



Title	1H NMR metabolomic and transcriptomic analyses reveal urinary metabolites as biomarker candidates in response to protein undernutrition in adult rats
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Supplementary Table S1. PCR primer and probe set information

NCBI Entrez Gene ID*	Gene Symbol	Gene Name	TaqMan Gene Expression Assay ID
59085	<i>Asl</i>	argininosuccinate lyase	Rn01480437_g1
25698	<i>Ass1</i>	argininosuccinate synthase 1	Rn00565808_g1
292804	<i>Gpi</i>	glucose-6-phosphate isomerase	Rn01475756_m1
25104	<i>Pc</i>	pyruvate carboxylase	Rn00562534_m1
361596	<i>Idh2</i>	isocitrate dehydrogenase 2	Rn01478119_m1
81718	<i>Cdo1</i>	cysteine dioxygenase type 1	Rn00583853_m1
25256	<i>Fmo1</i>	flavin containing monooxygenase 1	Rn00562945_m1
246248	<i>Fmo5</i>	flavin containing monooxygenase 5	Rn00595199_m1
81822	<i>Actb</i>	β -actin	Rn00667869_m1

*Gene IDs reference The National Center for Biotechnology Information database

Supplementary Table S2. Metabolite assignments and ¹H NMR data in urine samples of rat*

	Urine Metabolite	δ ¹ H (ppm)						
1	N-Methylnicotinamide	4.48(s)	8.18(t)	8.90(d)	8.97(d)			
2	Nicotinamide N-oxide	7.73(dd)	8.12(m)	8.48(m)				
3	Formate	8.46(s)						
4	Hippurate	3.97(d)	7.55(t)	7.64(m)	7.84(dd)	8.56(s)		
5	Tryptophan	3.30(dd)	3.47(dd)	4.05(dd)	7.20(m)	7.28(m)	7.50(d)	7.71(d)
6	Phenylalanine	3.11(dd)	3.28(dd)	3.99(dd)	7.36(m)	7.42(m)		
7	Tyrosine	3.04(dd)	3.19(dd)	3.93(dd)	6.89(m)	7.17(m)		
8	Fumarate	6.53(s)						
9	Allantoin	5.39(s)	6.05(s)	7.26(s)	8.01(s)			
10	Urea	5.80(s)						
11	Glucose	3.24(dd)	3.39(t)	3.40(t)	3.45(m)	3.48(t)	3.53(dd)	3.70(t)
		3.72(dd)	3.76(dd)	3.82(m)	3.84(dd)	3.89(dd)	4.65(d)	5.24(d)
12	Tartrate	4.36(s)						
13	Threonine	1.33(d)	3.58(d)	4.24(m)				
14	Creatinine	3.05(s)	4.06(s)					
15	Creatine	3.02(s)	3.95(s)					
16	Glycine	3.57(s)						
17	Taurine	3.27(t)	3.43(t)					
18	Choline	3.20(s)	3.51(m)	4.06(m)				
19	cis-Aconitate	3.12(d)	5.69(t)					
20	Cadaverine	1.46(m)	1.72(m)	3.01(t)				
21	N,N-Dimethylglycine	2.93(s)	3.71(s)					
22	Dimethylamine	2.72(s)						
23	Citrate	2.55(d)	2.69(d)					
24	2-Oxoglutarate	2.44(t)	3.01(t)					
25	Succinate	2.41(s)						
26	Acetoacetate	2.30(s)	3.45(s)					
27	Trimethylamine N-oxide	3.27(s)						
28	Acetate	1.92(s)						
29	Putrescine	1.77(m)	3.05(m)					
30	Alanine	1.48(d)	3.78(q)					
31	Lactate	1.33(d)	4.11(q)					
32	3-Hydroxybutyrate	1.18(d)	2.30(dd)	2.39(dd)	4.14(m)			
33	Isobutyrate	1.07(d)	2.38(m)					
34	Valine	0.99(d)	1.05(d)	2.26(m)	3.60(d)			

*Key: s, singlet; d, doublet; t, triplet; q, quartet; m, multiplet; dd, doublet of doublet.

Supplementary Table S3. Relative concentration of the metabolites in urea samples of rats fed control (CT) or low protein (LP) diets at weeks

0-4*

Metabolites	CT diet group		LP diet group		P value	Metabolites	CT diet group		LP diet group		P value
Phenylalanine	0w	0.0813 ± 0.0352	0w	0.0819 ± 0.0366	0.98	Cadaverine	0w	0.2120 ± 0.0056	0w	0.0189 ± 0.0052	0.48
	1w	0.0743 ± 0.0259	1w	0.0336 ± 0.0089	< 0.05		1w	0.0186 ± 0.0037	1w	0.0143 ± 0.0022	< 0.05
	2w	0.0732 ± 0.0235	2w	0.0410 ± 0.0137	< 0.05		2w	0.0175 ± 0.0036	2w	0.0126 ± 0.0020	< 0.05
	3w	0.0715 ± 0.0144	3w	0.0527 ± 0.0150	0.05		3w	0.0180 ± 0.0029	3w	0.0122 ± 0.0018	< 0.01
	4w	0.0693 ± 0.0429	4w	0.0556 ± 0.0196	0.50		4w	0.0152 ± 0.0025	4w	0.0114 ± 0.0021	< 0.05
Threonine	0w	0.0121 ± 0.0034	0w	0.0128 ± 0.0053	0.81	Putrescine	0w	0.0259 ± 0.0070	0w	0.0257 ± 0.0062	0.95
	1w	0.0172 ± 0.0043	1w	0.0125 ± 0.0073	0.21		1w	0.0252 ± 0.0022	1w	0.0227 ± 0.0024	0.09
	2w	0.0157 ± 0.0019	2w	0.0118 ± 0.0042	0.07		2w	0.0207 ± 0.0008	2w	0.0162 ± 0.0024	< 0.01
	3w	0.0177 ± 0.0032	3w	0.0095 ± 0.0027	< 0.001		3w	0.0197 ± 0.0021	3w	0.0125 ± 0.0017	< 0.001
	4w	0.0158 ± 0.0029	4w	0.0110 ± 0.0081	0.22		4w	0.0203 ± 0.0027	4w	0.0144 ± 0.0023	< 0.01
Tryptophan	0w	0.0443 ± 0.0176	0w	0.0525 ± 0.0190	0.45	Urea	0w	81.164 ± 11.752	0w	62.853 ± 27.71	0.18
	1w	0.0463 ± 0.0135	1w	0.0261 ± 0.0061	< 0.01		1w	64.175 ± 28.652	1w	19.856 ± 12.237	< 0.05
	2w	0.0487 ± 0.0217	2w	0.0310 ± 0.0111	0.11		2w	49.556 ± 24.065	2w	13.159 ± 6.864	< 0.05
	3w	0.0490 ± 0.0171	3w	0.0495 ± 0.0162	0.95		3w	49.287 ± 19.809	3w	11.994 ± 7.843	< 0.01
	4w	0.0461 ± 0.0170	4w	0.0472 ± 0.0161	0.91		4w	44.974 ± 24.440	4w	15.073 ± 6.749	< 0.05
Valine	0w	0.0044 ± 0.0016	0w	0.0048 ± 0.0009	0.55	Citrate	0w	0.4304 ± 0.1563	0w	0.5085 ± 0.1560	0.41
	1w	0.0062 ± 0.0044	1w	0.0036 ± 0.0009	0.21		1w	0.4282 ± 0.1729	1w	0.6411 ± 0.2603	0.13
	2w	0.0052 ± 0.0011	2w	0.0037 ± 0.0012	< 0.05		2w	0.3701 ± 0.1564	2w	0.8490 ± 0.2354	< 0.01
	3w	0.0053 ± 0.0007	3w	0.0035 ± 0.0005	< 0.001		3w	0.3850 ± 0.1378	3w	0.9208 ± 0.2860	< 0.01
	4w	0.0045 ± 0.0010	4w	0.0031 ± 0.0006	< 0.05		4w	0.5150 ± 0.1242	4w	0.8961 ± 0.3340	< 0.05
Isobutyrate	0w	0.0019 ± 0.0005	0w	0.0020 ± 0.0005	0.77	cis-Aconitate	0w	0.0457 ± 0.0036	0w	0.0512 ± 0.0082	0.18
	1w	0.0025 ± 0.0004	1w	0.0013 ± 0.0002	< 0.001		1w	0.0493 ± 0.0034	1w	0.0521 ± 0.0108	0.56
	2w	0.0023 ± 0.0004	2w	0.0013 ± 0.0001	< 0.001		2w	0.0433 ± 0.0074	2w	0.0620 ± 0.0072	< 0.01
	3w	0.0024 ± 0.0004	3w	0.0012 ± 0.0002	< 0.001		3w	0.0465 ± 0.0062	3w	0.0609 ± 0.0054	< 0.01
	4w	0.0024 ± 0.0005	4w	0.0011 ± 0.0003	< 0.001		4w	0.0476 ± 0.0038	4w	0.0574 ± 0.0129	0.13

*The relative concentration of each metabolite is its integral value normalized to TSP, which was added to the NMR buffer as an internal standard. Data are expressed as the mean ± standard deviation (n = 6) and were analyzed by Student's t-tests with Welch's correction.

