

1 Supplementary Table

Table S1. Co-occurrence or exclusive taxa information was analyzed using CoDiNA, and correlation coefficients for each breed. Correlation coefficients were analyzed based on SparCC

Node 1	Node 2	Correlation coefficients			Phi score ¹⁾	Phi tilde score ²⁾	Internal score ³⁾
		Hanwoo	Angus	Wagyu			
Hanwoo exclusive correlation							
<i>Bacteroides</i>	<i>Desulfovibrio</i>	-0.539	-	-	0.307	0.452	0.461
<i>Bifidobacterium</i>	<i>Streptococcus</i>	0.668	0.189	0.257	0.610	0.905	0.460
<i>Blautia</i>	<i>Faecalicatena</i>	0.668	-	0.288	0.590	0.875	0.440
<i>Capnocytophaga</i>	<i>Ureaplasma</i>	0.695	-	0.297	0.634	0.940	0.426
<i>Erysipelothrix</i>	<i>Bacteroides</i>	0.524	-	-0.255	0.373	0.550	0.540
<i>Olsenella</i>	<i>Desulfovibrio</i>	0.654	-	0.254	0.552	0.818	0.429
<i>Olsenella</i>	<i>Lacrimispora</i>	-0.556	-	-0.247	0.411	0.608	0.508
<i>Olsenella</i>	<i>Paenibacillus</i>	-0.703	0.177	-	0.587	0.870	0.345
<i>Paenibacillus</i>	<i>Enterocloster</i>	-0.510	0.286	-	0.376	0.555	0.568
<i>Prevotella</i>	<i>Ureaplasma</i>	-0.502	0.279	-	0.361	0.533	0.571
<i>Ruminiclostridium</i>	<i>Sporomusa</i>	0.568	-0.319	-	0.476	0.704	0.537
<i>Selenomonas</i>	<i>Capnocytophaga</i>	-0.709	-	-	0.563	0.834	0.291
<i>Streptococcus</i>	<i>Prevotella</i>	0.663	0.308	-0.280	0.674	1.000	0.536
<i>Streptococcus</i>	<i>Selenomonas</i>	0.573	0.215	0.229	0.479	0.709	0.530
<i>Ureaplasma</i>	<i>Treponema</i>	-0.727	-	-	0.590	0.874	0.273
Angus exclusive correlation							
<i>Acetivibrio</i>	<i>Dialister</i>	-0.104	-0.784	-0.210	0.727	0.727	0.319
<i>Acetivibrio</i>	<i>Prevotella</i>	-	-0.625	-	0.437	0.437	0.375
<i>Clostridium</i>	<i>Dialister</i>	-0.237	-0.802	-0.282	0.823	0.823	0.418
<i>Clostridium</i>	<i>Pedobacter</i>	-	0.592	0.289	0.488	0.488	0.500
<i>Dialister</i>	<i>Prevotella</i>	0.329	1.000	-	1.000	1.000	0.329
<i>Dialister</i>	<i>Treponema</i>	0.077	0.754	-	0.637	0.637	0.258
<i>Enterocloster</i>	<i>Prevotella</i>	-0.235	0.627	-	0.504	0.504	0.441
<i>Enterocloster</i>	<i>Sporomusa</i>	-	0.578	-0.293	0.472	0.472	0.513
<i>Erysipelothrix</i>	<i>Desulfovibrio</i>	-0.255	-0.605	-	0.485	0.485	0.470
<i>Erysipelothrix</i>	<i>Prevotella</i>	-	0.827	-	0.741	0.741	0.173
<i>Modestobacter</i>	<i>Dialister</i>	0.129	0.636	0.181	0.511	0.511	0.427
<i>Paenibacillus</i>	<i>Dialister</i>	-0.164	0.589	-	0.417	0.417	0.442
<i>Prevotella</i>	<i>Desulfovibrio</i>	-	-0.653	0.318	0.589	0.589	0.470
<i>Prevotella</i>	<i>Pedobacter</i>	-	-0.686	-	0.529	0.529	0.314
<i>Sporomusa</i>	<i>Dialister</i>	0.081	0.750	0.135	0.649	0.649	0.296
Wagyu exclusive correlation							
<i>Acetivibrio</i>	<i>Ruminiclostridium</i>	-0.288	-	0.572	0.461	0.461	0.515
<i>Acetivibrio</i>	<i>Ruminiclostridium</i>	-0.288	-	0.572	0.461	0.461	0.515
<i>Bacteroides</i>	<i>Treponema</i>	-	-	0.786	0.678	0.678	0.214
<i>Bifidobacterium</i>	<i>Capnocytophaga</i>	-	0.251	-0.582	0.450	0.450	0.488
<i>Bifidobacterium</i>	<i>Capnocytophaga</i>	-	0.251	-0.582	0.450	0.450	0.488
<i>Clostridium</i>	<i>Faecalicatena</i>	-	0.255	1.000	1.000	1.000	0.255
<i>Enterocloster</i>	<i>Capnocytophaga</i>	0.306	-	0.578	0.481	0.481	0.521
<i>Enterocloster</i>	<i>Capnocytophaga</i>	0.306	-	0.578	0.481	0.481	0.521
<i>Mogibacterium</i>	<i>Bacteroides</i>	-	-	-0.770	0.655	0.655	0.230

