protein
MUL_2864	Cell wall/cell processes	Conserved mce associated membrane protein
Mce3F	Cell wall/cell processes	Mce-family protein Mce3F
lprM	Cell wall/cell processes	Mce-family lipoprotein LprM
mce3D	Cell wall/cell processes	Mce-family protein Mce3D
mce3C	Cell wall/cell processes	Mce-family protein Mce3C
mce3B	Cell wall/cell processes	Mce-family protein Mce3B
mce3A	Cell wall/cell processes	Mce-family protein Mce3A
yrbE3B	Cell wall/cell processes	Conserved hypothetical integral membrane protein, YrbE family, probably part of mce3 operon
yrbE3A	Cell wall/cell processes	Conserved hypothetical integral membrane protein YrbE3A
MUL_2873	Intermediary metabolism	Ferredoxin, Fe-S protein involved in electron transfer
MUL_2874	Conserved hypothetical	Conserved hypothetical protein, has domain identity with ketosteroid isomerase-related proteins
Cyp278A1P	Pseudogene	Cytochrome P450, heme-thiolate monooxygenase
MUL_2876	Regulatory protein	Conserved hypothetical regulatory protein, has weak domain identity with 2-component response regulators
MUL_2877	Intermediary metabolism	Aldehyde dehydrogenase, probably oxidizing aliphatic and aromatic aldehydes
MUL_2878	Conserved hypothetical	Conserved hypothetical protein
mce3R	Regulatory protein	Transcriptional repressor Mce3R, probably TetR-family, repressor of the mce3 operon, probably also has regulatory action on the mce2 operon
MUL_2881	Detoxification	Multidrug transport integral membrane protein Mmr, export of multidrug substrates leading to multidrug resistance
MUL_2882	Conserved hypothetical	Conserved hypothetical protein
MUL_2884	Conserved hypothetical	Conserved hypothetical membrane protein
MUL_2885	Intermediary metabolism	Dehydrogenase/reductase, short-chain type
ribA1	Intermediary metabolism	Riboflavin biosynthesis protein, RibA1
MUL_2887	Intermediary metabolism	Conserved hypothetical oxidoreductase
ephB	Detoxification	Epoxide hydrolase, EphB, acts on epoxides (alkene oxides, oxiranes), involved in xenobiotic detoxification, determines steady-state levels of physiological mediators
MUL_2889	Intermediary metabolism	Oxygenase, probably involved in electron transfer
MUL_2890	Intermediary metabolism	Oxygenase
echA13	Pseudogene	Enoyl-CoA hydratase, EchA13, probably involved in oxidization of fatty acids
fadE17	Lipid metabolism	Acyl-CoA dehydrogenase FadE17, probably involved in lipid degradation
fadE18	Lipid metabolism	Acyl-CoA dehydrogenase FadE18, probably involved in lipid degradation
Tpx	Detoxification	Thiol peroxidase, Tpx, has antioxidant activity, probably removes peroxides
MUL_2895	Intermediary metabolism	Conserved hypothetical oxidoreductase, domain identity with Fe-S oxidoreductases
MUL_2896	IS, prophages	Transposase for IS*2404*
MUL_2897	Pseudogene	Conserved hypothetical protein
MUL_2898	IS, prophages	Transposase for IS*2606*
MUL_2900	Pseudogene	Short-chain fatty acid transporter
MUL_2901	IS, prophages	Transposase for IS*2404*
MUL_2902	Regulatory protein	Transcriptional regulatory protein
MUL_2903	Pseudogene	Conserved hypothetical protein
MUL_2904	Conserved hypothetical	Conserved hypothetical membrane protein
MUL_2905	Intermediary metabolism	Conserved hypothetical protein, contains dihydrofolate reductase domain
MUL_2906	Conserved hypothetical	Conserved hypothetical protein, has weak identity with hydrolase domains
MUL_2907	Conserved hypothetical	Conserved hypothetical protein
MUL_2908	Pseudogene	Dehydrogenase/reductase, short-chain type
MUL_2909	Conserved hypothetical	Conserved hypothetical protein
MUL_2910	Unique hypothetical	Unique hypothetical protein
MUL_2911	Intermediary metabolism	Alpha-L-fucosidase, involved in carbohydrate transport and metabolism
ahpC_1	Detoxification	Alkyl hydroperoxide reductase C protein, AhpC, involved in oxidative stress response
MUL_2913	IS, prophages	Transposase for IS*2606*
MUL_2914	Intermediary metabolism	Metal-dependent hydrolase
MUL_2915	IS, prophages	Transposase for IS*2404*

*RD, regions of difference; IS, insertion sequence. Gray shading indicates categories for which a biological function can be discussed.