Supplementary Materials

Domain-Dependent Phenotypic Positioning of Liaodan Black Pigs Relative to Liaoning Black and Duroc Populations at a Common Target Body Weight

This supplementary file contains Tables S1–S7 and Figures S1–S3 cited in the main manuscript. Abbreviations used throughout: LB, Liaoning Black; LDB, Liaodan Black; DR, Duroc.

Table S1. Ingredient composition and premix nutrient supply of the experimental diets

Panel A. Ingredient composition (% as-fed)

Ingredient	P1 (20–<50 kg)	P2 (50–<80 kg)	P3 (≥80 kg to slaughter)
Corn	8.68	21.74	36.08
Wheat middlings	3.79	4.87	5.93
Wheat flour	12.18	10.79	8.92
Rice bran meal	4.58	5.75	6.38
Extruded corn	22.33	17.46	10.24
Biscuit meal	13.50	11.67	9.86
Soybean meal	15.80	12.48	11.62
Extruded full-fat soybean	5.91	5.13	2.08
Fermented soybean meal	3.29	0.51	0.00
Fish meal	1.09	0.34	0.00
Sucrose	0.50	0.80	0.00
Peanut shell meal	0.00	1.43	1.93
Soybean oil	2.45	2.22	2.70
Limestone	1.02	1.11	1.11
Dicalcium phosphate	0.77	0.37	0.28
Monocalcium phosphate	0.15	0.24	0.05
Sodium chloride	0.32	0.34	0.36
Sodium bicarbonate	0.27	0.27	0.27
L-Lysine HCl (98.5%)	0.45	0.35	0.28
DL-Methionine (99%)	0.19	0.08	0.05
L-Threonine (98.5%)	0.26	0.15	0.10
L-Tryptophan (98%)	0.04	0.02	0.02
L-Valine (98%)	0.18	0.07	0.02
L-Isoleucine (98%)	0.12	0.04	0.01
Citric acid monohydrate	0.42	0.06	0.00
Vitamin-mineral premix	1.71	1.71	1.71
Total	100.00	100.00	100.00

Panel B. Premix nutrient supply per kg complete diet

Premix component	Supply per kg complete diet
Vitamin A	5000 IU
Vitamin D3	1600 IU
Vitamin E	50 IU
Vitamin K3	3 mg
Thiamine (B1)	2.2 mg
Riboflavin (B2)	8 mg
Niacin (B3)	50 mg
Pantothenic acid (B5)	28 mg
Pyridoxine (B6)	3.3 mg
Biotin (B7)	0.22 mg
Folic acid (B9)	1.3 mg
Vitamin B12	0.038 mg
Choline	500 mg
Fe	50 mg
Cu	4 mg
Zn	35 mg
Mn	10 mg
I	0.15 mg
Se	0.20 mg
Phytase	500 FTU

Ingredient inclusion is expressed as percentage of complete diet on an as-fed basis. The three phase formulations each sum to 100.00%. Analyzed and matrix-derived nutrient composition is reported in Table 1 of the main manuscript. P1, 20 to <50 kg body weight; P2, 50 to <80 kg; P3, ≥80 kg to slaughter; FTU, phytase units.

Table S2. Expanded growth-performance and carcass model output

Panel A. Population estimated marginal means from the primary model

Trait	LB	LDB	DR	*Ppop*	*Psex*	*Pint*
Initial BW, kg	21.19 ± 0.37[c]	25.01 ± 0.37[b]	29.01 ± 0.37[a]	<0.001	0.081	0.166
Final BW, kg	110.18 ± 0.48	109.87 ± 0.48	110.31 ± 0.48	0.801	0.706	0.884
Slaughter age, d	205.6 ± 0.98[a]	185.3 ± 0.98[b]	170.3 ± 0.98[c]	<0.001	1.000	1.000
Trial duration, d	135.60 ± 0.98[a]	115.30 ± 0.98[b]	100.30 ± 0.98[c]	<0.001	1.000	1.000
Body-weight gain, kg	88.99 ± 0.59[a]	84.86 ± 0.59[b]	81.30 ± 0.59[c]	<0.001	0.155	0.369
Total feed intake, kg	285.44 ± 1.97[a]	234.15 ± 1.97[b]	207.14 ± 1.97[c]	<0.001	<0.001	0.334
ADG, g/d	657.13 ± 10.94[c]	737.66 ± 10.94[b]	812.73 ± 10.94[a]	<0.001	0.511	0.804
ADFI, kg/d	2.107 ± 0.031	2.035 ± 0.031	2.071 ± 0.031	0.254	0.001	0.616
F/G, kg/kg	3.209 ± 0.020[a]	2.762 ± 0.020[b]	2.548 ± 0.020[c]	<0.001	<0.001	0.875
Cold carcass weight, kg	82.04 ± 0.55[b]	80.57 ± 0.55[b]	84.31 ± 0.55[a]	<0.001	0.572	0.182
Dressing percentage, %	74.45 ± 0.51[b]	73.37 ± 0.51[b]	76.44 ± 0.51[a]	<0.001	0.764	0.288
Straight length, cm	100.25 ± 0.85[a]	92.70 ± 0.85[b]	103.00 ± 0.85[a]	<0.001	0.564	0.199
Oblique length, cm	79.85 ± 1.04[b]	79.15 ± 1.04[b]	88.50 ± 1.04[a]	<0.001	0.411	0.382
Bone, %	12.42 ± 0.33[b]	15.31 ± 0.33[a]	12.88 ± 0.33[b]	<0.001	0.058	0.781
Skin, %	12.23 ± 0.21[a]	9.09 ± 0.21[b]	8.21 ± 0.21[c]	<0.001	0.376	0.331
Lean, %	50.84 ± 0.65[c]	59.81 ± 0.65[b]	66.99 ± 0.65[a]	<0.001	0.217	0.665
Fat, %	24.50 ± 0.76[a]	15.78 ± 0.76[b]	11.93 ± 0.76[c]	<0.001	0.037	0.463
Average BFT, mm	33.97 ± 0.94[a]	24.07 ± 0.94[b]	20.08 ± 0.94[c]	<0.001	0.130	0.627
Loin muscle area, cm²	40.03 ± 1.18[c]	47.04 ± 1.18[b]	55.97 ± 1.18[a]	<0.001	0.579	0.701
Skin thickness, mm	2.53 ± 0.09	2.03 ± 0.09	2.90 ± 0.09	<0.001	0.137	0.003

Values are Population estimated marginal means (EMMs) ± standard error (SE) (n = 20 pigs/source population; 10 barrows and 10 gilts) from the primary Population + Sex + Population × Sex model. *Ppop*, *Psex*, and *Pint* denote the main effects of Population and Sex and their interaction, respectively. Within a row, Population EMMs without a common superscript differ by Tukey-adjusted pairwise comparison ($P < 0.05$). Because the Population × Sex interaction was significant for skin thickness, the marginal Population means should not be interpreted alone; descriptive Population × Sex means (mm) were LB barrows 2.175, LB gilts 2.880, LDB barrows 2.103, LDB gilts 1.956, DR barrows 2.939, and DR gilts 2.859. Descriptive dissected tissue weights (mean ± SD, kg) were bone: 10.19 ± 0.96, 12.33 ± 1.50, and 10.86 ± 1.21; skin: 10.03 ± 0.85, 7.33 ± 0.88, and 6.93 ± 0.75; lean: 41.68 ± 2.53, 48.17 ± 2.79, and 56.49 ± 2.48; and fat: 20.14 ± 3.41, 12.74 ± 3.40, and 10.04 ± 1.90 for LB, LDB, and DR, respectively. Observed slaughter-age ranges were 201–211, 180–191, and 165–176 d for LB, LDB, and DR, respectively; thus, the ranges did not overlap. BW, body weight; ADG, average daily gain; ADFI, average daily feed intake; F/G, feed-to-gain ratio; BFT, backfat thickness.

