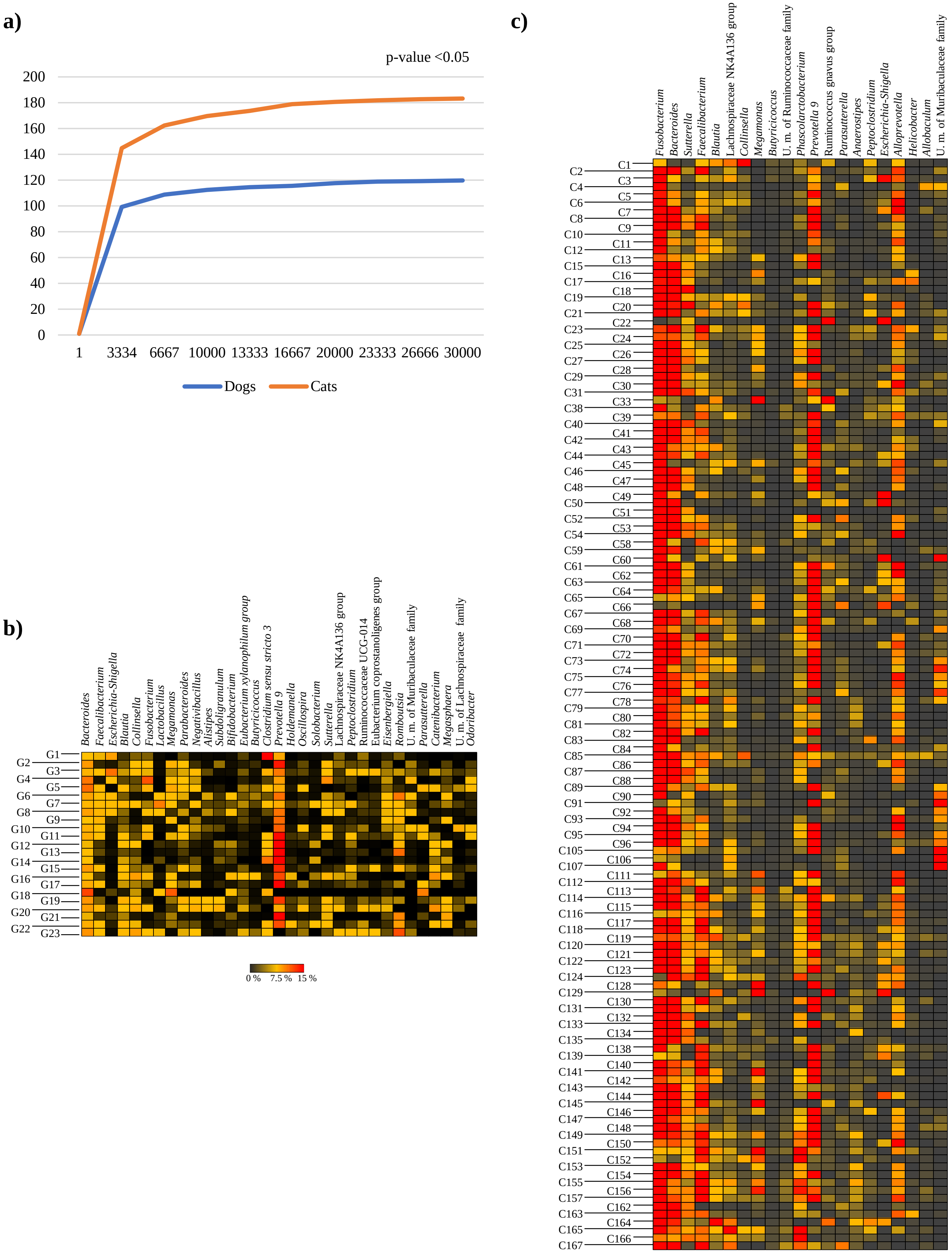


Figure S1. Evaluation of alpha-diversity and assessment of the core-gut microbial community of dogs and cats. Panel a reports alpha-diversity through rarefaction curves representing variation of the observed OTUs. Panels b and c represent the heat map illustrating the average relative abundance of the bacterial genera that constitute the core gut microbiota of cats and dogs, respectively. On the left hand, sample name is reported, while in the upper part of the heat maps the core-gut microbial genera are listed.