<i>Mogibacterium</i>	<i>Faecalicatena</i>	-	-	0.708	0.562	0.562	0.292
<i>Mogibacterium</i>	<i>Prevotella</i>	0.310	-0.309	-0.612	0.629	0.629	0.585
<i>Mogibacterium</i>	<i>Prevotella</i>	0.310	-0.309	-0.612	0.629	0.629	0.585
<i>Mogibacterium</i>	<i>Treponema</i>	-	-	-0.745	0.617	0.617	0.255
<i>Olsenella</i>	<i>Mogibacterium</i>	-	0.231	0.612	0.480	0.480	0.452

¹⁾ Measurements the consistency of the direction (positive or negative correlation) of an edge across different treatments or phenotypes
²⁾ A normalized version of the Phi score those accounts for the imbalance in edge
³⁾ The degree of connectivity of a node within its own condition-specific network
For selection of nodes and edges, the median values of external and internal scores were used as thresholds, and only edges with over 0.4 of phi score

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Table S2. Co-occurrence or exclusive predicted functions information was analyzed using CoDiNA, and correlation coefficients for each breed. Correlation coefficients were analyzed based on SparCC

Node 1	Node 2	Correlation coefficients			Phi score ¹⁾	Phi tilde score ²⁾	Internal score ³⁾
		Hanwoo	Angus	Wagyu			
Hanwoo exclusive correlation							
M00006	M00025	-0.669	-0.203	-	0.707	0.842	0.388
M00022	M00023	0.510	-	0.232	0.442	0.526	0.542
M00022	M00916	0.573	-0.153	-	0.505	0.601	0.453
M00025	M00169	0.525	-	-	0.374	0.445	0.475
M00064	M00170	0.548	0.253	-	0.525	0.625	0.518
M00095	M00925	0.591	-	0.241	0.591	0.704	0.474
M00114	M00365	-0.568	-0.227	-	0.541	0.644	0.488
M00115	M00365	-0.666	-0.320	-0.208	0.839	1.000	0.507
M00169	M00170	-0.571	-0.270	-	0.579	0.689	0.507
M00170	M00740	-0.587	-0.210	-0.247	0.654	0.779	0.525
M00849	M00925	0.587	-	0.314	0.643	0.766	0.519
Angus exclusive correlation							
M00003	M00365	-	-0.579	-0.178	0.528	0.521	0.457
M00006	M00023	-	-0.621	-0.254	0.654	0.655	0.456
M00006	M00028	-	-0.595	-	0.508	0.499	0.405
M00006	M00036	-	0.645	0.154	0.639	0.638	0.387
M00006	M00095	-	0.743	0.272	0.885	0.899	0.374
M00006	M00135	-	0.637	-	0.588	0.584	0.363
M00006	M00365	-	0.653	-	0.618	0.617	0.347
M00006	M00570	-0.282	-0.543	-	0.539	0.533	0.537
M00006	M00844	-	-0.624	-	0.563	0.558	0.376
M00006	M00845	-0.269	-0.632	-	0.684	0.686	0.456
M00006	M00849	-	0.706	0.329	0.862	0.874	0.441
M00023	M00032	-0.203	-0.635	-0.317	0.782	0.790	0.524
M00023	M00117	-	-0.721	-0.241	0.825	0.836	0.369
M00023	M00135	-0.296	-0.563	-	0.586	0.582	0.528
M00023	M00570	-	0.566	0.282	0.579	0.575	0.517
M00025	M00899	-	0.510	-0.198	0.415	0.401	0.529
M00026	M00609	-	0.599	0.329	0.679	0.680	0.519
M00028	M00064	-	0.543	-0.196	0.475	0.464	0.497
M00028	M00169	-	-0.543	0.176	0.461	0.450	0.490
M00028	M00609	-	0.545	0.156	0.453	0.441	0.481
M00028	M00916	0.307	0.707	-	0.845	0.857	0.425
M00029	M00064	-	0.553	-0.183	0.484	0.473	0.483
M00029	M00916	-	0.583	-0.156	0.525	0.517	0.445
M00036	M00916	-0.255	-0.681	-0.285	0.865	0.878	0.497
M00064	M00135	-0.301	-0.585	-	0.629	0.628	0.513
M00064	M00344	-0.263	-0.582	-0.161	0.629	0.628	0.519
M00064	M00845	-	0.554	-0.283	0.559	0.554	0.528
M00064	M00922	0.221	0.608	0.195	0.663	0.663	0.491
M00095	M00117	-	0.725	-	0.757	0.763	0.275
M00117	M00135	0.298	0.727	0.302	0.980	1.000	0.504

