

***Tritrichomonas musculus* XZH isolate ITS sequence:**

AATACGTCCCCTGCCCTTTGTACACACCGCCCGTCGCTCCTACCGATTGGATGACTCGGTGAAATTATCGGAGTTTTT
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Multiple sequence alignment of the selected ITS sequences as shown below using the EMBL-EBI search and sequence analysis tools APIs:

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1 T.muris AY886843 -----ATCAGTTTCGTA TAAATTTAAACACAAAAAT TTTTTTTT-TAAT
2 T.rainier MH370486 CGATGGATCAGTTTCG--TAAATTTAATCACAAACATA TTTTTTTT-AAAA
3 Tritrichomonas XZH isolateITS CGATGGATCAGTTTCG--TAAATTTAATCACAAACATA TTTTTTTT-AAAA
4 T.musculus KX000922 CGATGGATCAGTTTCG--TAAATTTAATCACAAACATA TTTTTTTTAAAA

1 T.muris AY886843 C T A T A T A A C C T T T T A A C A T A - C A A A C A A T A A A A A C A A A T A A A A A A A T T T
2 T.rainier MH370486 A A A T A T A A C C T T T T A T A C A A A T T A A A T A A T A A A A A C - - - - A A A A A A T T T
3 Tritrichomonas XZH isolateITS A A A A A T A T A T C T A A A A T A C A A A T T A A A T A A T A A A A A C - - - - A A A A A A T T T
4 T.musculus KX000922 A A A A A T T A T C T A A A A T A C A A A T T A A A T A A T A A A A A C - - - - A A A A A A T T T

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3 Tritrichomonas XZH isolateITS A G A C C T T A G G C A A T G G A T G T C T T G G C T T C T T A C A C G G G A A G A A C G T T G C
4 T.musculus KX000922 A G A C C T T A G G C A A T G G A T G T C T T G G C T T C T T A C A C G A G A A G A A C G T T G C

1 T.muris AY886843 A T A A T G C G A T A A G C G G C T G G A G T T G C T T T C T T T G C G A C A A G T T C G A T C T T
2 T.rainier MH370486 A T A A T G C G A T A A G C G G C T G G A G T T G C T T A C T T T G C G A C A A G T T C G A T C T T
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4 T.musculus KX000922 A T A A T G C G A T A A G C G G C T G G A G T T G C T T A C T T T G C G A C A A G T T C G A T C T T

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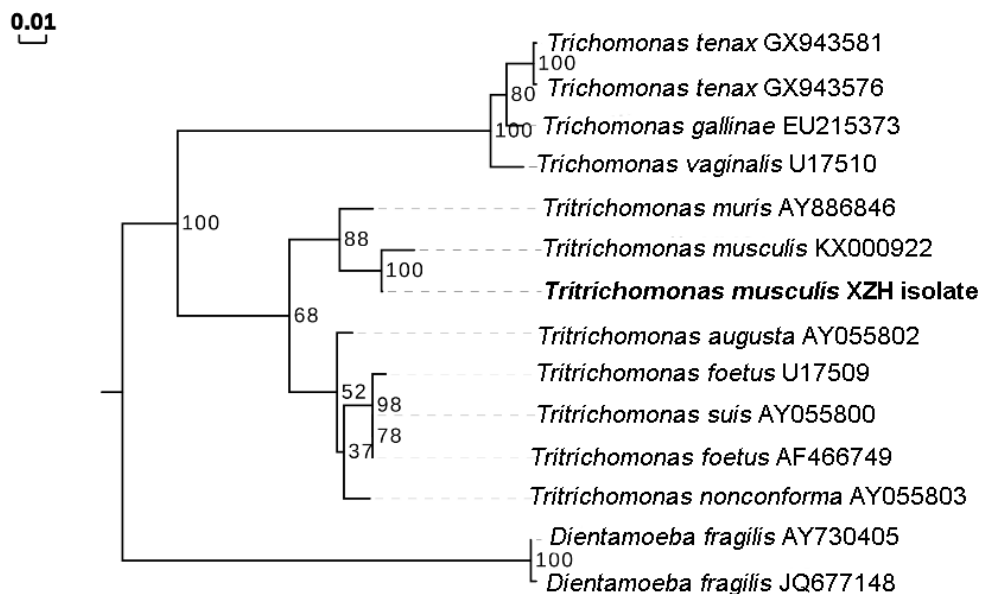
***Tritrichomonas musculus* XZH isolate 18S sequence:**

