

## Supplimentary Data

**Supplementary Table 1.** Details on sources of *Brucella melitensis* isolates and studies performed.

Sample	Source	Study
Bm IND1	Aborted goat fetus	MLST and whole genome analysis
Bm IND2	Vaginal swab of aborted goat	MLST
Bm IND3	Stomach content of aborted sheep fetus	MLST
Bm IND4	Vaginal swab of aborted sheep	MLST

**Supplementary Table 2.** SNPs identified using Next Generation Sequencing (NGS) data of Bm IND1 against completely sequenced *B. melitensis* strains. Only well-defined and characterized genome sequences of *B. melitensis* strains were used for the purpose of selecting closely related reference genome for Bm IND1.

<b>B. melitensis strains</b>	<b>Number of SNPs</b>
<i>Brucella melitensis</i> 16M	2976
<i>Brucella melitensis</i> M28	330
<i>Brucella melitensis</i> M5-90	442
<i>Brucella melitensis</i> NI	474
<i>Brucella melitensis</i> ATCC 23457	280
<i>Brucella melitensis</i> ether	3000
<i>Brucella abortus</i> 2308	6588

17 **Supplementary Table 3.** Repertoire of protein coding genes in different strains of *B. melitensis*  
18 and one *B. abortus* strain.

S. No	Organism	GenBank Assembly ID	Number of gene
1	<i>Brucella melitensis</i> bv. 1 str. 16M	GCA_000007125.1	3198
2	<i>Brucella melitensis</i> ATCC 23457	GCA_000022625.1	3136
3	<i>Brucella melitensis</i> bv. 1 str. Rev.1	GCA_000158695.1	3220
4	<i>Brucella melitensis</i> bv. 3 str. Ether	GCA_000158735.1	3237
5	<i>Brucella melitensis</i> bv. 1 str. 16M (1)	GCA_000160295.1	3083
6	<i>Brucella melitensis</i> bv. 2 str. 63/9	GCA_000182235.1	3207
7	<i>Brucella melitensis</i> M28	GCA_000192725.1	3363
8	<i>Brucella melitensis</i> M5-90	GCA_000192885.1	3360
9	<i>Brucella melitensis</i> NI	GCA_000227645.1	3229
10	<i>Brucella melitensis</i> F15/06-7	GCA_000365845.1	3154
11	<i>Brucella melitensis</i> B115	GCA_000365865.1	3144
12	<i>Brucella melitensis</i> UK22/06	GCA_000366585.1	3091
13	<i>Brucella melitensis</i> CNGB 1076	GCA_000366625.1	3140
14	<i>Brucella melitensis</i> 64/150	GCA_000366845.1	3147
15	<i>Brucella melitensis</i> 66/59	GCA_000366865.1	3143
16	<i>Brucella melitensis</i> CNGB 1120	GCA_000366885.1	3143
17	<i>Brucella melitensis</i> CNGB 290	GCA_000366905.1	3138

18	<i>Brucella melitensis</i> F10/05-2	GCA_000366925.1	3167
19	<i>Brucella melitensis</i> F2/06-6	GCA_000366945.1	3147
20	<i>Brucella melitensis</i> F3/02	GCA_000366965.1	3139
21	<i>Brucella melitensis</i> F5/07-239A	GCA_000366985.1	3153
22	<i>Brucella melitensis</i> F6/05-6	GCA_000367005.1	3140
23	<i>Brucella melitensis</i> R3/07-2	GCA_000367025.1	3152
24	<i>Brucella melitensis</i> UK19/04	GCA_000367045.1	3144
25	<i>Brucella melitensis</i> BG2 (S27)	GCA_000370625.1	3139
26	<i>Brucella melitensis</i> F1/06 B10	GCA_000370645.1	3146
27	<i>Brucella melitensis</i> F10/06-16	GCA_000370665.1	3143
28	<i>Brucella melitensis</i> F8/01-155	GCA_000370685.1	3147
29	<i>Brucella melitensis</i> F9/05	GCA_000370705.1	3144
30	<i>Brucella melitensis</i> UK14/06	GCA_000370725.1	3144
31	<i>Brucella melitensis</i> UK22/04	GCA_000370745.1	3158
32	<i>Brucella melitensis</i> UK23/06	GCA_000370765.1	3137
33	<i>Brucella melitensis</i> Uk24/06	GCA_000370785.1	3147
34	<i>Brucella melitensis</i> UK29/05	GCA_000370805.1	3156
35	<i>Brucella melitensis</i> UK3/06	GCA_000370825.1	3152
36	<i>Brucella melitensis</i> UK31/99	GCA_000370845.1	3164
37	<i>Brucella melitensis</i> UK37/05	GCA_000370865.1	3147