Supplementary Table S3, continued*

Metabolites		CT diet group		LP diet group	P value	Metabolites		CT diet group		LP diet group	P value
2-Oxoglutarate	0w	0.2594 ± 0.0964	0w	0.2612 ± 0.0618	0.97	Choline	0w	0.0094 ± 0.0026	0w	0.0083 ± 0.0010	0.35
	1w	0.2720 ± 0.0801	1w	0.4315 ± 0.1210	< 0.05		1w	0.0089 ± 0.0028	1w	0.1120 ± 0.0013	0.10
	2w	0.2085 ± 0.1213	2w	0.4296 ± 0.1409	< 0.05		2w	0.0084 ± 0.0012	2w	0.0094 ± 0.0016	0.22
	3w	0.2113 ± 0.0732	3w	0.4534 ± 0.0953	< 0.001		3w	0.0086 ± 0.0011	3w	0.0105 ± 0.0007	< 0.01
	4w	0.2207 ± 0.0550	4w	0.4116 ± 0.1234	< 0.01		4w	0.0079 ± 0.0015	4w	0.0100 ± 0.0014	< 0.05
Succinate	0w	0.0225 ± 0.0058	0w	0.0222 ± 0.0035	0.90	Tartrate	0w	0.7685 ± 0.3176	0w	0.7907 ± 0.2839	0.90
	1w	0.0251 ± 0.0061	1w	0.0308 ± 0.0125	0.34		1w	0.6536 ± 0.1449	1w	0.8066 ± 0.4344	0.44
	2w	0.0201 ± 0.0112	2w	0.0358 ± 0.0258	0.24		2w	0.6794 ± 0.1602	2w	0.7488 ± 0.1689	0.48
	3w	0.0205 ± 0.0047	3w	0.0346 ± 0.0049	< 0.001		3w	0.7275 ± 0.2203	3w	1.1332 ± 0.3873	< 0.05
	4w	0.0232 ± 0.0044	4w	0.0294 ± 0.0046	< 0.05		4w	0.5213 ± 0.1025	4w	0.8518 ± 0.3132	< 0.05
Fumarate	0w	0.0081 ± 0.0021	0w	0.0071 ± 0.0025	0.44	Trimethylamine N-oxide	0w	0.0330 ± 0.0111	0w	0.0367 ± 0.0032	0.47
	1w	0.0071 ± 0.0017	1w	0.0124 ± 0.0062	0.09		1w	0.0289 ± 0.0114	1w	0.0387 ± 0.0031	0.09
	2w	0.0050 ± 0.0024	2w	0.0111 ± 0.0028	< 0.01		2w	0.0346 ± 0.0075	2w	0.0518 ± 0.0107	< 0.01
	3w	0.0057 ± 0.0019	3w	0.0125 ± 0.0036	< 0.01		3w	0.0303 ± 0.0081	3w	0.0559 ± 0.0080	< 0.001
	4w	0.0062 ± 0.0019	4w	0.0133 ± 0.0048	< 0.05		4w	0.0277 ± 0.0114	4w	0.0536 ± 0.0153	< 0.01
Taurine	0w	1.0355 ± 0.3644	0w	1.1928 ± 0.1792	0.37						
	1w	0.9182 ± 0.4974	1w	0.1861 ± 0.0909	< 0.05						
	2w	1.0685 ± 0.4338	2w	0.0944 ± 0.0506	< 0.01						
	3w	1.0803 ± 0.3228	3w	0.0540 ± 0.0116	< 0.001						
	4w	1.1937 ± 0.4426	4w	0.0499 ± 0.0075	< 0.01						
N-Methylnicotinamide	0w	0.0961 ± 0.0226	0w	0.1022 ± 0.0236	0.65						
	1w	0.0679 ± 0.0207	1w	0.0523 ± 0.0103	0.13						
	2w	0.0850 ± 0.0162	2w	0.0335 ± 0.0081	< 0.001						
	3w	0.0785 ± 0.0262	3w	0.0200 ± 0.0049	< 0.01						
	4w	0.0793 ± 0.0232	4w	0.0306 ± 0.0087	< 0.01						

*The relative concentration of each metabolite is its integral value normalized to TSP, which was added to the NMR buffer as an internal standard. Data are expressed as the mean ± standard deviation (n = 6) and were analyzed by Student's t-tests with Welch's correction.

Supplementary Table S4. Metabolite assignments and ^1H NMR data in plasma samples of rat *

Plasma Metabolite		δ ^1H (ppm)						
1	3-Hydroxybutyrate	1.22(d)	2.32(dd)	2.37(dd)	4.14(m)			
2	Acetate	1.91(s)						
3	Acetoacetate	2.22(s)	3.43(s)					
4	Alanine	1.47(d)	3.78(q)					
5	Betaine	3.26(s)	3.92(s)					
6	Choline	3.21(s)	3.47(m)	4.06(m)				
7	Creatine	3.02(s)	3.93(s)					
8	Creatine phosphate	3.03(s)	3.94(s)					
9	Formate	8.44(s)						
10	Fumarate	6.52(s)						
11	Glucose	3.24(dd)	3.40(t)	3.41(t)	3.46(m)	3.48(t)	3.53(dd)	3.71(t)
		3.72(dd)	3.77(dd)	3.82(m)	3.84(dd)	3.90(dd)	4.64(d)	5.23(d)
12	Glutamine	2.12(m)	2.14(m)	2.42(m)	2.46(m)	3.77(t)	6.87(s)	
13	Glycine	3.57(s)						
14	Histidine	3.12(dd)	3.22(dd)	3.99(dd)	7.06(s)	7.82(s)		
15	Isoleucine	0.93(t)	1.00(d)	1.25(m)	1.46(m)	1.97(m)	3.66(d)	
16	Lactate	1.32(d)	4.11(q)					
17	Leucine	0.95(d)	0.96(d)	1.68(m)	1.70(m)	1.73(m)	3.73(dd)	
18	Methionine	2.11(m)	2.12(s)	2.19(m)	2.63(t)	3.84(dd)		
19	N,N-Dimethylglycine	2.91(s)	3.71(s)					
20	Phenylalanine	3.12(dd)	3.28(dd)	3.99(dd)	7.31(d)	7.35(m)	7.41(m)	
21	Pyruvate	2.36(s)						
22	Serine	3.83(dd)	3.94(dd)	3.98(dd)				
23	Succinate	2.40(s)						
24	Threonine	1.32(d)	3.58(d)	4.25(m)				
25	Tyrosine	3.04(dd)	3.19(dd)	3.93(dd)	6.88(m)	7.17(m)		
26	Urea	5.84(s)						
27	Valine	0.98(d)	1.03(d)	2.26(m)	3.61(d)			

*Key: s, singlet; d, doublet; t, triplet; q, quartet; m, multiplet; dd, doublet of doublet.