M00117	M00365	-	0.660	-	0.633	0.632	0.340
M00117	M00849	-	0.701	-	0.711	0.714	0.299
M00117	M00916	-	-0.620	-	0.556	0.550	0.380
M00135	M00169	0.308	0.650	-	0.747	0.753	0.466
M00365	M00609	-	-0.705	-	0.719	0.723	0.295
M00570	M00916	0.284	0.577	-	0.599	0.596	0.509
M00609	M00844	-	0.559	0.229	0.525	0.517	0.497
M00609	M00845	-	0.593	0.208	0.572	0.568	0.457
M00855	M00925	0.283	0.542	-	0.539	0.533	0.539
M00899	M00925	-	0.595	0.151	0.544	0.537	0.432
Wagyu exclusive correlation							
M00003	M00018	-	0.312	0.562	0.741	0.741	0.529
M00003	M00022	-	-	0.743	0.894	0.894	0.204
M00003	M00115	-	0.286	0.683	0.740	0.740	0.528
M00003	M00169	-	-	0.653	0.535	0.535	0.391
M00003	M00525	-	0.230	0.572	0.739	0.739	0.484
M00003	M00526	-	0.249	0.571	0.940	0.940	0.525
M00003	M00527	-	0.232	0.574	0.521	0.521	0.540
M00003	M00950	-0.301	-0.225	-0.685	0.823	0.823	0.436
M00006	M00010	-	-	0.547	0.648	0.648	0.432
M00006	M00012	-	0.279	0.538	0.658	0.658	0.432
M00006	M00740	-	-	0.614	0.656	0.656	0.415
M00006	M00899	-	-0.200	-0.542	0.690	0.690	0.428
M00007	M00015	-	0.173	0.613	0.718	0.718	0.368
M00007	M00018	-	-	0.773	0.750	0.750	0.398
M00007	M00022	-	0.282	0.624	0.734	0.734	0.372
M00007	M00026	-	-	0.619	0.623	0.623	0.422
M00007	M00029	-	-	0.740	0.740	0.740	0.455
M00007	M00045	-	-0.222	-0.665	0.472	0.472	0.505
M00007	M00525	-	-	0.798	0.625	0.625	0.344
M00007	M00526	-	-	0.796	0.787	0.787	0.260
M00007	M00527	-	-	0.795	0.660	0.660	0.326
M00007	M00570	0.224	0.229	0.695	0.566	0.566	0.462
M00007	M00909	0.275	-	0.535	0.743	0.743	0.434
M00010	M00849	0.288	-	0.615	0.629	0.629	0.585
M00012	M00916	-	-0.238	-0.681	0.780	0.780	0.456
M00015	M00718	-	-0.254	-0.538	0.731	0.731	0.491
M00015	M00909	-	-	0.668	0.542	0.542	0.387
M00016	M00034	-	0.312	0.667	0.553	0.553	0.533
M00016	M00036	-	-0.287	-0.542	0.554	0.554	0.485
M00016	M00344	-	-	0.738	0.416	0.416	0.453
M00016	M00573	-0.219	-	-0.504	0.629	0.629	0.501
M00016	M00718	-	-	-0.722	0.528	0.528	0.540
M00016	M00897	-	0.194	0.625	0.679	0.679	0.470
M00016	M00909	-	-	0.679	0.523	0.523	0.397
M00018	M00034	-	0.241	0.646	0.817	0.817	0.421
M00018	M00718	-	-	-0.674	0.475	0.475	0.500
M00018	M00897	-	0.294	0.653	0.588	0.588	0.424