Panel B. Population × Sex descriptive statistics for starting and slaughter timing variables

Population	Sex	*n*	Initial BW, kg	Final BW, kg	Slaughter age, d	Trial duration, d
LB	Barrow	10	21.31 ± 0.76	109.94 ± 2.41	205.60 ± 4.12	135.60 ± 4.12
LB	Gilt	10	21.07 ± 1.24	110.41 ± 1.93	205.60 ± 4.12	135.60 ± 4.12
LDB	Barrow	10	25.98 ± 1.39	109.70 ± 2.00	185.30 ± 4.50	115.30 ± 4.50
LDB	Gilt	10	24.04 ± 2.20	110.03 ± 2.18	185.30 ± 4.50	115.30 ± 4.50
DR	Barrow	10	29.07 ± 2.21	110.39 ± 1.98	170.30 ± 4.50	100.30 ± 4.50
DR	Gilt	10	28.95 ± 1.72	110.22 ± 2.31	170.30 ± 4.50	100.30 ± 4.50

Values are mean ± SD within each Population × Sex cell (n = 10 pigs/cell). These descriptive statistics show the six-cell distribution of initial BW, final BW, slaughter age, and trial duration. They are descriptive and are not intended as a separate inferential analysis.

Table S3. Intramuscular fatty-acid composition, class and derived summaries, and model output

Panel A. Individual fatty acids

Fatty acid	LB	LDB	DR	*Ppop*	*Psex*	*Pint*	*qpop*
C10:0	0.081 ± 0.004	0.087 ± 0.004	0.091 ± 0.004	0.164	0.186	0.022	0.187
C12:0	0.060 ± 0.002	0.064 ± 0.002	0.070 ± 0.002	0.008	0.171	0.002	0.014
C14:0	1.006 ± 0.048	1.082 ± 0.048	1.100 ± 0.048	0.347	0.040	0.005	0.370
C16:0	28.635 ± 0.619^{a}	27.525 ± 0.619^{a}	23.381 ± 0.619^{b}	<0.001	0.188	0.470	<0.001
C16:1	2.756 ± 0.123^{ab}	2.438 ± 0.123^{b}	2.976 ± 0.123^{a}	0.012	0.090	0.119	0.019
C18:0	14.565 ± 0.665	16.892 ± 0.665	15.050 ± 0.665	0.040	0.203	0.444	0.059
C18:1n-9c	33.056 ± 1.070^{a}	24.544 ± 1.070^{b}	30.571 ± 1.070^{a}	<0.001	0.433	0.486	<0.001
C18:2n-6	11.375 ± 0.711^{b}	17.950 ± 0.711^{a}	16.781 ± 0.711^{a}	<0.001	0.237	0.226	<0.001
C20:0	0.253 ± 0.015^{a}	0.276 ± 0.015^{a}	0.160 ± 0.015^{b}	<0.001	0.065	0.148	<0.001
C20:1	0.626 ± 0.042	0.688 ± 0.042	0.672 ± 0.042	0.548	0.210	0.240	0.548
C18:3n-3	0.159 ± 0.014^{b}	0.200 ± 0.014^{b}	0.301 ± 0.014^{a}	<0.001	0.326	0.250	<0.001
C20:2n-6	0.291 ± 0.020^{c}	0.390 ± 0.020^{b}	0.469 ± 0.020^{a}	<0.001	0.497	0.083	<0.001
C20:3n-6	0.270 ± 0.019	0.326 ± 0.019	0.302 ± 0.019	0.109	0.270	0.339	0.134
C20:4n-6	2.187 ± 0.198^{b}	3.131 ± 0.198^{a}	3.412 ± 0.198^{a}	<0.001	0.056	0.063	<0.001
C20:5n-3 (EPA)	0.058 ± 0.004	0.061 ± 0.004	0.049 ± 0.004	0.095	0.129	0.192	0.126
C22:6n-3 (DHA)	0.088 ± 0.009^{ab}	0.100 ± 0.009^{a}	0.059 ± 0.009^{b}	0.007	0.109	0.466	0.014

Values are Population estimated marginal means ± SE (n = 20 pigs/source population; 10 barrows and 10 gilts) and are expressed as percentage of total detected fatty acids. *Ppop*, *Psex*, and *Pint* denote the main effects of Population and Sex and their interaction; *qpop* is the Benjamini–Hochberg-adjusted q value for the Population effect across 16 individual fatty acids. For fatty acids with *qpop* < 0.05 and no supported Population × Sex interaction, Population EMMs without a common superscript differ by Tukey-adjusted pairwise comparison (P < 0.05). For C10:0, C12:0, and C14:0, Population × Sex interactions with nominal *Pint* < 0.05 (0.022, 0.002, and 0.005, respectively) preclude interpretation of marginal Population EMMs alone; descriptive cell means are therefore provided below. Population × Sex means (%) for LB barrows/LB gilts, LDB barrows/LDB gilts, and DR barrows/DR gilts were 0.081/0.081, 0.098/0.076, and 0.088/0.093 for C10:0; 0.060/0.060, 0.072/0.056, and 0.067/0.072 for C12:0; and 1.003/1.009, 1.273/0.890, and 1.087/1.114 for C14:0, respectively. Fatty-acid class and derived summaries were analyzed separately in Panel B. SFA, saturated fatty acids; MUFA, monounsaturated fatty acids; PUFA, polyunsaturated fatty acids; UFA, unsaturated fatty acids; EPA, eicosapentaenoic acid; DHA, docosahexaenoic acid.

