

1 **Supplemental information**

2 **Transcriptomic analysis of *Bifidobacterium longum* subsp. *longum* BBMN68 in response to**
3 **oxidative shock**

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16 **Supplementary Table S1.** Fold change in expression of up- and downregulated genes of *B. longum*
 17 BBMN68 under oxygen treatment.

Changes in mRNA level (30 min vs. control)	Number of genes (% of total) with indicated mRNA level change			
	FC \geq 2	2 \leq FC < 5	5 \leq FC < 10	FC \geq 10
Upregulated	241 (13.16)	206 (11.25)	23 (1.26)	12 (0.66)
Downregulated	99 (5.41)	94 (5.13)	5 (0.27)	0 (0)
Total	340 (18.57)	300 (16.38)	28 (1.53)	12 (0.66)

Changes in mRNA level (60 min vs. control)	Number of genes (% of total) with indicated mRNA level change			
	FC \geq 2	2 \leq FC < 5	5 \leq FC < 10	FC \geq 10
Upregulated	217 (11.84)	193 (10.53)	19 (1.04)	5 (0.27)
Downregulated	218 (11.90)	202 (11.03)	12 (0.66)	4 (0.22)
Total	435 (23.74)	395 (21.56)	31 (0.17)	9 (0.49)

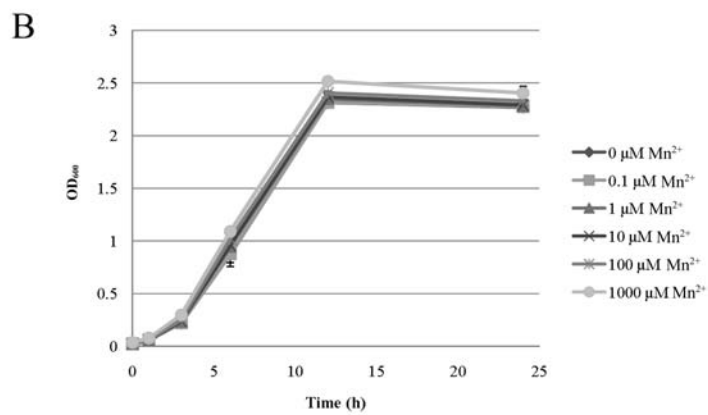
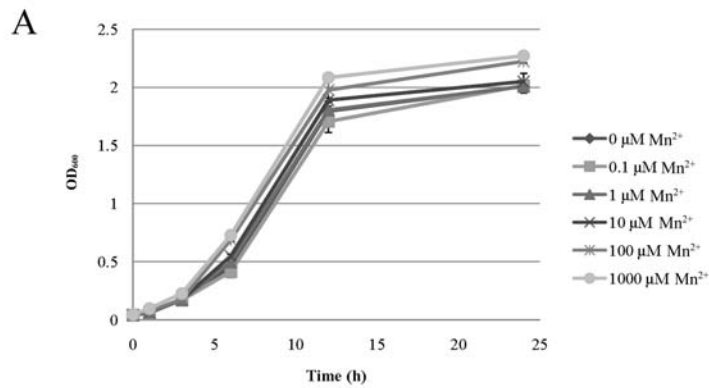
18 FC: fold change.