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GCTCGAGCATGCATCTAGAGGGCCCAATCGCC

Multiple sequence alignment of the selected 18S sequences as shown below using the EMBL-EBI search and sequence analysis tools APIs:

1 <i>T. muris</i> AY886846	GCAGTAAATTCGGTGCTAATACATGCCATTGTTTCACTACGTTGAGAAAT
2 <i>Tritrichomonas</i> XZH isolate	GCAGTAAATTCGGTGCTAATACATGCCATTGTTTCACTACGTTGAGAAAT
3 <i>T. musculus</i> KX000921	TTTCACTACGTTGAGAAAT
1 <i>T. muris</i> AY886846	AGTGGAAAAGTTGACCCTTACGGGCACACCAATCGATTGAGCGACCTATC
2 <i>Tritrichomonas</i> XZH isolate	AGTGGAAAAGTTGACCCTTACGGGCACACCAATCGATTGAGCGACCTATC
3 <i>T. musculus</i> KX000921	AGTGGAAAAGTTGACCCTTACGGGCACACCAATCGATTGAGCGACCTATC
1 <i>T. muris</i> AY886846	ATGCTTGTACTTAGGGTCTTTACCTAGGTAGGCATCACGGGTAACGGGC
2 <i>Tritrichomonas</i> XZH isolate	ATGCTTGTACTTAGGGTCTTTACCTAGGTAGGCATCACGGGTAACGGGC
3 <i>T. musculus</i> KX000921	ATGCTTGTACTTAGGGTCTTTACCTAGGTAGGCATCACGGGTAACGGGC
1 <i>T. muris</i> AY886846	GGTTACCFTCGGACTGCCGAGAAGGGCCGAGAGATAGCCACTATATC
2 <i>Tritrichomonas</i> XZH isolate	GGTTACCFTCGGACTGCCGAGAAGGGCCGAGAGATAGCCACTATATC
3 <i>T. musculus</i> KX000921	GGTTACCFTCGGACTGCCGAGAAGGGCCGAGAGATAGCCACTATATC
1 <i>T. muris</i> AY886846	CACGGGTAGCAGCAGGCCGCAAACTTACCCACTCGAGACTTCGGAGGTG
2 <i>Tritrichomonas</i> XZH isolate	CACGGGTAGCAGCAGGCCGCAAACTTACCCACTCGAGACTTCGGAGGTG
3 <i>T. musculus</i> KX000921	CACGGGTAGCAGCAGGCCGCAAACTTACCCACTCGAGACTTCGGAGGTG
1 <i>T. muris</i> AY886846	GTAATGACCAGTTCCATCTCATCCCTTTGGGGTATTTGGATAGGATCAC
2 <i>Tritrichomonas</i> XZH isolate	GTAATGACCAGTTCCATCTCATCCCTCACGGGTGTTTGGATAGGATCAC
3 <i>T. musculus</i> KX000921	GTAATGACCAGTTCCATCTCATCCCTCACGGGTGTTTGGATAGGATCAC
1 <i>T. muris</i> AY886846	ACTTTTCCAGTTCGGTGCATCTAGCAGAGGGCCAGTCTGGTCCAGCAG
2 <i>Tritrichomonas</i> XZH isolate	ACTTTTCCAGTTCGGTGCATCTAGCAGAGGGCCAGTCTGGTCCAGCAG
3 <i>T. musculus</i> KX000921	ACTTTTCCAGTTCGGTGCATCTAGCAGAGGGCCAGTCTGGTCCAGCAG
1 <i>T. muris</i> AY886846	CTGCGGTAATCCAGCTCTGCGAGTTTGCITCCCATATTGTTGCAGTTAAA
2 <i>Tritrichomonas</i> XZH isolate	CTGCGGTAATCCAGCTCTGCGAGTTTGCITCCCATATTGTTGCAGTTAAA
3 <i>T. musculus</i> KX000921	CTGCGGTAATCCAGCTCTGCGAGTTTGCITCCCATATTGTTGCAGTTAAA

18S sequence RAxML phylogenetic reconstruction (bootstrap score is indicated, branch length scale=0.01):