Panel B. Fatty-acid class and derived summaries

Summary	LB	LDB	DR	*Ppop*	*Psex*	*Pint*
SFA, %	44.60 ± 1.10[a]	45.92 ± 1.10[a]	39.85 ± 1.10[b]	0.001	0.104	0.324
MUFA, %	36.44 ± 0.99[a]	27.67 ± 0.99[b]	34.22 ± 0.99[a]	<0.001	0.561	0.626
PUFA, %	14.43 ± 0.82[b]	22.16 ± 0.82[a]	21.37 ± 0.82[a]	<0.001	0.126	0.129
UFA, %	50.86 ± 1.15[b]	49.83 ± 1.15[b]	55.59 ± 1.15[a]	0.002	0.113	0.250
Other FA, %	4.54 ± 0.22	4.25 ± 0.22	4.56 ± 0.22	0.538	0.866	0.335
UFA:SFA	1.189 ± 0.060[b]	1.104 ± 0.060[b]	1.414 ± 0.060[a]	0.002	0.149	0.294

Values are Population estimated marginal means ± SE (n = 20 pigs/source population; 10 barrows and 10 gilts). *Ppop*, *Psex*, and *Pint* denote the main effects of Population and Sex and their interaction, respectively. SFA, MUFA, PUFA, UFA, and Other FA are expressed as percentage of total detected fatty acids; UFA:SFA is unitless. Other FA was calculated as 100% minus the summed proportions of the 16 reported fatty acids; individual minor-peak identities were not archived. These summaries were analyzed separately and were not included in the 16-individual-fatty-acid FDR family. For summaries with *Ppop* < 0.05, Population EMMs without a common superscript differ by Tukey-adjusted pairwise comparison (P < 0.05). SFA, saturated fatty acids; MUFA, monounsaturated fatty acids; PUFA, polyunsaturated fatty acids; UFA, unsaturated fatty acids; FA, fatty acid; FAME, fatty-acid methyl ester.

Table S4. Protein-hydrolysate amino-acid composition, summary indices, and model output

Panel A. Individual protein-hydrolysate amino acids

Amino acid	LB	LDB	DR	*Ppop*	*qpop*
Asp	8.046 ± 0.089	7.803 ± 0.089	7.813 ± 0.089	0.102	0.282
Glu	13.705 ± 0.180	13.627 ± 0.180	13.522 ± 0.180	0.771	0.841
Ser	3.630 ± 0.043	3.627 ± 0.043	3.614 ± 0.043	0.958	0.958
Arg	6.760 ± 0.091	6.700 ± 0.091	6.947 ± 0.091	0.143	0.282
Gly	3.634 ± 0.059[a]	3.554 ± 0.059[a]	3.324 ± 0.059[b]	0.001	0.011
Thr	4.456 ± 0.061	4.433 ± 0.061	4.492 ± 0.061	0.792	0.841
Pro	4.631 ± 0.061[a]	4.353 ± 0.061[b]	4.244 ± 0.061[b]	<0.001	0.002
Ala	5.767 ± 0.072[a]	5.591 ± 0.072[ab]	5.431 ± 0.072[b]	0.007	0.040
Val	4.779 ± 0.052	4.674 ± 0.052	4.871 ± 0.052	0.034	0.144
Met	2.418 ± 0.036	2.516 ± 0.036	2.471 ± 0.036	0.166	0.282
Ile	4.358 ± 0.055	4.324 ± 0.055	4.448 ± 0.055	0.271	0.386
Leu	7.064 ± 0.103	7.281 ± 0.103	7.254 ± 0.103	0.272	0.386
His	3.388 ± 0.042	3.357 ± 0.042	3.405 ± 0.042	0.719	0.841
Phe	3.805 ± 0.047	3.851 ± 0.047	3.935 ± 0.047	0.155	0.282
Lys	7.873 ± 0.109	7.671 ± 0.109	7.673 ± 0.109	0.330	0.431
Tyr	3.207 ± 0.043	3.096 ± 0.043	3.226 ± 0.043	0.078	0.266
Cys	0.611 ± 0.017	0.658 ± 0.017	0.653 ± 0.017	0.116	0.282

Values are Population estimated marginal means ± SE (n = 20 pigs/source population; 10 barrows and 10 gilts) and are expressed as g/100 g protein. *Ppop* is the Population main-effect P value from the primary model; *qpop* is the Benjamini–Hochberg-adjusted q value for the Population effect across 17 protein-hydrolysate amino acids. For amino acids with *qpop* < 0.05, Population EMMs without a common superscript differ by Tukey-adjusted pairwise comparison (P < 0.05). At the nominal α = 0.05 level, a Sex main effect was detected only for isoleucine (*Psex* = 0.047; all other *Psex* ≥ 0.051), and no Population × Sex interaction was supported for any individual amino acid (all *Pint* ≥ 0.211). Tryptophan was not determined. Cys represents total cystine/cysteine determined after performic-acid oxidation and expressed on a Cys-equivalent basis. EAA8 = His + Ile + Leu + Lys + Met + Phe + Thr + Val; TAA, total measured amino acids.

Panel B. Amino-acid summary indices

Summary	LB	LDB	DR	*Ppop*	*Psex*	*Pint*
TAA, g/100 g protein	88.133 ± 0.572	87.116 ± 0.572	87.323 ± 0.572	0.419	0.445	0.779
EAA8, g/100 g protein	38.142 ± 0.273	38.106 ± 0.273	38.549 ± 0.273	0.449	0.476	0.835
EAA8:TAA, %	43.286 ± 0.152[b]	43.742 ± 0.152[ab]	44.141 ± 0.152[a]	0.001	0.958	0.710

Values are Population estimated marginal means ± SE from the primary Population + Sex + Population × Sex model (n = 20 pigs/source population; 10 barrows and 10 gilts). *Ppop*, *Psex*, and *Pint* denote the main effects of Population and Sex and their interaction, respectively. These summary indices were analyzed separately and were not included in the 17-individual-amino-acid FDR family. For EAA8:TAA, Population EMMs without a common superscript differ by Tukey-adjusted pairwise comparison (P < 0.05). EAA8 = His + Ile + Leu + Lys + Met + Phe + Thr + Val; TAA, total measured amino acids.

Table S5. Sensitivity analyses for key outcomes

Panel A. Sensitivity to centered final body weight

Outcome	LB primary → adjusted	LDB primary → adjusted	DR primary → adjusted	Max absolute shift
Cold carcass weight, kg	82.035 → 82.015	80.565 → 80.648	84.305 → 84.242	0.083 kg
Lean, %	50.838 → 50.833	59.808 → 59.826	66.991 → 66.976	0.018 pp
Fat, %	24.503 → 24.501	15.782 → 15.792	11.931 → 11.923	0.010 pp
Average BFT, mm	33.965 → 33.929	24.070 → 24.221	20.080 → 19.965	0.151 mm
Loin muscle area, cm^2	40.025 → 40.004	47.040 → 47.129	55.965 → 55.897	0.089 cm^2
IMF, %	4.189 → 4.188	3.311 → 3.317	2.575 → 2.570	0.006 pp
pH24	5.8220 → 5.8215	5.7515 → 5.7535	5.7045 → 5.7030	0.002
Drip loss, %	1.994 → 1.990	2.469 → 2.482	3.173 → 3.163	0.013 pp
Cooking loss, %	22.484 → 22.489	24.744 → 24.723	27.715 → 27.731	0.021 pp
Shear force, N	24.984 → 25.025	27.118 → 26.949	30.313 → 30.441	0.169 N

Values show the Population EMM from the primary model followed by the EMM after adding centered Final BW as a covariate. pp, percentage points.

A sensitivity model with SlaughterBatch nested within Population as a random intercept was fitted to the 20 selected postmortem outcomes shown below. Batch-aware Population EMMs were compared with the primary-model EMMs to assess sensitivity of effect magnitude and numeric ordering.