Supplementary Table S5. Relative concentration of the metabolites in plasma samples of rats fed control (CT) or low protein (LP) diets for 4 weeks*

Metabolite	CT diet group	LP diet group	Pvalue
Significantly higher in the LP diet group			
Betaine	0.050 ± 0.016	0.078 ± 0.014	< 0.05
Fumarate	0.002 ± 0.001	0.004 ± 0.001	< 0.05
Glutamine	0.439 ± 0.046	0.514 ± 0.062	< 0.05
Glycine	0.036 ± 0.006	0.045 ± 0.004	< 0.05
N,N-Dimethylglycine	0.003 ± 0.001	0.007 ± 0.002	< 0.001
Serine	0.141 ± 0.023	0.327 ± 0.072	< 0.001
Significantly lower in the LP diet group			
Isoleucine	0.062 ± 0.008	0.047 ± 0.005	< 0.01
Leucine	0.086 ± 0.013	0.062 ± 0.014	< 0.05
Phenylalanine	0.013 ± 0.001	0.010 ± 0.002	< 0.05
Threonine	0.196 ± 0.028	0.138 ± 0.032	< 0.01
Urea	0.667 ± 0.122	0.281 ± 0.063	< 0.001
Valine	0.164 ± 0.023	0.122 ± 0.007	< 0.01
Not significantly			
3-Hydroxybutyrate	0.013 ± 0.005	0.014 ± 0.003	0.80
Acetate	0.092 ± 0.085	0.095 ± 0.063	0.94
Acetoacetate	0.022 ± 0.009	0.022 ± 0.017	0.98
Alanine	0.404 ± 0.099	0.514 ± 0.092	0.07
Choline	0.051 ± 0.024	0.058 ± 0.018	0.59
Creatine	0.024 ± 0.008	0.032 ± 0.012	0.17
Creatine phosphate	0.005 ± 0.002	0.007 ± 0.002	0.15
Formate	1.069 ± 0.026	1.073 ± 0.026	0.80
Glucose	3.880 ± 0.500	4.731 ± 1.378	0.20
Histidine	0.053 ± 0.006	0.059 ± 0.007	0.15
Lactate	2.398 ± 0.815	2.716 ± 0.200	0.39
Methionine	0.014 ± 0.006	0.013 ± 0.007	0.77
Pyruvate	0.042 ± 0.012	0.047 ± 0.009	0.38
Succinate	0.007 ± 0.006	0.023 ± 0.025	0.18
Tyrosine	0.019 ± 0.004	0.023 ± 0.004	0.10

*The relative concentration of each metabolite is its integral value normalized to formic acid, which was added to the NMR buffer as an internal standard. Data are expressed as the mean ± standard deviation (n = 6) and were analyzed by Student's t-tests with Welch's correction.

Supplementary Table S6. Metabolite assignments and ^1H NMR data in liver sample of rat *

Liver Metabolite		δ ^1H (ppm)						
1	3-Hydroxybutyrate	1.20(d)	2.31(dd)	2.39(dd)	4.14(m)			
2	Acetate	1.92(s)						
3	Alanine	1.49(d)	3.77(q)					
4	β -alanine	2.56(t)	3.18(t)					
5	Betaine	3.24(s)	3.88(s)					
6	Choline	3.21(s)	3.51(m)	4.07(m)				
7	Creatine	3.03(s)	3.93(s)					
8	Creatine phosphate	3.04(s)	3.94(s)					
9	Cytidine	3.80(dd)	3.92(dd)	4.12(m)	4.20(t)	4.30(dd)	5.92(d)	6.07(d)
		7.85(d)						
10	Dimethylamine	2.72(s)						
11	Formate	8.46(s)						
12	Fumarate	6.52(s)						
13	Glucose	3.26(dd)	3.41(t)	3.42(t)	3.47(m)	3.50(t)	3.54(dd)	3.72(t)
		3.73(dd)	3.78(dd)	3.85(m)	3.86(dd)	3.90(dd)	4.66(d)	5.24(d)
14	Glutamate	2.05(m)	2.16(m)	2.33(m)	2.38(m)	3.75(dd)		
15	Glutamine	2.05(m)	2.13(m)	2.43(m)	2.48(m)	3.77(t)	6.92(s)	
16	Glycerol	3.56(dd)	3.65(dd)	3.78(m)				
17	Histidine	3.13(dd)	3.22(dd)	3.98(dd)	7.11(s)	7.92(s)		
18	Hypoxanthine	8.20(s)	8.22(s)					
19	Inosine	3.83(dd)	3.90(dd)	4.29(q)	4.45(dd)	4.77(t)	6.11(s)	8.25(s)
		8.36(s)						
20	Inosine monophosphate (IMP)	4.00(m)	4.03(m)	4.36(m)	4.50(m)	6.13(d)	8.22(s)	8.59(s)
21	Isoleucine	0.94(t)	1.02(d)	1.25(m)	1.46(m)	1.97(m)	3.66(d)	
22	Lactate	1.33(d)	4.12(q)					
23	Leucine	0.96(d)	0.97(d)	1.67(m)	1.70(m)	1.73(m)	3.73(dd)	
24	Lysine	1.43(m)	1.50(m)	1.71(m)	1.87(m)	1.91(m)	3.06(t)	3.75(t)
25	Methionine	2.11(m)	2.14(s)	2.19(m)	2.65(t)	3.85(dd)		
26	Niacinamide	7.60(m)	8.26(tt)	8.72(dd)	8.95(dd)			
27	Nicotinamide adenine dinucleotide (NAD ⁺)	4.20(m)	4.23(m)	4.25(m)	4.36(m)	4.37(m)	4.42(m)	4.48(t)
		4.50(m)	4.54(m)	4.76(t)	6.03(d)	6.09(d)	8.16(s)	8.19(q)
		8.42(s)	8.81(m)	9.10(m)	9.35(m)			
28	O-Phosphocholine	3.23(s)	3.59(m)	4.17(m)				
29	Phenylalanine	3.14(dd)	3.28(dd)	3.99(dd)	7.33(m)	7.38(m)	7.43(m)	
30	Succinate	2.41(s)						
31	Taurine	3.28(t)	3.42(t)					
32	Threonine	1.34(d)	3.57(d)	4.25(m)				
33	Trimethylamine N-oxide	3.26(s)						
34	Tryptophan	3.30(dd)	3.47(dd)	4.05(dd)	7.19(m)	7.28(m)	7.31(s)	7.54(d)
		7.74(d)						
35	Tyrosine	3.04(dd)	3.19(dd)	3.93(dd)	6.91(m)	7.20(m)		
36	Uracil	5.81(d)	7.55(d)					
37	Uridine	3.80(dd)	3.90(dd)	4.12(m)	4.24(t)	4.36(t)	5.91(d)	5.93(d)
		7.89(d)						
38	Valine	1.00(d)	1.05(d)	2.26(m)	3.60(d)			

*Key: s, singlet; d, doublet; t, triplet; q, quartet; m, multiplet; dd, doublet of doublet.

Supplementary Table S7. Relative concentration of the metabolites in liver samples of rats fed control (CT) or low protein (LP) diets for 4 weeks*

