

# The Impact of Microbiome and Microbiota-Derived Sodium Butyrate on *Drosophila* Transcriptome and Metabolome Revealed by Multi-Omics Analysis

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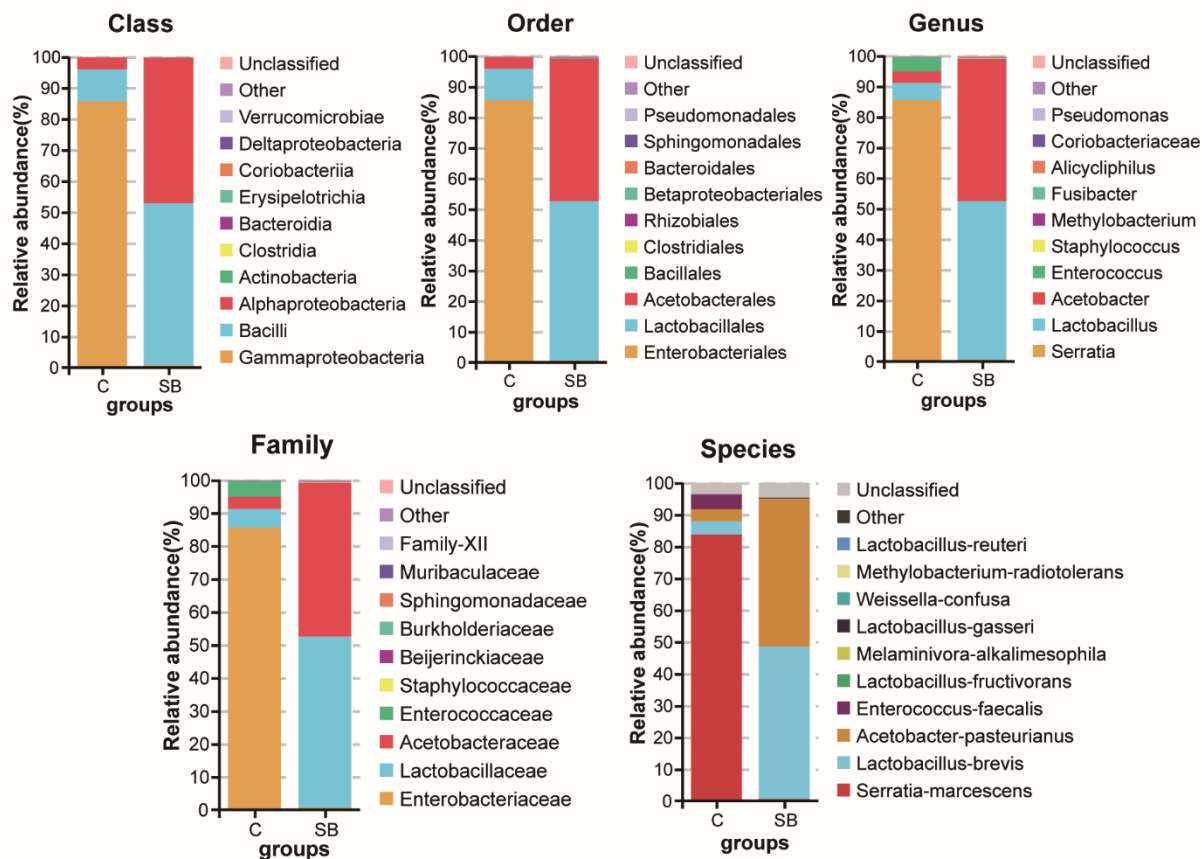
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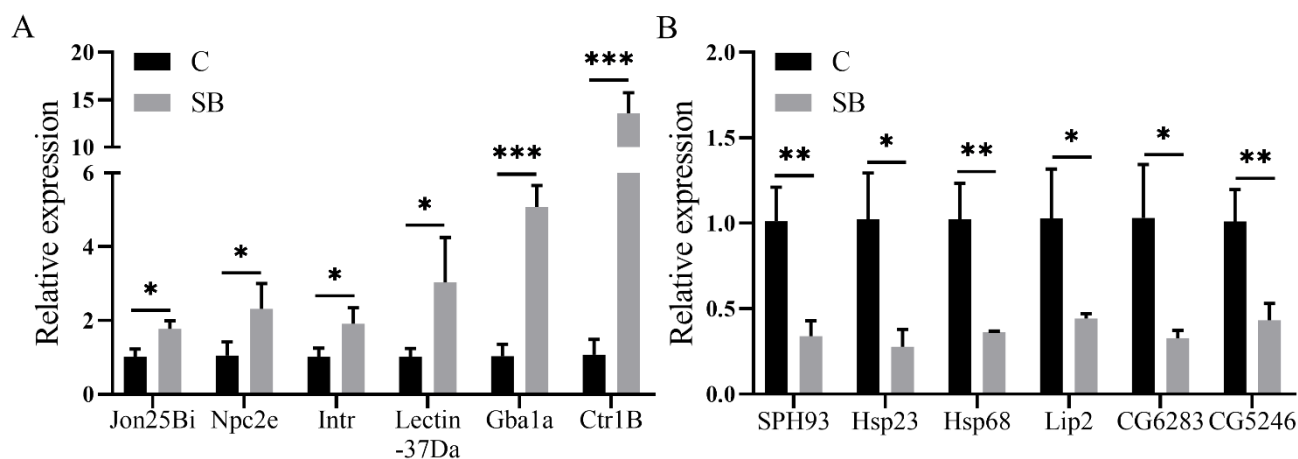
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**Supplementary Table S1.** Primer sequences used for RT-qPCR analysis in this study.

