

Table S1.Cytokine expression of dendritic cells after stimulation with OMVs purified from *B. melitensis* 16M and *B. melitensis* VTRM1. The cytokine expression is reported as fold change in mRNA expression

OMVs from <i>B. melitensis</i> VTRM1		OMVs from <i>B. melitensis</i> 16M			
Time (h)	Cytokine fold change IFN γ	Time (h)	Cytokine foldchange IFN γ	P value	P value per group
1	11.27	1	0.4467	0.05	0.05
3	6.111	3	1.007	Ns	
6	0.7433	6	1.537	Ns	
12	7.453	12	5.18	Ns	
Time (h)	Cytokine fold change IL-2	Time (h)	Cytokine fold change IL-2	P value	P value per group
1	19.12	1	0.16	0.05	Ns
3	7.653	3	1.49	Ns	
6	1.243	6	4.52	Ns	
12	8.463	12	8.733	Ns	
Time (h)	Cytokine fold change IL-6	Time (h)	Cytokine fold change IL-6	P value	P value per group
1	61.37	1	0.3567	0.001	Ns
3	7.253	3	5.753	Ns	
6	4.633	6	12.54	Ns	
12	5.267	12	67.37	Ns	
Time (h)	Cytokine fold change IL-12	Time (h)	Cytokine fold change IL-12	P value	P value per group
1	53.83	1	0.2767	0.001	0.05
3	5.6	3	1.653	Ns	
6	1.277	6	6.087	Ns	
12	1.16	12	9.6	Ns	
Time (h)	Cytokine fold change IL-4	Time (h)	Cytokine fold change IL-4	P value	P value per group
1	1.572	1	0.1867	Ns	Ns
3	3.343	3	0.6933	Ns	
6	1.353	6	3.197	Ns	
12	0.1433	12	13.38	Ns	
Time (h)	Cytokine fold change IL-10	Time (h)	Cytokine fold change IL-10	P value	P value per group
1	2.36	1	1.007	Ns	Ns
3	9.457	3	4.62	Ns	
6	4.33	6	25.71	Ns	
12	3.193	12	41.54	Ns	

Time (h)	Cytokine fold change IL-17	Time (h)	Cytokine fold change IL-17	P value	P value per group
1	11.27	1	0.16	0.05	Ns
3	6.09	3	0.44	Ns	
6	0.07667	6	2.24	Ns	
12	7.453	12	14.54	Ns	
Time (h)	Cytokine fold change TNF α	Time (h)	Cytokine fold change TNF α	P value	P value per group
1	71.5	1	0.8109	0.05	0.001
3	100.7	3	2.778	0.05	
6	56	6	11.2	0.05	
12	59.33	12	19.17	Ns	
Time (h)	Cytokine fold change TGF β	Time (h)	Cytokine fold change TGF β	P value	P value per group
1	26.5	1	0.1754	0.01	Ns
3	4.145	3	0.04006	Ns	
6	3.295	6	4.862	Ns	
12	13.71	12	10.74	Ns	
Time (h)	Cytokine fold change IL-23	Time (h)	Cytokine fold change IL-23	P value	P value per group
1	18.96	1	0.0003104	0.05	Ns
3	0.1574	3	0.001534	Ns	
6	0.06513	6	0.1167	Ns	
12	1.736	12	0.2051	Ns	

Table S2. *B. melitensis* 16M OMVs proteins identified by 1D-SDS-PAGE coupled to LC-MS/MS

