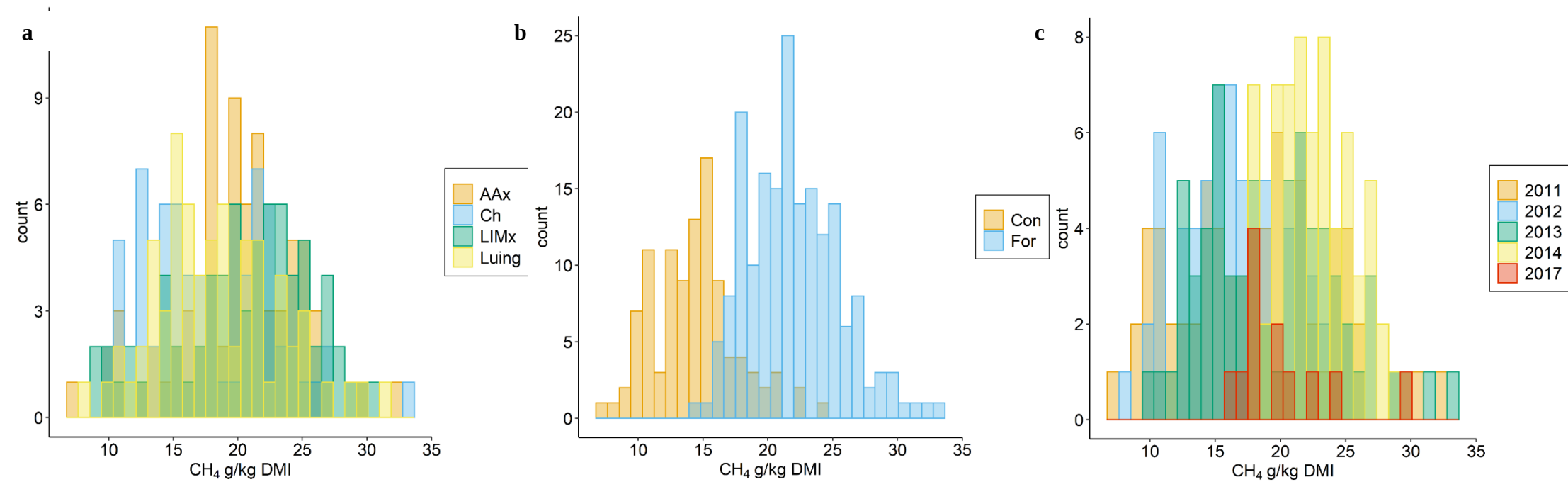
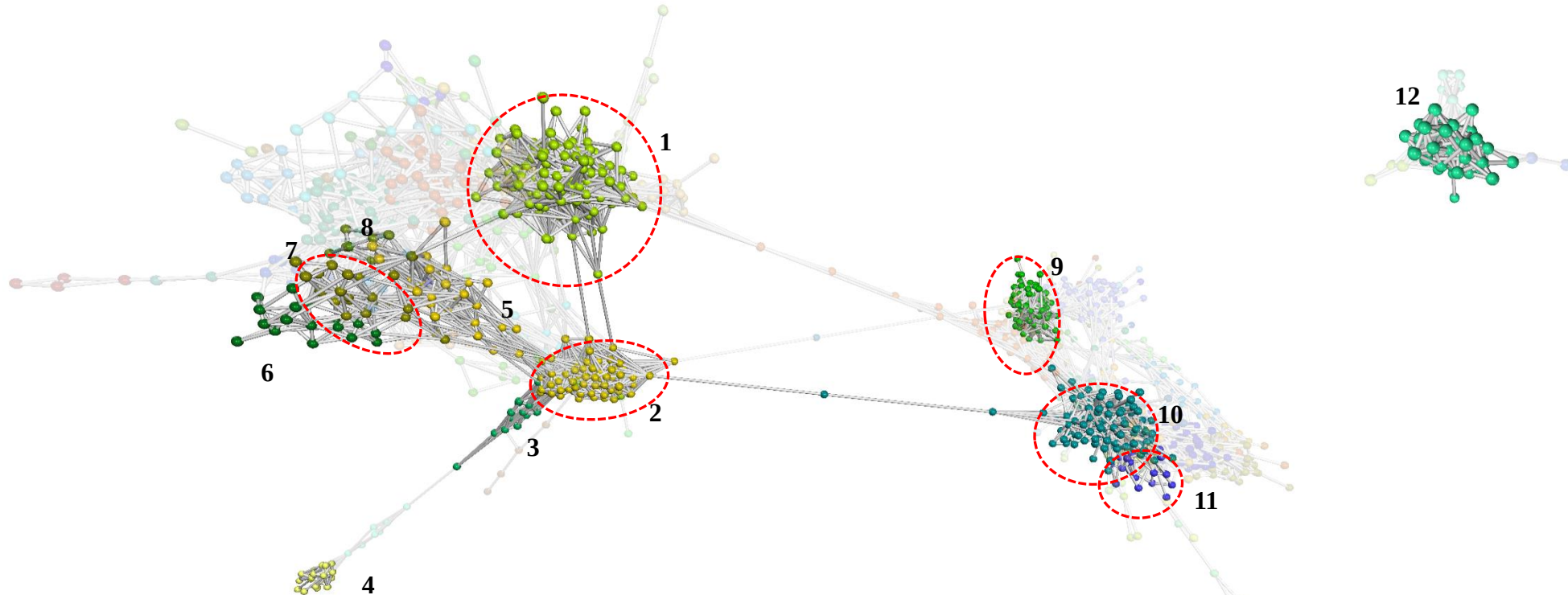