Panel B. Batch-aware random-intercept sensitivity

Outcome	LB EMM	LDB EMM	DR EMM	Batch ICC	Max absolute EMM shift
Cold carcass weight, kg	82.087	80.623	84.390	0.237	0.085 kg
Dressing percentage, %	74.493	73.427	76.506	0.241	0.066 pp
Lean, %	50.837	59.807	66.991	<0.001	<0.001 pp
Fat, %	24.503	15.782	11.931	<0.001	<0.001 pp
Average BFT, mm	34.013	24.084	20.108	0.083	0.048 mm
LMA, cm^2	40.004	47.100	55.860	0.054	0.105 cm^2
IMF, %	4.189	3.311	2.575	<0.001	<0.001 pp
pH45	6.435	6.382	6.205	<0.001	<0.001
pH24	5.822	5.751	5.705	0.015	<0.001
L*	48.870	50.570	52.733	<0.001	<0.001
a*	10.444	9.479	8.600	<0.001	<0.001
b*	6.119	6.444	6.549	0.107	0.016
Drip loss, %	1.993	2.469	3.172	<0.001	<0.001 pp
Cooking loss, %	22.513	24.773	27.720	0.107	0.029 pp
Shear force, N	24.970	27.118	30.359	0.055	0.046 N
MinFeret, µm	52.023	60.145	69.938	0.033	0.067 µm
Fiber density, fibers/mm^2	159.666	145.000	124.732	<0.001	<0.001 fibers/mm^2
SFA, % total FA	44.648	46.016	39.793	0.064	0.091 pp
MUFA, % total FA	36.436	27.669	34.219	<0.001	<0.001 pp
PUFA, % total FA	14.426	22.157	21.373	<0.001	<0.001 pp

EMMs are Population estimated marginal means from the random-intercept sensitivity model. Batch intraclass correlation coefficient (ICC) was calculated as the SlaughterBatch variance divided by the sum of the SlaughterBatch and residual variances; values <0.001 indicate a variance estimate at or near the boundary. Max absolute EMM shift is the largest absolute difference between primary and batch-aware Population EMMs across LB, LDB, and DR; pp, percentage points. Numerical Population ordering was retained for all 20 outcomes. Because slaughter batches were nested within Population, these models provide a sensitivity assessment but do not independently separate Population from slaughter calendar.

Panel C. Analysis of the nine slaughter-batch means

Outcome	*Ppop* (9-batch means)	Primary numeric ordering retained
Cold carcass weight	0.062	Yes
Dressing percentage	0.097	Yes
Lean, %	<0.001	Yes
Fat, %	<0.001	Yes
Average BFT	<0.001	Yes
LMA	<0.001	Yes
IMF	<0.001	Yes
pH45	<0.001	Yes
pH24	0.015	Yes
L*	<0.001	Yes
a*	<0.001	Yes
b*	0.281	Yes
Drip loss	0.002	Yes
Cooking loss	0.002	Yes
Shear force	0.047	Yes
MinFeret	<0.001	Yes
Fiber density	0.005	Yes
SFA	0.025	Yes
MUFA	<0.001	Yes
PUFA	<0.001	Yes

The nine-batch analysis used three slaughter-batch means per Population (nine batch means in total) and was treated as a cluster-level sensitivity analysis. Numerical Population ordering was retained for all 20 outcomes shown, but statistical support was attenuated for cold carcass weight (P = 0.062), dressing percentage (P = 0.097), and b* (P = 0.281). Because only three slaughter batches were available per source population and batches were nested within Population, this analysis has limited cluster-level power and cannot independently separate Population from slaughter calendar.

Panel D. Leave-one-out stability of key Population contrasts

Outcome	LDB − LB: full-data contrast [leave-one-out range]	LDB − DR: full-data contrast [leave-one-out range]	Ordering stable
ADG	+80.53 [75.40, 85.61] g/d	−75.07 [−80.21, −69.41] g/d	Yes
F/G	−0.447 [−0.459, −0.436]	+0.214 [0.205, 0.223]	Yes
Lean	+8.97 [8.59, 9.31] pp	−7.18 [−7.56, −6.90] pp	Yes
Average BFT	−9.90 [−10.42, −9.37] mm	+3.99 [3.59, 4.35] mm	Yes
IMF	−0.878 [−0.951, −0.796] pp	+0.736 [0.678, 0.788] pp	Yes
Shear force	+2.13 [1.74, 2.72] N	−3.20 [−3.59, −2.65] N	Yes
MinFeret	+8.08 [7.41, 8.67] μm	−9.88 [−10.60, −9.11] μm	Yes
PUFA	+7.73 [7.31, 8.16] pp	+0.784 [0.363, 1.190] pp	Yes

Each row reports the full-data raw Population contrast and the observed range of that contrast across 60 leave-one-out refits, each obtained after omitting one pig and refitting the primary Population + Sex + Population × Sex model. Population ordering was retained for all eight outcomes. pp, percentage points. Leave-one-out refits assess influence and directional stability and are not independent biological replicates.

Table S6. Growth performance over the shared 50–80 kg body-weight interval

Trait	LB	LDB	DR	*Ppop*	*Psex*	*Pint*
Days from 50 to 80 kg, d	42.778 ± 0.600[a]	37.647 ± 0.600[b]	33.666 ± 0.600[c]	<0.001	0.512	0.837
ADG, g/d	704.088 ± 12.875[c]	800.638 ± 12.875[b]	895.642 ± 12.875[a]	<0.001	0.504	0.838
ADFI, kg/d	1.959 ± 0.026	1.870 ± 0.026	1.875 ± 0.026	0.032	<0.001	0.484
F/G, kg/kg	2.789 ± 0.020[a]	2.339 ± 0.020[b]	2.094 ± 0.020[c]	<0.001	<0.001	0.714

Values are Population estimated marginal means ± SE from the Population + Sex + Population × Sex model (n = 20 pigs/source population). Trial days corresponding to 50 and 80 kg were estimated by linear interpolation between the nearest bracketing body-weight observations, without extrapolation; cumulative feed intake at each crossing time was interpolated from the daily cumulative feed record. Means without a common superscript differ by Tukey-adjusted pairwise comparison ($P < 0.05$). *Ppop*, *Psex*, and *Pint* denote Population, Sex, and Population × Sex effects, respectively. ADG, average daily gain; ADFI, average daily feed intake; F/G, feed-to-gain ratio.

