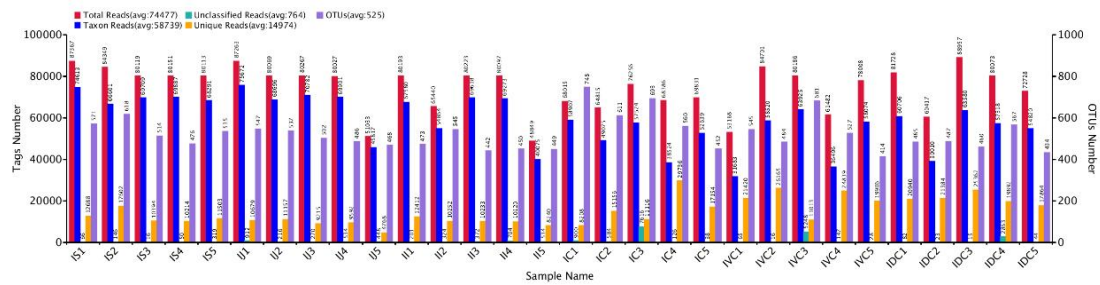


Additional File 1. OTUs clustering and annotation statistics.



Abscissa: sample name; First ordinate (reads Number) : reads Number; Total reads (red) : the Total number of reads per sample (valid data for subsequent analysis such as OTUs clustering per sample); Unique reads (orange) : refers to the number of reads with frequency 1 that cannot be clustered into OTUs (sequences that cannot be clustered into OTUs will not be used for subsequent analysis). Taxon reads (blue) : Number of reads used to build OTUs and obtain annotated information; Unclassified reads (tea green) : refers to the number of reads without any classified information; The second ordinate (OTUs Number) : refers to the Number of OTUs; OTUs (purple) : indicates the number of OTUs obtained for each sample.

Additional File 2. Breed comparisons for the relative abundance of LG and UG microbiota at the phylum level.

Phylum	The upper GIT	The lower GIT
Neocallimastigomycota	0.1966±0.5488 ^B	0.5384±0.3786 ^A
Basidiomycota	0.6002±0.1726 ^A	0.22914±0.2471 ^B
Ascomycota	0.3619±0.1628 ^a	0.2047±0.1802 ^b
Glomeromycota	0.0047±0.0059	0.0054±0.0138
Zygomycota	0.0051±0.0064	0.0028±0.0030
Chytridiomycota	0.0030±0.0042	0.0008±0.0011

Note: Different uppercase letters means the significance at $P < 0.01$, Different lowercase letters means the significance at $P < 0.05$ and blank indicates no significant difference $P > 0.05$.

Additional File 3. Comparison of relative abundance of gastrointestinal fungi at phylum level.

Phylum	Stomach (IS)	Jejunum (IJ)	Ileum (II)	Cecum (IC)	Ventral colon (IVC)	Dorsal colon (IDC)
Neocallimastigomycota	0.0466±0.0956 ^C	0.0041±0.0013 ^C	0.0083±0.0058 ^C	0.2491±0.2817 ^{Bb}	0.5731±0.4080 ^{ABa}	0.7931±0.2620 ^A
Basidiomycota	0.7140±0.1908 ^A	0.6140±0.1406 ^A	0.4727±0.1064 ^A	0.3757±0.2619 ^{Ba}	0.2474±0.2850 ^{Bb}	0.0644±0.0520 ^C
Ascomycota	0.2347±0.1341 ^{Ab}	0.3560±0.1398 ^{Aa}	0.4949±0.1137 ^{Aa}	0.3376±0.1727 ^{Aa}	0.1589±0.1500 ^B	0.1175±0.1647 ^B
Glomeromycota	0.0007±0.0004	0.0064±0.0080	0.0070±0.0051	0.0024±0.0013	0.0015±0.0010	0.0124±0.0241
Zygomycota	0.0019±0.0025	0.0057±0.0043	0.0077±0.0010	0.004±0.0043	0.0016±0.0013	0.0022±0.0020
Chytridiomycota	0.0005±0.0007 ^B	0.0067±0.0056 ^A	0.0019±0.0013 ^B	0.0011±0.0084 ^B	0.0011±0.0017 ^B	0.0004±0.0006 ^B

Note: Different uppercase letters means the significance at $P < 0.01$, Different lowercase letters means the significance at $P < 0.05$ and blank indicates no significant difference $P > 0.05$.

Additional File 4. Breed comparisons for the relative abundance of LG and UG microbiota at the genus level.