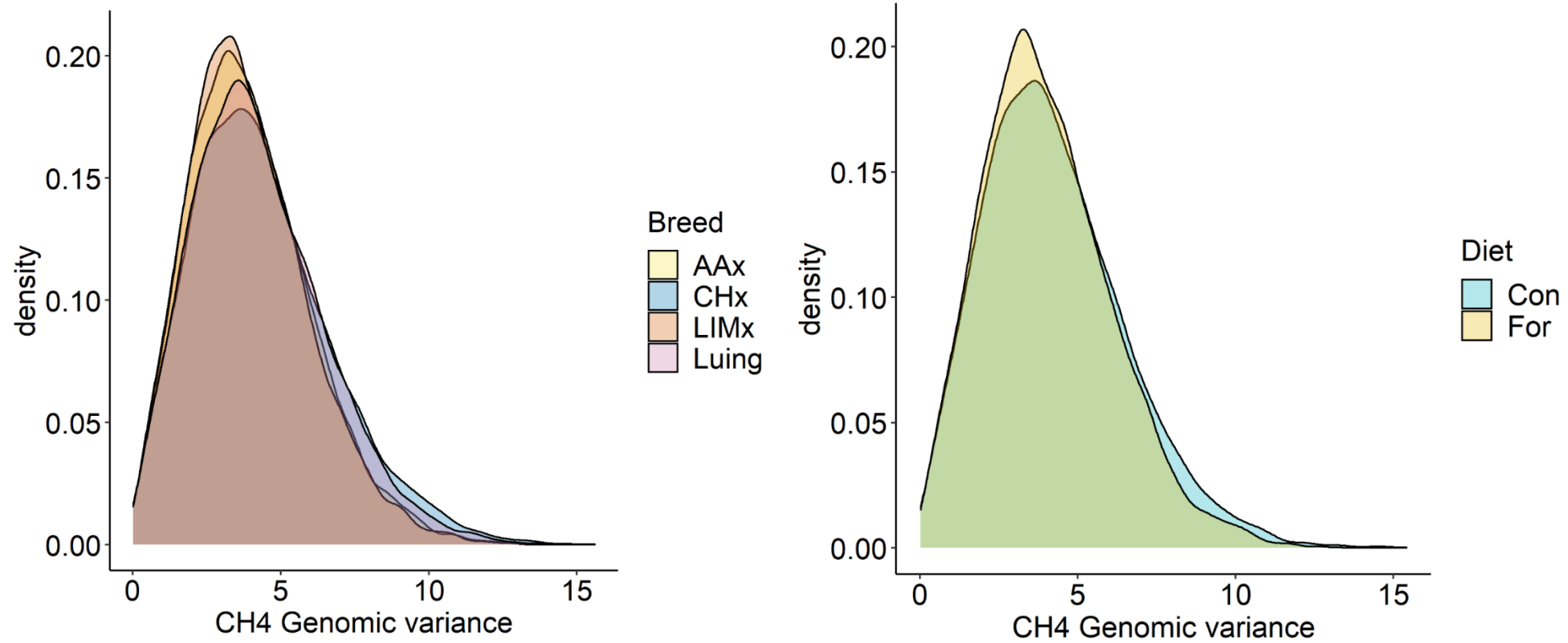




