

Supplementary Tables:

Table S1. Differences of ADG and other performance traits between groups of high (n = 6) and low ADG steers (n = 6) of the three breeds.

Trait	Angus			Charolais			KC		
	L_ADG±SE	H_ADG±SE	P-value	L_ADG±SE	H_ADG±SE	P-value	L_ADG±SE	H_ADG±SE	P-value
ADG/kg/day	1.54±0.02	2.1±0.09	8.06E-04*	1.48±0.02	1.93±0.05	7.2E-05*	1.23±0.04	1.88±0.09	4.8E-05*
RFI/kg/day	0.63±0.35	0.37±0.39	0.63	-0.032±0.40	0.33±0.28	0.48	-0.65±0.3	-0.06±0.56	0.37
DMI/kg/day	12.2±0.34	13.45±0.34	0.03	11.06±0.48	11.7±0.34	0.30	9.57±0.31	11.12±0.78	0.10
MWT/kg	115±2.33	120.26±2.19	0.13	122.31±2.06	117.76±2.25	0.22	98.45±1.66	103.53±3.02	0.17
FUREA/cm2	83.08±2.89	82.88±2.95	0.96	94.78±4.91	91.59±3.83	0.73	65.34±1.62	74.45±1.49	0.002*
FUFAT/mm	10.57±0.93	10.18±0.98	0.78	6.38±0.71	5.73±0.37	0.44	8.28±0.94	8.83±0.32	0.59
HCW/lb	752.95±21.68	786.53±16.14	0.24	859.33 ±21.22	836.17±16.34	0.41	657.67±20.83	703.33±26.7	0.21
AFAT/mm	12±1.13	11.33±1.31	0.71	6.67±0.67	7.17±0.4	0.53	11.17±1.78	9.83±0.95	0.52
CREA/cm2	73.17±2.87	75.5±4.09	0.65	95.33±3.17	90.33±5.18	0.43	66.83±3.33	77.17±2.98	0.04
LMY/%	55.08±1.17	55.61±1.66	0.80	62.01±0.79	60.93±0.84	0.37	55.55±1.36	58.02±0.94	0.17
Marbling	448.33±24.96	416.67±24.32	0.39	365±19.05	381.67±25.23	0.58	372.5±9.64	380±18.08	0.72
Slaughter age/day	491.67±7.52	493.5±4.43	0.84	525.5 ±1.28	504±8.98	0.06	470.83±8.35	448.5±6.14	0.06

“*” indicates significant difference (P-value < 0.0042, Bonferroni Correction for 12 multiple testing analyses at P<0.05). ADG = average daily gain, RFI = residual feed intake, DMI = daily dry matter intake, MWT = metabolic body weight, FUREA = final ultrasound ribeye area at the end of feedlot test; FUFAT = final ultrasound backfat at the end of feedlot test; HCW = hot carcass weight; AFAT = carcass average backfat; REA = carcass ribeye area; LMY = lean meat yield; Marbling score (100–399 = trace marbling or less, 400–499 = slight marbling, 500–799 = small to moderate marbling, and 800–1199 = slightly abundant or more marbling). L_ADG ± SE= trait mean values for the low ADG group± standard error (SE); H_ADG ± SE= trait mean values for the high ADG steer group ± standard error (SE).

Table S2. Differences of DMI and other performance traits between groups of high (n = 6) and low DMI steers (n = 6) of the three breeds.

Trait	Angus			Charolais			KC		
	L_DMI±SE	H_DMI±SE	P-value	L_DMI±SE	H_DMI±SE	P-value	L_DMI±SE	H_DMI±SE	P-value
DMI/kg/day	10.88±0.21	13.61±0.29	1.87E-05*	9.96±0.08	12.44±0.13	1.81E-08*	8.83±0.16	12.8±0.32	6.47E-07*
RFI/kg/day	-0.7±0.03	0.84±0.42	0.014	-1.06±0.1	1.02±0.19	2.03E-06*	-1.18±0.14	1.4±0.17	3.77E-07*
ADG/kg/day	1.72±0.03	1.97±0.14	0.13	1.64±0.08	1.65±0.07	0.95	1.39±0.11	1.61±0.08	0.14
MWT/kg	110.29±2.8	119.68±2.42	0.03	118±1.72	123.72±1.93	0.05	96.28±1.43	106.11±1.88	0.002*
FUREA/cm2	84.24±1.3	83.81±3.52	0.91	94.42±2.52	94.08±2.53	0.93	68.78±3.26	74±1.64	0.18
FUFAT/mm	9.06±1.01	10.29±0.87	0.38	5.82±0.71	6.54±0.64	0.46	9.39±0.83	9.07±0.46	0.74
HCW/lb	721.87±22.92	786.1±17.96	0.05	824.5±11.68	872±15.67	0.04	624.33±7.85	701.17±22.54	0.02
AFAT/mm	11.17±1.47	12.33±1.45	0.58	6.83±0.79	7.5±0.43	0.48	13.17±1.62	9.67±0.49	0.03
CREA/cm2	76.17±2.75	76.5±4.46	0.95	94.17±2.77	94.67±2.11	0.89	65.83±2.89	75.83±2.51	0.03
LMY/%	56.66±1.55	55.12±1.74	0.52	62.08±0.73	61.13±0.5	0.31	54.35±1.09	57.89±0.53	0.02
Marbling	423.33±28.49	450±16.74	0.44	376.67±36.86	390±25.3	0.77	373.33±21.09	361.67±12.5	0.64
Slaughter age/day	505.83±5.77	490.67±4.69	0.07	518.5±6.88	525.67±3.4	0.37	461.17±5.45	446.67±2.83	0.04

“*” indicates significant difference (P-value < 0.0042, Bonferroni Correction for 12 multiple testing analyses at P<0.05). DMI = daily dry matter intake, RFI = residual feed intake, ADG = average daily gain, MWT = metabolic body weight, FUREA = final ultrasound ribeye area at the end of feedlot test; FUFAT = final ultrasound backfat at the end of feedlot test; HCW = hot carcass weight; AFAT = carcass average backfat; REA = carcass ribeye area; LMY = lean meat yield; Marbling score (100–399 = trace marbling or less, 400–499 = slight marbling, 500–799 = small to moderate marbling, and 800–1199 = slightly abundant or more marbling). L_DMI ± SE= trait mean values for the low DMI group± standard error (SE); H_DMI ± SE= trait mean values for the high DMI steer group ± standard error (SE).

Table S3. Differences of MWT and other performance traits between groups of high (n = 6) and low MWT steers (n = 6) of the three breeds.