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38	<i>Brucella melitensis</i> 02-7258	GCA_000479975.1	3151
39	<i>Brucella melitensis</i> 02-5863-1	GCA_000480095.1	3151
40	<i>Brucella melitensis</i> 11-1823-3434	GCA_000480215.1	3156
41	<i>Brucella melitensis</i> bv. 3 str. Ether (1)	GCA_000740355.1	3090
42	<i>Brucella melitensis</i> bv. 2 str. 63/9	GCA_000740395.1	3118
43	<i>Brucella melitensis</i> bv. 1 str. 16M (2)	GCA_000740415.1	3110
44	<i>Brucella melitensis</i> Human/CT/US/1995	GCA_000988815.1	3024
45	<i>Brucella melitensis</i> Bme20236	GCA_001431745.1	3155
46	<i>Brucella melitensis</i> BRUC048	GCA_001608355.1	2994
47	<i>Brucella melitensis</i> BRUC101	GCA_001608425.1	3000
48	<i>Brucella melitensis</i> bv. 3 IND1	In this study	3313
49	<i>Brucella melitensis</i> biovar Abortus 2308	GCA_000054005.1	3034

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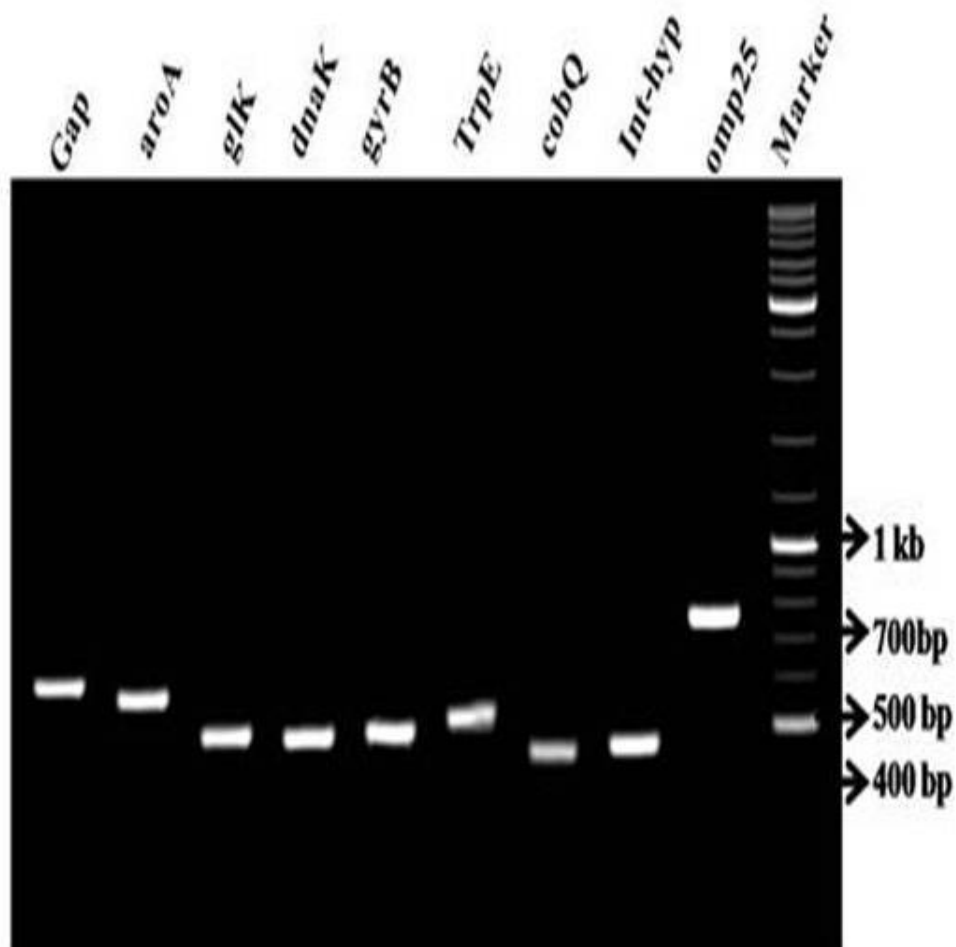
27 **Supplementary Table 4.** VNTRs detected in the genome of Bm IND1 and their comparison with other *B.melitensis* strains.