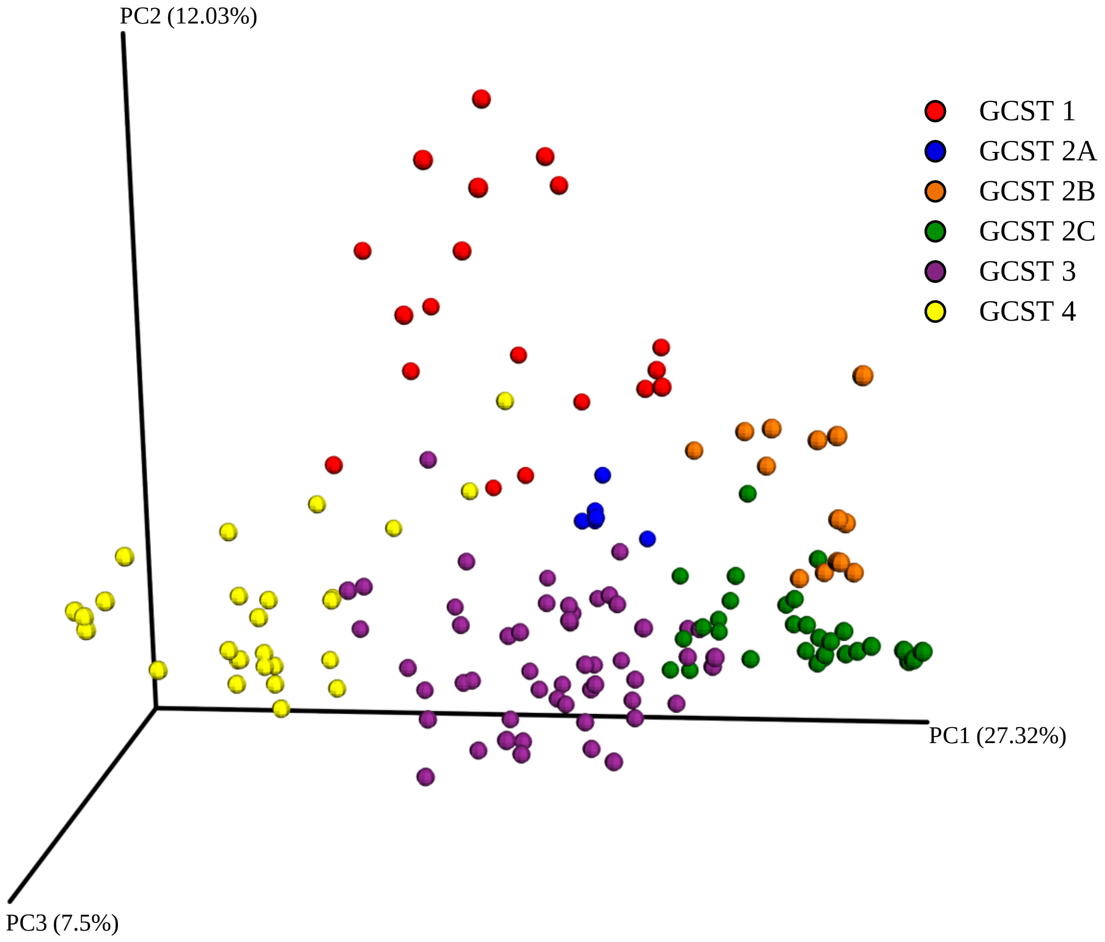


Figure S2. Evaluation of beta-diversity based on the CGST classification. The predicted PCoA illustrates the division of samples into the identified CGSTs.

