Figure S2. Similarity of 136 \textit{M. agalactiae} CDSs with their best BLAST hits in \textit{M. mycoides} subsp. \textit{mycoides SC} and \textit{M. capricolum} subsp. \textit{capricolum}. Each of the 136 CDS from \textit{M. agalactiae} inherited from the mycoides cluster is represented as a dot positioned in function of the percentage of similarity (amino acid sequence, global alignment) with its best BLAST hit in \textit{M. mycoides} subsp. \textit{mycoides SC} and \textit{M. capricolum} subsp. \textit{capricolum}. Most dots are positioned on the diagonal line, which indicates a similar proximity of the corresponding CDSs with its Bi Directional Best Hit (BDBH) in \textit{M. mycoides} subsp. \textit{mycoides SC} and \textit{M. capricolum} subsp. \textit{capricolum}. However, some CDSs have only a BDBH in \textit{M. mycoides} subsp. \textit{mycoides SC} (blue symbol) or in \textit{M. capricolum} subsp. \textit{capricolum} (green symbol). MSC, \textit{M. mycoides} subsp. \textit{mycoides SC}; MCA, \textit{M. capricolum} subsp. \textit{capricolum}. Detail of the symbols are indicated under the graph.

\* 38 correspond to truncated products