Trait	Angus			Charolais			KC		
	L_MWT±SE	H_MWT±SE	P-value	L_MWT±SE	H_MWT±SE	P-value	L_MWT±SE	H_MWT±SE	P-value
MWT/kg	105.99±2.12	124.57±2.2	1.20E-04*	114.57 ±0.83	125.56±1.08	1.05E-05*	94.24±0.72	107.93±1.47	7.97E-06*
RFI/kg/day	0.11±0.39	0.31±0.51	0.77	0.24 ±0.36	-0.11±0.44	0.55	-0.07±0.51	0.57±0.53	0.41
DMI/kg/day	11.26±0.37	13.49±0.35	1.47E-03*	11.22 ±0.38	11.42±0.47	0.75	9.75±0.54	12.22±0.62	0.013
ADG/kg/day	1.66±0.04	1.98±0.13	0.06	1.8 ±0.07	1.63±0.06	0.10	1.56±0.13	1.64±0.07	0.57
FUREA/cm2	81.75±2.01	83.14±3.01	0.71	86.81 ±3.67	96.33±1	0.03	68.52±2.35	73.94±1.54	0.08
FUFAT/mm	8.75±0.53	10.02±0.73	0.19	5.97 ±0.43	7.01±0.85	0.30	8.26±0.36	9.16±0.39	0.12
HCW/lb	683.5±17.77	827.62±21.4	4.13E-04*	803.33 ±6.97	898.17±14.31	1.4E-04*	641.17±17.59	727.67±16.62	5.07E-03
AFAT/mm	10.83±1.11	11.33±1.23	0.77	7.33 ±0.61	8.17±1.14	0.53	10.67±0.71	8.83±0.6	0.08
CREA/cm2	74.33±2.62	75.67±4.33	0.80	88.17 ±3.74	96.5±3.92	0.15	69±3.51	78.5±1.63	0.03
LMY/%	56.99±1.04	55.14±1.67	0.37	60.78 ±0.77	60.71±1.04	0.96	56.54±0.59	58.69±0.56	0.02
Marbling	391.67±16	413.33±20.92	0.43	353.33 ±17.44	363.33±26.28	0.76	372.5±22.05	375±6.71	0.92
Slaughter age/day	487.83±7.19	497.5±2.46	0.23	503 ±8.22	525±4.42	0.04	460.17±11.3	448.67±3.4	0.37

“*” indicates significant difference (P-value < 0.0042, Bonferroni Correction for 12 multiple testing analyses at P<0.05). MWT = metabolic body weight, DMI = daily dry matter intake, RFI = residual feed intake, ADG = average daily gain, FUREA = final ultrasound ribeye area at the end of feedlot test; FUFAT = final ultrasound backfat at the end of feedlot test; HCW = hot carcass weight; AFAT = carcass average backfat; REA = carcass ribeye area; LMY = lean meat yield; Marbling score (100–399 = trace marbling or less, 400–499 = slight marbling, 500–799 = small to moderate marbling, and 800–1199 = slightly abundant or more marbling). L_MWT ± SE= trait mean values for the low MWT group± standard error (SE); H_MWT ± SE= trait mean values for the high MWT steer group ± standard error (SE).

Table S4. Top five enriched functions and the DE genes involved in the functions for ADG, DMI and MWT within Angus, Charolais and KC populations.

	Molecular and Cellular Functions	No. DE Genes	DE Genes involved in the Function
ADG			
Angus	Cellular Movement	36	<i>ABHD6, ANO6, ANXA5, BCL3, CCL24, CD44, CORO1A, CUL7, CXCL2, CYP7A1, EZR, F2R, GBP1, GPC3, GPNMB, HMGCR, HP, IGF1, IL20RA, ITGA4, KIAA0319, LBP, MGP, MX1, PIP5K1A, PLA2G7, RAP1GAP, S100A2, SAA1, SERPINA3, SERPINE1, SLC1A2, SOCS2, SOCS3, SPNS2, VCAMI</i>
	Lipid Metabolism	29	<i>ABHD6, AKR1B10, ANXA5, CD44, CYP2C19, CYP51A1, CYP7A1, ELOVL5, F2R, GPC3, HMGCR, HMGCS1, HP, IGF1, IL1R2, LBP, NR0B2, PGAP1, PIP5K1A, PLA2G7, SAA1, SERPINE1, SLC1A2, SOCS3, SPNS2, SQLE, SULT2A1, UGT2B17, VCAMI</i>
	Small Molecule Biochemistry	32	<i>ABHD6, AKR1B10, ANXA5, CD44, CYP2C19, CYP51A1, CYP7A1, ELOVL5, F2R, GPC3, HMGCR, HMGCS1, HP, IGF1, IL1R2, LBP, NR0B2, PGAP1, PIP5K1A, PLA2G7, SAA1, SERPINE1, SLC16A10, SLC1A2, SLC25A15, SLC3A1, SOCS3, SPNS2, SQLE, SULT2A1, UGT2B17, VCAMI</i>
	Vitamin and Mineral Metabolism	13	<i>AKR1B10, CYP2C19, CYP51A1, CYP7A1, GPC3, HMGCR, HMGCS1, IGF1, NR0B2, SAA1, SQLE, SULT2A1, UGT2B17</i>
	Cell-To-Cell Signaling and Interaction	27	<i>ANO6, ANXA5, BCL3, CCL24, CD44, CMAH, CORO1A, CXCL2, EZR, F2R, GPC3, GPNMB, HMGCR, IGF1, IL1R2, IL20RA, ITGA4, LBP, PIP5K1A, RAP1GAP, SAA1, SERPINE1, SOCS2, SOCS3, SPTB, TOP2A, VCAMI</i>
Charolais	Lipid Metabolism	33	<i>ACSS2, AKR1B10, ALDH3B1, APOA1, APOA4, CCDC80, CPT1B, CS, CYP2B6, CYP2C19, EGR1, ELOVL2, FASN, GNMT, GPC3, GSTA1, HMOX1, IL1R2, MFSD2A, MGLL, MID1IP1, NOCT, PDK4, PIP5K1A, PPP1R3C, RXRG, SAA1, SCD, SOAT2, SQLE, STEAP4, STS, SULT1E1</i>
	Molecular Transport	44	<i>AKR1B10, APOA1, APOA4, ARG1, CCDC80, CD22, CDH17, CPT1B, CRYAB, CXCL2, CYP2B6, EGLN3, EGR1, ELOVL2, FASN, GNMT, GPC3, GSTA1, HMOX1, HOOK1, IFI27, IL1R2, MFSD2A, MGLL, MID1IP1, NOCT, PDK4, PIP5K1A, PNP, PPP1R3C, RXRG, S100A10, SAA1, SCD, SLC13A2, SLC17A9, SLC23A4, SLC3A1, SOAT2, STEAP4, STS, SULT1E1, TPH1, TTC7A</i>
	Small Molecule Biochemistry	45	<i>ACSS2, AKR1B10, ALDH3B1, APOA1, APOA4, CCDC80, CNDP2, CPT1B, CS, CSAD, CYP2B6, CYP2C19, DDO, EGLN3, EGR1, ELOVL2, FASN, GNMT, GPC3, GPX3, GSTA1, HMOX1, IL1R2, MFSD2A, MGLL, MID1IP1, NOCT, PDK4, PIP5K1A, PPP1R3C, RXRG, S100A10, SAA1, SCD, SDS, SHMT2, SLC17A9, SLC3A1, SOAT2, SQLE, STEAP4, STS, SULT1E1, TPH1</i>
	Vitamin and Mineral Metabolism	15	<i>AKR1B10, APOA1, APOA4, CYP2B6, CYP2C19, FASN, GPC3, GSTA1, SAA1, SCD, SHMT2, SOAT2, SQLE, STS, SULT1E1</i>
	Amino Acid Metabolism	13	<i>ARG1, CNDP2, CS, CSAD, DDO, EGR1, GNMT, PDK4, RXRG, SDS, SHMT2, SLC3A1, TPH1</i>