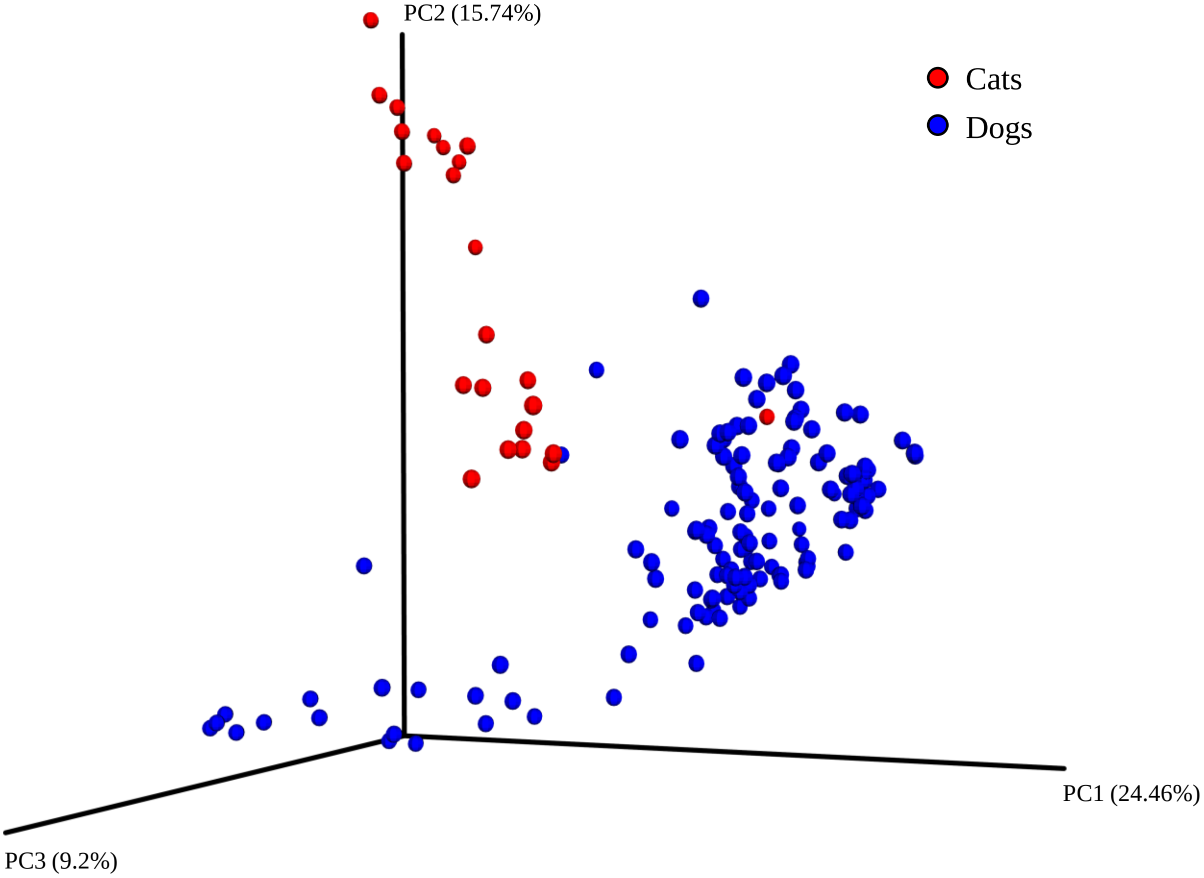


Figure S3. Evaluation of beta-diversity of the assessed bifidobacterial profiling from the collected fecal samples. The predicted PCoA depicts the three-dimension arrangement of the collected samples based on their bifidobacterial community.