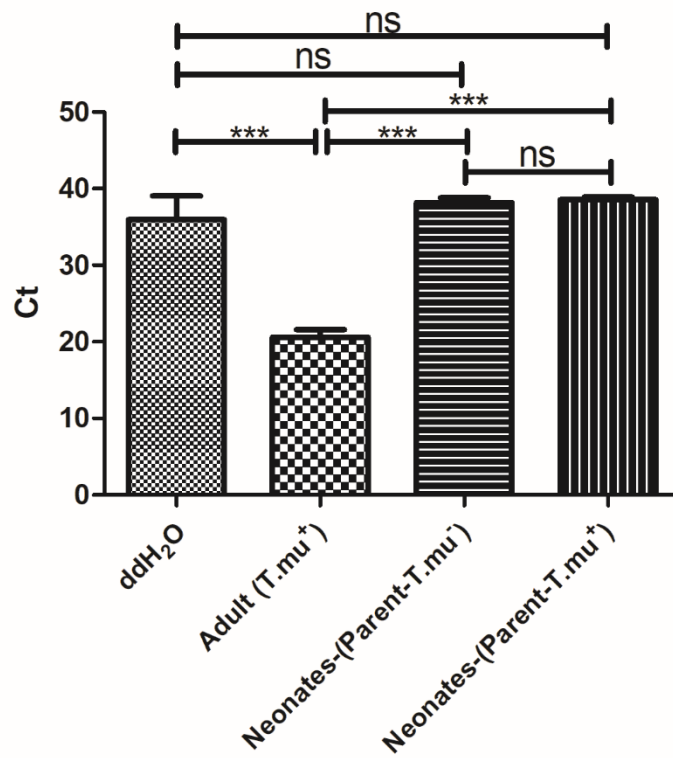


Figure S1. Neonatal mice are *T. mu*-free. qPCR was performed to determine the relative abundance of *T. mu*. Total DNA was isolated from cecal content of the indicated mice. Autoclaved water was used as protozoan-free control. Neonates were born either of mothers without protozoan colonization (Parent-*T. mu*⁻) or of mothers that orally administered with *T. mu* (Parent-*T. mu*⁺). n=3-6 per group, ***, $P < 0.001$; ns, no statistical significance.

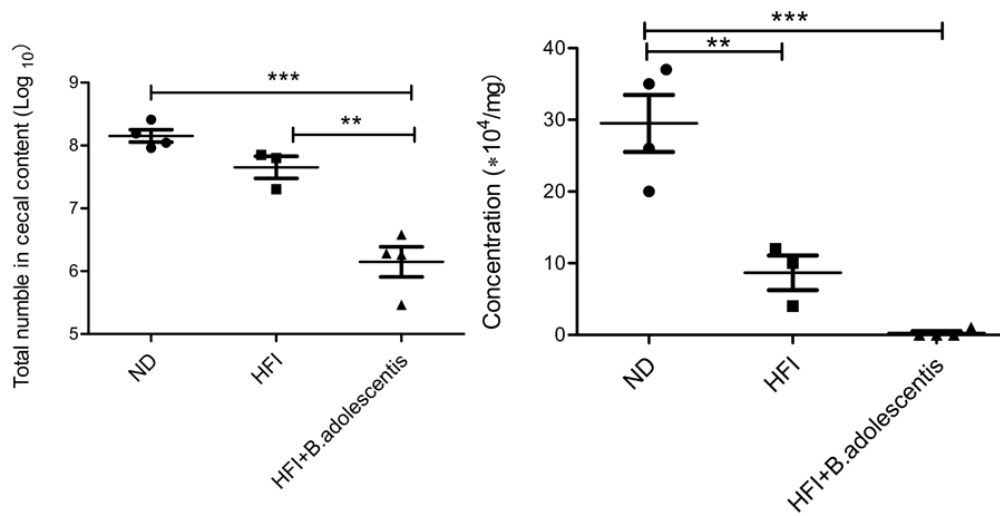


Figure S2. *B. adolescentis* (ATCC 15703) inhibits *T. mu* colonization in inulin-enriched environment. WT B6 mice were treated similarly as depicted in Figure 6A, except that *B. longum* JDM301 was replaced by *B. adolescentis* (ATCC 15703). The total number and concentration of *T. mu* in the cecal content from the mice fed either with ND, HFI, or HFI+B. *adolescentis* were monitored 7 days post *T. mu* administration. N=3-4/group. **, $P < 0.01$; ***, $P < 0.001$.