Metabolite	CT diet group	LP diet group	P value
Significantly higher in the LP diet group			
β-alanine	0.087 ± 0.009	0.110 ± 0.016	< 0.05
Choline	0.066 ± 0.020	0.107 ± 0.025	< 0.05
Dimethylamine	0.002 ± 0.0005	0.005 ± 0.002	< 0.05
Hypoxanthine	0.101 ± 0.015	0.250 ± 0.105	< 0.05
Inosine monophosphate (IMP)	0.017 ± 0.004	0.027 ± 0.006	< 0.05
Trimethylamine N-oxide	0.101 ± 0.054	0.183 ± 0.052	< 0.05
Significantly lower in the LP diet group			
Inosine	0.176 ± 0.037	0.092 ± 0.025	< 0.001
Nicotinamide adenine dinucleotide (NAD ⁺)	0.012 ± 0.002	0.008 ± 0.002	< 0.01
o-Phosphocholine	0.311 ± 0.062	0.192 ± 0.055	< 0.01
Taurine	1.468 ± 0.278	0.278 ± 0.106	< 0.001
Uridine	0.142 ± 0.031	0.102 ± 0.022	< 0.05
Not significantly			
3-Hydroxybutyrate	0.059 ± 0.018	0.054 ± 0.020	0.67
Acetate	0.229 ± 0.089	0.176 ± 0.078	0.30
Alanine	0.983 ± 0.209	1.180 ± 0.197	0.12
Betaine	0.084 ± 0.065	0.104 ± 0.027	0.50
Creatine	0.030 ± 0.005	0.032 ± 0.010	0.72
Creatine phosphate	0.026 ± 0.005	0.028 ± 0.007	0.56
Cytidine	0.023 ± 0.003	0.029 ± 0.009	0.13
Formate	0.020 ± 0.019	0.012 ± 0.009	0.35
Fumarate	0.025 ± 0.006	0.019 ± 0.007	0.13
Glucose	9.115 ± 3.622	12.564 ± 3.498	0.12
Glutamate	0.417 ± 0.097	0.542 ± 0.209	0.21
Glutamine	0.823 ± 0.182	0.807 ± 0.093	0.85
Glycerol	0.289 ± 0.037	0.317 ± 0.070	0.40
Histidine	0.104 ± 0.015	0.089 ± 0.016	0.14
Isoleucine	0.062 ± 0.007	0.060 ± 0.022	0.82
Lactate	1.798 ± 0.310	2.316 ± 0.539	0.07
Leucine	0.147 ± 0.024	0.130 ± 0.035	0.37
Lysine	0.073 ± 0.006	0.076 ± 0.027	0.80
Methionine	0.049 ± 0.009	0.043 ± 0.012	0.38
Niacinamide	0.125 ± 0.032	0.145 ± 0.012	0.21
Phenylalanine	0.071 ± 0.009	0.071 ± 0.020	0.99
Succinate	0.107 ± 0.034	0.120 ± 0.063	0.67
Threonine	0.176 ± 0.040	0.153 ± 0.033	0.30
Tryptophan	0.014 ± 0.002	0.014 ± 0.004	0.71
Tyrosine	0.078 ± 0.015	0.078 ± 0.020	1.00
Uracil	0.010 ± 0.004	0.032 ± 0.022	0.06
Valine	0.126 ± 0.017	0.114 ± 0.035	0.45

*The relative concentration of each metabolite is its integral value normalized to TSP, which was added to the NMR buffer as an internal standard. Data are expressed as the mean ± standard deviation (n = 6) and were analyzed by Student's t-tests with Welch's correction.

Supplementary Table S8. Hepatic genes showing statistically significant expression changes and up- or down-regulation by more than 1.5-fold by mRNA microarray in rats fed a low-protein (LP) diet compared to a control (CT) diet for 4 weeks

NCBI Entrez Gene ID ^{a)}	Gene Symbol	Gene Name	Fold Change	CT diet group (raw intensity) ^{b)}	LP diet group (raw intensity)	P value
58835	Phgdh	phosphoglycerate dehydrogenase	123.5	166.2	21998.5	0.0000
399475	Adm2	adrenomedullin 2	42.9	17.9	824.4	0.0000
25612	Asns	asparagine synthetase (glutamine-hydrolyzing)	27.4	193.0	5676.8	0.0000
293820	Psat1	phosphoserine aminotransferase 1	20.1	283.2	6088.2	0.0000
170580	Fgf21	fibroblast growth factor 21	17.5	277.5	5196.9	0.0000
680308	Mthfd2	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2	14.3	115.6	1773.9	0.0000
25334	Bhlha15	basic helix-loop-helix family, member a15	11.5	105.6	1297.2	0.0000
361637	Acsm5	acyl-CoA synthetase medium-chain family member 5	11.3	194.3	2343.8	0.0020
81919	Fut1	fucosyltransferase 1	9.1	43.8	427.5	0.0000
361755	Aldh18a1	aldehyde dehydrogenase 18 family, member A1	8.1	15.2	131.9	0.0000
287877	Pycr1	pyrroline-5-carboxylate reductase 1	7.3	105.3	820.5	0.0000
494500	Gsta3	glutathione S-transferase alpha 3	7.1	23.6	180.0	0.0012
300719	Cib2	calcium and integrin binding family member 2	6.0	735.3	4728.2	0.0004
140942	Ddit4	DNA-damage-inducible transcript 4	5.9	255.9	1604.9	0.0000
361424	RGD1309651	similar to 1190005106Rik protein	5.4	35.1	205.0	0.0016
685612	Col26a1	collagen type XXVI alpha 1 chain	5.0	12.9	69.4	0.0000
29142	Vnn1	vanin 1	5.0	308.2	1654.5	0.0000
100910829	LOC100910829	probable N-acetyltransferase CML2-like	4.8	458.3	2334.6	0.0000
362835	Reep6	receptor accessory protein 6	4.3	151.8	703.6	0.0001
26760	Akr7a3	aldo-keto reductase family 7 member A3	4.3	2360.6	10788.7	0.0001
302507	Efhc2	EF-hand domain containing 2	4.1	15.6	68.6	0.0000
100363433	Srrm5	serine/arginine repetitive matrix 5	3.9	11.7	49.1	0.0020
113992	Ugt1a6	UDP glucuronosyltransferase family 1 member A6	3.8	63.6	261.4	0.0000
24188	Aldh1a1	aldehyde dehydrogenase 1 family, member A1	3.8	4897.0	19893.7	0.0001
50567	Slc3a2	solute carrier family 3 member 2	3.8	1037.0	4192.6	0.0000
498416	Grb10	growth factor receptor bound protein 10	3.7	13.2	53.0	0.0000
305166	Gpat3	glycerol-3-phosphate acyltransferase 3	3.5	53.9	202.0	0.0003
290277	Cryl1	crystallin, lambda 1	3.3	943.9	3385.8	0.0002
246248	Fmo5	flavin containing monooxygenase 5	3.3	182.1	645.6	0.0001
500237	Cml2	camello-like 2	3.2	466.7	1620.6	0.0011
54193	Pbsn	probasin	3.2	33.0	113.6	0.0059
361659	Plekha1	pleckstrin homology domain containing A1	3.1	1667.9	5620.4	0.0000
246273	Trib3	tribbles pseudokinase 3	3.1	212.8	707.1	0.0000
361042	Pck2	phosphoenolpyruvate carboxykinase 2 (mitochondrial)	3.0	622.0	1986.2	0.0000
81806	Serpina7	serpin family A member 7	3.0	215.6	682.6	0.0042
499010	Syne1	spectrin repeat containing nuclear envelope protein 1	2.9	10.3	32.3	0.0002
64679	Tgm4	transglutaminase 4	2.8	27.4	83.3	0.0000
171026	Akap5	A-kinase anchoring protein 5	2.8	34.9	105.8	0.0018
100360982	Relb	RELB proto-oncogene, NF-kB subunit	2.8	20.1	60.2	0.0001
360857	Rgs16	regulator of G-protein signaling 16	2.8	4531.3	13540.0	0.0193
64570	Nat8	N-acetyltransferase 8	2.8	912.7	2700.9	0.0060
102556148	LOC102556148	probable N-acetyltransferase CML2-like	2.7	437.1	1265.2	0.0014
24443	Hdc	histidine decarboxylase	2.7	320.2	926.0	0.0046
297096	Snx10	sorting nexin 10	2.7	192.8	557.4	0.0002
117271	Hrk	harakiri, BCL2 interacting protein	2.6	27.7	77.2	0.0199
690130	Rhof	ras homolog family member F, filopodia associated	2.6	62.7	174.2	0.0006
294708	Sgtb	small glutamine rich tetratricopeptide repeat containing beta	2.5	31.9	86.4	0.0000

a) Gene IDs reference The National Center for Biotechnology Information database.

b) Data are expressed as the mean ($n = 6$), analyzed by Moderated t -tests using GeneSpring GX ver. 14.9.