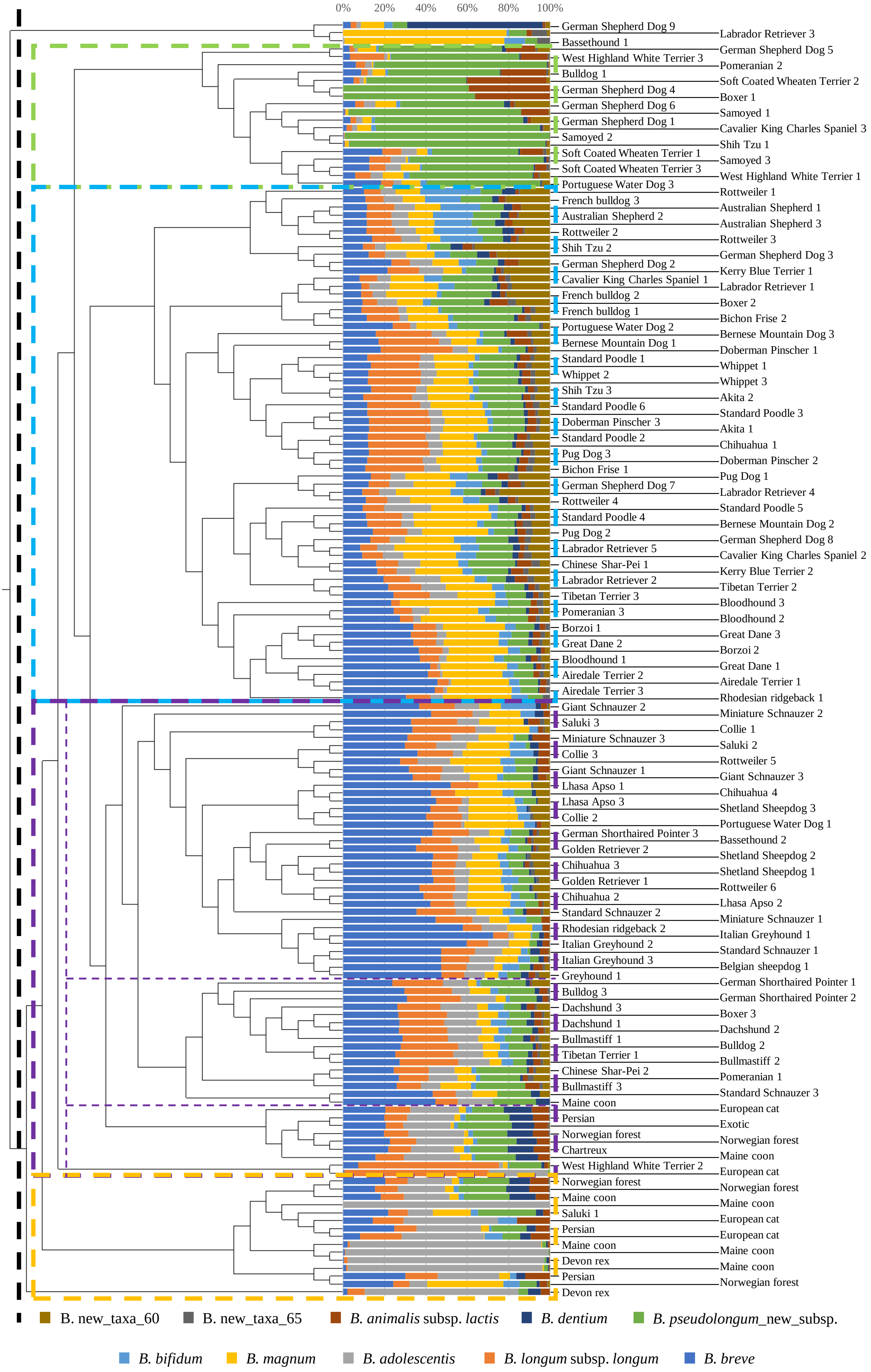


Figure S4. Evaluation of the breed-related effect on the bifidobacterial population of dogs and cats. The cladogram on the left depicts the hierarchical clustering of canine and feline fecal samples bsed on their average bifidobaterial relative abundance. The barplot in the centre reports the bifidobacterial relative abundance of the 10 most abundant bifidobacterial species.