M00018	M00909	-	-	0.690	0.532	0.532	0.392
M00022	M00034	-	-	0.588	0.897	0.897	0.202
M00022	M00117	-0.249	-	-0.590	0.495	0.495	0.540
M00022	M00123	-0.227	-0.179	-0.591	0.678	0.678	0.214
M00022	M00377	-	0.160	0.670	0.865	0.865	0.491
M00022	M00573	-0.241	-0.257	-0.666	1.000	1.000	0.255
M00022	M00577	-0.228	-0.171	-0.588	0.617	0.617	0.255
M00022	M00609	-	-	0.695	0.592	0.592	0.361
M00022	M00897	-	-	0.551	0.711	0.711	0.299
M00022	M00909	-	0.233	0.720	0.595	0.595	0.480
M00022	M00950	-0.297	-	-0.549	0.480	0.480	0.452
M00025	M00029	-	0.196	0.702	0.543	0.543	0.540
M00025	M00034	-	0.290	0.801	0.577	0.577	0.461
M00025	M00045	-	-	-0.656	0.764	0.764	0.357
M00025	M00135	-	-	-0.541	0.686	0.686	0.399
M00025	M00344	-	0.161	0.559	0.543	0.543	0.447
M00025	M00570	-	0.204	0.657	0.465	0.465	0.507
M00025	M00896	-0.185	0.225	-0.548	0.491	0.491	0.535
M00026	M00718	-	-	-0.564	1.000	1.000	0.351
M00026	M00909	-	-	0.615	0.891	0.891	0.205
M00028	M00897	-	0.162	0.530	0.586	0.586	0.488
M00029	M00344	-	-0.253	0.583	0.818	0.818	0.364
M00029	M00718	-	-	-0.744	0.482	0.482	0.470
M00032	M00525	-	-0.264	-0.560	0.601	0.601	0.538
M00032	M00526	-	-0.273	-0.551	0.787	0.787	0.427
M00032	M00527	-	-0.265	-0.557	0.562	0.562	0.496
M00034	M00525	-	0.223	0.630	0.554	0.554	0.514
M00034	M00526	-	0.228	0.633	0.546	0.546	0.525
M00034	M00527	-	0.206	0.640	0.549	0.549	0.516
M00036	M00718	-	0.203	0.536	0.550	0.550	0.486
M00045	M00344	-	-	-0.595	0.595	0.595	0.446
M00045	M00527	-	-0.284	-0.549	0.507	0.507	0.527
M00095	M00899	-0.193	-	-0.659	0.421	0.421	0.542
M00096	M00123	-0.211	-	-0.589	0.629	0.629	0.585
M00096	M00573	-0.225	-	-0.638	0.562	0.562	0.292
M00096	M00577	-0.209	-	-0.586	0.461	0.461	0.515
M00096	M00909	-	0.293	0.697	0.695	0.695	0.513
M00096	M00950	-0.290	-	-0.586	0.655	0.655	0.230
M00115	M00123	-0.167	-	-0.591	0.632	0.632	0.463
M00115	M00169	0.274	-	0.663	0.571	0.571	0.491
M00115	M00573	-0.169	-	-0.633	0.669	0.669	0.481
M00115	M00577	-0.168	-	-0.587	0.578	0.578	0.489
M00115	M00950	-0.308	-	-0.624	0.481	0.481	0.521
M00122	M00916	0.314	0.199	0.618	0.811	0.811	0.485
M00123	M00176	0.250	-	0.580	0.481	0.481	0.521
M00123	M00308	-0.279	-0.233	-0.617	0.702	0.702	0.486
M00123	M00609	-	-	-0.603	0.783	0.783	0.262
M00169	M00308	-	0.174	0.588	0.688	0.688	0.367