Supplementary Table S8, continued

NCBI Entrez Gene ID ^{a)}	Gene Symbol	Gene Name	Fold Change	CT diet group (raw intensity) ^{b)}	LP diet group (raw intensity)	P value
246263	Acsm2	acyl-CoA synthetase medium-chain family member 2	2.5	859.4	2314.3	0.0006
297113	Gars	glycyl-tRNA synthetase	2.5	7947.2	21151.8	0.0000
360642	Kansl1	KAT8 regulatory NSL complex subunit 1	2.5	22.5	59.4	0.0123
690315	Derl3	derlin 3	2.5	193.4	508.1	0.0102
85332	Cavin3	caveolae associated protein 3	2.4	6734.9	17630.1	0.0000
116636	Eif4ebp1	eukaryotic translation initiation factor 4E binding protein 1	2.4	6325.6	16485.5	0.0000
362899	Nipal2	NIPA-like domain containing 2	2.4	18.9	48.6	0.0001
619561	Acsf2	acyl-CoA synthetase family member 2	2.4	16.3	42.0	0.0006
679091	Mettl1	methyltransferase like 1	2.4	49.4	124.6	0.0001
313560	Ctsp1	CTP synthase 1	2.3	623.4	1557.8	0.0000
307395	Ablim3	actin binding LIM protein family, member 3	2.3	238.3	591.9	0.0359
685448	Pcp4l1	Purkinje cell protein 4-like 1	2.3	181.7	450.1	0.0004
287450	Slc16a11	solute carrier family 16, member 11	2.3	949.3	2348.0	0.0004
84422	Gfra3	GDNF family receptor alpha 3	2.3	33.2	81.5	0.0004
83509	Slc7a7	solute carrier family 7 member 7	2.3	10.9	26.6	0.0000
314462	Trmt61a	tRNA methyltransferase 61A	2.3	533.8	1297.9	0.0003
59320	Adcy10	adenylate cyclase 10 (soluble)	2.3	40.3	98.0	0.0086
57033	Adam22	ADAM metalloproteinase domain 22	2.3	24.7	59.6	0.0026
311428	RGD1311739	similar to RIKEN cDNA 1700037H04	2.3	688.9	1661.7	0.0000
291541	Cidea	cell death-inducing DFFA-like effector a	2.2	136.9	329.3	0.0409
293638	Cars	cysteinyl-tRNA synthetase	2.2	463.5	1109.8	0.0000
685679	Nme4	NME/NM23 nucleoside diphosphate kinase 4	2.2	25.6	61.2	0.0001
288499	Slc29a4	solute carrier family 29 member 4	2.2	171.7	411.0	0.0004
313047	Yars	tyrosyl-tRNA synthetase	2.2	311.4	740.1	0.0000
287818	Cd300lf	Cd300 molecule-like family member F	2.2	72.0	170.0	0.0000
306804	Iars	isoleucyl-tRNA synthetase	2.2	1620.4	3814.8	0.0000
100912108	Nupr1	nuclear protein 1, transcriptional regulator	2.2	4555.4	10689.6	0.0000
25586	Alpl	alkaline phosphatase, liver/bone/kidney	2.2	207.0	485.8	0.0000
363465	Pir	pirin	2.2	480.0	1117.1	0.0001
294072	Slc35g1	solute carrier family 35, member G1	2.2	56.3	130.4	0.0001
681337	Acot4	acyl-CoA thioesterase 4	2.2	2724.6	6311.8	0.0000
652928	Rbm12	RNA binding motif protein 12	2.2	26.6	61.5	0.0125
365901	Gnat2	G protein subunit alpha transducin 2	2.2	41.6	96.2	0.0055
304429	Psph	phosphoserine phosphatase	2.1	554.0	1258.7	0.0000
29455	Gdf15	growth differentiation factor 15	2.1	44.8	101.5	0.0228
310376	Nim1k	NIM1 serine/threonine protein kinase	2.1	587.3	1317.1	0.0095
291317	Rpp38	ribonuclease P/MRP subunit p38	2.1	103.2	229.6	0.0000
116509	Slc6a9	solute carrier family 6 member 9	2.1	489.8	1086.4	0.0000
65035	Nr1i3	nuclear receptor subfamily 1, group I, member 3	2.1	994.3	2198.9	0.0002
308584	Plekha4	pleckstrin homology domain containing A4	2.1	167.8	369.4	0.0001
366593	Dus4l	dihydrouridine synthase 4-like	2.0	30.0	65.8	0.0000
29739	Gclm	glutamate cysteine ligase, modifier subunit	2.0	92.9	203.6	0.0000
305826	Samd4a	sterile alpha motif domain containing 4A	2.0	119.4	261.3	0.0011
25146	Cyp17a1	cytochrome P450, family 17, subfamily a, polypeptide 1	2.0	566.3	1236.7	0.0072
364838	Reep5	receptor accessory protein 5	2.0	21.1	46.1	0.0000
499129	Kctd15	potassium channel tetramerization domain containing 15	2.0	17.2	37.6	0.0000
64526	Ech1	enoyl-CoA hydratase 1	2.0	3614.4	7880.1	0.0001
309122	H19	H19, imprinted maternally expressed transcript (non-protein coding)	2.0	26.8	58.4	0.0014
60630	Unc5b	unc-5 netrin receptor B	2.0	276.9	599.6	0.0080
308602	Tmem86a	transmembrane protein 86A	2.0	1643.0	3552.8	0.0145

a) Gene IDs reference The National Center for Biotechnology Information database.

b) Data are expressed as the mean ($n = 6$), analyzed by Moderated t -tests using GeneSpring GX ver. 14.9.

Supplementary Table S8, continued

NCBI Entrez Gene ID ^{a)}	Gene Symbol	Gene Name	Fold Change	CT diet group (raw intensity) ^{b)}	LP diet group (raw intensity)	P value
314304	Acot3	acyl-CoA thioesterase 3	2.0	95.6	206.6	0.0001
299851	Mars	methionyl-tRNA synthetase	2.0	2599.5	5617.0	0.0000
24536	Lepr	leptin receptor	2.0	202.2	432.8	0.0001
26989	Cadps	calcium dependent secretion activator	2.0	40.1	85.9	0.0000
64316	Srpx	sushi-repeat-containing protein, X-linked	2.0	161.2	343.5	0.0049
64157	Ddah1	dimethylarginine dimethylaminohydrolase 1	2.0	5189.5	10943.4	0.0037
361441	Fam89a	family with sequence similarity 89, member A	2.0	2886.9	6063.2	0.0006
315759	Igdcc3	immunoglobulin superfamily, DCC subclass, member 3	2.0	102.0	213.7	0.0362
192267	Obp1f	odorant binding protein I f	2.0	84.5	177.0	0.0041
291624	Lars	leucyl-tRNA synthetase	1.9	3421.6	7112.7	0.0000
291773	Taf4b	TATA-box binding protein associated factor 4b	1.9	39.8	82.5	0.0000
680493	Cd3eap	CD3e molecule associated protein	1.9	268.7	557.4	0.0000
24552	Me1	malic enzyme 1	1.9	7733.7	16005.7	0.0031
100911757	Tshz2	teashirt zinc finger homeobox 2	1.9	117.7	242.3	0.0006
298699	Ppan	peter pan homolog (Drosophila)	1.9	1636.8	3358.7	0.0001
192272	Acot2	acyl-CoA thioesterase 2	1.9	35.6	72.4	0.0007
60356	Csad	cysteine sulfinic acid decarboxylase	1.9	1396.0	2833.6	0.0001
24627	Pde4d	phosphodiesterase 4D	1.9	9.6	19.5	0.0036
309145	RGD1311946	similar to RIKEN cDNA 1810055G02	1.9	87.9	177.8	0.0007
102553031	LOC102553031	zinc finger and SCAN domain-containing protein 20-like	1.9	102.8	207.3	0.0055
499709	Gar1	GAR1 ribonucleoprotein	1.9	116.2	233.9	0.0001
89820	Prmt3	protein arginine methyltransferase 3	1.9	24.0	48.2	0.0002
294007	Pprc1	peroxisome proliferator-activated receptor gamma, coactivator-related 1	1.9	209.8	419.9	0.0000
289533	Ugt2a3	UDP glucuronosyltransferase family 2 member A3	1.9	185.0	369.8	0.0005
29740	Eci1	enoyl-CoA delta isomerase 1	1.8	5682.5	11214.2	0.0011
297436	Chchd6	coiled-coil-helix-coiled-coil-helix domain containing 6	1.8	60.0	118.3	0.0001
298031	Susd1	sushi domain containing 1	1.8	34.0	66.5	0.0000
171093	Shank2	SH3 and multiple ankyrin repeat domains 2	1.8	20.8	40.6	0.0014
365192	Zfp324	zinc finger protein 324	1.8	20.2	39.3	0.0111
298541	Dhdds	dehydrodolichyl diphosphate synthase subunit	1.8	594.1	1154.2	0.0043
102552326	LOC102552326	late cornified envelope protein 5A-like	1.8	24.0	46.6	0.0001
286989	Ugt2b7	UDP glucuronosyltransferase family 2 member B7	1.8	574.1	1113.9	0.0013
81008	Itga7	integrin subunit alpha 7	1.8	35.7	69.2	0.0004
295228	Gpatch4	G patch domain containing 4	1.8	160.8	311.7	0.0081
298594	Rcc2	regulator of chromosome condensation 2	1.8	152.2	294.9	0.0000
79255	Atf4	activating transcription factor 4	1.8	9581.1	18524.8	0.0000
300862	Irak1bp1	interleukin-1 receptor-associated kinase 1 binding protein 1	1.8	31.4	60.6	0.0392
500707	Tc2n	tandem C2 domains, nuclear	1.8	142.4	274.3	0.0000
117024	Crym	crystallin, mu	1.8	1624.3	3114.5	0.0010
364827	Zscan30	zinc finger and SCAN domain containing 30	1.8	11.8	22.7	0.0105
54261	Kcnn1	potassium calcium-activated channel subfamily N member 1	1.8	14.3	27.3	0.0172
85255	Hacl1	2-hydroxyacyl-CoA lyase 1	1.8	8519.2	16277.1	0.0072
288053	Ropn1	rhopilin associated tail protein 1	1.8	47.9	91.1	0.0287
314405	Otub2	OTU deubiquitinase, ubiquitin aldehyde binding 2	1.8	2675.5	5065.4	0.0079
362287	Slc17a9	solute carrier family 17 member 9	1.8	216.4	409.5	0.0031
171347	Mat2a	methionine adenosyltransferase 2A	1.8	2123.6	4005.8	0.0000
266975	Sars	seryl-tRNA synthetase	1.8	665.4	1255.0	0.0000
85262	Slc25a27	solute carrier family 25, member 27	1.8	15.1	28.3	0.0049
308911	Rrp8	ribosomal RNA processing 8	1.7	73.6	136.6	0.0000
288622	Zbed5	zinc finger, BED-type containing 5	1.7	30.1	55.7	0.0079