KC	Amino Acid Metabolism	8	<i>AASS, ACMSD, ARG1, CARNS1, DUSP1, GNMT, MYC, TAT</i>
	Small Molecule Biochemistry	31	<i>AASS, ACMSD, ALOX15B, ARFGEF3, ARG1, CARNS1, CES1, CYP7A1, DUSP1, EXTL1, FGF21, GNMT, GSTM1, GSTM4, IGFBP1, LPIN1, MFSD2A, MX1, MYC, NOCT, OAS1, PIP5K1A, S100A12, SCD, SLC17A9, SLC4A4, SOD3, STS, TAT, USP2, WFS1</i>
	Carbohydrate Metabolism	21	<i>ARFGEF3, CES1, CYP7A1, DUSP1, FGF21, GLCE, GNMT, IGFBP1, LPIN1, MFSD2A, MYC, NOCT, NUDT5, OAS1, PIP5K1A, SCD, SLC5A8, SOD3, TAT, USP2, WFS1</i>
	Molecular Transport	28	<i>ALOX15B, ARFGEF3, ARG1, CA7, CES1, CXCL2, CYP7A1, DUSP1, EXTL1, FGF21, GNMT, GSTM1, IFI27, IGFBP1, LPIN1, MFSD2A, MX2, MYC, NOCT, PIP5K1A, RSAD2, S100A12, SCD, SLC17A9, SLC4A4, SLC5A8, STS, WFS1</i>
	Lipid Metabolism	17	<i>ALOX15B, CES1, CYP7A1, DUSP1, EXTL1, FGF21, GNMT, GSTM4, LPIN1, MFSD2A, MX1, MYC, PIP5K1A, S100A12, SCD, SLC4A4, STS</i>
DMI			
Angus	Lipid Metabolism	29	<i>ABHD6, AKR1B10, APOA4, ARNTL, BAG3, BCL6, CCDC80, CDKN1A, CREM, CYP2C19, CYP7A1, DDIT4, DUSP1, FCGR2B, GNAI1, GNMT, GPC3, HP, LPIN1, MTHFR, MX1, NOCT, NR1D1, PIP5K1A, SAA1, SCD, SLC1A2, STEAP4, VCAM1</i>
	Molecular Transport	41	<i>ABHD6, AKR1B10, ANXA2, APOA4, ARNTL, BAG3, BCL6, CA7, CCDC80, CDKN1A, CORO1A, CREM, CXCL2, CYP7A1, DUSP1, FCGR2B, GNAI1, GNMT, GPC3, HAMP, HERPUD1, HP, IFI27, LPIN1, MTHFR, MX2, NOCT, NR1D1, PIP5K1A, PTGER3, RSAD2, SAA1, SCD, SLC17A9, SLC1A2, SLC22A2, SLC2A5, SLC3A1, SPTB, STEAP4, VCAM1</i>
	Small Molecule Biochemistry	42	<i>ABHD6, AK8, AKR1B10, ANXA2, APOA4, ARNTL, BAG3, BCL6, CCDC80, CDKN1A, CMPK2, CREM, CYP2C19, CYP7A1, DDIT4, DDO, DUSP1, FCGR2B, GNAI1, GNMT, GPC3, GPX3, HP, KYAT3, LPIN1, MTHFR, MX1, NOCT, NR1D1, PIP5K1A, PSPH, SAA1, SCD, SDS, SLC17A9, SLC1A2, SLC2A5, SLC3A1, SPTB, STEAP4, TAT, VCAM1</i>
	Cell Death and Survival	44	<i>AKR1B10, ANXA2, BAG3, BCL6, BTG2, CCDC80, CDKN1A, CORO1A, CRELD1, CREM, CXCL2, CYP7A1, CYR61, DDIT4, DHX58, DUSP1, FCGR2B, FKBP5, GADD45B, GNMT, GPC3, GPNMB, HERPUD1, HLA-B, HSPH1, HTRA3, IFIT2, ISG15, MICAL2, MTHFR, MX1, NR1D1, NUF2, PRAP1, SAA1, SCD, SFRP2, SLC1A2, SLC22A2, SOCS2, SPTB, VCAM1, ZFAND5, ZNF385B</i>
	Carbohydrate Metabolism	16	<i>APOA4, ARNTL, CCDC80, CYP7A1, DUSP1, FCGR2B, GNMT, LPIN1, NOCT, PIP5K1A, RGL1, SCD, SDS, SLC2A5, STEAP4, TAT</i>
Charolais	Lipid Metabolism	49	<i>ABCA1, ABCG5, ABCG8, AHR, AKR1C3, ALDH3B1, CIQTNF5, CCDC80, CES1, CYP11A1, CYP2C19, CYP7A1, CYR61, EGR1, ERBB2, F2R, FGF21, FOS, GNMT, HMGCR, HMGCS1, HP, HSPG2, IDI1, IL1B, IL1R2, JUN, LPIN1, LTF, NAAA, NOS3, NPC1, NR0B2, PIP5K1A, PMVK, RGS16, SAA1, SAA2-SAA4, SFTPD, SLC1A1, SLC22A2, SLC22A7, SLC27A6, SLC4A4, SQLE, SULT1E1, THBS1, UGT2B17, VWF</i>
	Small Molecule Biochemistry	60	<i>AASS, ABCA1, ABCG5, ABCG8, AHR, AKR1C3, ALDH3B1, CIQTNF5, CARNS1, CCDC80,</i>

			<i>CES1, CYP11A1, CYP2C19, CYP7A1, CYR61, EGR1, ERBB2, F2R, FGF21, FOS, GLDC, GNMT, HAL, HMGCR, HMGCS1, HP, HSPG2, ID11, IL1B, IL1R2, JUN, LPIN1, LTF, NAAA, NOS3, NPC1, NR0B2, OAT, PIP5K1A, PMVK, PRODH2, RGS16, SAA1, SAA2-SAA4, SFTPD, SLC11A1, SLC16A10, SLC1A1, SLC22A2, SLC22A7, SLC25A15, SLC27A6, SLC3A1, SLC4A4, SLC7A2, SQLE, SULT1E1, THBS1, UGT2B17, VWF</i>
	Vitamin and Mineral Metabolism	26	<i>ABCA1, ABCG5, ABCG8, AHR, AKR1C3, CES1, CYP11A1, CYP2C19, CYP7A1, HMGCR, HMGCS1, HSPG2, ID11, IL1B, NAAA, NPC1, NR0B2, PMVK, SAA1, SFTPD, SLC22A2, SQLE, SULT1E1, UGT2B17</i>
	Cellular Movement	63	<i>ABCA1, ACTA2, ADGRG6, AHR, ASCL1, CAMK2D, CCND1, CD93, CES1, CLDN4, COL1A1, COL1A2, CORO1A, CXCL2, CYP7A1, CYR61, EGR1, ERBB2, F2R, FBLN1, FOS, GADD45A, GLCE, GRB7, HMGCR, HOOK1, HP, HSPG2, HTRA3, IL1B, JAM3, JCHAIN, JUN, JUNB, KIAA0319, LTF, LUM, MMP11, NAAA, NOS3, NPC1, PAQR3, PIP5K1A, PRAP1, PTPRZI, RGS16, S100A2, S100A10, SAA1, SELL, SERPINA3, SFRP1, SFTPD, SLC11A1, SLC17A3, SULT1E1, TAGLN, TDP2, THBS1, TMEM176B, TNFRSF8, VWF, WASF3</i>
	Molecular Transport	54	<i>ABCA1, ABCG5, ABCG8, AHR, CIQTNF5, CAMK2D, CCDC80, CDH17, CES1, COL1A1, CORO1A, CXCL2, CYP11A1, CYP7A1, EGR1, ERBB2, F2R, FGF21, FOS, GNMT, GRIN3A, HMGCR, HOOK1, HP, IFI27, IL1B, IL1R2, JUN, LPIN1, LTF, NAAA, NNAT, NOS3, NPC1, NR0B2, PIP5K1A, PPY, SAA1, SAA2-SAA4, SELL, SFTPD, SLC11A1, SLC16A10, SLC17A3, SLC1A1, SLC22A2, SLC22A7, SLC25A15, SLC27A6, SLC3A1, SLC4A4, SLC7A2, SULT1E1, THBS1</i>
KC	Cellular Function and Maintenance	51	<i>ADA, APCS, BCL6, CACNG1, CD274, CD3D, CD3E, CDKN1A, CORO1A, CR2, CXCL10, DRAM1, FCGR2B, FGR, GIMAP4, HCK, HLA-DQB1, IDO1, IFI6, IFIH1, IRF1, ISG15, ITGAL, LCP1, LCP2, LSP1, MPZL2, NFIL3, NLRC5, OAS1, ORAI2, PIM1, PIP5K1A, PKM, PSMB8, PSMB9, PSMB10, PYCR1, RAC2, RGS16, RSAD2, SGK1, STAT1, TAP1, TGM2, TLR3, TRPV2, UBD, USP18, VCAM1, WFS1</i>
	Cell-To-Cell Signaling and Interaction	49	<i>ADA, APCS, ARHGAP24, BCL6, CD180, CD274, CD3D, CD3E, CDKN1A, COL1A1, CORO1A, CR2, CTGF, CXCL10, CXCL9, CYP2C19, FCGR2B, FGR, HCK, HLA-DQB1, IDO1, IGFBP1, IGFBP2, IL20RA, IRF1, ISG15, ITGAL, LCP1, LCP2, LSP1, MFSD2A, NFIL3, PIM1, PIP5K1A, PKM, PLTP, PSMB10, PSMB8, PSMB9, PTPRZI, RAC2, RGS16, SGK1, STAT1, TAP1, TGM2, TLR3, TOP2A, TRPV2, USP18, VCAM1, ZBP1</i>
	Cell Death and Survival	76	<i>ADA, AKR1B10, APCS, APMAP, BCL6, CD274, CD3E, CD53, CDKN1A, COL1A1, CORO1A, CR2, CRELD1, CTGF, CXCL10, CXCL9, CYP2B6, DIRAS3, DRAM1, ENCI, FCGR2B, FETUB, FGR, GBP1, GIMAP4, HCK, HEBP2, HLA-B, HLA-DQB1, HTRA3, IDO1, IFI6, IFIH1, IFIT2, IFRD1, IGFBP1, IGFBP2, INPP1, INSIG1, IRF1, ISG15, ITGAL, LCP2, LMNB1, LSP1, NFIL3, OAS1, PDE9A, PIM1, PKM, PLTP, PPP1R17, PSMB10, PSMB8, PTPRZI, RAC2, REV3L, RGS16, RRM2, SFRP2, SGK1, SLFN11, STAT1, STMN1, TAP1, TGM2, TLR3, TOP2A, TRPV2, UBA7, UBD, USP18, VCAM1, WFS1, XAF1, ZNF385B</i>
	Cellular Movement	58	<i>ABCA1, ABCG5, ABCG8, AHR, AKR1C3, ALDH3B1, CIQTNF5, CCDC80, CES1, CYP11A1, CYP2C19, CYP7A1, CYR61, EGR1, ERBB2, F2R, FGF21, FOS, GNMT, HMGCR, HMGCS1, HP,</i>