ID	Locus	Copy number			Consensus Size	Consensus Sequence
		BmIND1	Bm 28	Bm ADMAS-G1		
<b>VNTR-01</b>	chr1:1036719	2.5	2.5	2.5	11	CAGCGACAGGC
<b>VNTR-02</b>	chr1:105775	2.1	2.1	NA	19	CGCTTCCTTCAACCGCGAT
<b>VNTR-03</b>	chr1:107329	2.8	2.8	NA	12	ATGAAACCCGCA
<b>VNTR-04</b>	chr1:1085260	3.3	3.3	3.3	15	TTGAAGTTGCCAATA
<b>VNTR-05</b>	chr1:1085272	2.8	2.8	2.8	15	ATATTGAAATTGCCA
<b>VNTR-06</b>	chr1:1141914	1.9	1.9	NA	16	CGCTGGCGCTTTCATG
<b>VNTR-07</b>	chr1:1142833	2	2	NA	21	GTATGGTAAGTGACGCAAGCT
<b>VNTR-08</b>	chr1:1184601	2.8	2.8	NA	18	GAACAGAATGATTGGCCA
<b>VNTR-09</b>	chr1:1185243	2.2	2.2	NA	18	GATGAAGATTTCTTCAAC
<b>VNTR-10</b>	chr1:1206886	2.4	2.4	NA	18	AAGAAGGCGGCGCCGAAG
<b>VNTR-11</b>	chr1:1221963	2	2	NA	14	GCGGATAGTTTTTC
<b>VNTR-12</b>	chr1:1260282	1.9	1.9	1.9	15	GCCCCTGTGATTTTC
<b>VNTR-13</b>	chr1:1283476	2.4	3.4	NA	12	GGCAACAGCAAG
<b>VNTR-14</b>	chr1:1289514	2	2	NA	13	GCATTGCTTCGGG
<b>VNTR-15</b>	chr1:1322149	2.1	2.1	2.1	15	GGCGCTGCTGATGGC
<b>VNTR-16</b>	chr1:134832	2.9	2.9	NA	15	CGGAGGACATGGTGG
<b>VNTR-17</b>	chr1:147602	1.9	1.9	NA	18	GACCATCATCACGACCAT
<b>VNTR-18</b>	chr1:1575849	1.9	1.9	NA	20	TAGAGCATTTCCAGCAAATC
<b>VNTR-19</b>	chr1:1632045	2	2	NA	15	GGCGATCACAAGGGC
<b>VNTR-20</b>	chr1:164304	3.3	3.3	NA	12	TGATCGTGATGA
<b>VNTR-21</b>	chr1:1676829	2	2	NA	15	GCGTCTGGGTTTCGG
<b>VNTR-22</b>	chr1:1733517	1.9	1.9	NA	16	TCCCCTACTCCCTTAT
<b>VNTR-23</b>	chr1:1733551	4.2	4.2	NA	8	TACTGCCT
<b>VNTR-24</b>	chr1:1733554	2.1	2.1	NA	16	TGCCTTACTGCCCTAT
<b>VNTR-25</b>	chr1:1763142	2.8	2.8	NA	13	TGGCTAACCTTTC