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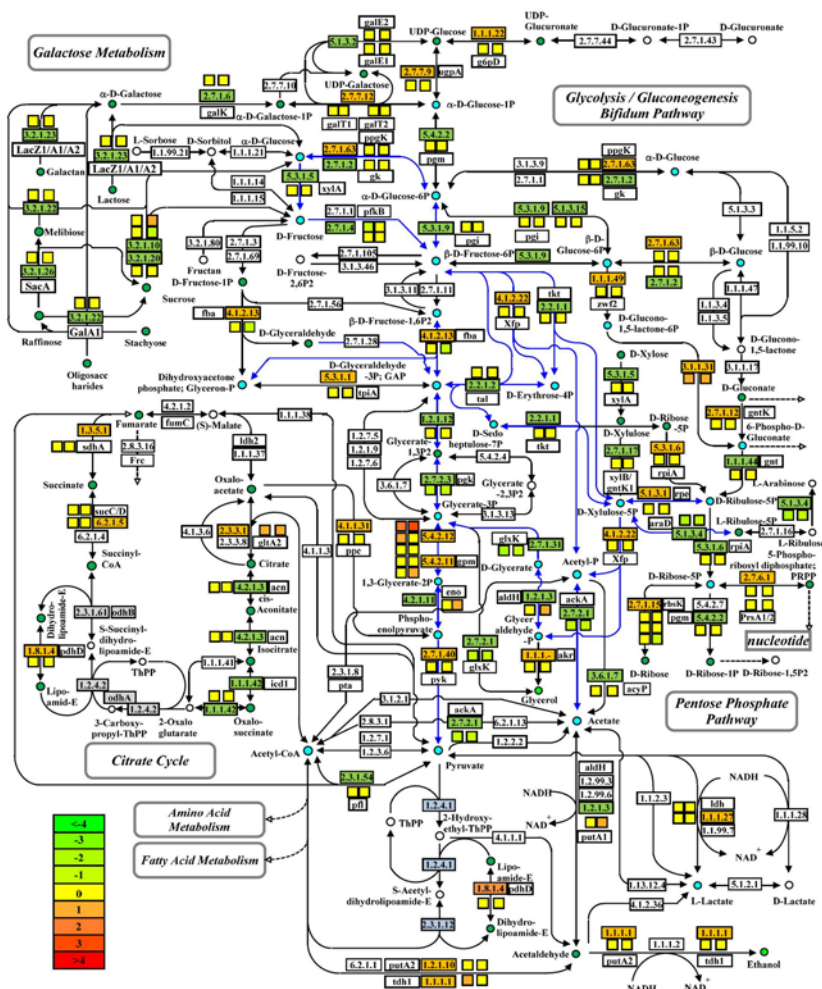
21 **Supplementary Table S2.** Genes that were upregulated or downregulated by \geq 2-fold in the transcriptome
 22 of *B. longum* BBMN68 exposed to 3% (v/v) oxygen (see Excel file).

23 **Supplementary Figure S1.** Growth of *B. longum* BBM68 under modified MRS broth supplemented with
24 MnSO_4 (at 0 to 1000 μM). *B. longum* BBM68 overnight culture was inoculated at 1% into an injection
25 vial containing modified MRS broth and grown upon exposure to 3% (v/v) oxygen (A) or under anaerobic
26 conditions (B).