Table S7. IMF-adjusted and compositional fatty-acid sensitivity analyses

Panel A. IMF-adjusted fatty-acid outcomes and Population × IMF slope-homogeneity check

Fatty acid / summary	LB	LDB	DR	*Ppop*	*Pint*	*qpop*	*Ppop×IMF*
C10:0	0.077 ± 0.005	0.087 ± 0.004	0.094 ± 0.005	0.099	0.030	0.132	0.167
C12:0	0.059 ± 0.003	0.064 ± 0.002	0.070 ± 0.003	0.055	0.002	0.079	0.142
C14:0	0.992 ± 0.063	1.082 ± 0.049	1.114 ± 0.062	0.460	0.007	0.460	0.134
C16:0	27.578 ± 0.783	27.585 ± 0.601	24.377 ± 0.765	0.006	0.578	0.013	0.135
C16:1	2.749 ± 0.162	2.438 ± 0.124	2.982 ± 0.158	0.017	0.124	0.030	0.225
C18:0	14.022 ± 0.868	16.922 ± 0.666	15.561 ± 0.847	0.027	0.515	0.043	0.045
C18:1n-9c	33.748 ± 1.401	24.504 ± 1.076	29.918 ± 1.369	<0.001	0.497	<0.001	0.522
C18:2n-6	12.063 ± 0.925	17.910 ± 0.710	16.131 ± 0.903	<0.001	0.279	<0.001	0.200
C20:0	0.253 ± 0.020	0.276 ± 0.016	0.160 ± 0.020	<0.001	0.154	<0.001	0.573
C20:1	0.600 ± 0.054	0.689 ± 0.042	0.696 ± 0.053	0.429	0.250	0.458	0.609
C18:3n-3	0.165 ± 0.019	0.199 ± 0.014	0.296 ± 0.018	<0.001	0.272	<0.001	0.966
C20:2n-6	0.296 ± 0.027	0.390 ± 0.020	0.464 ± 0.026	0.002	0.095	0.004	0.847
C20:3n-6	0.285 ± 0.024	0.325 ± 0.019	0.287 ± 0.024	0.242	0.387	0.277	0.169
C20:4n-6	2.455 ± 0.254	3.116 ± 0.195	3.159 ± 0.248	0.126	0.089	0.156	0.014
C20:5n-3 (EPA)	0.064 ± 0.005	0.061 ± 0.004	0.043 ± 0.005	0.013	0.235	0.027	0.084
C22:6n-3 (DHA)	0.104 ± 0.011	0.099 ± 0.009	0.043 ± 0.011	<0.001	0.558	0.002	0.030
SFA, %	42.981 ± 1.407	46.017 ± 1.080	41.377 ± 1.375	0.015	0.424	—	0.028
MUFA, %	37.096 ± 1.301	27.631 ± 0.998	33.596 ± 1.271	<0.001	0.638	—	0.578
PUFA, %	15.433 ± 1.061	22.100 ± 0.815	20.423 ± 1.037	<0.001	0.176	—	0.062
Other FA, %	4.489 ± 0.287	4.252 ± 0.220	4.604 ± 0.281	0.533	0.355	—	0.472

Values are EMM ± SE from models adding centered IMF to Population + Sex + Population × Sex. For the 16 individual fatty acids, *qpop* is the BH-FDR-adjusted Population q value within the IMF-adjusted family; class summaries were analyzed separately. *Ppop×IMF* is the nominal P value for a Population × centered-IMF term used to assess homogeneity of the IMF association. When *Ppop×IMF* < 0.05, common-slope adjusted EMMs are descriptive and are not interpreted as a uniform Population contrast. *Pint* denotes the Population × Sex interaction. When *Pint* < 0.05, marginal Population EMMs should likewise not be interpreted alone.

Panel B. Centered-log-ratio sensitivity for individual fatty acids and fatty-acid classes

CLR coordinate	LB	LDB	DR	*Ppop*	*Pint*	*qpop*
CLR(C10:0)	-2.392 ± 0.042	-2.447 ± 0.042	-2.381 ± 0.042	0.492	0.034	0.613
CLR(C12:0)	-2.691 ± 0.034	-2.750 ± 0.034	-2.636 ± 0.034	0.065	0.005	0.104
CLR(C14:0)	0.121 ± 0.045	0.060 ± 0.045	0.121 ± 0.045	0.536	0.008	0.613
CLR(C16:0)	3.477 ± 0.030	3.331 ± 0.030	3.188 ± 0.030	<0.001	0.662	<0.001
CLR(C16:1)	1.136 ± 0.041	0.886 ± 0.041	1.102 ± 0.041	<0.001	0.096	<0.001
CLR(C18:0)	2.745 ± 0.064	2.836 ± 0.064	2.743 ± 0.064	0.512	0.314	0.613
CLR(C18:1n-9c)	3.612 ± 0.046	3.204 ± 0.046	3.451 ± 0.046	<0.001	0.244	<0.001
CLR(C18:2n-6)	2.523 ± 0.042	2.892 ± 0.042	2.847 ± 0.042	<0.001	0.263	<0.001
CLR(C20:0)	-1.259 ± 0.063	-1.317 ± 0.063	-1.879 ± 0.063	<0.001	0.387	<0.001
CLR(C20:1)	-0.365 ± 0.054	-0.394 ± 0.054	-0.400 ± 0.054	0.886	0.326	0.886
CLR(C18:3n-3)	-1.755 ± 0.057	-1.632 ± 0.057	-1.187 ± 0.057	<0.001	0.542	<0.001
CLR(C20:2n-6)	-1.130 ± 0.045	-0.934 ± 0.045	-0.752 ± 0.045	<0.001	0.081	<0.001
CLR(C20:3n-6)	-1.222 ± 0.054	-1.142 ± 0.054	-1.172 ± 0.054	0.575	0.291	0.614
CLR(C20:4n-6)	0.832 ± 0.064	1.113 ± 0.064	1.253 ± 0.064	<0.001	0.081	<0.001
CLR(C20:5n-3 [EPA])	-2.799 ± 0.063	-2.813 ± 0.063	-2.983 ± 0.063	0.081	0.092	0.118
CLR(C22:6n-3 [DHA])	-2.470 ± 0.091	-2.346 ± 0.091	-2.830 ± 0.091	0.001	0.138	0.002
CLR4(SFA)	0.910 ± 0.031	0.909 ± 0.031	0.748 ± 0.031	<0.001	0.472	—
CLR4(MUFA)	0.705 ± 0.035	0.397 ± 0.035	0.595 ± 0.035	<0.001	0.285	—
CLR4(PUFA)	-0.244 ± 0.042	0.172 ± 0.042	0.117 ± 0.042	<0.001	0.156	—
CLR4(Other FA)	-1.372 ± 0.038	-1.478 ± 0.038	-1.460 ± 0.038	0.120	0.193	—

The 17-part composition comprised the 16 identified fatty acids plus Other FA; all component values were strictly positive, so no zero replacement was required. *qpop* is BH-FDR-adjusted across the 16 identified-fatty-acid CLR coordinates. The four class-level coordinates (SFA, MUFA, PUFA, Other FA) were derived from a mutually exclusive four-part composition and analyzed separately, so *qpop* is not assigned to those rows. *Pint* denotes the Population × Sex interaction. When *Pint* < 0.05, marginal Population CLR coordinates should be interpreted cautiously rather than as uniform Population contrasts. CLR, centered log ratio.