M00169	M00609	-	-0.217	0.593	0.729	0.729	0.372
M00176	M00573	0.250	-	0.611	0.461	0.461	0.515
M00176	M00577	0.248	-	0.577	0.450	0.450	0.488
M00176	M00909	-0.322	-	-0.639	0.538	0.538	0.446
M00308	M00573	-0.253	-0.205	-0.633	0.560	0.560	0.464
M00308	M00577	-0.286	-0.226	-0.617	0.623	0.623	0.405
M00308	M00855	0.321	0.286	0.698	0.544	0.544	0.442
M00344	M00525	-	-	0.701	0.793	0.793	0.256
M00344	M00526	-	-	0.694	0.554	0.554	0.381
M00344	M00527	-	-	0.699	0.850	0.850	0.227
M00344	M00570	-	-	0.592	0.429	0.429	0.497
M00525	M00573	-0.253	-	-0.528	0.620	0.620	0.505
M00525	M00718	-	-	-0.644	0.544	0.544	0.386
M00525	M00897	-	-	0.609	0.403	0.403	0.459
M00525	M00909	-	0.183	0.680	0.683	0.683	0.392
M00526	M00573	-0.261	-	-0.527	0.663	0.663	0.426
M00526	M00718	-	-	-0.639	0.448	0.448	0.436
M00526	M00897	-	0.209	0.606	0.710	0.710	0.402
M00526	M00909	-	0.196	0.683	0.621	0.621	0.381
M00527	M00573	-0.254	-	-0.535	0.619	0.619	0.501
M00527	M00718	-	-	-0.644	0.508	0.508	0.405
M00527	M00897	-	-	0.613	0.502	0.502	0.408
M00527	M00909	-	0.198	0.685	0.687	0.687	0.386
M00535	M00909	-	-	0.579	0.707	0.707	0.301
M00570	M00718	-0.190	-0.271	-0.608	0.835	0.835	0.442
M00570	M00909	-	-0.205	0.539	0.556	0.556	0.538
M00573	M00609	-	-	-0.608	0.751	0.751	0.278
M00577	M00609	-	-	-0.600	0.601	0.601	0.356
M00609	M00950	-0.129	-	-0.641	0.749	0.749	0.533
M00740	M00916	-0.310	-	-0.693	0.563	0.563	0.540
M00844	M00909	-	-	0.586	0.697	0.697	0.306
M00845	M00909	-	-	0.541	0.601	0.601	0.356
M00849	M00899	-0.188	-	-0.662	0.503	0.503	0.530

¹⁾ Measurements the consistency of the direction (positive or negative correlation) of an edge across different treatments or phenotypes

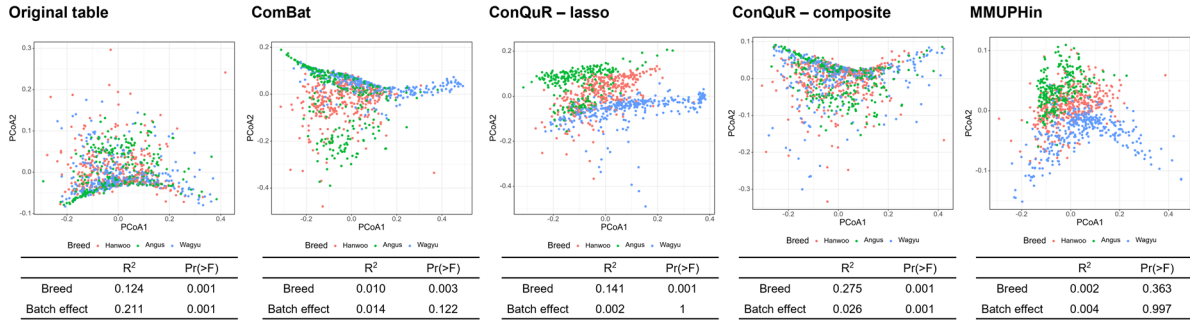
²⁾ A normalized version of the Phi score those accounts for the imbalance in edge

³⁾ The degree of connectivity of a node within its own condition-specific network