			<i>HSPG2, ID11, IL1B, IL1R2, JUN, LPINI, LTF, NAAA, NOS3, NPC1, NR0B2, PIP5K1A, PMVK, RGS16, SAA1, SAA2-SAA4, SFTPD, SLC1A1, SLC22A2, SLC22A7, SLC27A6, SLC4A4, SQLE, SULT1E1, THBS1, UGT2B17, VWF</i>
	Cellular Development	48	<i>ADA, APCS, BCL6, CD180, CD274, CD3D, CD3E, CDKN1A, COL1A1, CORO1A, CR2, CTGF, CXCL10, FCGR2B, GBP2, GIMAP4, HCK, HLA-DQB1, IDO1, IFRD1, IGFBP1, IGFBP2, IL20RA, IRF1, ISG15, ITGAL, LCP1, LCP2, LMNB1, LSP1, MPZL2, NFIL3, PIMI, PKM, PSMB10, PSMB8, PSMB9, RAC2, RSAD2, Sectm1b, SFRP2, STAT1, STMN1, TGM2, TLR3, UBD, USP18, VCAM1</i>
MWT			
Angus	Amino Acid Metabolism	9	<i>CSAD, GNMT, IGF1, IGFBP2, MTHFR, OAT, PSPH, SDS, SLC3A1</i>
	Small Molecule Biochemistry	27	<i>ABHD6, AKR1B10, CCL24, CSAD, CTGF, CYP2B6, CYP2C19, ETNPPL, GNMT, GPC3, HMGCR, HMGCS1, IGF1, IGFBP2, IL1R2, ITPR1, LBP, MTHFR, OAT, PIP5K1A, PLCD4, PSPH, SDS, SLC3A1, SPTB, SULT1E1, SULT2A1</i>
	Lipid Metabolism	16	<i>ABHD6, AKR1B10, CYP2B6, CYP2C19, ETNPPL, GNMT, GPC3, HMGCR, HMGCS1, IGF1, IGFBP2, LBP, PIP5K1A, PLCD4, SULT1E1, SULT2A1</i>
	Vitamin and Mineral Metabolism	11	<i>AKR1B10, CYP2B6, CYP2C19, GPC3, HMGCR, HMGCS1, IGF1, IGFBP2, MTHFR, SULT1E1, SULT2A1</i>
	Cell Morphology	11	<i>CRYAB, CTGF, CYR61, GPX3, IGF1, IGFBP2, ISG15, ITPR1, OAT, PIP5K1A, RAP1GAP</i>
Charolais	Lipid Metabolism	26	<i>AOAH, CIQA, CIQTNF5, CSF2RB, CYP2B6, FADS1, FGF21, HCK, HMOX1, IL1B, KCNE1B, LPINI, NRBF2, PDK4, PLTP, PLVAP, PPP1R3C, PTGS1, S100A10, SDC3, SOAT2, SULT1E1, TBXAS1, THRSP, UCP2, VCAM1</i>
	Small Molecule Biochemistry	33	<i>AOAH, CIQA, CIQTNF5, CSF2RB, CTGF, CYP2B6, FADS1, FGF21, HCK, HMOX1, IL1B, KCNE1B, LPINI, NRBF2, PDK4, PLTP, PLVAP, PPP1R3C, PPY, PTGS1, S100A10, SDC3, SFRP1, SLC3A1, SLC7A5, SLCO4A1, SOAT2, SULT1E1, TBXAS1, THRSP, TSHB, UCP2, VCAM1</i>
	Cellular Movement	27	<i>CD22, CRYAB, CSF1R, CSF2RB, CTGF, FBLN2, HCK, HMOX1, IL1B, KIAA0319, MACF1, MMP11, PDK4, PILRA, PLTP, PLVAP, PRAP1, S100A10, SDC3, SELL, SERPINA3, SFRP1, SLC7A5, SULT1E1, TBXAS1, UCP2, VCAM1</i>
	Molecular Transport	35	<i>CIQA, CIQTNF5, CD22, CRYAB, CSF2RB, CTGF, CYP2B6, FADS1, FGF21, GRIN3A, HCK, HMOX1, IL1B, KCNE1B, LILRB2, LPINI, NRBF2, PDK4, PLTP, PLVAP, PPP1R3C, PPY, PTGS1, S100A10, SDC3, SLC13A2, SLC23A4, SLC3A1, SLC7A5, SOAT2, SULT1E1, THRSP, TSHB, UCP2, VCAM1</i>
	Cell-To-Cell Signaling and Interaction	23	<i>CSF2RB, CRYAB, IL1B, CIQA, CD22, CSF1R, CTGF, SELL, HCK, HMOX1, FGF21, HLA-DQB1, VCAM1, PLTP, UCP2, SFRP1, S100A10, PDK4, SDC3, PTGS1, LILRB2, SLC7A5, PILRA</i>
KC	Cell Death and Survival	32	<i>BCL6, CAMK2D, CDH11, CES1, CLTC, COL1A1, CTGF, CXCL10, CXCL9, ECE1, ENC1, GADD45B, GIMAP4, GNMT, GRIN3A, HLA-B, HLA-DQB1, HOPX, IFI6, IFRD1, LY9, PIMI, PRAP1, REV3L, RNF13, SGK1, SOCS3, TGM2, TOP2A, TRIB2, WFS1, ZNF385B</i>

