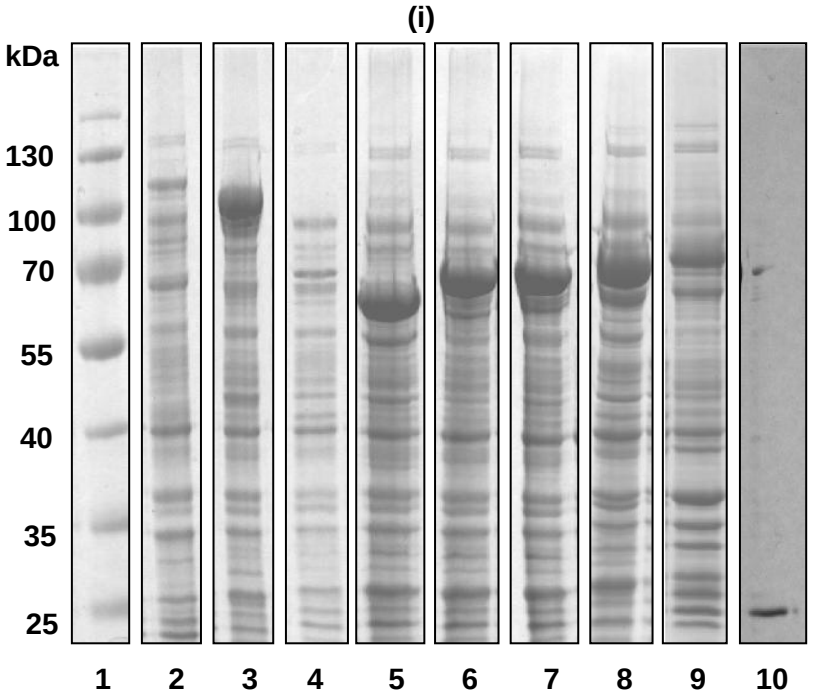
(i)
kDa
130
100
70
55
40
35
25
1
2
3
4
5
6
7
8
9
10

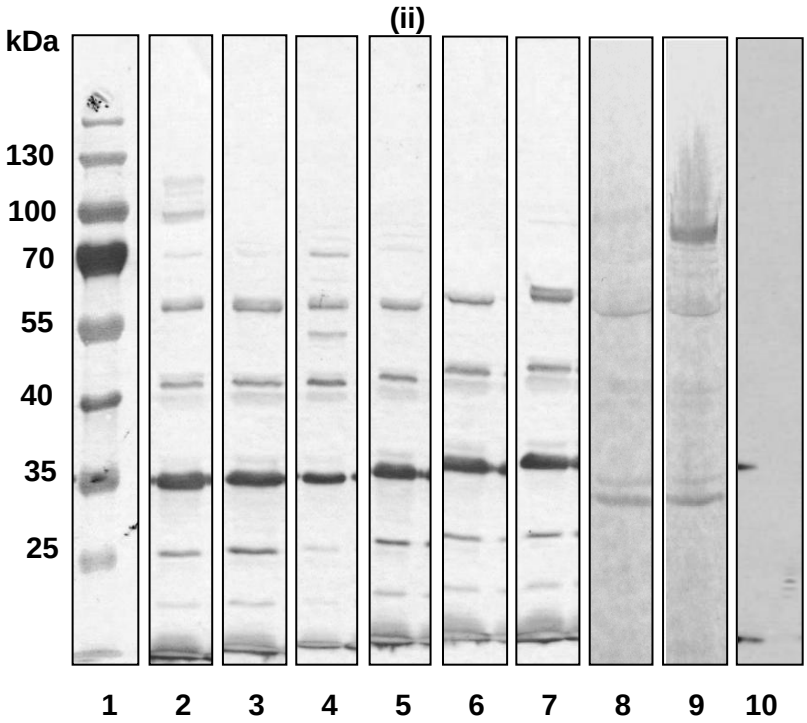
(ii)
kDa
130
100
70
55
40
35
25
1
2
3
4
5
6
7
8
9
10

FIG. S1 Expression of recombinant proteins in *E. coli* JM 109 cells. (i) Whole cell proteins of induced clones stained with Coomassie blue, (ii) Western blots of whole cell proteins of induced clones probed with *M. bovis*-specific calf sera. Lanes: 1, PageRuler prestained protein ladder (Thermo Scientific); 2, pGEX-4T-1-*milA*-AB (125.5 kDa); 3, pGEX-4T-1-*milA*-CD (127 kDa); 4, pGEX-4T-1-*milA*-A (72.8 kDa); 5, pGEX-4T-1-*milA*-B (69 kDa); 6, pGEX-4T-1-*milA*-C (71.9 kDa); 7, pGEX-4T-1-*milA*-D (73.3 kDa); 8, pGEX-4T-1-*milA*-cd (94.3 kDa); 9, pGEX-4T-1-*milA*-ab (92.9 kDa); 10, purified GST (26 kDa).