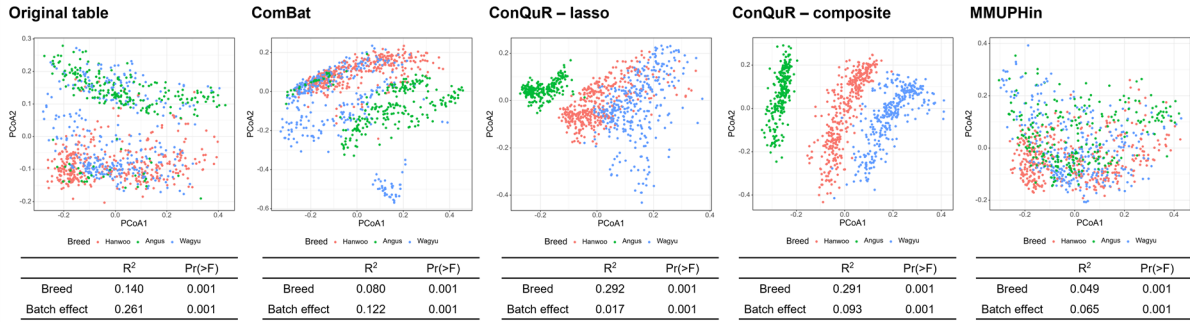
For selection of nodes and edges, the median values of external and internal scores were used as thresholds, and only edges with over 0.4 of phi score

5 **Supplementary Figure**

A. Bacteria | Phylum



B. Bacteria | Genus



C. Bacteria | KEGG ortholog

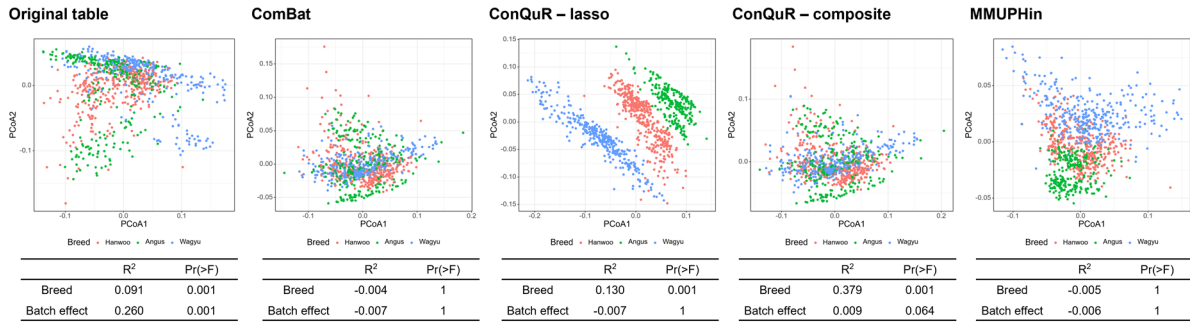
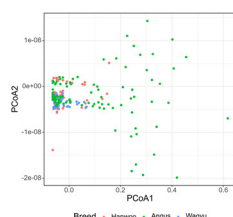


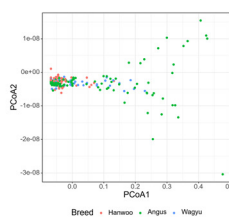
Fig. S1. The overall microbial community was analyzed using the total sum scaling normalized table, with raw data classified at the phylum (A) and genus (B) levels for taxonomy and Kyoto Encyclopedia of Genes and Genomes (KEGG) orthologs (C) for functional prediction in bacteriome. The proportion of variance explained (R²) indicates the coefficient of determination, representing the proportion of variance explained. Principal coordinates analysis (PCoA) and Bray–Curtis dissimilarity analyses were performed for visualization. Statistical analysis was conducted using permutational multivariate analysis of variance (PERMANOVA).

A. Archaea | Phylum**Original table**

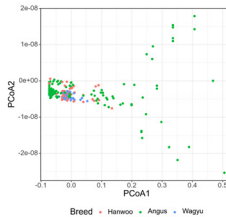
	R ²	Pr(>F)
Breed	0.187	0.001
Batch effect	0.068	0.003

ComBat

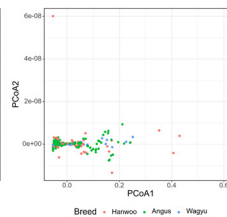
The analysis could not be performed due to the extremely low number of microbial taxa

ConQuR – lasso

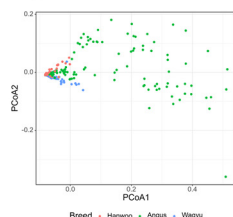
	R ²	Pr(>F)
Breed	0.123	0.001
Batch effect	3.83E-05	1