	Cellular Movement	14	<i>BCL6, CES1, CLTC, COL1A1, CTGF, CXCL10, CXCL9, HP, JCHAIN, PGLYRP2, PRAP1, SGK1, SOCS3, TGM2</i>
	Cell Morphology	8	<i>CAMK2D, CTGF, CXCL10, CXCL9, GPX3, MEX3C, PIMI, SGK1</i>
	Cell-To-Cell Signaling and Interaction	12	<i>CDH11, CES1, CLTC, COL1A1, CTGF, CXCL10, CXCL9, CYP2B6, CYP2C19, GPX3, SGK1, TGM2</i>
	Drug Metabolism	2	<i>CYP2B6, CYP2C19</i>

Table S5. Enriched biological processes within amino acid metabolism biological functions associated with ADG in Angus, Charolais and KC steers.

Categories	Functions Annotation	P-Value	Activation z-score	Molecules (DE genes)
Angus				
	Uptake of leucine	9.66E-04		<i>IGF1, SLC3A1</i>
	Uptake of cystine	5.67E-04		<i>IGF1, SLC3A1</i>
	Uptake of aromatic amino acid	1.47E-03		<i>SLC16A10, SLC3A1</i>
	Uptake of amino acids	8.09E-04	-0.744	<i>IGF1, SLC16A10, SLC1A2, SLC3A1</i>
	Transport of glutamine family amino acid	2.33E-03		<i>SLC1A2, SLC25A15, SLC3A1</i>
	Transport of essential amino acids	1.47E-03		<i>SLC16A10, SLC25A15</i>
	Transport of arginine	1.47E-03		<i>SLC25A15, SLC3A1</i>
	Transport of amino acids	1.16E-03	-1.27	<i>IGF1, SLC16A10, SLC1A2, SLC25A15, SLC3A1</i>
	Transport of L-amino acid	3.06E-03		<i>SLC16A10, SLC1A2, SLC25A15</i>
	Metabolism of L-tetrahydrofolic acid	2.40E-03		<i>MTHFD1L, MTHFR</i>
Charolais				
	Metabolism of amino acids	5.67E-08	-0.391	<i>ARG1, CNDP2, CS, CSAD, DDO, EGR1, GNMT, SDS, SHMT2, SLC3A1</i>
	Synthesis of L-amino acid	4.51E-05		<i>ARG1, CNDP2, CS, SHMT2</i>
	Metabolism of L-amino acid	5.63E-05		<i>CSAD, DDO, GNMT, SDS, SHMT2</i>
	Synthesis of amino acids	6.91E-05	0	<i>ARG1, CNDP2, CS, EGR1, SHMT2</i>
	Abnormal quantity of amino acids	1.64E-04		<i>ARG1, DDO, GNMT, PDK4</i>
	Metabolism of amino acid analogs	1.85E-04		<i>CSAD, EGR1, GNMT, SHMT2</i>
	Metabolism of sulfur amino acid	3.60E-04		<i>CSAD, GNMT, SHMT2</i>
	Metabolism of serine family amino acid	3.95E-04		<i>CSAD, SDS, SHMT2</i>
	Quantity of amino acids	5.48E-04		<i>ARG1, DDO, GNMT, PDK4, RXRG, SHMT2</i>
	Transport of arginine	1.07E-03		<i>ARG1, SLC3A1</i>
KC				

	Metabolism of essential amino acids	3.67E-07		<i>AASS, ACMSD, CARNSI, GNMT, TAT</i>
	Metabolism of amino acids	1.27E-05		<i>AASS, ACMSD, ARG1, CARNSI, GNMT, MYC, TAT</i>
	Catabolism of amino acids	1.57E-05		<i>AASS, ARG1, CARNSI, MYC, TAT</i>
	Metabolism of L-amino acid	1.75E-05		<i>AASS, ACMSD, CARNSI, GNMT, TAT</i>
	Catabolism of basic amino acid	3.31E-05		<i>AASS, ARG1, CARNSI</i>
	Catabolism of essential amino acids	1.76E-04		<i>AASS, CARNSI, TAT</i>
	Synthesis of L-proline	4.35E-04		<i>ARG1, MYC</i>
	Metabolism of glutamine family amino acid	5.74E-04		<i>ARG1, MYC, TAT</i>
	Catabolism of L-amino acid	6.50E-04		<i>AASS, CARNSI, TAT</i>
	Catabolism of glutamine family amino acid	2.02E-03		<i>ARG1, MYC</i>

Table S6: Enriched biological processes within carbohydrate metabolism biological functions associated with ADG in Angus, Charolais and KC steers.

	Subfunctions/ processes	P-Value	Activation z-score	Molecules
Angus				
	Uptake of sugar acid	7.54E-04		<i>IGF1, UGT2B17</i>
	Synthesis of proteoglycan	1.95E-03		<i>IGF1, IL1R2, SOCS3</i>
	Internalization of carbohydrate	1.37E-03	-0.555	<i>CD44, GPC3, IGF1, SLC1A2</i>
	Interaction of carbohydrate	1.80E-03	1.236	<i>ANXA5, CD44, IGF1, LBP</i>
	Binding of phosphatidylinositol	2.76E-03		<i>IGF1, LBP</i>
Charolais				
	Oxidation of carbohydrate	1.26E-04		<i>APOA1, CRYAB, FASN, PDK4</i>
	Quantity of carbohydrate	1.50E-04	-0.674	<i>APOA4, CCDC80, FASN, GNMT, MFSD2A, MGLL, NOCT, PDK4, PIP5K1A, PPP1R3C, SCD, STEAP4</i>
	Incorporation of carbohydrate	2.37E-04		<i>FASN, PPP1R3C, SCD</i>
	Uptake of D-glucose	2.43E-04	1.432	<i>APOA1, EGLN3, EGRI, PDK4, PPP1R3C, SCD, STEAP4</i>
	Synthesis of carbohydrate	5.34E-03	-0.252	<i>APOA1, CD22, GLCE, GPC3, IL1R2, MFSD2A, PIP5K1A, PPP1R3C, SCD</i>
	Depletion of carbohydrate	4.74E-04		<i>APOA1, PPP1R3C, SCD</i>
	Depletion of glycogen	8.76E-04		<i>PPP1R3C, SCD</i>
	Concentration of D-glucose	9.67E-04	-0.2	<i>APOA4, CCDC80, GNMT, NOCT, PDK4, PPP1R3C, SCD, STEAP4</i>