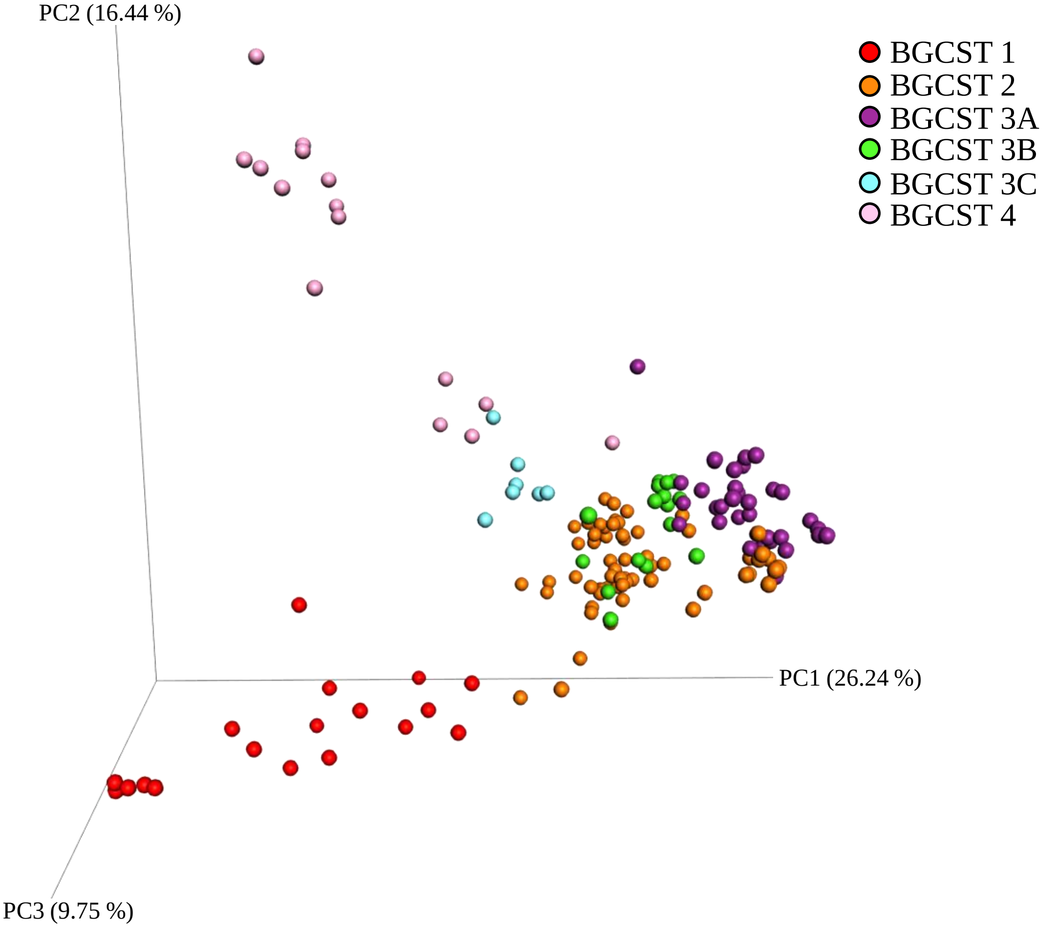
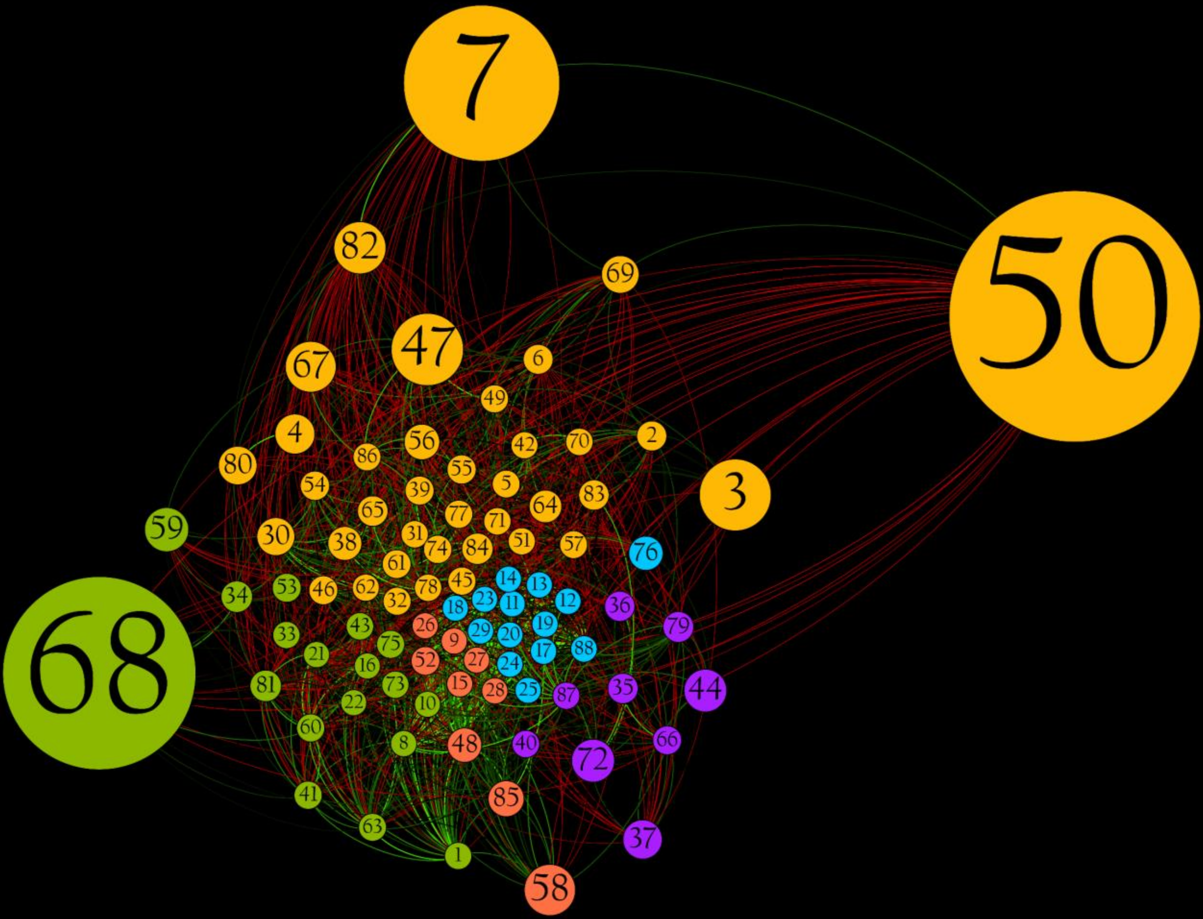


Figure S5. Assessment of the beta-diversity based on the BCGST classification. The predicted PCoA shows the three-dimensional separation of samples according to the identified BCGSTs.



