

**Fig. S1:** Relative abundance of taxa at greater than 5% at phylum (**A**) and family (**B**) levels. All taxa with less than 5% relative abundance were grouped into the "Other" category. FMT: fecal matter transplantation, IH: intermittent hypoxia, RA: room air

**Fig. S2:** EMPress plot depicting the phylogenetic tree of all features detected by 16S rRNA amplicon sequencing with concentric circles describing the following feature metadata from the innermost layer out: phylum, relative abundance within treatment group, W-score produced by ANCOM, Benjamini Hochberg-corrected p value of ALDEx2 generalized linear model and features significantly differing identified by ALDEx2 or ALDEx2 and ANCOM. FMT: fecal matter transfer, IH: intermittent hypoxia, PRO: probiotic, RA: room air

**Fig. S3:** Hierarchical cluster analysis of the 50 consistently detected ASVs in the gut microbiota. FMT: fecal matter transfer, IH: intermittent hypoxia, ASV: amplicon sequence variant, PRO: probiotic, RA: room air

**Fig. S4: FMT from IH-exposed mice impairs aortic function in naïve mice and VSL3 probiotic administration prevents such effects.** Cumulative concentration response curve of U46619 (A), acetylcholine (ACh) (B), and sodium nitroprusside (SNP) (C). Values are displayed as mean  $\pm$  S.D (n = 9 -10) mice. Statistical analysis was done using two-way ANOVA followed by Tukey post-test \*p < 0.05 vs. IH-FMT-PRO, #p < 0.05 vs. RA-FMT, \$p < 0.05 vs. RA-FMT-PRO. FMT: fecal matter transplantation, IH: intermittent hypoxia, PRO: probiotic, RA: room air, VEH: vehicle

## Supplementary materials

**Table S1:** Significant relative abundance taxa in in gut microbiome composition in naïve mice subjected to FMT from mice exposed to RA and IH and treated with VSL3

Taxon	Relative Abundance (Mean ± SD)				ANCOM W score	ALDEx2	
	RA FMT	RA FMT PRO	IH FMT	IH FMT PRO		glm.ep	glm.eBH
d__Bacteria; p__Firmicutes; c__Bacilli; o__Erysipelotrichales; f__Erysipelotrichaceae; g__Dubosiella; s__uncultured_bacterium	3.75% ± 1.23%	0.44% ± 0.27%	1.77% ± 0.89%	15.05% ± 5.65%		6.96E-09	4.05E-06
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Muribaculaceae; g__Muribaculaceae; s__uncultured_Bacteroidales	0.59% ± 0.17%	0.91% ± 0.26%	0.69% ± 0.05%	0.32% ± 0.02%		8.86E-08	2.11E-05
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Muribaculaceae; g__Muribaculaceae; s__uncultured_bacterium	0.08% ± 0.03%	0.15% ± 0.04%	0.41% ± 0.04%	0.26% ± 0.07%		8.94E-08	2.24E-05
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Muribaculaceae; g__Muribaculaceae; s__uncultured_Bacteroidales	0.72% ± 0.29%	0.19% ± 0.05%	0.07% ± 0.04%	0.16% ± 0.07%		5.72E-07	1.13E-04
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Muribaculaceae; g__Muribaculaceae; s__uncultured_bacterium	0.41% ± 0.16%	0.33% ± 0.02%	0.00% ± 0.00%	0.00% ± 0.00%	1700	1.25E-06	1.67E-04
d__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Streptococcaceae; g__Lactococcus; s__Lactococcus_lactis	0.00% ± 0.00%	0.11% ± 0.10%	0.00% ± 0.00%	0.26% ± 0.30%	1591	7.52E-06	5.09E-04
d__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Burkholderiales; f__Sutterellaceae; g__Parasutterella; s__uncultured_organism	0.25% ± 0.13%	1.00% ± 0.17%	0.11% ± 0.10%	0.16% ± 0.04%		4.14E-06	5.30E-04
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Muribaculaceae; g__Muribaculaceae; s__uncultured_organism	0.67% ± 0.36%	0.01% ± 0.01%	0.26% ± 0.09%	0.17% ± 0.09%	1623	7.93E-06	6.13E-04
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Muribaculaceae; g__Muribaculaceae; s__uncultured_bacterium	19.29% ± 4.36%	17.86% ± 4.95%	8.05% ± 1.08%	6.76% ± 3.20%		4.97E-06	6.58E-04
d__Bacteria; p__Actinobacteriota; c__Actinobacteria; o__Bifidobacteriales; f__Bifidobacteriaceae; g__Bifidobacterium; s__Bifidobacterium_animalis	0.00% ± 0.00%	0.13% ± 0.06%	0.00% ± 0.00%	0.15% ± 0.09%	1631	2.05E-05	1.09E-03
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Muribaculaceae; g__Muribaculaceae; s__uncultured_bacterium	0.35% ± 0.11%	0.30% ± 0.05%	0.11% ± 0.03%	0.36% ± 0.13%		2.28E-05	1.83E-03
d__Bacteria; p__Firmicutes; c__Bacilli;	0.65% ±	0.04% ±	0.16% ±	2.40% ±		5.17E-05	2.93E-03