	Glycogenolysis	1.51E-03		<i>PPP1R3C, SCD</i>
	Transport of choline-phospholipid	1.51E-03		<i>APOA1, MFSD2A</i>
	Metabolism of carbohydrate	1.68E-03	-0.252	<i>APOA1, APOA4, CD22, CS, GLCE, GNMT, GPC3, IL1R2, MFSD2A, PIP5K1A, PPP1R3C, SCD</i>
KC				
	Quantity of carbohydrate	3.68E-07	-0.76	<i>CES1, CYP7A1, DUSP1, FGF21, GNMT, IGFBP1, LPIN1, MFSD2A, MYC, NOCT, PIP5K1A, SCD, SOD3, WFS1</i>
	Concentration of D-glucose	4.07E-06	-0.256	<i>CES1, CYP7A1, FGF21, GNMT, IGFBP1, LPIN1, MYC, NOCT, SCD, WFS1</i>
	Gluconeogenesis	6.36E-06		<i>DUSP1, FGF21, GNMT, IGFBP1, SCD, TAT</i>
	Transport of monocarboxylic acid	5.36E-05		<i>MYC, SLC16A6, SLC5A8</i>
	Metabolism of carbohydrate	1.82E-04	-1.964	<i>FGF21, GLCE, GNMT, IGFBP1, LPIN1, MFSD2A, MYC, OAS1, PIP5K1A, SCD, SOD3, USP2</i>
	Synthesis of D-glucose	4.67E-04	-1.982	<i>FGF21, MYC, SCD, USP2</i>
	Quantity of glycogen	6.88E-04	-1	<i>DUSP1, FGF21, MYC, SCD</i>
	Regulation of D-glucose	9.33E-04		<i>FGF21, MYC</i>
	Synthesis of carbohydrate	1.01E-03	-2.219	<i>FGF21, GLCE, IGFBP1, LPIN1, MFSD2A, MYC, PIP5K1A, SCD, USP2</i>
	Homeostasis of D-glucose	2.84E-03		<i>ARFGEF3, FGF21, OAS1, SCD, WFS1</i>

Table S7. Predicted activated and deactivated gene expression regulators associated with ADG, DMI and MWT in Angus, Charolais and KC.

A	Upstream Regulator	Molecule Type	Predicted Activation	Activation z-score	P-Value	Target DE genes
ADG_Angus	<i>SREBF1</i>	Transcription regulator		0.27	9.41E-11	<i>AK4, CYP51A1, CYP7A1, GPNMB, GPX3, HMGCR, HMGCS1, IFI30, IL1R2, NR0B2, OAT, SERPINA3, SERPINE1, SOLE</i>
	<i>IFNAR1</i>	Transmembrane receptor		1.3	7.43E-09	<i>CCL24, CXCL2, HMGCR, HMGCS1, IFI6, PLA2G7, SERPINE1, SOCS3, SOLE, VCAM1</i>
	<i>IL1B</i>	Cytokine	Activated	2.06	1.2E-08	<i>BCL3, CCL24, CD44, CXCL2, CYP2C19, CYP7A1, GBP1, HP, IGF1, IL1R2, LBP, MX1, NR0B2, SAA1, SERPINA3, SERPINE1, SLC1A2, SLC3A1, SOCS2, SOCS3, VCAM1</i>
	<i>OSM</i>	Cytokine	Activated	2.06	3.1E-08	<i>AKR1B10, CCL24, CXCL2, GBP1, GPNMB, HLA-B, HP, IL1R2, LBP, MX1, SAA1, SERPINA3, SERPINE1, SOCS3, TOP2A, VCAM1</i>
	<i>IL1A</i>	Cytokine		1.03	2.38E-08	<i>BCL3, CD44, CXCL2, GBP1, IGF1, IL1R2, SAA1, SERPINA3, SERPINE1, UGT2B17, VCAM1</i>

ADG_Charolais	<i>POR</i>	Enzyme			1.86E-12	<i>ACTG1, APOA4, CSAD, CYP2B6, ELOVL2, GADD45B, HMOX1, NOCT, PDK4, SCD, SDS, SERPINA3, SQLE</i>
	<i>PPARA</i>	Ligand-dependent nuclear receptor		1.64	2.05E-12	<i>ACSS2, APOA1, APOA4, ARG1, CPT1B, CS, CSAD, CYP2B6, FASN, GNMT, HMOX1, LAMB3, MGLL, PDK4, SAA1, SCD, SOCS2, SQLE</i>
	<i>IL1B</i>	Cytokine		-0.84	5.96E-11	<i>ARG1, CISH, CRYAB, CXCL2, CYP2B6, CYP2C19, EGLN3, EGR1, FKBP5, GADD45B, GSTA1, HMOX1, IL1R2, ISG15, LAMB3, NOCT, S100A10, SAA1, SERPINA3, SLC3A1, SOCS2, SULT1E1</i>
	<i>NFE2L2</i>	Transcription regulators		-0.21	6.60E-11	<i>ACTG1, AKR1B10, APOA4, CXCL2, FKBP5, GPX3, GSTA1, HMOX1, INMT, MGLL, NOCT, SAA1, SERPINA3, SHMT2, SLC3A1, SULT1E1</i>
	<i>TNF</i>	Cytokine		-0.29	6.16E-10	<i>AKR1B10, APOA1, ARG1, CCDC80, CISH, CPT1B, CRYAB, CXCL2, EGLN3, EGR1, EPCAM, FASN, GADD45B, GSTA1, HLA-B, HMOX1, IL1R2, ISG15, LAMB3, MFSD2A, NOCT, PPP1R3C, SAA1, SCD, SERPINA3, SOCS2, SQLE, STEAP4, TAGLN</i>
ADG_KC	<i>IFN Beta</i>	Group	Inhibited	-3.08	5.63E-14	<i>DUSP1, HLA-B, IFI44, IFI6, ISG15, MX1, MX2, MYC, OAS1, RSAD2, SLC16A6, USP18</i>
	<i>IFNL1</i>	Cytokine	Inhibited	-3.10	4.45E-13	<i>HERC6, HLA-B, IFI44, IFI44L, IFI6, ISG15, MX1, OAS1, RSAD2, USP18</i>
	<i>Interferon alpha</i>	Group	Inhibited	-2.86	2.34E-12	<i>CXCL2, FOSL2, GLI1, HERC6, HLA-B, Ifi27, IFI44, IFI44L, IFI6, ISG15, MX1, MX2, MYC, OAS1, RSAD2, USP18</i>
	<i>IL1RN</i>	Cytokine	Activated	3.16	2.54E-11	<i>CYP7A1, HERC6, IFI44, IFI44L, IFI6, MX1, MX2, OAS1, RSAD2, USP18</i>
	<i>IFNA2</i>	Cytokine	Inhibited	-2.94	3.28E-11	<i>HERC6, HLA-B, IFI44, IFI44L, IFI6, ISG15, MX1, MX2, MYC, OAS1, RSAD2, USP18</i>
B						
DMI_Angus	<i>Interferon alpha</i>	Group		-0.65	3.11E-14	<i>BCL6, BTG2, CDKN1A, CXCL2, DDIT4, DHX58, FCGR2B, HERC6, HLA-B, Ifi27, IFI44, IFI44L, IFIT2, ISG15, MX1, MX2, RSAD2, RTP4, SOCS2, VCAM1</i>
	<i>PRL</i>	Cytokine	Inhibited	-3.20	4.78E-12	<i>ANXA2, BCL6, CDKN1A, CMPK2, DHX58, GPNMB, HERC6, HERPUD1, IFI44, IFI44L, ISG15, MX2, RSAD2, SFRP2, SOCS2</i>
	<i>IL1B</i>	Cytokine		-0.38	5.32E-12	<i>BCL6, BTG2, CDKN1A, CMPK2, CREM, CXCL2, CYP2C19, CYP7A1, DDIT4, DUSP1, FCGR2B, FKBP5, GADD45B, HP, ISG15, MX1, NOCT, NR1D1, RSAD2, SAA1, SLC1A2, SLC3A1, SOCS2, VCAM1</i>
	<i>IFNL1</i>	Cytokine	Inhibited	-2.61	1.23E-11	<i>CMPK2, HERC6, HLA-B, IFI44, IFI44L, IFIT2, ISG15, MX1, RSAD2, RTP4</i>
	<i>NR3C1</i>	Ligand-dependent nuclear receptor	Activated	2.40	7.30E-11	<i>BAG3, BCL6, CDKN1A, CXCL2, CYP2C19, CYP7A1, CYR61, DDIT4, DUSP1, FKBP5, GADD45B, GNMT, GPX3, HERPUD1, IFIT2, ISG15, SDS, SLC2A5, TAT, VCAM1</i>
DMI_Charolais	<i>FGF19</i>	Growth factor			2.30E-16	<i>AMY2A, CCND1, CXCL2, CYP7A1, EGR1, FOS, GADD45A, GAS2, HLA-DQB1, HMGCRCR, NNAT, NR0B2, RGS16, SERPINA3, SQLE</i>
	<i>FGF2</i>	Growth factor	Activated		3.32E-13	<i>ACTA2, ASCL1, CCND1, COL1A1, COL1A2, CXCL2, CYP11A1, CYR61, EGR1, FOS, GADD45A, IL1B, JUN, JUNB, NOS3, S100A10, SFRP1, TAGLN, THBS1, TOP2A, UGT2B17, VWF</i>
	<i>NR5A2</i>	Ligand-dependent nuclear receptor			4.20E-13	<i>ABCG5, ABCG8, CCND1, CYP11A1, CYP7A1, FOS, HMGCRCR, HP, IL1B, JUN, JUNB, NR0B2, SAA1</i>