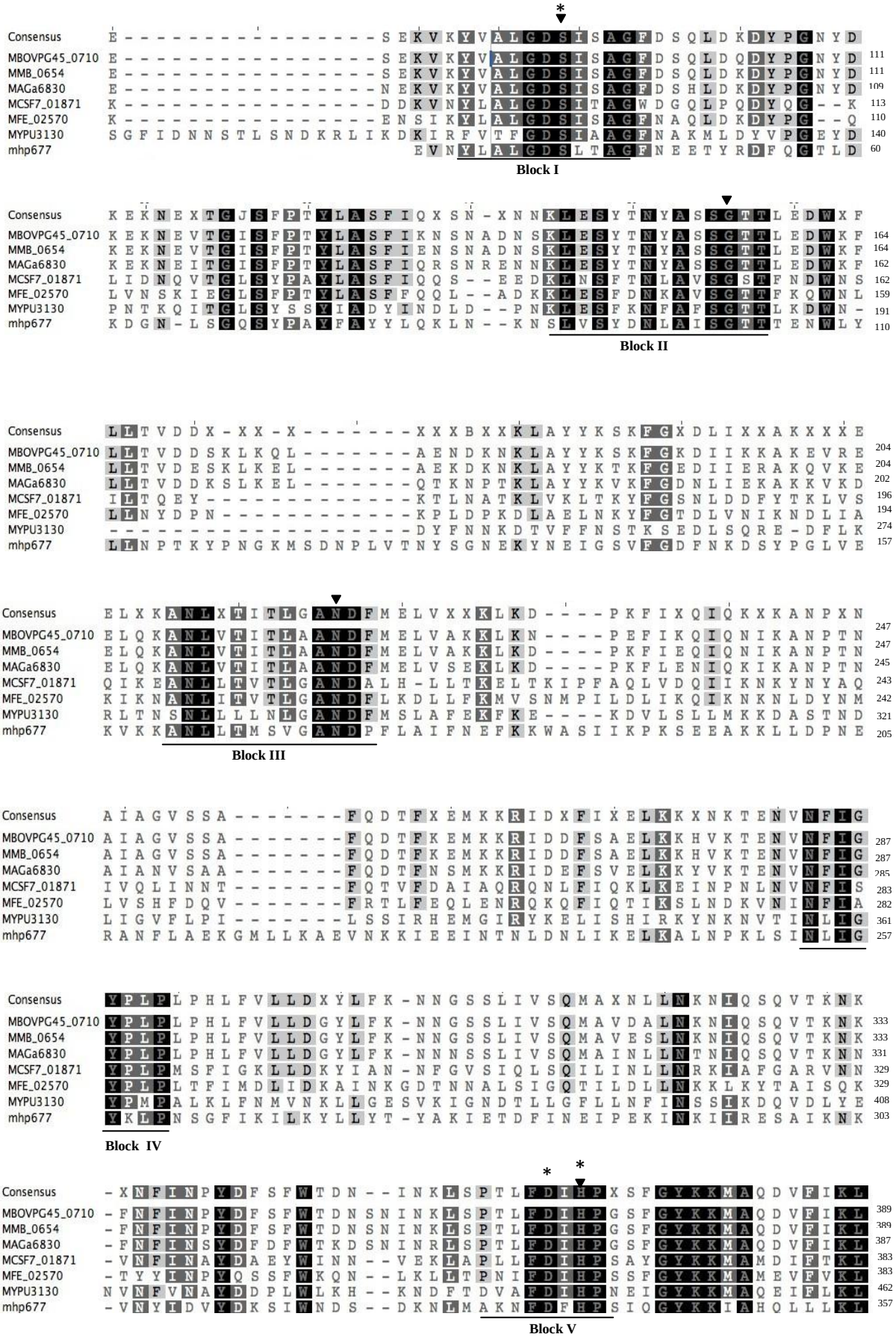
Block I
Block II
Block III
Block IV
Block V

FIG. S2 Multiple sequence alignment of region 1 of mycoplasma immunogenic lipase (MilA) with homologues in other mycoplasmas and the mycoplasma GDSL carboxyesterases.

Numbers on the right indicate the position of the adjacent amino acid. Identical amino acids are shaded black. Grey shading indicates at least one substitution with a very similar amino acid. Light grey shading indicates at least one substitution with a similar amino acid. Dashed lines indicate gaps in the amino acid sequence alignment. GDSL-like lipase conserved sequence blocks are underlined. Asterisks (*) indicate the active site residues and the arrowheads indicate the conserved amino acids of the SGNH_hydrolase family. The sequences included in the alignment are: MBOVPG45_0710 (MilA), *M. bovis* PG45; MMB_0654, *M. bovis* strain Hubei-1; MAGa6830, *M. agalactiae* PG2; MCSF7_01871, *M. columbinum* SF7; MFE_02570, *M. fermentans* JER; MYPU3130, *M. pulmonis*; and mhp677, *M. hyopneumoniae.*