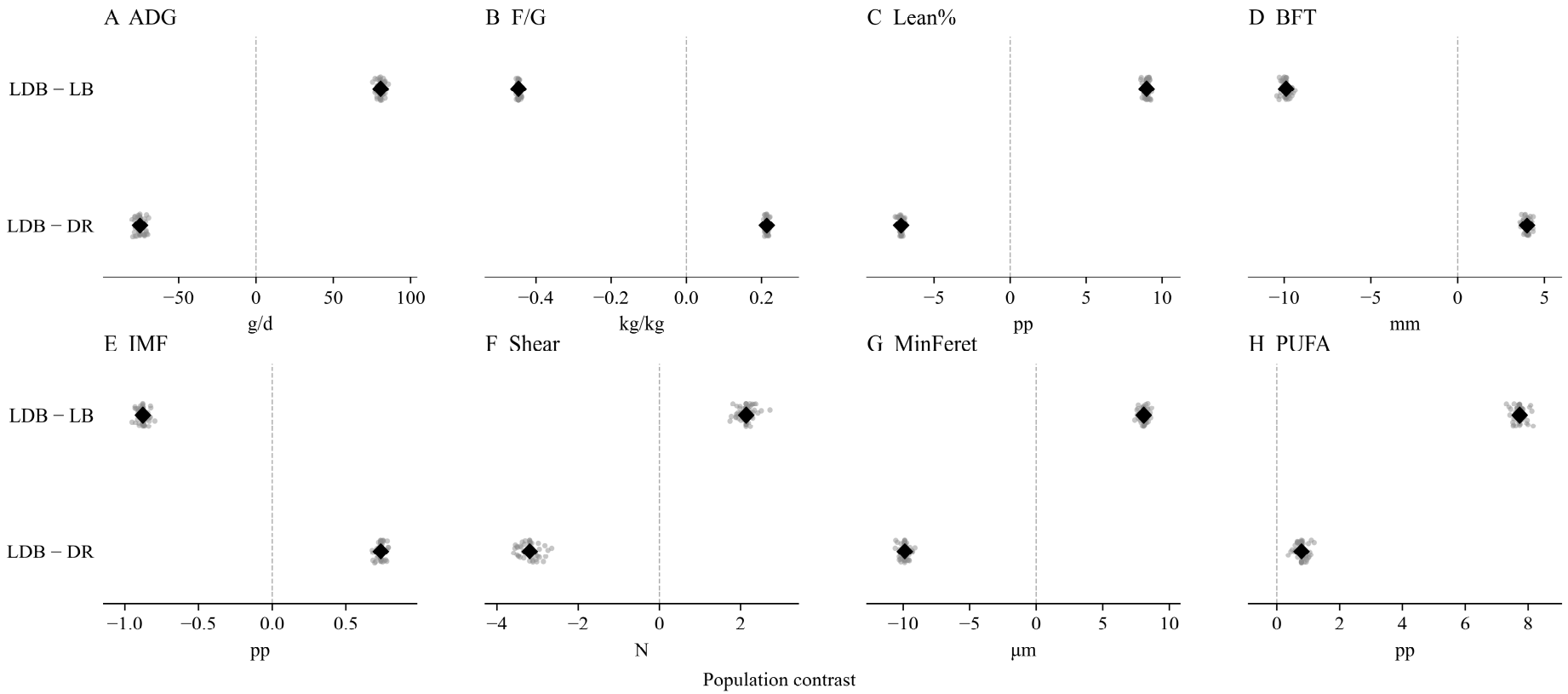


Figure S1. Leave-one-out stability of key Population contrasts. Each panel shows the 60 leave-one-out refit values for the LDB − LB and LDB − DR contrasts after omitting one pig at a time and refitting the primary Population + Sex + Population × Sex model. Panels are shown for average daily gain (ADG), feed-to-gain ratio (F/G), carcass lean percentage, average backfat thickness (BFT), intramuscular fat (IMF), shear force, minimum Feret diameter (MinFeret), and polyunsaturated fatty acids (PUFA), each in its natural unit. Gray points are leave-one-out refit values, and the black diamond denotes the corresponding full-data contrast in each group. The figure assesses influence and directional stability; leave-one-out refits are not independent biological replicates.