	<i>AHR</i>	Ligand-dependent nuclear receptor	Inhibited		1.00E-12	<i>ACTA2, CCND1, COL12A1, COL1A1, COL1A2, COL27A1, COL6A3, FGF21, FOS, GADD45A, HMGCR, HP, IL1B, JUN, JUNB, MMD2, SAA1, SLC16A10, SLC1A1, SLC22A7, THBS1</i>
	<i>IL1B</i>	Cytokine	Activated		5.09E-12	<i>ACTA2, COL1A1, CXCL2, CYP11A1, CYP2C19, CYP7A1, EGR1, ERBB2, FKBP5, FOS, GADD45A, GRB7, HP, HSPG2, IL1B, IL1R2, JUN, JUNB, MEKV, MMP11, NOS3, NR0B2, RGS16, S100A10, SAA1, SAA2-SAA4, SERPINA3, SLC3A1, SULT1E1, THBS1, TMEM176B</i>
DMI_KC	<i>Interferon alpha</i>	Group	Activated	3.86	9.83E-31	<i>BCL6, CDKN1A, CXCL10, CXCL9, EPSTI1, FCGR2B, GBP1, GBP2, GIMAP4, HERC6, HLA-B, IDO1, Iff27, IFI44, IFI44L, IFI6, IFIH1, IFIT2, IFITM1, IRF1, ISG15, MX2, NFIL3, OAS1, PIM1, PSMB8, PSMB9, RSAD2, RTP4, SAMD9, STAT1, TAP1, TLR3, UBA7, USP18, VCAM1, WARS, ZBP1</i>
	<i>IFNA2</i>	Cytokine	Activated	4.59	2.06E-29	<i>CDKN1A, CXCL10, CXCL9, GBP1, GBP2, HERC6, HLA-B, IDO1, IFI44, IFI44L, IFI6, IFIH1, IFIT2, IFITM1, IRF1, ISG15, MX2, OAS1, REC8, RSAD2, SAMD9, STAT1, TAP1, TGM2, TLR3, UBA7, UBD, USP18, XAF1, ZBP1</i>
	<i>IFNAR2</i>	Transmembrane receptor	Activated	3.00	4.84E-28	<i>CXCL10, IDO1, IFI44, IFI6, IFIH1, IFITM1, ISG15, MX2, OAS1, PSMB10, PSMB8, PSMB9, TGM2, TLR3, UBA7, UBD, USP18, XAF1</i>
	<i>STAT1</i>	Transcription regulator	Activated	4.21	6.10E-28	<i>BCL6, CD274, CDKN1A, CXCL10, CXCL9, FCGR2B, GBP1, GBP2, GBP6, HAPLN3, HERC6, IDO1, IFI6, IFIH1, IFIT2, IFITM1, IRF1, ISG15, NLRC5, OAS1, PIM1, PSMB10, PSMB8, PSMB9, RSAD2, RTP4, STAT1, TAP1, TLR3, UBD, USP18, WARS, XAF1</i>
	<i>IFNL1</i>	Cytokine	Activated	4.51	4.93E-27	<i>CXCL10, CXCL9, EPSTI1, GBP1, HERC6, HLA-B, IFI44, IFI44L, IFI6, IFIH1, IFIT2, IFITM1, ISG15, OAS1, PSMB9, RSAD2, RTP4, SAMD9, STAT1, USP18, XAF1</i>
C						
MWT_Angus	<i>RORA</i>	Ligand-dependent nuclear receptor			5.29E-07	<i>CCL24, CYP2B6, HMGCR, IGF1, ITPR1, SLC13A2, SULT1E1, SULT2A1</i>
	<i>IFNAR1</i>	Transmembrane receptor			1.12E-06	<i>CCL24, CXCL2, HMGCR, HMGCS1, IFI6, ISG15, OASL</i>
	<i>HMGCR</i>	Enzyme			1.63E-06	<i>CTGF, CYR61, HMGCR</i>
	<i>SREBF1</i>	Transcription regulator	Inhibited	-2.16	3.89E-06	<i>AK4, CSAD, GPNMB, GPX3, HMGCR, HMGCS1, IL1R2, OAT</i>
	<i>CEBPA</i>	Transcription regulator		-1.66	5.51E-06	<i>AKR1B10, CKAP4, CYP2B6, HBD, HMGCR, HP, IFI6, IGF1, ISG15, SULT2A1</i>
MWT_Charolais	<i>IFNG</i>	Cytokine		1.22	5.32E-08	<i>C1QA, C1QC, CSF1R, CSF2RB, CTGF, HCK, HLA-B, HLA-DQB1, HMOX1, IL1B, KCTD12, MMP11, S100A10, SELL, SFRP1, SLC3A1, SLC7A5, TBXAS1, THEMIS2, VCAM1</i>
	<i>IL1B</i>	Cytokine		1.19	6.83E-07	<i>CRYAB, CSF2RB, CTGF, CYP2B6, HMOX1, IL1B, MMP11, PTGS1, S100A10, SERPINA3, SLC3A1, SULT1E1, THRSP, TMEM176B, VCAM1</i>
	<i>Immunoglobulin</i>	Complex		-2.00	1.22E-06	<i>CSF1R, CSF2RB, HCK, HLA-DQB1, HMOX1, IL1B, KCTD12, LILRB2, VCAM1</i>
	<i>EGFR</i>	Kinase		0.28	1.90E-06	<i>COL8A1, CRYAB, CTGF, FBLN2, IL1B, MACF1, PTGS1, SERPINA3, SFRP1, TBXAS1</i>
	<i>NFEE2L2</i>	Transcription		0.07	2.93E-06	<i>CTGF, GAS2, HMOX1, IL1B, SERPINA3, SLC3A1, SULT1E1, TBXAS1,</i>

		regulator				<i>THRSP, VCAMI</i>
MWT_KC	<i>IL6</i>	Cytokine		-1.27	5.69E-08	<i>BCL6, CES1, COL1A1, CTGF, CXCL10, CYP2B6, GADD45B, HP, JCHAIN, PIMI, SGK1, SOCS3, STEAP4, TGM2, TOP2A</i>
	<i>Alpha catenin</i>	Group		0.06	2.83E-07	<i>CDH11, COL1A1, CXCL10, SGK1, SOCS3, STEAP4, TGM2</i>
	<i>Interferon alpha</i>	Group		0.34	5.70E-07	<i>BCL6, CXCL10, CXCL9, GIMAP4, HERC6, HLA-B, Ifi27, IFI6, PIMI, SOCS3, TRIB2</i>
	<i>IFNL1</i>	Cytokine	Activated	2.42	7.31E-07	<i>CXCL10, CXCL9, HERC6, HLA-B, IFI6, OASL</i>
	<i>STAT3</i>	Transcription regulator		-1.81	1.13E-06	<i>BCL6, COL1A1, CTGF, CXCL10, CXCL9, HERC6, HP, IFI6, OASL, PIMI, SGK1, SOCS3</i>

A = ADG, B = DMI and C = MWT

Table S8. Enriched biological processes within the topmost enriched molecular and cellular functions associated with MWT in Angus, Charolais and KC.