Gel section	Protein	Gene	Accession number (a.a)	Score (%) [*]	Coverage (%) ^{**}
1	Bacterial surface antigen	<i>omp1</i>	YP_221860	71	4
	Iron-Regulated outer membrane protein FRPB	<i>bhuA</i>	NP_541082	100	13
	Metal chelate outer membrane receptor	ND	NP_539574	90	3
2	Sugar binding protein	<i>sp39</i>	NP_541568	90	7
	Outer surface protein	ND	YP_223106	91	18
	D-Ribose binding periplasmic protein precursor	<i>rbsB</i>	NP_541413	99	50
	Hypothetical protein BMEI0542	ND	NP_539459	99	42
3	25 kDa outer-membrane immunogenic protein precursor	<i>omp2b</i>	NP_539924	99	28
	25 kDa outer-membrane immunogenic protein precursor	<i>omp25</i>	NP_540166	100	19
	25 kDa outer-membrane immunogenic protein precursor	<i>omp25c</i>	NP_540746	96	18
	25 kDa outer-membrane immunogenic protein precursor	<i>omp25d</i>	NP_540747	99	50
	31 kDa outer-membrane immunogenic protein precursor	<i>omp31</i>	NP_541822	99	32
	BP26	<i>bp26</i>	ABC17803	91	10
	Protein YBIS precursor	ND	AAL52550.	100	22
	OmpA family protein	<i>ompA</i>	NP_698208	99	17
	Ribosome recycling factor	<i>frr</i>	NP_698164	100	38
4	22 kDa outer-membrane immunogenic protein precursor	<i>omp22</i>	NP_539634	100	43
	DNA starvation/stationary phase protection protein Dps	<i>dps</i>	NP_699124	100	25
	Hypothetical lipoprotein	ND	NP_539702	90	14
	Hypothetical Membrane Associated Protein (BMEII0692)	<i>ialB</i>	NP_541670	90	14
5	Invasion protein B	<i>invB</i>	YP_221125	53	12
	Peptidoglycan-associated lipoprotein	<i>omp16</i>	NP_539257	99	40
	Chain A , -Cu-Zn superoxide dismutase	<i>sodC</i>	2AQM_A	100	48
	Co-chaperonin GroES	<i>groES</i>	NP_542025	99	42
	Thioredoxin C-1	<i>trxC</i>	NP_540939	98	16
	Outer membrane lipoprotein	<i>omp19</i>	NP_539053	97	26
6	DNA-binding protein HU	<i>hu</i>	YP_221813	95	20
	Hypothetical lipoprotein	ND	YP_221486	100	43
	Hypothetical protein BMEI0287	ND	NP_539204	100	50

ND. None designated

* The percentage of detection is the value assigned on the identity of a protein. **The percentage of coverage corresponds to the length of the sequence covering by the peptides obtained in the LC-MS/MS for this sequence.

Table S3. *In silico* analyses of proteins and annotation of identified vesicular proteins based on hypothetical function by software database (ProLinks and Gene Ontology).