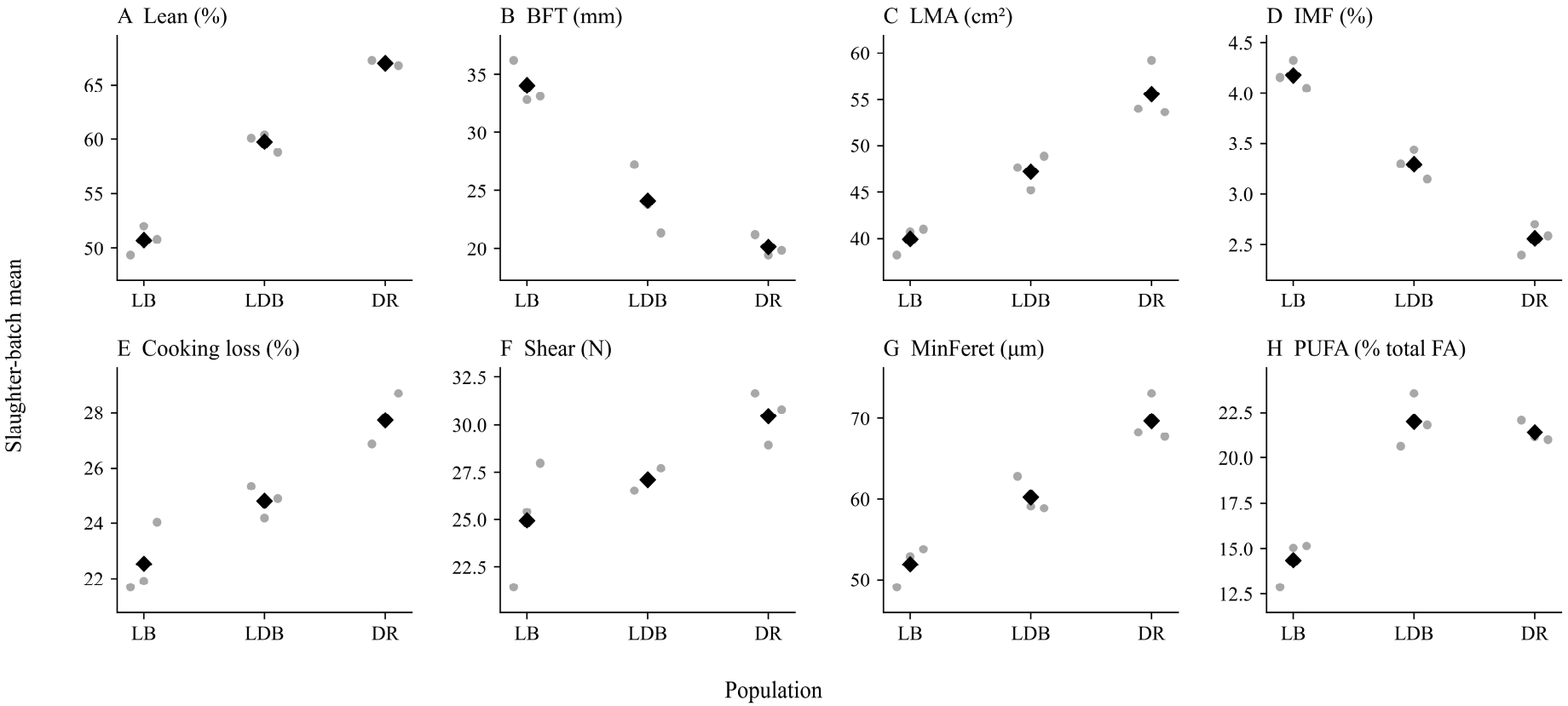
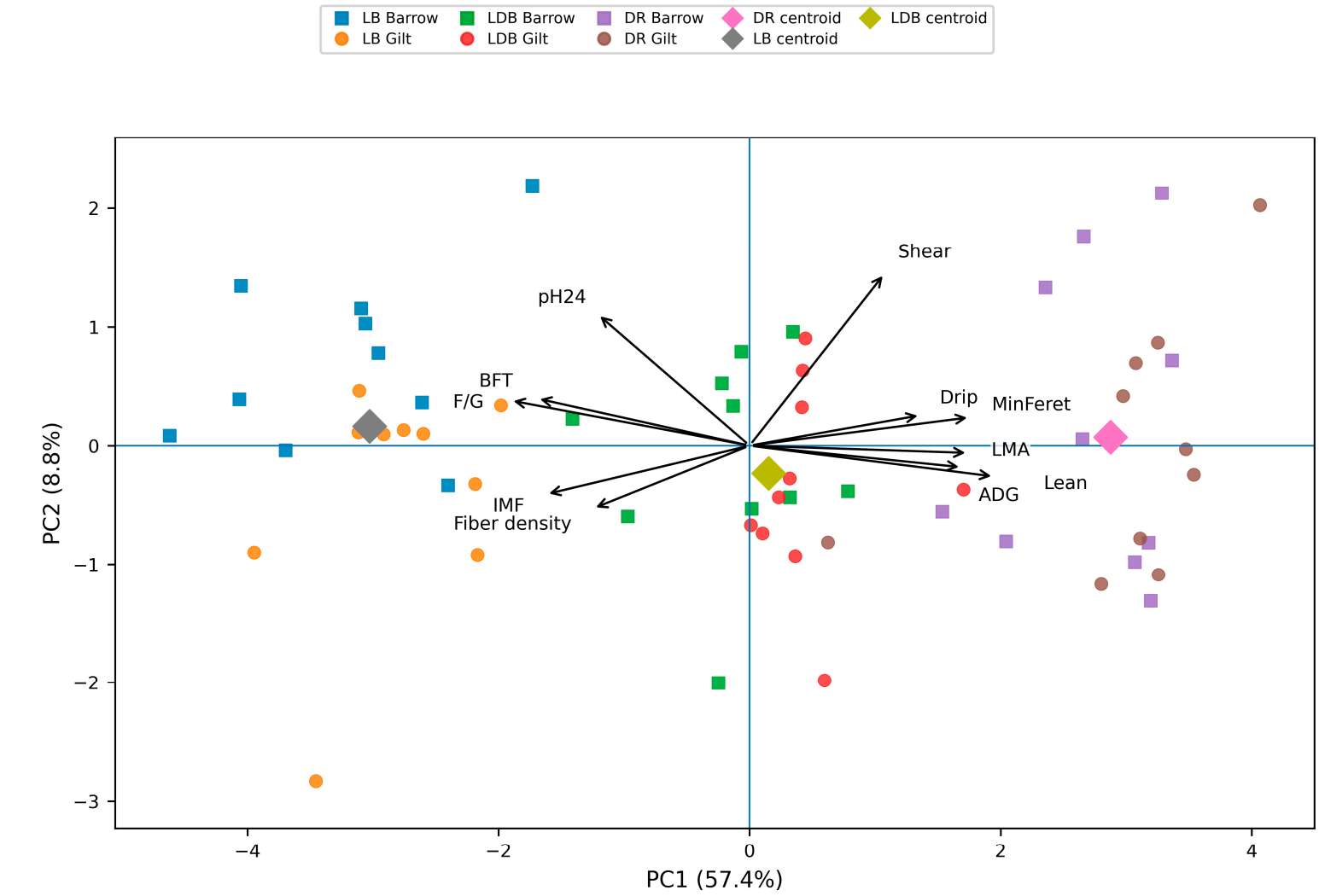
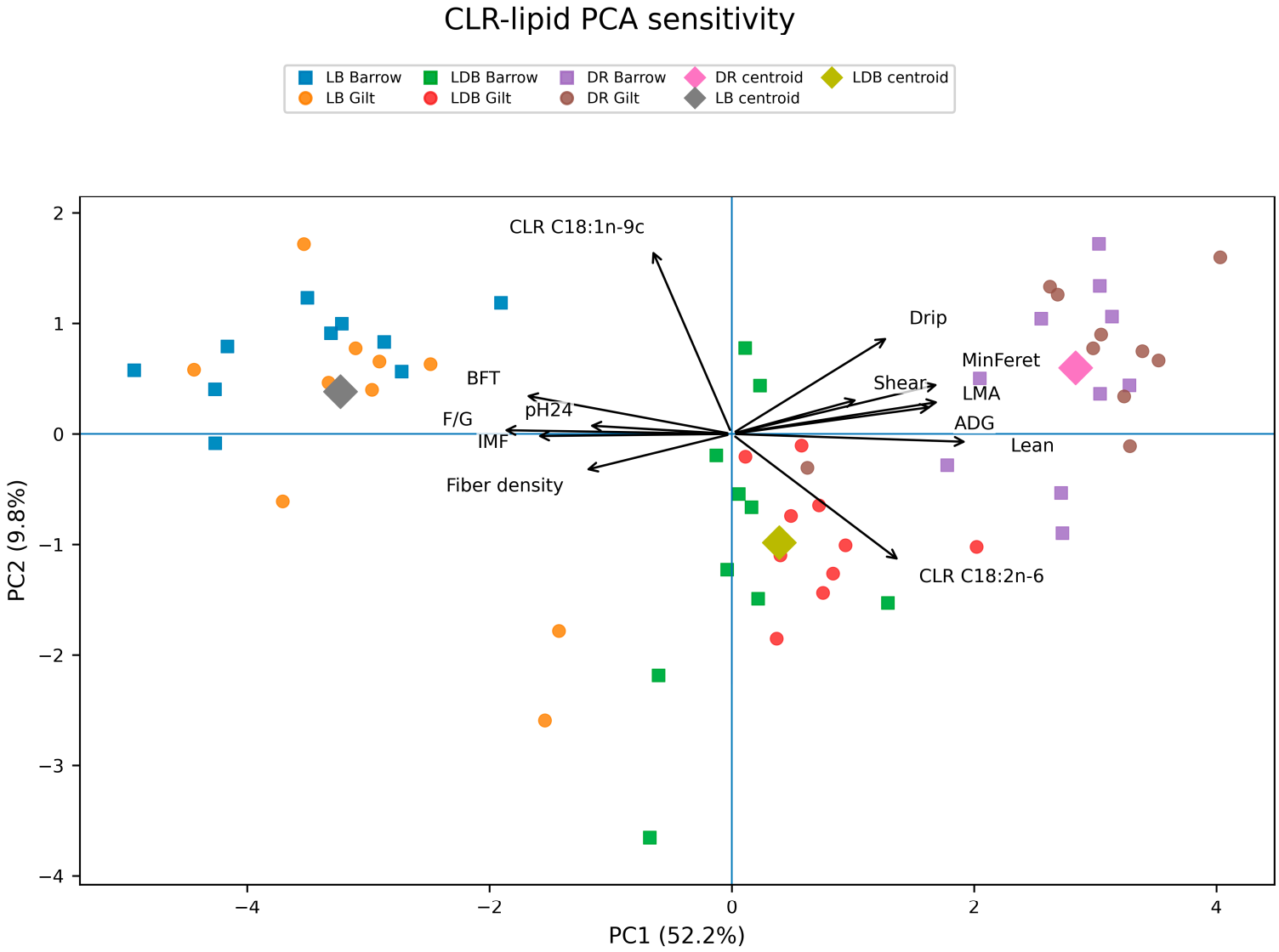


