

Supplementary File S1 : Raw FASTA sequences (n=11) obtained from 10 badger stool samples (ID=Mm.n) at the β -giardin (bg; number of sequences=8) and the triose phosphate isomerase (tpi; number of sequences=3) loci

>Mm.3_bg (identified as Assemblage A, sub assemblage All)

TCCATAACGACGCCATCGCGGCTCTCAGGAAGGAGGCCCTCAAGAGCyTGAACGAyCTCGAGACGGGCATTGCCACG
GAGAACGCAGAAAGGAAGAAGATGTACGACCAGCTCAACGAGAAGGTCGAGAGGGCTTCGCCCCGATCTCCGCCG
CGATCGAGAAGGAGACGATCGCCCGGAGAGGGCCGTTAGTGCTGCCACGACAGAAGCGCTCACAAACACGAAGCT
CGTCGAGAAGTGCGTCAACGAGCAGCTCGAGAACGTGCGCTCGGAGATCCGCGCTATCCAGGAGGAGATCGACCGC
GAGAAGCCCGAGCGCAAGGA

>Mm.5_bg (identified as mixed Assemblage A and B infection)

CATAACGACGCCATCGCGGCTCTCAGGAAGGAGGCCCTCAAGAGCyTGAACGACCTCGAGACRGGCATyGCCACGGA
GAACGCMGARAGGAAGAAGATGTAYGACCAGCTCAACGAGAARGTCGAGAGGGCTTCGCCCCGATCTCCGCCGS
ATCGAGAAGGAGACGATCGCCCGGAGAGGGCCGTYAGYGCTGCCACGACAGARGCSCTCACAAACACGAAGCTCGT
CGAGAAGTGCGTCAACGAGCAGCTCGAGAACGTGCGCTCGGAGATCCGCGCYATCCAGGAGGAGATCGACCGCGAG
AAGGCCGAGCGCAAGGA

>Mm.11_bg (identified as Assemblage A, sub assemblage All)

TccATAACGACGCCATCGCGGCTCTCAGGAAGGAGGCCCTCAAGAGCyTGAACGAyCTCGAGACGGGCATTGCCACG
GAGAACGCAGAAAGGAAGAAGATGTACGACCAGCTCAACGAGAAGGTCGAGAGGGCTTCGCCCCGATCTCCGCCG
CGATCGAGAAGGAGACGATCGCCCGGAGAGGGCCGTTAGTGCTGCCACGACAGAAGCGCTCACAAACACGAAGCT
CGTCGAGAAGTGCGTCAACGAGCAGCTCGAGAACGTGCGCTCGGAGATCCGCGCTATCCAGGAGGAGATCGACCGC
GAGAAGGCCGAGCGCAaGGA

>Mm.14_bg (identified as Assemblage A, sub assemblage All)

tcCATAACGACGCCATCGCGGCTCTCAGGAAGGAGGCCCTCAAGAGCyTGAACGAyCTCGAGACGGGCATTGCCACG
GAGAACGCAGAAAGGAAGAAGATGTACGACCAGCTCAACGAGAAGGTCGAGAGGGCTTCGCCCCGATCTCCGCCG
CGATCGAGAAGGAGACGATCGCCCGGAGAGGGCCGTTAGTGCTGCCACGACAGAAGCGCTCACAAACACGAAGCT
CGTCGAGAAGTGCGTCAACGAGCAGCTCGAGAACGTGCGCTCGGAGATCCGCGCTATCCAGGAGGAGATCGACCGC
GAGAAGGCCGAGCGCAAGGA

>Mm.16_bg (identified as Assemblage A, sub assemblage All)

TCCATAACGACGCCATCGCGGCTCTCAGGAAGGAGGCCCTCAAGAGCCTGAACGAyCTCGAGACGGGCATTGCCACG
GAGAACGCAGAAAGGAAGAAGATGTACGACCAGCTCAACGAGAAGGTCGAGAGGGCTTCGCCCCGATCTCCGCCG
CGATCGAGAAGGAGACGATCGCCCGGAGAGGGCCGTTAGTGCTGCCACGACAGAAGCGCTCACAAACACGAAGCT
CGTCGAGAAGTGCGTCAACGAGCAGCTCGAGAACGTGCGCTCGGAGATCCGCGCTATCCAGGAGGAGATCGACCGC
GAGAAGGCCGAGCGCAaGGA

>Mm.22_bg (identified as Assemblage A, sub assemblage All)

TcCATAACGACGCCATCGCGGCTCTCAGGAAGGAGGCCCTCAAGAGCCTGAACGAyCTCGAGACGGGCATTGCCACG
GAGAACGCAGAAAGGAAGAAGATGTACGACCAGCTCAACGAGAAGGTCGAGAGGGCTTCGCCCCGATCTCCGCCG
CGATCGAGAAGGAGACGATCGCCCGGAGAGGGCCGTTAGTGCTGCCACGACAGAAGCGCTCACAAACACGAAGCT
CGTCGAGAAGTGCGTCAACGAGCAGCTCGAGAACGTGCGCTCGGAGATCCGCGCTATCCAGGAGGAGATCGACCGC
GAGAAGGCCGAGCGCAAGGACGCAGACG