Angus	Processes	P-Value	Z-score	DE genes involved
Amino acid metabolism	Metabolism of amino acids	1.27E-05		<i>CSAD, GNMT, MTHFR, OAT, PSPH, SDS, SLC3A1</i>
	Metabolism of L-amino acid	1.75E-05		<i>CSAD, GNMT, MTHFR, PSPH, SDS</i>
	Metabolism of sulfur amino acid	1.76E-04		<i>CSAD, GNMT, MTHFR</i>
	Incorporation of L-proline	1.82E-04		<i>IGF1, IGFBP2</i>
	Metabolism of serine family amino acid	1.94E-04		<i>CSAD, PSPH, SDS</i>
	Uptake of cystine	2.55E-04		<i>IGF1, SLC3A1</i>
Lipid Metabolism				
	Metabolism of terpenoid	1.65E-05	0	<i>AKR1B10, CYP2B6, CYP2C19, GPC3, HMGCR, HMGCS1, IGF1, SULT1E1, SULT2A1</i>
	Steroid metabolism	1.77E-04	-0.662	<i>CYP2B6, CYP2C19, HMGCR, HMGCS1, IGF1, SULT1E1, SULT2A1</i>
	Synthesis of testosterone	7.33E-04		<i>IGF1, IGFBP2, SULT1E1</i>
	Steroidogenesis of hormone	1.56E-04	1.008	<i>HMGCR, IGF1, IGFBP2, SULT1E1</i>
	Metabolism of membrane lipid derivative	1.71E-03	0.13	<i>ABHD6, ETNPPL, HMGCR, HMGCS1, IGF1, PIP5K1A, PLCD4, SULT2A1</i>
Charolais				
Lipid Metabolism	Modification of prostaglandin h2	5.4E-08	0.415	<i>CYP2B6, IL1B, PTGSI, TBXAS1</i>

	Concentration of triacylglycerol	5.38E-07	0.39	<i>CIQA, FGF21, IL1B, LPINI, PDK4, PLTP, PLVAP, PPP1R3C, SOAT2, THRSP, UCP2</i>
	Concentration of fatty acid	1.32E-06	-0.169	<i>FGF21, HMOX1, IL1B, LPINI, PDK4, PLTP, PPP1R3C, PTGS1, THRSP, UCP2</i>
	Concentration of lipid	1.33E-06	-0.232	<i>CIQA, FGF21, HMOX1, IL1B, KCNE1B, LPINI, NRBF2, PDK4, PLTP, PLVAP, PPP1R3C, PTGS1, SOAT2, SULT1E1, THRSP, UCP2, VCAMI</i>
	Accumulation of lipid	2.49E-06	-0.36	<i>CSF2RB, FGF21, HCK, HMOX1, IL1B, LPINI, PDK4, PLTP, SULT1E1, UCP2</i>
Cellular Movement	Cellular infiltration	8.35E-08	0.605	<i>CRYAB, CSF1R, CSF2RB, CTGF, HCK, HMOX1, IL1B, PDK4, PLTP, S100A10, SELL, SFRP1, UCP2, VCAMI</i>
	Cellular infiltration by leukocytes	1.36E-07	0.837	<i>CRYAB, CSF1R, CTGF, HCK, HMOX1, IL1B, PDK4, PLTP, S100A10, SELL, SFRP1, UCP2, VCAMI</i>
	Leukocyte migration	1.45E-07	0.904	<i>CD22, CRYAB, CSF1R, CSF2RB, CTGF, HCK, HMOX1, IL1B, PDK4, PILRA, PLTP, PRAP1, S100A10, SDC3, SELL, SERPINA3, SFRP1, SLC7A5, UCP2, VCAMI</i>
	Cell movement of myeloid cells	1.97E-07	1.357	<i>CRYAB, CSF1R, CTGF, HCK, HMOX1, IL1B, PDK4, PILRA, PLTP, PRAP1, S100A10, SELL, SERPINA3, SFRP1, VCAMI</i>
	Cellular infiltration by myeloid cells	4.28E-07	0.52	<i>CRYAB, CSF1R, CTGF, HCK, HMOX1, IL1B, PDK4, PLTP, S100A10, SELL, SFRP1</i>
KC				
Cellular Movement	Migration of cytotoxic type 1 T lymphocytes	3.77E-05		<i>CXCL10, CXCL9</i>
	Attraction of plasmacytoid dendritic cells	3.77E-05		<i>CXCL10, CXCL9</i>
	Attraction of Th1 cells	7.52E-05		<i>CXCL10, CXCL9</i>
	Cell movement of monocytes	9.06E-05	1.446	<i>COL1A1, CTGF, CXCL10, CXCL9, HP, PRAP1</i>
	Migration of mononuclear leukocytes	1.00E-04	2.244	<i>CLTC, COL1A1, CTGF, CXCL10, CXCL9, PGLYRP2, PRAP1, SOCS3, TGM2</i>
	Cell movement of mononuclear leukocytes	1.33E-04	1.943	<i>CLTC, COL1A1, CTGF, CXCL10, CXCL9, HP, PGLYRP2, PRAP1, SOCS3, TGM2</i>
Cell Death and Survival	Necrosis	1.38E-05	-0.397	<i>BCL6, CAMK2D, CDH11, CES1, CLTC, COL1A1, TOP2A CTGF, CXCL10, CXCL9, ECEL1, ENCI, GADD45B, WFS1 GIMAP4, GNMT, GRIN3A, HLA-B, HLA-DQB1, IFI6, TGM2 IFRD1, LY9, PIMI, PRAP1, REV3L, RNF13, SGK1, SOCS3, TRIB2, ZNF385B</i>
	Cell death	2.90E-04	-0.646	<i>BCL6, CAMK2D, CDH11, CES1, CLTC, COL1A1, CTGF, CXCL10, CXCL9, CYP2B6, ECEL1, ENCI,</i>

				<i>GADD45B, GIMAP4, GNMT, GRIN3A, HLA-B, WFS1, HLA-DQB1, HP, IFI6, IFRD1, LY9, PIM1, PRAP1, SGK1, REV3L, RNF13, SOCS3, TGM2, TOP2A, TRIB2, ZNF385B</i>
	Cell death of immune cells	4.15E-04	0.202	<i>BCL6, COL1A1, CXCL10, GADD45B, GIMAP4, LY9, PIM1, PRAP1, TGM2, TOP2A, TRIB2</i>
	Cell death of hematopoietic cells	6.92E-04	-0.186	<i>COL1A1, GADD45B, GIMAP4, PIM1, TGM2, TOP2A</i>
	Cell viability of tumor cell lines	1.02E-03	-0.549	<i>BCL6, CAMK2D, CES1, COL1A1, CTGF, CXCL9, HOPX, PIM1, REV3L, SGK1, SOCS3, TGM2, TRIB2</i>