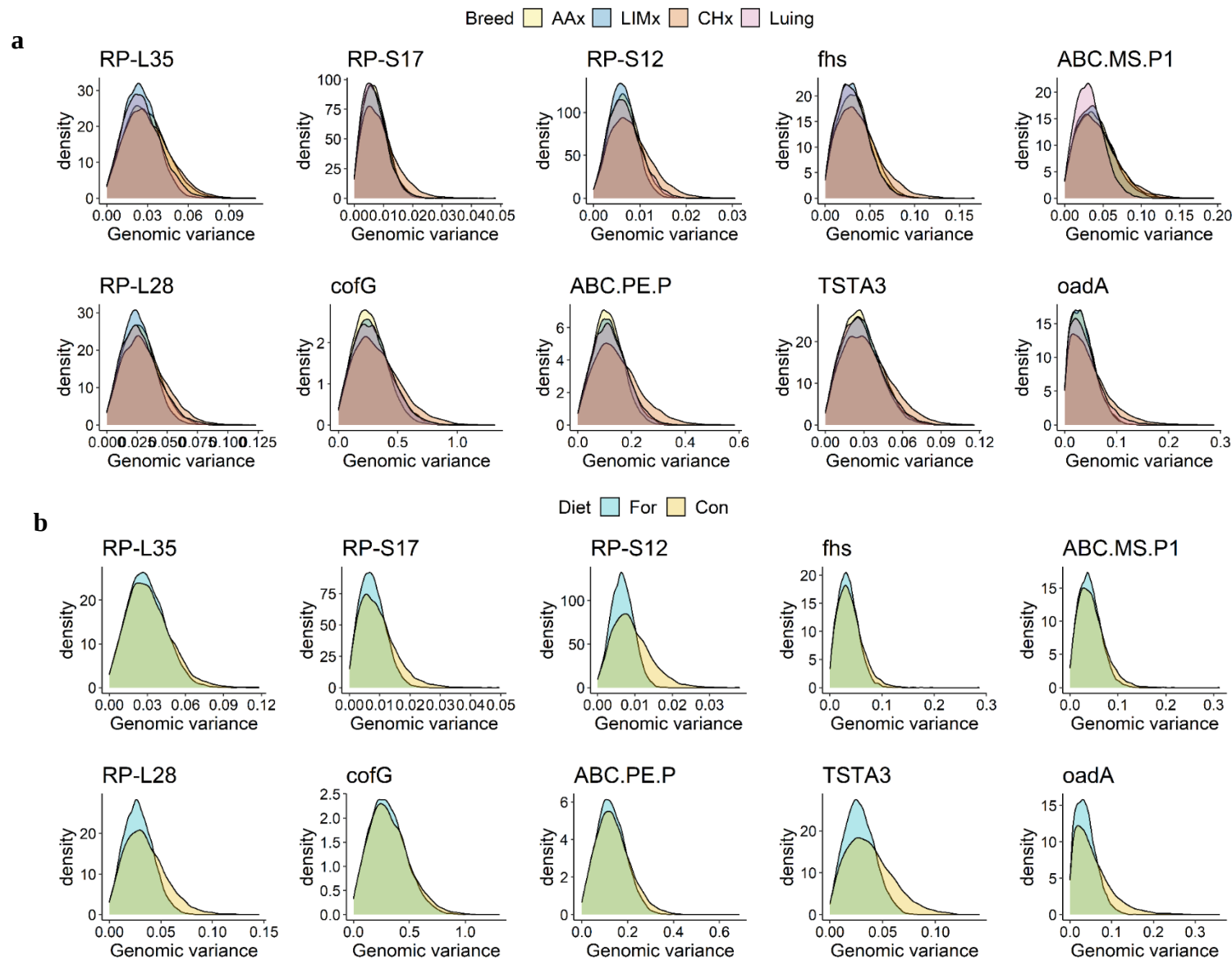
Supplementary Figure 1 | Phenotypic variability observed in methane emissions (CH₄). Variability within animals from (a) the same breed (Aberdeen Angus (AAx), Charolais (Ch), Limousin (LIMx) or Luing), (b) offered the same diet (concentrate (Con) or forage (For) based) or (c) from the same experiment (2011, 2012, 2013, 2014 and 2017). Coefficient of variation within animals from the same breeds are AAx 23.9%, Ch 28.5%, LIMx 23.2%, Luing 28.3%; within animals offered the same diet are 16.3% for forage-based and 22.6% for concentrate-based; and within animals belonging to the same experiment: 31.1% 2011, 25.5% 2012, 27.2% 2013, 13.36% 2014 and 18.8% 2017



