

Additional file 4 The Top 10 genes of highly variable genes in *M. abscessus* subsp. *abscessus* and *M. abscessus* subsp. *massiliense*.

<i>M. abscessus</i> subsp	node	domain_summary_url
<i>M. abscessus</i> subsp. <i>abscessus</i>	ANO24454.1	Branched-chain amino acid ABC transporter; Derived by automated computational analysis using gene prediction method: Protein Homology; Belongs to the binding-protein-dependent transport system permease family.
<i>M. abscessus</i> subsp. <i>abscessus</i>	ANO25759.1	Mycofactocin system glycosyltransferase; Derived by automated computational analysis using gene prediction method: Protein Homology.
<i>M. abscessus</i> subsp. <i>abscessus</i>	ANO25761.1	Alpha-hydroxy-acid oxidizing enzyme; Derived by automated computational analysis using gene prediction method: Protein Homology.
<i>M. abscessus</i> subsp. <i>abscessus</i>	ANO25762.1	Mycofactocin radical SAM maturase; Derived by automated computational analysis using gene prediction method: Protein Homology.
<i>M. abscessus</i> subsp. <i>abscessus</i>	ANO25763.1	Mycofactocin system protein MftB; Derived by automated computational analysis using gene prediction method: Protein Homology.
<i>M. abscessus</i> subsp. <i>abscessus</i>	ANO25764.1	Mycofactocin system transcriptional regulator; Derived by automated computational analysis using gene prediction method: Protein Homology.
<i>M. abscessus</i> subsp. <i>abscessus</i>	livF	ABC transporter ATP-binding protein; Derived by automated computational analysis using gene prediction method: Protein Homology.
<i>M. abscessus</i> subsp. <i>abscessus</i>	livH_1 MAB_2625c	Branched-chain amino acid ABC transporter permease; Derived by automated computational analysis using gene prediction method: Protein Homology; Belongs to the binding-protein-dependent transport system permease family.
<i>M. abscessus</i> subsp. <i>abscessus</i>	lptB	ABC transporter ATP-binding protein; Derived by automated computational analysis using gene prediction method: Protein Homology.
<i>M. abscessus</i> subsp. <i>abscessus</i>	mftE	Mycofactocin system creatininase family protein; Derived by automated computational analysis using gene prediction method: Protein Homology.

<i>M. abscessus</i> subsp. massiliense	ANO22843.1	Hypothetical protein; Derived by automated computational analysis using gene prediction method: Protein Homology.
<i>M. abscessus</i> subsp. massiliense	ANO22845.1	Hypothetical protein; Derived by automated computational analysis using gene prediction method: Protein Homology.
<i>M. abscessus</i> subsp. massiliense	ANO22846.1	Hypothetical protein; Derived by automated computational analysis using gene prediction method: Protein Homology.
<i>M. abscessus</i> subsp. massiliense	ANO22847.1	Hypothetical protein; Derived by automated computational analysis using gene prediction method: Protein Homology.
<i>M. abscessus</i> subsp. massiliense	ANO24000.1	Polyketide synthase; Derived by automated computational analysis using gene prediction method: Protein Homology.
<i>M. abscessus</i> subsp. massiliense	mbtB_1	Non-ribosomal peptide synthetase; Derived by automated computational analysis using gene prediction method: Protein Homology.
<i>M. abscessus</i> subsp. massiliense	srfAB_1 MAB_2123	Non-ribosomal peptide synthetase; Derived by automated computational analysis using gene prediction method: Protein Homology.
<i>M. abscessus</i> subsp. massiliense	ANO22848.1	Hypothetical protein; Derived by automated computational analysis using gene prediction method: Protein Homology.
<i>M. abscessus</i> subsp. massiliense	ANO26522.1	AMP-dependent synthetase; Derived by automated computational analysis using gene prediction method: Protein Homology.
<i>M. abscessus</i> subsp. massiliense	mbtB_3 2121C	Thioesterase; Derived by automated computational analysis using gene prediction method: Protein Homology.