o__Erysipelotrichales; f__Erysipelotrichaceae; g__Dubosiella; s__uncultured_bacterium	0.22%	0.06%	0.08%	0.89%			
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Muribaculaceae; g__Muribaculaceae; s__uncultured_bacterium	0.42% ± 0.13%	0.12% ± 0.02%	0.30% ± 0.10%	0.41% ± 0.21%		5.08E-05	3.52E-03
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Rikenellaceae; g__Alistipes; s__uncultured_bacterium	0.24% ± 0.14%	0.66% ± 0.19%	0.19% ± 0.09%	0.55% ± 0.10%		6.14E-05	4.14E-03
d__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Lactobacillaceae; g__Lactobacillus	5.89% ± 2.04%	1.99% ± 0.41%	10.49% ± 8.26%	2.20% ± 0.45%		6.79E-05	4.72E-03
d__Bacteria; p__Actinobacteriota; c__Coriobacteriia; o__Coriobacteriales; f__Atopobiaceae; g__Coriobacteriaceae_UCG-002; s__uncultured_bacterium	0.13% ± 0.09%	0.21% ± 0.15%	0.07% ± 0.02%	0.69% ± 0.31%		1.22E-04	6.89E-03
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Muribaculaceae; g__Muribaculaceae; s__uncultured_Bacteroidales	0.45% ± 0.27%	0.83% ± 0.22%	0.05% ± 0.05%	1.92% ± 0.89%		2.62E-04	9.45E-03
d__Bacteria; p__Actinobacteriota; c__Coriobacteriia; o__Coriobacteriales; f__Eggerthellaceae; g__Enterorhabdus	0.10% ± 0.05%	0.05% ± 0.02%	0.17% ± 0.04%	0.19% ± 0.02%		2.33E-04	9.79E-03
d__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__Rhodospirillales; f__uncultured; g__uncultured; s__Azospirillum_sp.	0.00% ± 0.00%	0.00% ± 0.00%	0.00% ± 0.00%	0.11% ± 0.05%	1577	5.48E-04	1.21E-02
d__Bacteria; p__Firmicutes; c__Clostridia; o__Lachnospirales; f__Lachnospiraceae; g__Lachnospiraceae_NK4A136_group	0.00% ± 0.00%	0.00% ± 0.00%	0.13% ± 0.12%	0.00% ± 0.00%	1557	5.36E-04	1.27E-02
d__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Burkholderiales; f__Sutterellaceae; g__Parasutterella; s__uncultured_bacterium	0.70% ± 0.22%	0.43% ± 0.09%	0.97% ± 0.18%	1.15% ± 0.22%		3.64E-04	1.47E-02
d__Bacteria; p__Firmicutes; c__Bacilli; o__RF39; f__RF39; g__RF39	0.01% ± 0.00%	0.00% ± 0.00%	0.02% ± 0.01%	0.05% ± 0.05%		7.27E-04	1.51E-02
d__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridia_UCG-014; f__Clostridia_UCG-014; g__Clostridia_UCG-014	0.00% ± 0.01%	0.01% ± 0.02%	0.17% ± 0.08%	0.03% ± 0.02%		5.52E-04	1.60E-02
d__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridia_UCG-014; f__Clostridia_UCG-014; g__Clostridia_UCG-014	0.01% ± 0.02%	0.19% ± 0.13%	0.18% ± 0.07%	0.02% ± 0.03%		6.09E-04	1.67E-02
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Muribaculaceae; g__Muribaculaceae; s__uncultured_bacterium	0.21% ± 0.13%	0.08% ± 0.02%	0.08% ± 0.02%	0.03% ± 0.02%		5.29E-04	1.73E-02
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Muribaculaceae; g__Muribaculaceae; s__uncultured_bacterium	1.20% ± 0.28%	2.24% ± 0.93%	2.72% ± 0.96%	3.39% ± 0.56%		5.48E-04	1.98E-02
d__Bacteria; p__Firmicutes; c__Clostridia;	0.00% ±	0.01% ±	0.04% ±	0.03% ±		1.28E-03	2.05E-02