Genera/Species	Label	Genera/Species	Label	Genera/Species	Label
Alistipes	"1"	*Butyricicoccus*	"31"	*Megasphaera*	"60"
Allobaculum	"2"	CAG-56	"32"	*Negativibacillus*	"61"
Alloprevotella	"3"	*Campylobacter*	"33"	*Oscillospira*	"62"
Anaerobiospirillum	"4"	*Catenibacterium*	"34"	*Parabacteroides*	"63"
Anaeroplasma	"5"	*Cetobacterium*	"35"	*Parasutterella*	"64"
Anaerostipes	"6"	Clostridium sensu stricto 1	"36"	*Peptoclostridium*	"65"
Bacteroides	"7"	Clostridium sensu stricto 3	"37"	*Peptostreptococcus*	"66"
B. adolescentis	"8"	*Collinsella*	"38"	*Phascolarctobacterium*	"67"
B. animalis subsp. *lactis*	"9"	*Coprococcus* 1	"39"	*Prevotella* 9	"68"
B. asteroides	"10"	*Coprococcus* 3	"40"	Prevotellaceae Ga6A1 group	"69"
B. bifidum	"11"	*Dialister*	"41"	Prevotellaceae UCG-004	"70"
B. breve	"12"	*Dysgonomonas*	"42"	Rikenellaceae RC9 gut group	"71"
B. catenulatum	"13"	*Eisenbergiella*	"43"	*Romboutsia*	"72"
B. cuniculi	"14"	*Escherichia-Shigella*	"44"	*Roseburia*	"73"
B. dentium	"15"	Eubacterium fissicatena group (Lachnospiraceae family)	"45"	Ruminococcaceae UCG-005	"74"
B. gallinarum	"16"	Eubacterium xylanophilum group (Lachnospiraceae family)	"46"	Ruminococcaceae UCG-014	"75"
B. longum subsp. *longum*	"17"	*Faecalibacterium*	"47"	Ruminococcus gnavus group (Lachnospiraceae family)	"76"
B. longum subsp. *suis*	"18"	*Faecalibaculum*	"48"	Ruminococcus torques group (Lachnospiraceae family)	"77"
B. magnum	"19"	*Fournierella*	"49"	*Slackia*	"78"
B. new_taxa_2	"20"	*Fusobacterium*	"50"	*Streptococcus*	"79"
B. new_taxa_50	"21"	GCA-900066575	"51"	*Succinatimonas*	"80"
B. new_taxa_55	"22"	Gram-negative bacterium cTPY-13	"52"	*Succinivibrio*	"81"
B. new_taxa_60	"23"	*Helicobacter*	"53"	*Sutterella*	"82"
B. new_taxa_65	"24"	*Holdemanella*	"54"	*Turicibacter*	"83"
B. new_taxa_89	"25"	*Lachnospira*	"55"	U. m. of Erysipelotrichaceae family	"84"
B. pseudocatenulatum	"26"	Lachnospiraceae NK4A136 group	"56"	U. m. of Muribaculaceae family	"85"
B. pseudolongum subsp. *globosum*	"27"	Lachnospiraceae UCG-007	"57"	U. m. of Ruminococcaceae family	"86"
B. pseudolongum subsp. *pseudolongum*	"28"	*Lactobacillus*	"58"	*Veillonella*	"87"
B. scardovii	"29"	*Megamonas*	"59"	*B. pseudolongum*_new_subsp.	"88"
Blautia	"30"				

Figure S6. Co-variance of bifidobacterial species and other microbial players of the canine and feline gut microbiota. The force-driven network shows the predicted co-variances with a p-value of < 0.05 between the bacterial genera with an average relative abundance of >1 % of the derived gut microbiota of dogs and cats, and the bifidobacterial ITS profiling data normalized for the *Bifidobacterium* genus relative abundance of each sample, obtained from the 16S rRNA gene sequencing. The node size is proportional to the average relative abundance of each microbial taxa, while the node color corresponds to the five observed clusters.