ConQuR – composite

	R ²	Pr(>F)
Breed	0.096	0.001
Batch effect	0.005	0.951

MMUPHin

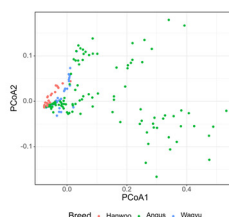
	R ²	Pr(>F)
Breed	0.007	0.348
Batch effect	0.043	0.051

B. Archaea | Genus**Original table**

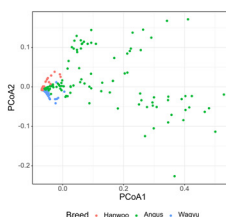
	R ²	Pr(>F)
Breed	0.303	0.001
Batch effect	0.089	0.001

ComBat

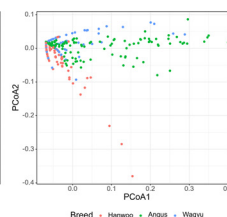
The analysis could not be performed due to the extremely low number of microbial taxa

ConQuR – lasso

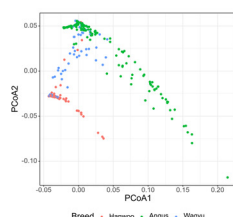
	R ²	Pr(>F)
Breed	0.276	0.001
Batch effect	0.004	0.989

ConQuR – composite

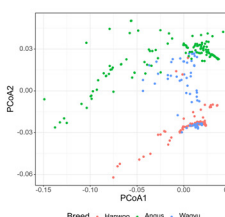
	R ²	Pr(>F)
Breed	0.317	0.001
Batch effect	0.012	0.457

MMUPHin

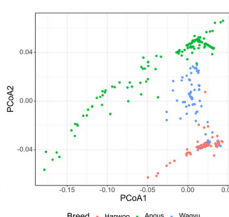
	R ²	Pr(>F)
Breed	0.171	0.001
Batch effect	0.040	0.009

C. Archaea | KEGG ortholog**Original table**

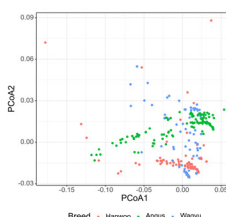
	R ²	Pr(>F)
Breed	0.378	0.001
Batch effect	0.142	0.001

ComBat

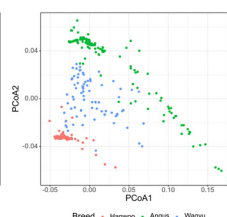
	R ²	Pr(>F)
Breed	0.248	0.001
Batch effect	0.085	0.001

ConQuR – lasso

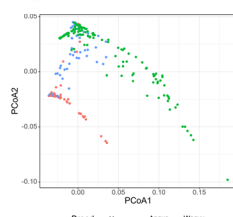
	R ²	Pr(>F)
Breed	0.393	0.001
Batch effect	0.00015	1

ConQuR – composite

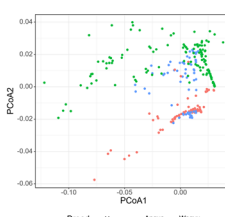
	R ²	Pr(>F)
Breed	0.374	0.001
Batch effect	0.007	0.862

MMUPHin

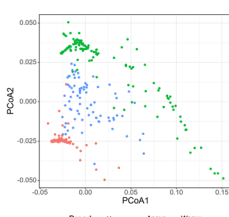
	R ²	Pr(>F)
Breed	0.069	0.001
Batch effect	0.057	0.002

D. Archaea | Enzyme Commission numbers**Original table**

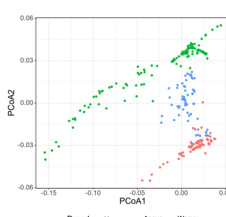
	R ²	Pr(>F)
Breed	0.376	0.001
Batch effect	0.066	0.001

ComBat

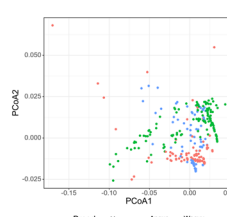
	R ²	Pr(>F)
Breed	0.238	0.001
Batch effect	0.045	0.001