Genus	The upper GIT	The lower GIT
<i>Cryptococcus</i>	0.1154±0.1520 ^a	0.0234±0.0361 ^b
<i>Cladosporium</i>	0.0966±0.077 ^A	0.0236±0.0340 ^B
<i>Lysurus</i>	0.0215±0.0483	0.0010±0.0014
<i>Alternaria</i>	0.0465±0.0350 ^A	0.0139±0.0183 ^B
<i>Gibberella</i>	0.0184±0.0158	0.0095±0.0299
<i>Bipolaris</i>	0.0137±0.0298	0.0011±0.0011
<i>Candida</i>	0.0012±0.0017	0.0083±0.0223
<i>Bullera</i>	0.0206±0.0255	0.0064±0.0085
<i>Sarocladium</i>	0.0212±0.0224 ^A	0.0030±0.0040 ^B
<i>Hannaella</i>	0.0215±0.0212	0.0094±0.0114
<i>Fusarium</i>	0.0187±0.0205 ^a	0.0044±0.0060 ^b

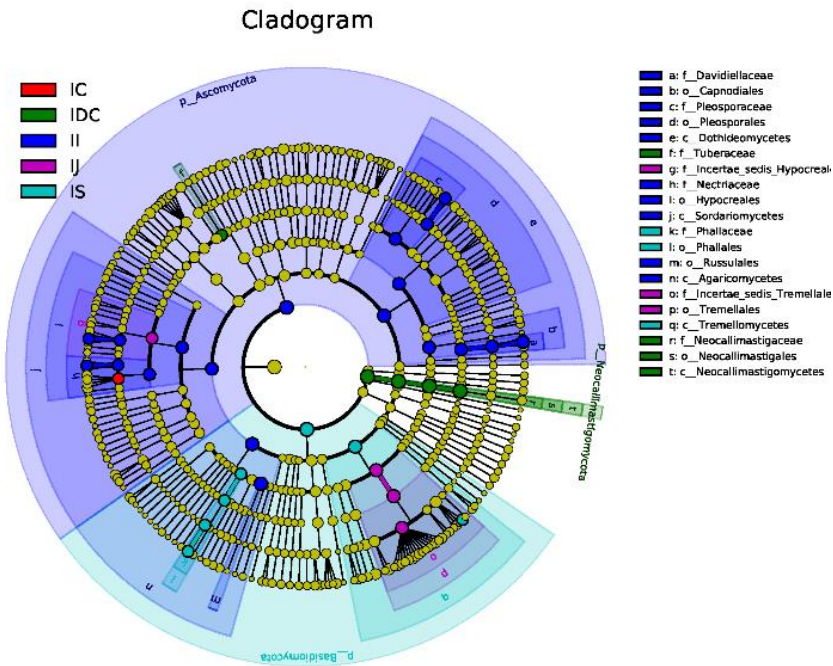
Note: Different uppercase letters means the significance at $P < 0.01$, Different lowercase letters means the significance at $P < 0.05$ and blank indicates no significant difference $P > 0.05$.

Additional File 5. Comparison of relative abundance of gastrointestinal fungi at the genus level.

Genus	Stomach (IS)	Jejunum (IJ)	Ileum (II)	Cecum (IC)	Ventral colon (IVC)	Dorsal colon (IDC)
<i>Cryptococcus</i>	0.1251±0.1701	0.1459±0.1756	0.0751±0.1332	0.0448±0.0591	0.0181±0.0114	0.0072±0.0024
<i>Cladosporium</i>	0.0575±0.0293 ^{Ab}	0.0810±0.0526 ^{Aa}	0.1511±0.1045 ^{Aa}	0.0242±0.0191 ^B	0.0419±0.0530 ^B	0.0047±0.0023 ^B
<i>Lysurus</i>	0.0389±0.0843	0.0061±0.0056	0.0196±0.01833	0.0018±0.0023	0.0008±0.0003	0.0005±0.0001
<i>Alternaria</i>	0.0385±0.0158 ^{Aa}	0.0324±0.0205 ^{Aa}	0.0686±0.5180 ^{Aa}	0.0143±0.0091 ^B	0.0236±0.0290 ^{Ab}	0.0037±0.0012 ^B
<i>Gibberella</i>	0.0115±0.0123	0.0194±0.0147	0.0244±0.0201	0.0262±0.0511	0.0018±0.0018	0.0006±0.0003
<i>Bipolaris</i>	0.0012±0.0010	0.0153±0.0297	0.0247±0.0433	0.0014±0.0010	0.0014±0.0015	0.0004±0.0001
<i>Candida</i>	0.0005±0.0003	0.0020±0.0028	0.0012±0.0007	0.0045±0.0055	0.0016±0.0015	0.0188±0.0387
<i>Bullera</i>	0.0224±0.0339	0.0245±0.0286	0.0148±0.0157	0.0080±0.0069	0.0100±0.0124	0.0011±0.0004
<i>Sarocladium</i>	0.0154±0.0140 ^a	0.0230±0.0309 ^a	0.0251±0.0226 ^a	0.0055±0.0051 ^a	0.0029±0.0039 ^b	0.0008±0.0006 ^b
<i>Hannaella</i>	0.0324±0.0293 ^{Aa}	0.0224±0.0167 ^{Ab}	0.0097±0.0106 ^{Aa}	0.0120±0.0076 ^{Aa}	0.0149±0.0166 ^{Aa}	0.0015±0.0008 ^B
<i>Fusarium</i>	0.0116±0.0187 ^{ab}	0.0183±0.0181 ^{ab}	0.0263±0.0256 ^a	0.0083±0.0078 ^{ab}	0.0039±0.0057 ^b	0.0009±0.0008 ^b

Note: Different uppercase letters means the significance at $P < 0.01$, Different lowercase letters means the significance at $P < 0.05$ and blank indicates no significant difference $P > 0.05$.

Additional File 6. Evolutionary branching diagram.



Additional File 7. LDA value distribution histogram (only the genera LDA scores above 4 are shown).