<b>VNTR-26</b>	chr1:1942686	3.2	2.2	NA	12	GCGGGTAAACGG
<b>VNTR-27</b>	chr1:2031740	2.6	2.6	2.6	15	CGATTCTGGTTGCCA
<b>VNTR-28</b>	chr1:209539	2	2	NA	14	GAATTGCAAATGGC
<b>VNTR-29</b>	chr1:2104903	2	NA	2	15	CCCACCGGACTTGGC
<b>VNTR-30</b>	chr1:349456	3.2	3.2	NA	12	GGCGGGAGAAAG
<b>VNTR-31</b>	chr1:356129	1.9	1.9	NA	18	TTTTGAAAGGGTTTCGCC
<b>VNTR-32</b>	chr1:374624	2	NA	NA	29	TAAGGCAATAGGGCAATAGGGCAGTATGT
<b>VNTR-33</b>	chr1:374718	4.1	9.1	NA	8	ACTGCCCT
<b>VNTR-34</b>	chr1:376516	1.9	1.9	NA	29	TTAAGGCAATAGGGCAATAAGGCAGTATG
<b>VNTR-35</b>	chr1:376546	1.9	1.9	1.9	16	TAAGGGAATAGGGGAA
<b>VNTR-36</b>	chr1:376618	10.4	8.4	NA	8	ACTGCCCT
<b>VNTR-37</b>	chr1:405288	1.9	1.9	NA	18	TCGCGCTTGCCGCTTCCA
<b>VNTR-38</b>	chr1:48954	2.2	2.2	NA	15	CCCATGCCGGTCACG
<b>VNTR-39</b>	chr1:509677	2.4	2.4	NA	17	GCGCAGCCTTGCCCGCC
<b>VNTR-40</b>	chr1:589765	2.8	2.8	NA	24	AAGGATGGCAGAAAATGCCCGACC
<b>VNTR-41</b>	chr1:605931	1.9	1.9	NA	18	CCGTAGCTGCCGCTTCCC
<b>VNTR-42</b>	chr1:639735	2	2	NA	24	TTGTTGAAGGCGCTTGCCAGGGCA
<b>VNTR-43</b>	chr1:671856	2	2	NA	22	GTTTGCCCCTGCTTGCGGGTTT
<b>VNTR-44</b>	chr1:762258	3.2	3.2	NA	30	GGCCAGACTGGCCGCGTCTGAAAATAATGG
<b>VNTR-45</b>	chr1:771875	1.9	1.9	NA	16	TAAGGGAATAGGGGAA
<b>VNTR-46</b>	chr1:771946	5.5	6.5	NA	8	TACTGCCC
<b>VNTR-47</b>	chr1:778994	2	2	NA	20	TACCGCGCGAGGCGGCCCGT
<b>VNTR-48</b>	chr1:799043	2	2	NA	15	CTTGCTGGTTCTGGG
<b>VNTR-49</b>	chr1:828925	2	2	NA	21	AGGAAGCGAAAGCGCGCTTGC
<b>VNTR-50</b>	chr1:85345	3	3	NA	13	GCAGAGTTAGTGG
<b>VNTR-51</b>	chr1:881282	2.2	2.2	2.2	16	GTAAGGCAATAAGGCA
<b>VNTR-52</b>	chr1:891503	3.8	3.8	3.8	8	AGGGGAAT
<b>VNTR-53</b>	chr1:949475	1.9	1.9	1.9	16	CATGGAACAGCAGCGC
<b>VNTR-54</b>	chr2:1007937	2.1	2.1	2.1	17	ACACAGGGCCGGTACAA