ConQuR – lasso

	R ²	Pr(>F)
Breed	0.176	0.001
Batch effect	0.005	0.990

ConQuR – composite

	R ²	Pr(>F)
Breed	0.333	0.001
Batch effect	0.048	0.001

MMUPHin

	R ²	Pr(>F)
Breed	0.032	0.001
Batch effect	0.030	0.064

Fig. S2. The overall microbial community was analyzed using the total sum scaling normalized table, with raw data classified at the phylum (A) and genus (B) levels for taxonomy and Kyoto Encyclopedia of Genes and Genomes (KEGG) orthologs (C) and enzyme commission numbers for functional prediction in archaeome. The proportion of variance explained (R^2) indicates the coefficient of determination, representing the proportion of variance explained. Principal coordinates analysis (PCoA) and Bray–Curtis dissimilarity analyses were performed for visualization. Statistical analysis was conducted using permutational multivariate analysis of variance (PERMANOVA).

Archaea | KEGG module

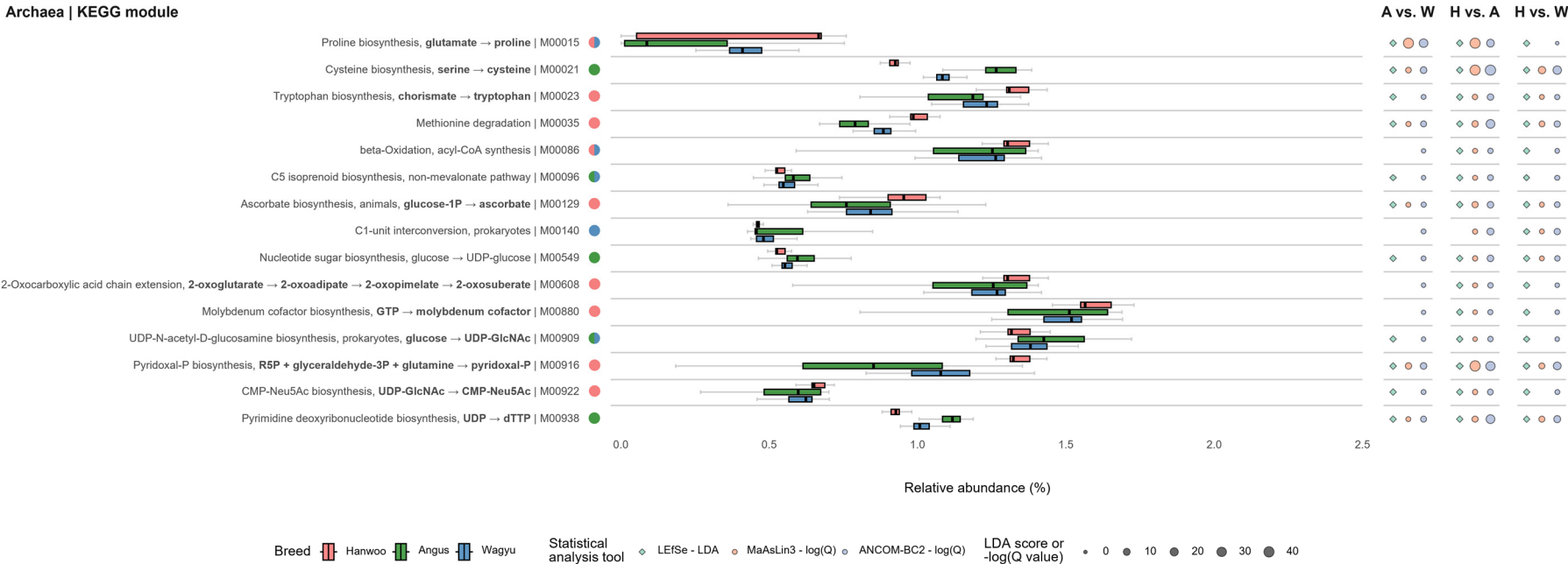


Fig. S3. Differentially abundant major predicted functions barplot (at least $\geq 0.1\%$ average relative abundance across all samples), excluding those related to methane metabolism. Statistical significance was determined only when all three statistical methods produced consistent results in pairwise comparisons. The significance determined based on LDA score ≥ 2 for LEfSe and $Q \leq 0.05$ for MaAsLin3 and ANCOM-BC2. Circular markers (red: Hanwoo, blue: Angus, green: Wagyu) indicate the breed where each microbial taxon exhibits dominant abundance. A, Angus; H, Hanwoo; W, Wagyu.