o__Clostridiales; f__Clostridiaceae; g__Clostridium_sensu_stricto_1	0.00%	0.01%	0.01%	0.01%			
d__Bacteria; p__Firmicutes; c__Clostridia; o__Oscillospirales; f__Oscillospiraceae; g__uncultured; s__uncultured_Clostridiales	0.19% ± 0.10%	0.24% ± 0.11%	0.33% ± 0.09%	0.73% ± 0.30%		7.03E-04	2.27E-02
d__Bacteria; p__Firmicutes; c__Bacilli; o__Erysipelotrichales; f__Erysipelotrichaceae; g__Ileibacterium; s__Ileibacterium_valens	28.57% ± 5.19%	28.77% ± 13.01%	39.26% ± ± 7.85%	16.60% ± ± 5.86%		6.82E-04	2.35E-02
d__Bacteria; p__Firmicutes; c__Clostridia; o__Oscillospirales; f__Oscillospiraceae; g__Colidextribacter	0.06% ± 0.03%	0.00% ± 0.00%	0.03% ± 0.04%	0.05% ± 0.03%		1.64E-03	2.66E-02
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Rikenellaceae; g__Alistipes; s__uncultured_bacterium	0.04% ± 0.02%	0.22% ± 0.14%	0.43% ± 0.33%	0.32% ± 0.16%		8.68E-04	2.68E-02
d__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridia_UCG-014; f__Clostridia_UCG-014; g__Clostridia_UCG-014	0.00% ± 0.00%	0.03% ± 0.02%	0.15% ± 0.05%	0.01% ± 0.01%		1.70E-03	2.99E-02
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Muribaculaceae; g__Muribaculaceae; s__uncultured_bacterium	1.61% ± 0.66%	1.11% ± 0.10%	2.83% ± 1.25%	3.75% ± 0.78%		1.06E-03	3.14E-02
d__Bacteria; p__Firmicutes; c__Bacilli; o__Erysipelotrichales; f__Erysipelatoclostridiaceae; g__Erysipelatoclostridium; s__unidentified	0.09% ± 0.06%	0.07% ± 0.02%	0.00% ± 0.01%	0.00% ± 0.00%		2.08E-03	3.31E-02
d__Bacteria; p__Actinobacteriota; c__Coriobacteriia; o__Coriobacteriales; f__Eggerthellaceae; g__Enterorhabdus; s__uncultured_bacterium	0.05% ± 0.03%	0.15% ± 0.01%	0.04% ± 0.03%	0.05% ± 0.01%		1.45E-03	3.44E-02
d__Bacteria; p__Firmicutes; c__Clostridia; o__Lachnospirales; f__Lachnospiraceae	0.00% ± 0.00%	0.00% ± 0.00%	0.00% ± 0.00%	0.03% ± 0.01%		2.58E-03	3.78E-02
d__Bacteria; p__Firmicutes; c__Clostridia; o__Lachnospirales; f__Lachnospiraceae	0.10% ± 0.08%	0.00% ± 0.00%	0.03% ± 0.03%	0.00% ± 0.00%		3.20E-03	3.80E-02
d__Bacteria; p__Firmicutes; c__Clostridia; o__Oscillospirales; f__UCG-010; g__UCG-010; s__unidentified	0.04% ± 0.02%	0.09% ± 0.03%	0.01% ± 0.01%	0.00% ± 0.00%		3.93E-03	3.84E-02
d__Bacteria; p__Firmicutes; c__Bacilli; o__Erysipelotrichales; f__Erysipelotrichaceae; g__Faecalibaculum; s__uncultured_bacterium	0.14% ± 0.04%	0.62% ± 0.36%	0.30% ± 0.15%	0.14% ± 0.01%		1.60E-03	3.91E-02
d__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Streptococcaceae; g__Streptococcus; s__Streptococcus_danieliae	0.00% ± 0.00%	0.00% ± 0.00%	0.03% ± 0.01%	0.00% ± 0.00%		2.39E-03	4.16E-02
d__Bacteria; p__Firmicutes; c__Clostridia; o__Oscillospirales; f__[Eubacterium]_coprostanoligenes_group; g__[Eubacterium]_coprostanoligenes_group; s__uncultured_bacterium	0.00% ± 0.00%	0.00% ± 0.00%	0.06% ± 0.05%	0.01% ± 0.01%		3.15E-03	4.34E-02
d__Bacteria; p__Firmicutes; c__Clostridia;	0.04% ±	0.33% ±	0.05% ±	0.00% ±		2.80E-03	4.66E-02

o__Oscillospirales; f__Ruminococcaceae; g__Incertae_Sedis; s__uncultured_bacterium	0.05%	0.12%	0.06%	0.00%			
d__Bacteria; p__Firmicutes; c__Clostridia; o__Peptococcales; f__Peptococcaceae; g__uncultured; s__unidentified	0.04% ± 0.05%	0.00% ± 0.00%	0.03% ± 0.02%	0.07% ± 0.03%		5.07E-03	4.76E-02
d__Bacteria; p__Actinobacteriota; c__Coriobacteriia; o__Coriobacteriales; f__Eggerthellaceae; g__Gordonibacter; s__uncultured_bacterium	0.13% ± 0.08%	0.19% ± 0.04%	0.08% ± 0.05%	0.05% ± 0.01%		2.54E-03	4.91E-02