Gene	Forward Primer	Reverse Primer
<i>Pten</i>	AACCTGCTCGGTTGGAACAT	ACACTATCAGCACCACACGAA
<i>Set1</i>	AAAAC TTCAACCGCCAGTGC	GGCGGTGCATTTCCTAAAAGT
<i>Cyp6a8</i>	GAAAGCAAGGCACCGTTTGT	GGCACCGTCCAGATTGAAGA
<i>LysD</i>	CTGCAACGCTCTCCTGACC	TGCGCAATCGTTTTAATCGGG
<i>Jon25Bi</i>	GCGGTGGTTCTATCATCGCC	GGCCAGTTGTGGTTCTGGAT
<i>Mal-A1</i>	AGTGGTGGGAGAGTGGAACT	GCCGATGTCTTTCAGGTAATG
<i>Mal-A4</i>	TTCAAAGACAGTGACGGAAATGG	TTTCAGAAAAGGAGACAGCCAG
<i>Mal-A6</i>	GCAGCGATACTCGTTTTGGG	TGCCACTTGCCACCAATCTC
<i>Gba1a</i>	CAGGGACTTCGGTTCTCCAC	GACAGGATTGTTCGATTTCGC
<i>LysB</i>	TCTTGACCGACGACATCACC	CGAAGAGGAGATGCTGGTGTTA
<i>LysE</i>	TAAGGGCCCCATTGCGAGGA	CCAATTGGTTCACGAGGAACG
<i>SPH93</i>	GCAATCGGAATCTACTCTTAGC	TGGAGCGGTAATCAAATGTTGG
<i>Hsp23</i>	ATTCCATTGTTGTTGAGCCTTGC	GGCCAAGTAGGGATTCTCTTG
<i>Hsp68</i>	CGACAACGGCAAACCAAAGAT	TAGTGCCCAGGTAGGCTTCTG
<i>Lip2</i>	CGGCAGCACATCGACTTGA	GGAGTGTCCAATTAGTACCACCT
<i>CG6283</i>	GCTCCGTTCTCTACTACGCC	GTAGGTGCTTCGCGAGTTCT
<i>CG5246</i>	CTGTCTCAATGTTCCGGCGAAA	CCTCCAATCACACGGGTCTC
<i>Jon25Bi</i>	GCGGTGGTTCTATCATCGCC	GGCCAGTTGTGGTTCTGGAT
<i>Npc2e</i>	CACTTCCTGGGCAATAACAACA	GACACTTCGTCGGGTAGGG
<i>Intr</i>	GACCGCTCCGCAGTTTAATGT	CTCTGGTAGGGATAGGGCACT
<i>Lectin-37Da</i>	AAACCCGTACAACCTGACCGT	TTCTCGTAGGCGACATACCAA
<i>Gba1a</i>	CAGGGACTTCGGTTCTCCAC	GACAGGATTGTTCGATTTCGC
<i>Ctr1B</i>	TGGTGTCTTCCTGTATGAGG	CTCGTTCTTCCTACGCTGCT
<i>SPH93</i>	GCAATCGGAATCTACTCTTAGC	TGGAGCGGTAATCAAATGTTGG
<i>Rp49</i>	GCCCAAGGGTATCGACAACA	ACCTCCAGCTCGCGCACGTT



**Supplementary Figure S1.** Gut microbiome analysis of bacterial structure at the class, order, family, genus, species level, respectively. 16S rDNA sequencing data from conventional *Drosophila* (C) and sodium butyrate-treated *Drosophila* (SB) were used,  $n=3$ .



**Supplementary Figure S2.** Quantitative RT-PCR validation of genes from conventional *Drosophila* (C) and sodium butyrate-treated *Drosophila* (SB). **(A)** Relative expression of up-regulated transcripts in the transcriptome data. **(B)** Relative expression of down-regulated transcripts in the transcriptome data. Significant differences are determined by the unpaired Student's *t*-test. \* $P < 0.05$ , \*\* $P < 0.01$ .