Identified protein	Antigenic region	I. P.	*Signal peptide	Related to (with ProLinks)	GO terms (Process or function)
Bacterial surface antigen	[+7.627]:SGRRLRDVI; [+5.862]:ETLRRFYYN; [+4.107]:LSAGFDVFR	5.37	Yes	Membrane proteins	Membrane, transmembrane, outer membrane
Iron-Regulated outer membrane protein FRPB	[+6.969]:PGKTFGARI; [+3.994]:AGASRTWLG [+4.461]:APGRFTFQ	5.54	Yes	Membrane proteins	Membrane, transmembrane, outer membrane
Metal chelate outer membrane receptor	[+6.223]: RTASATSGS; [+6.164]: LQGSFNFAL [+5.277]: QYDATAPAF; [+8.431]: TIDYDETGR	5.00	No	Membrane proteins	Receptor, transporter, membrane
Sugar binding protein	[+5.349]:IESPAFQSA; [+11.014]: AIYDVVTRQ	4.97	Yes	Sugar transport	Sugar transport, periplasmic
Outer surface protein	[+5.263]:GAGIGAAYV; [+4.550]:YGYDEQDRQ [+4.643]:VINQYQQGA	5.28	Yes		Membrane, transmembrane, outer membrane
D-Ribose binding periplasmic protein precursor	[+10.821]:AANIPVFLI; [+4.572]:ANIPVFLIN [+2.382]:ANWDRTQGH	5.60	No	Sugar transport	D-ribose transport, outer membrane-bounded periplasmic space, sugar binding
Hypothetical protein BMEI0542	[+3.159]:SKVEWTDPF; [+3.446]:DINDRWNI F [+4.666]:DIGGFGAGT	4.83	Yes		
25 kDa outer-membrane immunogenic protein precursor	[+5.837]:GVDSKLRWS; [+3.644]:DFSVVDGDL	4.72	Yes	Membrane proteins	Membrane, transmembrane, outer membrane
25 kDa outer-membrane immunogenic protein precursor	[+3.213]:WAGGYTGLY; [+12.005]:NYDLAGTTV	8.58	Yes		Membrane, transmembrane, outer membrane
25 kDa outer-membrane immunogenic protein precursor	[+2.813]:ATGANAADA; [+2.005]:APVVVAPTF	4.78	Yes	Membrane proteins	Membrane, transmembrane, outer membrane
25 kDa outer-membrane immunogenic protein precursor	[+4.891]:EPAPIAIAP; [+4.062]:NNLKKSRDF	9.28	Yes	Membrane proteins	Membrane, transmembrane, outer membrane
31 kDa outer-membrane immunogenic protein precursor	[+5.082]:KHPFSSFDK; [+4.300]: RLGYTATER	5.21	Yes	Membrane proteins	Membrane, transmembrane, outer membrane
BP26	[+1.069]: TMLAAAPDN**	7.93	Yes		Periplasmic space
Precursor YBIS protein	[+2.858]:KRQWPRWP; [+8.867]:ALYIFKDGGK	8.49	No		
OmpA family protein	[+4.455]:GAGIGALGG; [+2.212]:DTDQDQVKS	9.55	Yes		Outer membrane component, transmembrane
Hypothetical lipoprotein	[+6.979]: RGGWFNNQ; [+7.882]: DAIHFIGWY [+5.847]:ADAIHFIGW	10.48	Yes		Lytic endotransglycosylase activity
Ribosome recycling factor	[+4.144]:RIAARHVRR	5.98	No	Translation	Translation, translation termination
Hypothetical membrane-associated protein(BMEII0692)	[+2.166]: MLASATMPA; [+2.363]: PNPIPVALT	9.00	No		
22 kDa outer membrane protein precursor	[+7.382]: QVNGIEQRN	8.59	No	Membrane proteins	Membrane, transmembrane, outer membrane
DNA starvation/stationary phase protection protein Dps	[+7.137]: ITKQAHWNL; [+8.278]: RLKPYPPTDI [+4.828]: LKPYPPTDIY	5.25	No	Aminoacid transport	Metal ion binding, redox activity, ferric iron binding
Peptidoglycan associated lipoprotein	[+8.084]: ASKKNLPNN; [+3.394]: RTISYGNER	9.92	Yes	Toluene transport	Membrane, transmembrane, outer membrane
Invasion protein B	[+4.700]:KIDDTAGPNN; [+2.813]:QETYQDWTV	8.98	Yes		Membrane
Outer membrane lipoprotein	[+5.631]: ASAPDLTPG; [+4.541]: ISKASLLSL [+4.923] : LLSSLAAAGI	8.91	Yes		Membrane, transmembrane, outer membrane
Chain A, Cu-Zn superoxide dismutase	[+1.343]: TGPGKEVGT**	6.11	No		Ion binding, redox activity
Thioredoxin C-1	[+10.205]:WAEWCGPK; [+3.554]: MFKDGEA	4.53	No	A transketolase	Cellular protein metabolic process, generation of precursor metabolites and energy, nucleotide metabolic process
Co-chaperonin GroES	[+4.231]:VRRVESEAK	5.41	No		Protein folding, chaperone binding, chaperone regulator activity
DNA binding protein HU	[+1.540]: AEKGGLTKA**	9.77	No	The primosome	DNA binding
Hypothetical lipoprotein	[+2.847]: AGGAIIGGI	10.50	Yes		
Hypothetical protein BMEI0287	[+2.729]: RTAGYGVGG	9.02	Yes		

I. P. Isoelectric point.

*Signal P: used for the identification of the signal peptide into the protein sequence.

** Unique antigenic region into the sequence.