Supplementary Figure 2 | Network clusters of commonly host-genomically affected abundances of microbial genera/RUGs/genes identified in the bovine rumen. Nodes represent microbial genus/RUG/genes, and edges represent Pearson correlations among deregressed genomic effects of log-ratio transformed genera/RUGs/gene abundances > 0.70 ($n = 359$ animals). Clusters numbered from 1 to 12 are those including ≥ 3 methanogenic archaea genera, RUGs and microbial genes involved in methane (CH_4) metabolism pathway according to KEGG database or microbial genera/RUGs/genes host-genomically correlated with CH_4 emissions (probability of the host-genomic correlation being higher or lower than 0 (P_0) ≥ 0.95). Red dashed circles indicate the clusters including a combination of methanogenic archaea genera or RUGs and microbial genes involved in the CH_4 metabolism pathway and microbial genera, RUGs and genes significantly ($P_0 \geq 0.95$) host-genomically correlated with CH_4 emissions. 1) Cluster 01 containing 272 microbial genes from which 9 are involved in CH_4 metabolism (*serA*, *serC*, *glyA*, *pta*, *ackA*, *fbaA*, *gpmA*, *acs*); and 11 show positive r_{gCH_4} from 0.71 to 0.85 ($P_0 \geq 0.95$) mainly representing the ribosomal small and large protein biosynthesis (*RP-L3*, *RP-L6*, *RP-L23*, *RP-L28*, *RP-L34*, *RP-S10*, *RP-S12*); 2) Cluster 02 containing *Methanobrevibacter* genera and 194 microbial genes; from which 43 encode proteins required for methanogenesis (e.g. *methyl-coenzyme M* (*mcrA*, *mcrB*, *mcrC*, *mcrG*), *coenzyme F₄₂₀* (*frhA*, *frhB*, *frhG*), *tetrahydromethanopterin S-methyltransferase* (*mtrA*, *mtrD*, *mtrE*, *mtrG*, *mtrH*)) and 2 which display strong negative r_{gCH_4} of -0.71 and -0.73 with $P_0 \geq 0.95$ (*cofG* in CH_4 metabolism and *queD* in folate biosynthesis); 3) Cluster 21 with 13 out of 19 microbial genes with negative r_{gCH_4} from -0.71 to -0.88 ($P_0 \geq 0.96$) representing arginine (*argD*) and phenylalanine metabolism (*paaH*), pyrimidine metabolism (*upp*), peptide/nickel quorum sensing transport (*ABC.PE.P*), protein export (*secD* and *secF*), nitrogen fixation (*nifU*), copper transport (*copB*), and bacterial conversion of bile acids (*choloalglycine hydrolase*); 4) Cluster 19 made from 20 microbial genes from which 11 are negatively host-genomically correlated to CH_4 emissions with r_{gCH_4} from -0.82 to -0.93, $P_0 \geq 0.96$ involved in e.g., ABC transport (*livH*, *livK* and *livG*) and biosynthesis (*ilvA*) of branched-chain amino acids, propionogenesis by lactaldehyde route (*fucO*) and sucrose metabolism (*sucrose phosphorylase*); 5) Cluster 14 with 38 microbial genes including 17 with negative r_{gCH_4} (-0.69 to -0.91, $P_0 \geq 0.95$) associated to cobalt/nickel transport (*cbiQ*, *cbiO*) amino acid biosynthesis (*trpA*, *trpE*, *lysA*), porphyrin metabolism (*hemC*) and histidine metabolism (*hisA*, *hisF*); 6) Cluster 22 built by 18 microbial genes from which 9 show negative r_{gCH_4} (-0.78 to -0.92, $P_0 \geq 0.96$, e.g. associated to peptide/nickel transport (*ABC.PE.S*, *ABC.PE.P1*, *ABC.PE.A*), polar amino acid transport (*ABC.PA.A*), or aminoacyl-tRNA biosynthesis (*gatC*, *gata*); 7) Cluster 18 composed of 20 microbial genes including 6 with negative r_{gCH_4} from -0.76 to -0.87 ($P_0 \geq 0.95$) involved in methionine transport (*metE*, *metN* and *metQ*), oxocarboxylic chain extension (ACO), propionigenesis (*pccB*) and arginine biosynthesis (*argF*) and one microbial gene encoding for *enolase* in CH_4 metabolism; 8) Cluster 42 composed by 7 microbial genes including 4 with r_{gCH_4} from -0.80 to -0.85 ($P_0 \geq 0.95$), e.g., *cobL* in porphyrin metabolism, *baiN* in secondary bile acids biosynthesis and neurotransmitter:Na⁺ symporter (*TC.NSS*); 9) Cluster 04 with 163 microbial genera from which 117 are fungi including *Moniliophthora*, *Histoplasma* and *Metschnikowia* ($r_{\text{gCH}_4} = 0.74$ -0.83, $P_0 \geq 0.95$) and 5 are methanogenic archaea (*Methanocaldococcus*, *Methanococcus*, *Methanosarcina*, *Methanothermococcus* and *Methanotorris*); 10) Cluster 03 composed by 175 microbial genera containing *Methanocella* and *Candidatus Methanoplasma* methanogenic genera together with Proteobacteria *Ottowia* which showed a r_{gCH_4} of 0.85 ($P_0 = 0.95$); 11) Cluster 16 composed of 24 microbial genera mainly from Proteobacteria phyla but also including including *Syntrophobotulus* Firmicutes ($r_{\text{gCH}_4} = -0.79$, $P_0 = 0.95$) and methanogens *Methanomassiliicoccus* and *Methanosaeta*; 12) Cluster 11 built with 62 RUGs, 9 annotated as uncultured *Methanobrevibacter* sp. from which 5 are host-genomically correlated to CH_4 emissions, positively ($r_{\text{gCH}_4} = 0.91$, $P_0 = 0.99$) and negatively ($r_{\text{gCH}_4} = -0.72$ to -0.86, $P_0 \geq 0.95$); and 22 annotated as uncultured *Prevotellaceae bacterium* from which 5 are positively host-genomically correlated with CH_4 emissions ($r_{\text{gCH}_4} = 0.83$ to 0.92, $P_0 \geq 0.97$).