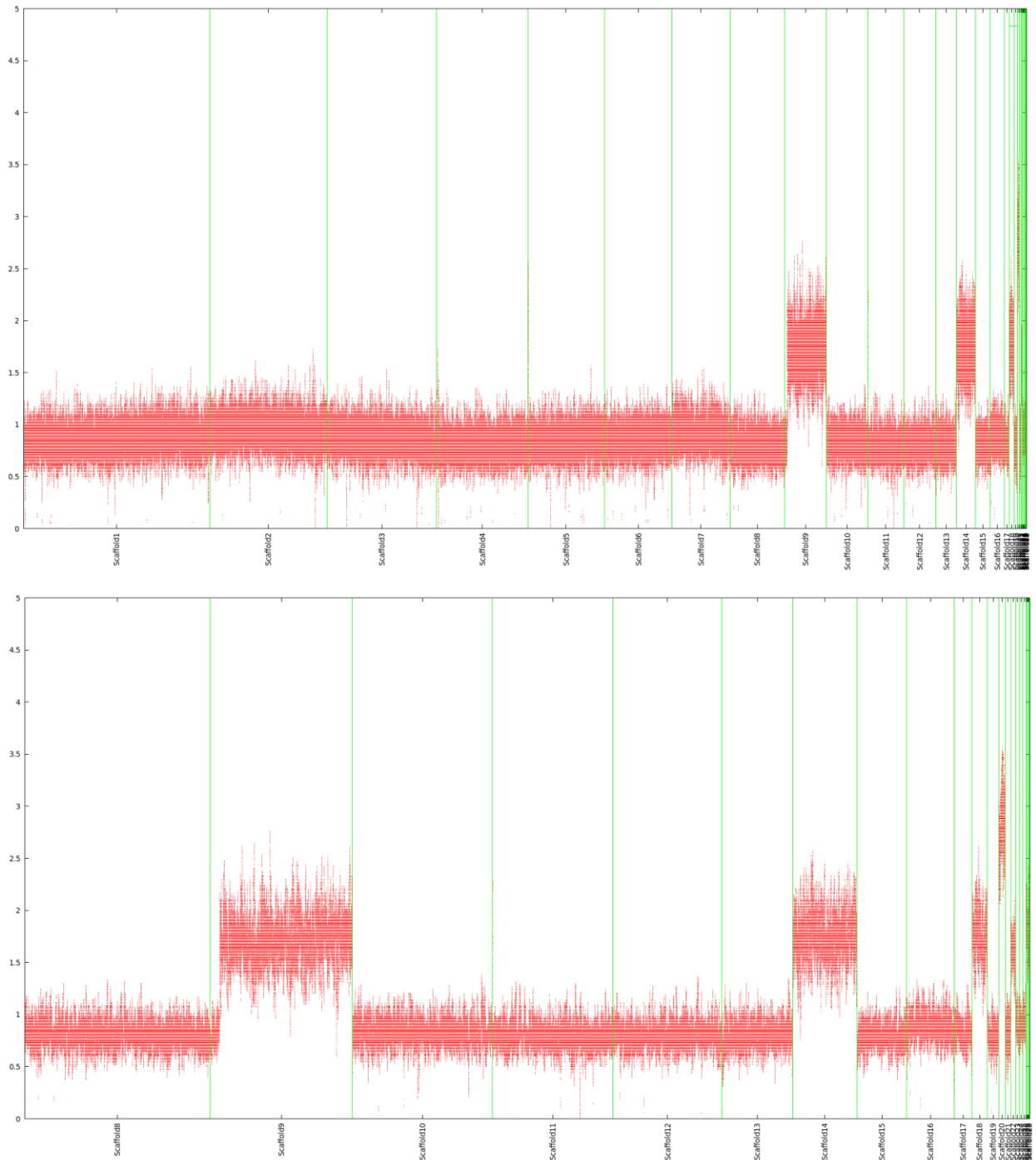
<b>VNTR-55</b>	chr2:1036911	2.7	NA	NA	12	GCCTTGGGGGGG
<b>VNTR-56</b>	chr2:1045666	11	7	NA	8	GGGCAGTG
<b>VNTR-57</b>	chr2:1045821	4.4	4.4	NA	8	TACTGCCT
<b>VNTR-58</b>	chr2:1050460	2.9	2.9	NA	17	GATCATCATCACCATGG
<b>VNTR-59</b>	chr2:1050463	2.2	2.2	NA	15	CATCATCACCATGGG
<b>VNTR-60</b>	chr2:1050493	2.6	2.6	NA	15	CATGACCATCACCAT
<b>VNTR-61</b>	chr2:1051972	6	9	NA	8	GGGCAGTG
<b>VNTR-62</b>	chr2:1052060	1.9	1.9	NA	16	TCCCCTACTCCCTTAT
<b>VNTR-63</b>	chr2:1086220	2.1	2.1	2.1	18	GCAGGCAGCACAGAACAG
<b>VNTR-64</b>	chr2:1089799	2.5	2.5	2.5	28	GCACGCTCATCGTGCCGTAATAAAAGAA
<b>VNTR-65</b>	chr2:115304	3.8	3.8	NA	15	TTCATGGCGTCGCCT
<b>VNTR-66</b>	chr2:164963	2.1	2.1	NA	12	CGATCTTGCCGT
<b>VNTR-67</b>	chr2:170184	8.1	6.1	NA	8	ATTCCCCT
<b>VNTR-68</b>	chr2:217770	1.9	1.9	NA	18	GCAATGACCAGAAAGGAA
<b>VNTR-69</b>	chr2:290120	2	2	NA	20	GAAGCAGAAAGCGCCAGCAA
<b>VNTR-70</b>	chr2:330625	2.2	2.2	NA	21	TGCTGAAATAGCCGATGACCA
<b>VNTR-71</b>	chr2:453544	3.1	NA	NA	12	GTTCATCGCCGC
<b>VNTR-72</b>	chr2:667985	2	2	2	22	CGATATCGAGCGCACCAACGGT
<b>VNTR-73</b>	chr2:711337	1.9	1.9	1.9	13	TGTGAAGATGCGA
<b>VNTR-74</b>	chr2:826002	5.4	4.4	NA	8	TAAGGGAG
<b>VNTR-75</b>	chr2:832157	2.3	3.3	2.3	12	GGCATCATGGCG
<b>VNTR-76</b>	chr2:93813	2	2	NA	20	ATCAACTATCTGCGCGAAAG
<b>VNTR-77</b>	chr2:93819	2.3	2.3	NA	20	TATCTGCGCGAAAGACCAAC
<b>VNTR-78</b>	chr2:958168	2	2	2	21	TCGGATTGGTTTATCAAAATG