a) Gene IDs reference The National Center for Biotechnology Information database.

b) Data are expressed as the mean ($n = 6$), analyzed by Moderated t -tests using GeneSpring GX ver. 14.9.

Supplementary Table S8, continued

NCBI Entrez Gene ID ^{a)}	Gene Symbol	Gene Name	Fold Change	CT diet group (raw intensity) ^{b)}	LP diet group (raw intensity)	P value
114483	Cdk6	cyclin-dependent kinase 6	1.7	16.7	30.8	0.0051
84596	Srm	spermidine synthase	1.7	1421.4	2626.0	0.0000
292757	Fbxo17	F-box protein 17	1.7	49.7	91.8	0.0349
288741	Ficd	FIC domain containing	1.7	322.6	594.3	0.0063
313610	Extl1	exostosin-like glycosyltransferase 1	1.7	2199.9	4052.3	0.0010
59115	Ninj2	ninjurin 2	1.7	118.0	217.2	0.0008
679127	Rrp12	ribosomal RNA processing 12 homolog	1.7	117.0	215.4	0.0001
362703	Wdr43	WD repeat domain 43	1.7	730.1	1342.8	0.0001
60335	Tgm1	transglutaminase 1	1.7	11.8	21.7	0.0166
299316	Slc25a47	solute carrier family 25, member 47	1.7	13494.0	24704.3	0.0076
363328	Ticam1	toll-like receptor adaptor molecule 1	1.7	25.1	45.9	0.0093
498196	Cyp3a85-ps	cytochrome P450, family 3, subfamily a, polypeptide 85, pseudogene	1.7	2821.9	5158.2	0.0005
25283	Gclc	glutamate-cysteine ligase, catalytic subunit	1.7	5831.2	10647.5	0.0004
500292	Cidec	cell death-inducing DFFA-like effector c	1.7	1103.4	2014.7	0.0001
300211	Fkbp11	FK506 binding protein 11	1.7	978.7	1786.5	0.0001
498206	Tnfrsf11a	TNF receptor superfamily member 11A	1.7	15.1	27.6	0.0165
300888	Tmed3	transmembrane p24 trafficking protein 3	1.7	458.9	835.0	0.0035
362976	Trmu	tRNA 5-methylaminomethyl-2-thiouridylate methyltransferase	1.7	91.9	166.9	0.0029
690297	Pwp2	PWP2, small subunit processome component	1.7	432.2	783.3	0.0000
171145	Eif2b3	eukaryotic translation initiation factor 2B subunit gamma	1.7	229.4	415.5	0.0001
316421	Aox2	aldehyde oxidase 2	1.7	11.3	20.4	0.0021
362979	Panx2	pannexin 2	1.7	25.1	45.4	0.0011
295384	Prmt6	protein arginine methyltransferase 6	1.7	16.1	28.9	0.0001
311849	Crat	carnitine O-acetyltransferase	1.7	3571.8	6408.8	0.0008
25458	Gss	glutathione synthetase	1.7	620.1	1112.7	0.0020
289338	Disp1	dispatched RND transporter family member 1	1.7	146.0	261.9	0.0038
498678	Ccdc71	coiled-coil domain containing 71	1.7	17.6	31.5	0.0057
314128	RGD1304624	similar to RIKEN cDNA 2700097O09	1.7	38.5	69.0	0.0036
291553	Nedd4l	neural precursor cell expressed, developmentally down-regulated 4-like	1.7	38.3	68.4	0.0383
29508	Nfya	nuclear transcription factor Y subunit alpha	1.7	14.6	26.1	0.0036
290686	Tma16	translation machinery associated 16 homolog	1.7	159.9	284.8	0.0000
313245	Polr1e	RNA polymerase I subunit E	1.7	97.3	173.3	0.0001
689232	Nxn12	nucleoredoxin-like 2	1.7	23.3	41.5	0.0159
360482	Tfap4	transcription factor AP-4	1.7	93.0	165.2	0.0000
60373	Nop58	NOP58 ribonucleoprotein	1.7	923.9	1637.4	0.0010
685474	Zfp385a	zinc finger protein 385A	1.7	1169.8	2069.9	0.0054
25062	Gpd2	glycerol-3-phosphate dehydrogenase 2	1.6	393.9	696.6	0.0072
309673	Rrp1b	ribosomal RNA processing 1B	1.6	13.5	23.9	0.0105
171179	Glyatl2	glycine-N-acyltransferase-like 2	1.6	5039.5	8904.1	0.0006
25413	Cpt2	carnitine palmitoyltransferase 2	1.6	3975.0	7008.0	0.0002
303569	Rundc3a	RUN domain containing 3A	1.6	19.4	34.3	0.0192
300994	Ifrd2	interferon-related developmental regulator 2	1.6	276.2	486.5	0.0036
300120	Fam118a	family with sequence similarity 118, member A	1.6	38.8	68.4	0.0009
140665	Rab3d	RAB3D, member RAS oncogene family	1.6	40.2	70.6	0.0044
361221	Nol8	nucleolar protein 8	1.6	249.2	437.5	0.0001
362495	Ndufaf4	NADH:ubiquinone oxidoreductase complex assembly factor 4	1.6	41.0	71.8	0.0046
100360406	Tsr1	TSR1, ribosome maturation factor	1.6	111.1	194.8	0.0044
291057	Eef1e1	eukaryotic translation elongation factor 1 epsilon 1	1.6	15.8	27.6	0.0075
294091	Ifit2	interferon-induced protein with tetratricopeptide repeats 2	1.6	335.5	587.2	0.0155
114555	Casp4	caspase 4	1.6	777.0	1357.8	0.0000

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Supplementary Table S8, continued