>Mm.23_bg (identified as Assemblage A, sub assemblage All)

TcCATAACGACGCCATCGCGGCTCTCAGGAAGGAGGCCCTCAAGAGCCTGAACGAyCTCGAGACGGGCATTGCCACG
GAGAACGCAGAAAGGAAGAAGATGTACGACCAGCTCAACGAGAAGGTCGCAGAGGGCTTCGCCCCGCATCTCCGCCG
CGATCGAGAAGGAGACGATCGCCCGCAGAGGGCCGTTAGTGCTGCCACGACAGAAGCGCTCACAAACACGAAGCT
CGTCGAGAAGTGCGTCAACGAGCAGCTCGAGAACGTCGCCTCGGAGATCCGCGCTATCCAGGAGGAGATCGACCGC
GAGAAGGCCGAGCGCAAGGAC

>**Mm.25_bg** (identified as Assemblage A, sub assemblage All)

CATAACGACGCCATCGCGGCTCTCAGGAAGGAGGCCCTCAAGAGCyTGAACGAyCTCGAGACGGGCATTGCCACGGA
GAACGCAGAAAGGAAGAAGATGTACGACCAGCTCAACGAGAAGGTCGCAGAGGGCTTCGCCCCGCATCTCCGCCGCG
ATCGAGAAGGAGACGATCGCCCGCAGAGGGCCGTTAGTGCTGCCACGACAGAAGCGCTCACAAACACGAAGCTCG
TCGAGAAGTGCGTCAACGAGCAGCTCGAGAACGTCGCCTCGGAGATCCGCGCTATCCAGGAGGAGATCGACCGCGA
GAAGGCCGAGCGCAAGGA

>**Mm.20_tpi** (identified as Assemblage A, sub assemblage All)

GGCAAACACGTCAAAACAGTTGAGGATAGCAGCGCAGAATGTGTACCTAGAGGGGAACGGGGCGTGGAATGGCGA
GACAAGTGTGAGATGCTTCAGGACATGGGTTTGAAGCATGTGATAGTAGGGCACTCTGAAAGACGCAGAATCATGG
GGGAGACCGACGAGCAAAGCGCCAAGAAGGCTAAGCGTGCCCTGGAAAAGGGGATGACGGTCATCTTCTGCGTCGG
AGAGACCTTGATGAGCGCAAGGCCAACCGCACCATGGAGGTGAACATCGCCCAGCTTGAGGCGCTTGGAAGGAG
CTCGGAGAGTCCAAGATGCTCTGGAAGGAGGTTGTCATTG

>**Mm.15a_tpi** (identified as Assemblage A, sub assemblage All)

GtCCCTTCATCGGGGGTAACtCAAGTGTAACGGCTCTCTTGACTTTATCAAGAGCCACGTGGCGGCAATTGCTGCCCA
TAAGATCCCTGATTCCGTGGACGTCGCCATTGCCCCCTCCGCCGTACACCTGTCAACAGCCACTGCGGCAAACACGTCA
AAACAGTTGAGGATAGCAGCGCAGAATGTGTACCTAGAGGGGAACGGGGCGTGGAATGGCGAGACAAGTGTTGAG
ATGCTTCAGGACATGGGTTTGAAGCATGTGATAGTAGGGCACTCTGAAAGACGCAGAATCATGGGGGAGACCGACG
AGCAAAGCGCCAAGAAGGCTAAGCGTGCCCTGGAAAAGGGGATGACGGTCATCTTCTGCGTCGGAGAGACCTTGGA
TGAGCGCAAGGCCAACCGCACCATGGAGGTGAACATCGCCCAGCTTGAGGCGCTTGGAAGGAGCTCGGAGAGTCC
AAGATGCTCTGGAAGGAGGTTGTCATT

>**Mm.16_tpi** (identified as mixed Assemblage A and B infection)

tccgtggacgtGTyGTTGCTCCCTCCGTTGTACACCTTTCTACAGCYATTGCGGCRAACAcTTCGAARyGTcTGArrAtaGCA
GCRCAAGAyGTGTAYcTGGAGggGAACGGkGCATGgaCyGGCGAGACAAGCGTyGAGAtGCTkCtGGACATGGGkyTGA
rsCATGTAATArTAGGaCACTcTGAAAGACGyAGAATCATGGGsGAGACCAAyGAGCArAgTGCyAaGAAGGckAAGCGt
GCyCTGGAmAArGgkAtGACKGTyaTCTTyTGCrycGGAGAGACCCTGgATgaACGCAagGCCCAyaACaCTAtGgAGgTG
AAmATtgCTCAGCTTGAGgCTcTTAaCAAGGaGaTTGGAGAAtCmAAGAAgCTmtgGAAGAAGGTTgTAATTg