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**Supplementary Figure 1.** Gel photo showing the amplification of nine loci from *B. melitensis* IND1 strain. Amplification of nine loci from *B. melitensis* IND1 strain for MLST analysis.

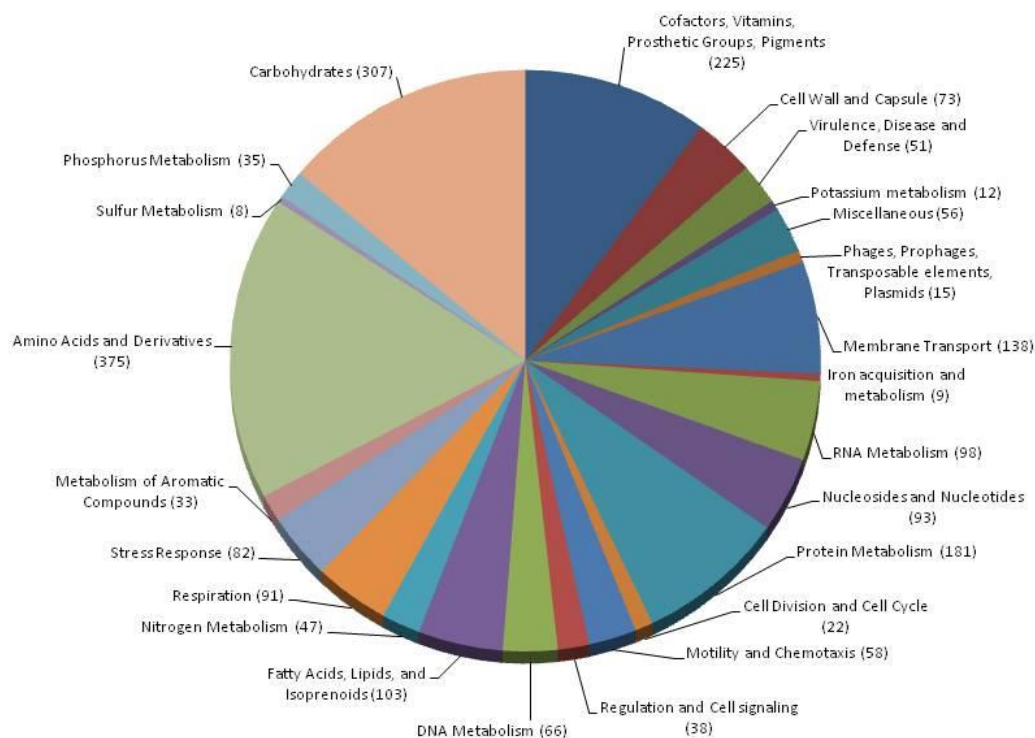




**Supplementary Figure 2. The depth coverage of each scaffold of Bm IND1 genome.** (a) X-axis shows the relative length of scaffolds and Y axis represents each position covered with number of reads on a scale of 100. Chart was generated using GNUplot. Scaffold 9, scaffold 14 and scaffold 18 are showing higher coverage. Scaffold 20 was showing maximum coverage. (b) Re-plot of the data (A) with X-axis shifted right to highlight smaller scaffolds.

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50 **Supplementary Figure 3. The distribution of genes containing SNPs in *B. melitensis* IND1**

51 **against other *B. melitensis* strains. *B. melitensis* IND1 genes carrying SNPs with respect to**

52 **any of the seven *B. melitensis* strains (*B. melitensis* 16M, *B. melitensis* Ether, *B. melitensis* NI, *B.***

53 ***melitensis* M5-90, *B. melitensis* M28, *B. melitensis* ATCC 23457) or *B. abortus* 2308 are**

54 **organized as per SEED sub-system annotation**