NCBI Entrez Gene ID ^{a)}	Gene Symbol	Gene Name	Fold Change	CT diet group (raw intensity) ^{b)}	LP diet group (raw intensity)	P value
317395	Spin2a	spindlin family, member 2A	1.6	55.7	97.2	0.0001
296302	Eif2s2	eukaryotic translation initiation factor 2 subunit beta	1.6	818.6	1426.6	0.0001
314879	Xpot	exportin for tRNA	1.6	1156.4	2010.5	0.0000
117020	Mcf2l	MCF.2 cell line derived transforming sequence-like	1.6	38.4	66.7	0.0002
291556	Nars	asparaginyl-tRNA synthetase	1.6	372.2	644.6	0.0000
297508	Nampt	nicotinamide phosphoribosyltransferase (NAMPT)	1.6	21.8	37.7	0.0414
501582	Gspt2	G1 to S phase transition 2	1.6	26.8	46.3	0.0018
292804	Gpi	glucose-6-phosphate isomerase	1.6	3634.9	6271.4	0.0011
362214	Nop56	NOP56 ribonucleoprotein	1.6	872.0	1504.1	0.0001
500595	Smim1	small integral membrane protein 1	1.6	1564.2	2694.2	0.0126
290558	Nt5dc2	5'-nucleotidase domain containing 2	1.6	169.8	292.3	0.0001
501283	Plin5	perilipin 5	1.6	16.0	27.6	0.0053
311441	Trmt6	tRNA methyltransferase 6	1.6	157.5	270.9	0.0000
58822	Csnk1e	casein kinase 1, epsilon	1.6	52.7	90.6	0.0010
26203	ND6	NADH dehydrogenase subunit 6	1.6	807.5	1385.7	0.0211
303372	Nle1	notchless homolog 1	1.6	181.4	311.0	0.0001
287451	Slc16a13	solute carrier family 16, member 13	1.6	371.6	636.9	0.0001
307253	Katnal2	katanin catalytic subunit A1 like 2	1.6	40.6	69.5	0.0004
316533	Chpf	chondroitin polymerizing factor	1.6	371.3	635.7	0.0048
83582	Polr1b	RNA polymerase I subunit B	1.6	98.6	168.6	0.0003
289827	Ugp2	UDP-glucose pyrophosphorylase 2	1.6	14721.6	25168.6	0.0024
689933	Syce3	synaptonemal complex central element protein 3	1.6	62.4	106.6	0.0067
81522	Mtr	5-methyltetrahydrofolate-homocysteine methyltransferase	1.6	44.7	76.3	0.0006
266764	Tbkbp1	TBK1 binding protein 1	1.6	620.6	1057.8	0.0008
266770	Soat2	sterol O-acyltransferase 2	1.6	289.0	491.7	0.0001
117242	Tenm2	teneurin transmembrane protein 2	1.6	57.6	97.9	0.0009
682457	Txlna	taxilin alpha	1.6	22.8	38.7	0.0025
499155	Fancl	Fanconi anemia, complementation group F	1.6	17.9	30.4	0.0001
170509	Cyp3a62	cytochrome P450, family 3, subfamily a, polypeptide 62	1.6	434.7	736.3	0.0206
298096	Wdr31	WD repeat domain 31	1.6	69.3	117.2	0.0003
290228	Ipo4	importin 4	1.6	1972.8	3334.9	0.0000
25009	Vars	valyl-tRNA synthetase	1.6	10.3	17.4	0.0010
114021	Ebna1bp2	EBNA1 binding protein 2	1.6	2795.8	4723.8	0.0000
361205	Lect2	leukocyte cell-derived chemotaxin 2	1.6	4932.7	8330.2	0.0001
292792	Tmem147	transmembrane protein 147	1.6	1600.1	2701.6	0.0000
313200	Hsd12	hydroxysteroid dehydrogenase like 2	1.6	1456.2	2456.6	0.0002
317382	Foxp3	forkhead box P3	1.6	13.0	21.9	0.0046
295394	Dph5	diphthamide biosynthesis 5	1.6	141.4	238.0	0.0002
305540	Slc1a4	solute carrier family 1 member 4	1.6	14.7	24.7	0.0067
362850	Angptl4	angiopoietin-like 4	1.6	18435.2	31008.6	0.0070
361935	Spata5	spermatogenesis associated 5	1.6	33.3	56.0	0.0187
303211	Mmgt2	membrane magnesium transporter 2	1.6	66.1	111.1	0.0050
685560	Mogat3	monoacylglycerol O-acyltransferase 3	1.6	30.2	50.7	0.0153
289352	Eprs	glutamyl-prolyl-tRNA synthetase	1.6	5622.7	9450.4	0.0000
501396	LOC501396	hypothetical protein LOC501396	1.6	59.8	100.4	0.0005
314969	Nop2	NOP2 nucleolar protein	1.6	1177.2	1975.4	0.0001
315212	Alg12	ALG12, alpha-1,6-mannosyltransferase	1.6	64.4	108.0	0.0013
79116	Apex1	apurinic/aprimidinic endodeoxyribonuclease 1	1.6	2077.3	3483.9	0.0002
171134	Lgals2	galectin 2	1.6	89.3	149.7	0.0148
60571	Mybbp1a	MYB binding protein 1a	1.6	253.9	424.7	0.0000

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Supplementary Table S8, continued

NCBI Entrez Gene ID ^{a)}	Gene Symbol	Gene Name	Fold Change	CT diet group (raw intensity) ^{b)}	LP diet group (raw intensity)	P value
309646	Slc26a8	solute carrier family 26 member 8	1.6	32.8	54.9	0.0217
171139	Timm9	translocase of inner mitochondrial membrane 9	1.6	1091.6	1824.3	0.0004
117544	Ppat	phosphoribosyl pyrophosphate amidotransferase	1.6	276.0	461.2	0.0003
363017	Taf1d	TATA-box binding protein associated factor, RNA polymerase I subunit D	1.6	96.5	161.0	0.0187
314243	Wdr89	WD repeat domain 89	1.6	103.0	171.6	0.0000
685697	Supt3h	SPT3 homolog, SAGA and STAGA complex component	1.6	71.9	119.5	0.0351
298384	RGD1559786	similar to RIKEN cDNA 0610037L13	1.6	24.7	41.2	0.0011
300652	Sorl1	sortilin related receptor 1	1.6	16.2	27.0	0.0447
102553962	LOC102553962	KRAB domain-containing protein ZNF747-like	1.5	507.7	842.9	0.0016
361783	Zfp57	zinc finger protein 57	1.5	39.5	65.5	0.0004
117041	Nln	neurolysin	1.5	807.0	1336.9	0.0002
84484	Slc4a4	solute carrier family 4 member 4	1.5	804.4	1331.2	0.0076
688966	Borcs8	BLOC-1 related complex subunit 8	1.5	141.6	234.3	0.0013
362224	Kat14	lysine acetyltransferase 14	1.5	27.1	44.8	0.0435
25623	Gys2	glycogen synthase 2	1.5	13653.3	22551.8	0.0040
315994	Mapkapk3	mitogen-activated protein kinase-activated protein kinase 3	1.5	474.9	783.6	0.0204
25256	Fmo1	flavin containing monooxygenase 1	1.5	3997.0	6590.7	0.0033
171047	Dnph1	2'-deoxynucleoside 5'-phosphate N-hydrolase 1	1.5	1947.5	3210.5	0.0000
300114	Rtl6	retrotransposon Gag like 6	1.5	281.6	464.2	0.0004
301544	Farsb	phenylalanyl-tRNA synthetase, beta subunit	1.5	173.7	285.1	0.0011
308652	Smox	spermine oxidase	1.5	24.0	39.4	0.0222
291469	Srfbp1	serum response factor binding protein 1	1.5	135.0	221.6	0.0001
367384	B3gnt1	UDP-GlcNAc:betaGal beta-1,3-N-acetylgalactosaminyltransferase-like 1	1.5	174.7	285.7	0.0004
100911224	LOC100911224	zinc finger protein interacting with ribonucleoprotein K-like	1.5	46.8	76.5	0.0005
81683	Mif	macrophage migration inhibitory factor (glycosylation-inhibiting factor)	1.5	10071.7	16460.6	0.0078
297784	Rrs1	ribosome biogenesis regulator homolog	1.5	157.3	256.7	0.0253
293738	Ccdc86	coiled-coil domain containing 86	1.5	311.0	507.1	0.0021
245981	Rpl15	ribosomal protein L15	1.5	165.6	270.0	0.0001
308568	Fv1	Friend virus susceptibility 1	1.5	13.6	22.1	0.0152
291540	Cep76	centrosomal protein 76	1.5	224.3	365.1	0.0000
29681	C1qbp	complement C1q binding protein	1.5	13227.7	21531.0	0.0000
24214	Atp1b2	ATPase Na ⁺ /K ⁺ transporting subunit beta 2	1.5	51.0	83.1	0.0040
361596	Idh2	isocitrate dehydrogenase (NADP(+)) 2, mitochondrial	1.5	5218.3	8478.2	0.0013
503049	Acot5	acyl-CoA thioesterase 5	1.5	2522.3	4094.8	0.0107
499756	Lcn10	lipocalin 10	1.5	10.8	17.6	0.0240
300839	Lysmd2	LysM domain containing 2	1.5	498.8	808.4	0.0040
360569	Mrm3	mitochondrial rRNA methyltransferase 3	1.5	104.1	168.6	0.0013
363134	Rrp9	ribosomal RNA processing 9, U3 small nucleolar RNA binding protein	1.5	169.3	273.7	0.0006
362058	Miga1	mitoguardin 1	1.5	55.9	90.3	0.0012
310625	Rhbg	Rh family B glycoprotein	1.5	31.8	51.4	0.0100
500981	Zfp202	zinc finger protein 202	1.5	85.3	137.8	0.0001
303343	Abhd15	abhydrolase domain containing 15	1.5	15.4	24.8	0.0177
29477	Mapt	microtubule-associated protein tau	1.5	85.4	137.6	0.0030
288176	Cmss1	cms1 ribosomal small subunit homolog (yeast)	1.5	73.2	117.9	0.0001
363237	Wdr12	WD repeat domain 12	1.5	1478.2	2380.9	0.0014
287273	Nhp2	NHP2 ribonucleoprotein	1.5	1103.1	1776.5	0.0000
362983	Dennd6b	DENN domain containing 6B	1.5	18.6	29.9	0.0031
363029	Swsap1	SWIM-type zinc finger 7 associated protein 1	1.5	90.3	145.3	0.0003
681037	Preli2	PRELI domain containing 2	1.5	1133.5	1822.8	0.0003
681023	Qsox2	quiescin sulfhydryl oxidase 2	1.5	90.1	144.9	0.0000