Supplementary Figure 4 | Marginal posterior distributions of genomic variances of methane emissions (g/kg DMI) partitioned across breeds (AAx, Aberdeen Angus, CHx, Charolais, LIMx, Limousin, LuIng, LuIng breed) and across different basal diets (For=Forage or Con=Concentrate).



Supplementary Figure 5 | Marginal posterior distributions of the genomic variances of 10 microbial gene abundances selected for microbiome-driven breeding. a. Genomic variances partitioned across breeds (AAx, Aberdeen Angus, CHx, Charolais, LIMx, Limousin, Luig, Luig breed) and **b.** across different basal diets (For=Forage or Con=Concentrate).

Supplementary Table 1. Descriptive statistics of methane emissions (CH₄, g/kg DMI) by breeds, computed using raw data or adjusted data by the interaction of breed, diet and experiment.

	Before adjustment (raw data)				After adjustment by breed x diet x experiment		
	n	Mean ¹	Sd ²	CV(%)	Mean	Sd ³	CV(%)
Aberdeen Angus X	75	19.8	4.7	23.9	13.47	3.20	23.75
Limousin X	71	18	5.1	28.5	13.47	3.26	24.18
Charolais X	69	20.6	5.2	25.2	13.47	3.58	26.59
Luining	70	18.4	4.8	26	13.47	3.61	26.83

¹A one-way ANOVA analysis using CH₄ as a trait and fitting breed as fixed effect resulted in breed explaining 4.5% of total CH₄ phenotypic variance (P-val=0.006).

²The Levene test indicated that phenotypic variance of CH₄ emissions was non-significantly different among breeds (P-val = 0.4749)

³The Levene test indicated that phenotypic variance of CH₄ emissions data after adjustment was non-significantly different among breeds (P-val = 0.5763)

Supplementary Table 2. Descriptive statistics of methane emissions (CH₄, g/kg DMI) by diets, computed using raw data or adjusted data by the interaction of breed, diet and experiment

	Before adjustment (raw data)				After adjustment by breed x diet x experiment		
	n	Mean ¹	Sd ²	CV(%)	Mean	Sd ³	CV(%)
Forage-based	182	22	3.6	16.3	13.47	3.41	25.34
Concentrate-based	103	14.3	3.2	22.6	13.47	3.09	22.95

¹One-way ANOVA analysis using CH₄ as a trait and fitting diet as fixed effect revealed that diet explained 52.7% of total CH₄ phenotypic variance (P-val<2.2x10⁻¹⁶).

²The Levene test indicated that phenotypic variance of CH₄ emissions was non-significantly different between diets (P-val = 0.1886)

³The Levene test indicated that phenotypic variance of CH₄ emissions data after adjustment was non-significantly different between diets (P-val = 0.3816)