Figure S2. Slaughter-batch-level sensitivity of selected postmortem outcomes. Gray points represent individual slaughter-batch means (three batches per Population; nine batches total) for eight outcomes spanning carcass composition, pork quality, muscle morphology, and intramuscular lipid composition: carcass lean percentage, average backfat thickness (BFT), loin muscle area (LMA), intramuscular fat (IMF), cooking loss, shear force, minimum Feret diameter (MinFeret), and polyunsaturated fatty acids (PUFA). Black diamonds show the mean of the three batch means within each Population for orientation. Because slaughter batch was nested within Population, the figure is a sensitivity visualization and does not independently separate Population from slaughter date.

A


Non-lipid PCA sensitivity
LB Barrow
LB Gilt
LDB Barrow
LDB Gilt
DR Barrow
DR Gilt
DR centroid
LB centroid
LDB centroid
Shear
pH24
BFT
F/G
Drip
MinFeret
LMA
Lean
ADG
IMF
Fiber density
PC2 (8.8%)
PC1 (57.4%)
2
1
0
−1
−2
−3
−4
−2
0
2
4

B


CLR-lipid PCA sensitivity
LB Barrow
LB Gilt
LDB Barrow
LDB Gilt
DR Barrow
DR Gilt
DR centroid
LB centroid
LDB centroid
CLR C18:1n-9c
Drip
MinFeret
Shear
LMA
ADG
Lean
CLR C18:2n-6
BFT
pH24
F/G
IMF
Fiber density
PC1 (52.2%)
PC2 (9.8%)
2
1
0
−1
−2
−3
−4
−4
−2
0
2
4

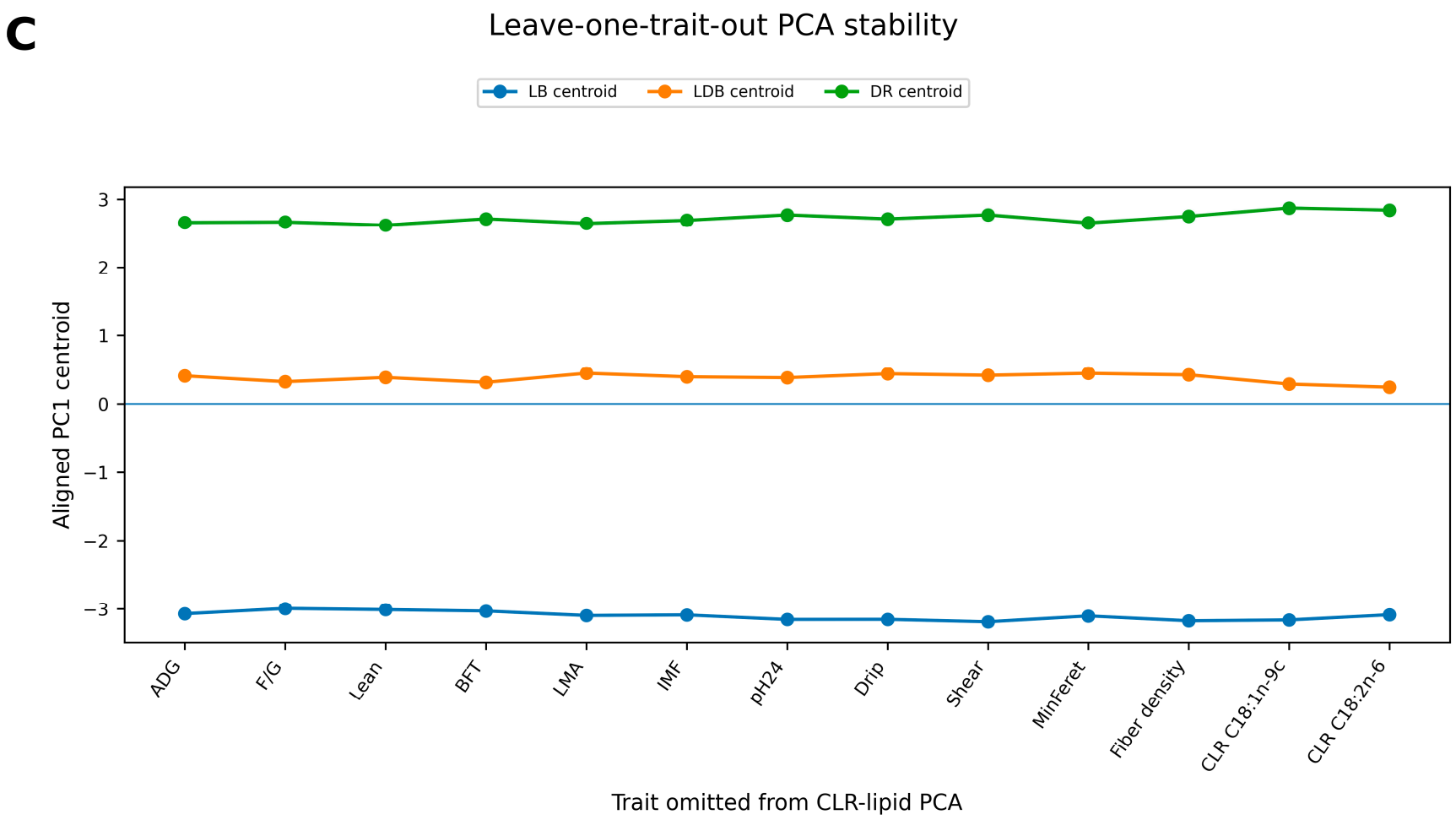


Figure S3. PCA sensitivity to lipid representation and trait selection. Panel A: non-lipid PCA excluding C18:1n-9c and C18:2n-6 retained LB–LDB–DR centroid ordering on PC1, which explained 57.4% of variance (PC2, 8.8%). Panel B: CLR-lipid PCA replacing the two raw fatty-acid percentages with their 17-part CLR coordinates retained the LB–LDB–DR PC1 ordering (52.2%) while LDB remained displaced along PC2 (9.8%). Panel C: leave-one-trait-out stability analysis of the CLR-lipid PCA. Because PCA axis signs are arbitrary, PC1 directions were aligned to the full CLR-lipid solution before comparing centroids; the LB–LDB–DR PC1 centroid ordering was retained in all 13 one-trait-omission specifications. Squares and circles denote barrows and gilts in Panels A and B, diamonds denote Population centroids, and vectors show trait loadings. CLR, centered log ratio; PCA, principal component analysis.