

1 **Table S4. Microbial genes associated with feed conversion efficiency.** Partial least squares (PLS) estimates of effects of microbial genes characterised by
2 the Kyoto Encyclopedia of Genes and Genomes (KEGG) database in an analysis where the PLS factors explained 80.6% of the variation in model effects and
3 88.3% of the variation in feed conversion ratio (kg feed intake/kg growth).

KEGG-ID, breed, diet	Description	Estimate	VIP	P-value	R ²
Breed AA	Aberdeen Angus	-0.12465	1.777	0.361	0.139
Breed LIM	Limousin	0.12465	1.777	0.361	0.139
K02008	cobalt/nickel transport system permease protein	0.10440	1.542	0.030	0.798
K00766	anthranilate phosphoribosyltransferase [EC:2.4.2.18]	0.08849	1.346	0.002	0.950
K02377	GDP-L-fucose synthase [EC:1.1.1.271]	-0.07758	1.297	0.004	0.924
K02907	large subunit ribosomal protein L30	0.05671	1.149	0.074	0.693
K00941	hydroxymethylpyrimidine/phosphomethylpyrimidine kinase [EC:2.7.1.49 2.7.4.7]	0.05850	1.117	0.046	0.753
K01195	beta-glucuronidase [EC:3.2.1.31]	-0.06401	1.111	0.090	0.664
K03694	ATP-dependent Clp protease ATP-binding subunit ClpA	-0.07025	1.079	0.066	0.707
K07588	LAO/AO transport system kinase [EC:2.7.-.-]	-0.06256	1.068	0.094	0.656
K00179	indolepyruvate ferredoxin oxidoreductase, alpha subunit [EC:1.2.7.8]	-0.07399	1.065	0.099	0.650
K00375	GntR family transcriptional regulator / MocR family aminotransferase	0.02972	0.959	0.041	0.765
K01876	aspartyl-tRNA synthetase [EC:6.1.1.12]	-0.05720	0.951	0.004	0.926
K06921	Putative ATPase	0.03796	0.951	0.052	0.739
K00075	UDP-N-acetylmuramate dehydrogenase [EC:1.1.1.158]	-0.01437	0.948	0.093	0.658
K01493	dCMP deaminase [EC:3.5.4.12]	0.02527	0.946	0.038	0.773
K00868	pyridoxine kinase [EC:2.7.1.35]	0.02290	0.942	0.045	0.756
K07139	Putative Fe-S oxidoreductase	-0.01605	0.937	0.065	0.710
K02006	cobalt/nickel transport system ATP-binding protein	0.03217	0.934	0.079	0.682
K00394	adenylylsulfate reductase, subunit A [EC:1.8.99.2]	0.02695	0.932	0.068	0.703
K01814	phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase [EC:5.3.1.16]	0.03485	0.928	0.093	0.659

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	DNA helicase II / ATP-dependent DNA helicase PcrA				
K03657	[EC:3.6.4.12]	-0.00217	0.925	0.071	0.698
K01784	UDP-glucose 4-epimerase [EC:5.1.3.2]	-0.02960	0.925	0.067	0.707
K09811	cell division transport system permease protein	-0.00675	0.919	0.053	0.736
K04517	prephenate dehydrogenase [EC:1.3.1.12]	0.03268	0.919	0.075	0.690
K03581	exodeoxyribonuclease V alpha subunit [EC:3.1.11.5]	0.01700	0.917	0.051	0.739
	diaminohydroxyphosphoribosylaminopyrimidine deaminase / 5-amino-6-(5-phosphoribosylamino)uracil reductase [EC:3.5.4.26 1.1.1.193]	-0.01062	0.916	0.088	0.667
K11752					
K01269	aminopeptidase [EC:3.4.11.-]	0.01317	0.916	0.056	0.728
K02313	chromosomal replication initiator protein	-0.00515	0.915	0.084	0.673
K03426	NAD ⁺ diphosphatase [EC:3.6.1.22]	0.02591	0.915	0.087	0.669
K00773	queuine tRNA-ribosyltransferase [EC:2.4.2.29]	-0.02257	0.910	0.073	0.694
	uroporphyrinogen III methyltransferase / synthase [EC:2.1.1.107 4.2.1.75]	0.02152	0.910	0.064	0.713
K13542					
K03631	DNA repair protein RecN (Recombination protein N)	0.01067	0.905	0.048	0.747
K08602	oligoendopeptidase F [EC:3.4.24.-]	0.01777	0.904	0.083	0.676
K00956	sulfate adenylyltransferase subunit 1 [EC:2.7.7.4]	0.00927	0.902	0.090	0.663
K01924	UDP-N-acetylmuramate--alanine ligase [EC:6.3.2.8]	-0.01173	0.901	0.087	0.668
	tRNA nucleotidyltransferase (CCA-adding enzyme) [EC:2.7.7.72 3.1.3.- 3.1.4.-]	0.01214	0.886	0.092	0.661
K00974					
K01818	L-fucose isomerase [EC:5.3.1.25]	-0.04998	0.884	0.067	0.707
K01129	dGTPase [EC:3.1.5.1]	-0.01655	0.881	0.043	0.760
K08483	phosphotransferase system, enzyme I, PtsI [EC:2.7.3.9]	0.00303	0.880	0.077	0.686
K03458	nucleobase:cation symporter-2, NCS2 family	0.01331	0.873	0.090	0.663
K03111	single-strand DNA-binding protein	0.02467	0.869	0.010	0.883
K00278	L-aspartate oxidase [EC:1.4.3.16]	-0.02361	0.868	0.082	0.678
K03501	glucose inhibited division protein B [EC:2.1.-.-]	-0.02020	0.862	0.066	0.707
K02343	DNA polymerase III subunit gamma/tau [EC:2.7.7.7]	0.02796	0.850	0.008	0.891
K01104	protein-tyrosine phosphatase [EC:3.1.3.48]	0.01502	0.843	0.025	0.815

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K07082	UPF0755 protein	-0.00521	0.837	0.076	0.687
K01928	UDP-N-acetylmuramoylalanyl-D-glutamate--2,6-diaminopimelate ligase [EC:6.3.2.13]	-0.01444	0.830	0.023	0.820
Diet CON	Concentrate based diet	-0.05925	0.829	0.429	0.107
Diet FOR	Forage based diet	0.05925	0.829	0.429	0.107
K03615	electron transport complex protein RnfC	0.03462	0.819	0.049	0.745
K01613	phosphatidylserine decarboxylase [EC:4.1.1.65]	0.01464	0.799	0.009	0.888
K01358	ATP-dependent Clp protease, protease subunit [EC:3.4.21.92]	-0.03591	0.731	0.020	0.833

Two factors were significant in the partial least squares analysis. Without considering diet and breed in the model, , the microbial genes explained 83.9% of the variation of model effects and 85.5% of the variation in feed conversion ratio. The PLS estimates were based on predictors and responses centered and scaled to have mean 0 and standard deviation 1. Variable Importance for Projection (VIP) statistic of Wold, which summarizes the contribution of a variable maker to the model were used to identify the significant microbial genes associated with feed conversion ratio. The P-value and R^2 were obtained by fitting a model including the gene and diet effects only.