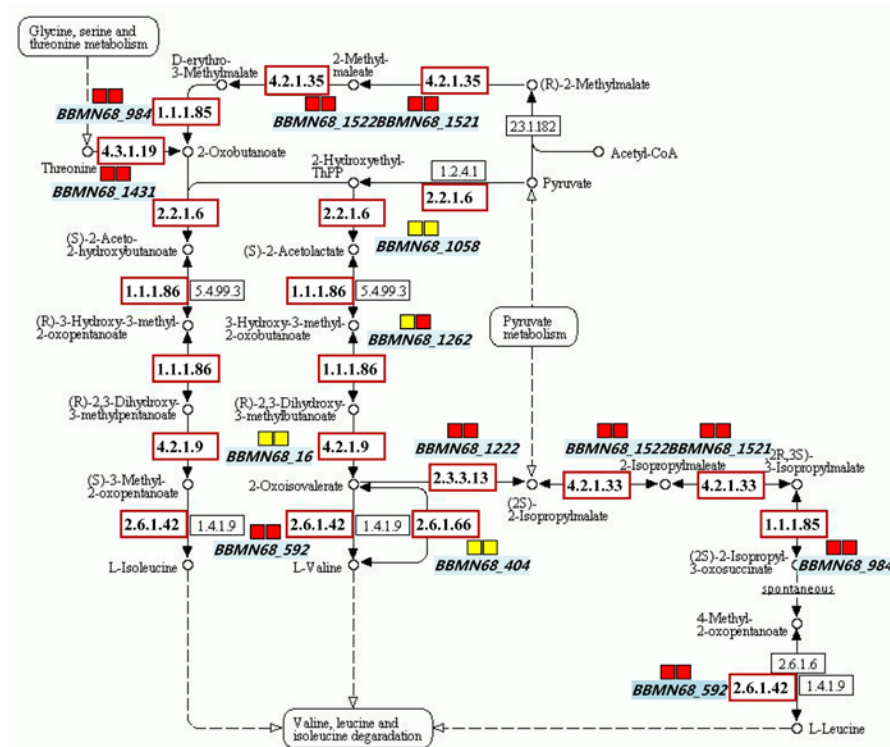
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28 **Supplementary Figure S2.** Global transcriptome profile of carbohydrate metabolism (adapted from KEGG
 29 pathway blb00010, blb00020, blb00030, and blb00052)⁴⁹ of *B. longum* BBMN68 exposed to 3% (v/v)
 30 oxygen. The gene designation and enzyme code are shown in and adjacent to the boxes, respectively. The
 31 small colored squares adjacent to genes indicate increased expression fold change for 3% oxygen for 30
 32 min treatment vs. control (left), and 3% oxygen for 60 min treatment vs. control (right). Square colors
 33 indicate the extent of the fold changes according to color key at bottom left.



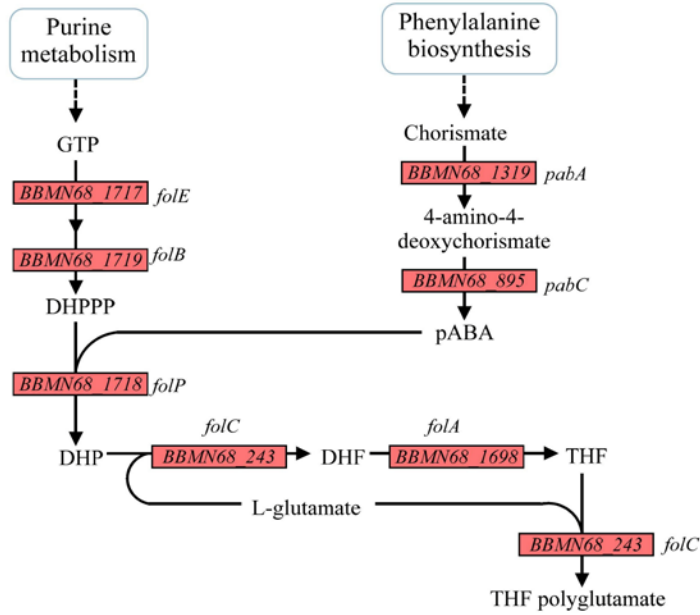
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35 **Supplementary Figure S3.** Genes involved in branched-chain amino acid (BCAA) synthesis (adapted
 36 from KEGG pathway blb00290)⁴⁹ were upregulated in *B. longum* BBM68 upon exposure to 3% (v/v)
 37 oxygen. Gene name and enzyme code are shown. The small colored squares adjacent to genes indicate
 38 increased (red) or non-significantly increased (yellow) mRNA expression for 3% oxygen treatment for 30
 39 min vs. control (left), and 3% oxygen treatment for 60 min vs. control (right).



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41 **Supplementary Figure S4.** Genes involved in tetrahydrofolate (THF) synthesis (adapted from KEGG
 42 pathway blb00790)⁴⁹ were upregulated in *B. longum* BBMN68 upon exposure to 3% (v/v) oxygen. Red
 43 gene names indicate upregulation in BBMN68 exposed to 3% oxygen for 60 min vs. control.



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59 **Reference**

- 60 49. Kanehisa, M. & Goto, S. KEGG: Kyoto Encyclopedia of Genes and Genomes. *Nucleic Acids Res.* **28**,
61 27-30 (2000).