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Supplementary Table S8, continued

NCBI Entrez Gene ID ^{a)}	Gene Symbol	Gene Name	Fold Change	CT diet group (raw intensity) ^{b)}	LP diet group (raw intensity)	P value
102551435	LOC102551435	endothelin-converting enzyme 2-like	1.5	215.3	345.6	0.0001
64846	Slc13a3	solute carrier family 13 member 3	1.5	2678.5	4297.0	0.0024
307989	Ablim1	actin-binding LIM protein 1	1.5	778.0	1247.7	0.0002
282840	Atf5	activating transcription factor 5	1.5	9153.1	14678.5	0.0004
29224	Cbr1	carbonyl reductase 1	1.5	573.5	919.5	0.0000
25315	Ephx1	epoxide hydrolase 1	1.5	1705.2	2732.0	0.0100
360463	Mpv17	MpV17 mitochondrial inner membrane protein	1.5	3929.7	6295.5	0.0000
311391	Cep152	centrosomal protein 152	1.5	88.9	142.5	0.0331
497978	Dgke	diacylglycerol kinase epsilon	1.5	30.1	48.2	0.0076
266682	Cyp3a2	cytochrome P450, family 3, subfamily a, polypeptide 2	1.5	50933.2	81387.4	0.0007
294230	Mrps18b	mitochondrial ribosomal protein S18B	1.5	371.0	592.5	0.0001
685545	Mcrip2	MAPK regulated co-repressor interacting protein 2	1.5	2788.3	4451.6	0.0072
364755	Ero1b	endoplasmic reticulum oxidoreductase 1 beta	1.5	68.4	109.1	0.0004
303333	Slc46a1	solute carrier family 46 member 1	1.5	426.0	680.0	0.0215
306768	Nop16	NOP16 nucleolar protein	1.5	2990.0	4767.5	0.0000
24908	Dnajb9	DnaJ heat shock protein family (Hsp40) member B9	1.5	991.0	1575.9	0.0239
114300	Gtpbp4	GTP binding protein 4	1.5	358.0	569.2	0.0045
84491	Qsox1	quiescin sulphydryl oxidase 1	1.5	1269.8	2018.2	0.0000
140946	Paics	phosphoribosylaminoimidazole carboxylase	1.5	4619.0	7331.1	0.0000
362883	Slc35e3	solute carrier family 35, member E3	1.5	23.2	36.7	0.0029
300554	Olr1229	olfactory receptor 1229	1.5	25.4	40.2	0.0338
360811	Naa25	N(alpha)-acetyltransferase 25, NatB auxiliary subunit	1.5	30.4	48.1	0.0016
103693432	Ptges3l	prostaglandin E synthase 3 like	1.5	20.4	32.2	0.0012
29660	Pnck	pregnancy up-regulated nonubiquitous CaM kinase	1.5	35.1	55.5	0.0040
311279	Arl14ep	ADP-ribosylation factor like GTPase 14 effector protein	1.5	704.1	1112.8	0.0013
315554	Pus3	pseudouridylate synthase 3	1.5	243.1	384.2	0.0002
290783	Tusc3	tumor suppressor candidate 3	1.5	169.4	267.6	0.0039
171439	Bzw2	basic leucine zipper and W2 domains 2	1.5	766.5	1209.4	0.0002
24763	Acsm3	acyl-CoA synthetase medium-chain family member 3	1.5	199.4	314.4	0.0434
304054	Prdm15	PR/SET domain 15	1.5	13.5	21.2	0.0038
311257	Nat10	N-acetyltransferase 10	1.5	55.7	87.7	0.0013
500909	Cdc134	coiled-coil domain containing 134	1.5	484.8	763.2	0.0020
311835	Ddx31	DEAD-box helicase 31	1.5	22.3	35.1	0.0084
363924	Rad9b	RAD9 checkpoint clamp component B	1.5	128.9	202.7	0.0009
116684	Oplah	5-oxoprolinase (ATP-hydrolysing)	1.5	727.8	1143.3	0.0064
499106	RGD1560854	similar to FLJ41131 protein	1.5	113.3	177.9	0.0003
289758	Pold2	DNA polymerase delta 2, accessory subunit	1.5	275.2	431.8	0.0021
308850	Klhl35	kelch-like family member 35	1.5	34.1	53.5	0.0054
24468	Hspa8	heat shock protein family A (Hsp70) member 8	1.5	32107.1	50365.3	0.0031
310244	Zc2hc1a	zinc finger, C2HC-type containing 1A	1.5	19.0	29.7	0.0020
303772	Slc16a6	solute carrier family 16, member 6	1.5	36.4	57.0	0.0211
290596	Ghitm	growth hormone inducible transmembrane protein	1.5	3324.9	5210.9	0.0011
302680	Txlng	taxilin gamma	1.5	920.7	1442.3	0.0007
360970	Cabp7	calcium binding protein 7	1.5	12.3	19.3	0.0002
688637	LOC688637	similar to WD repeat domain 36	1.5	39.3	61.6	0.0012
58958	Nup210	nucleoporin 210	1.5	650.0	1016.8	0.0001
29407	Tas1r1	taste 1 receptor member 1	1.5	96.8	151.3	0.0041
498385	Lcorl	ligand dependent nuclear receptor corepressor-like	1.5	14.4	22.5	0.0311
116641	Lgals8	galectin 8	1.5	926.4	1444.8	0.0011
498297	Cnst	consortin, connexin sorting protein	1.5	90.2	140.5	0.0013

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Supplementary Table S8, continued

NCBI Entrez Gene ID ^{a)}	Gene Symbol	Gene Name	Fold Change	CT diet group (raw intensity) ^{b)}	LP diet group (raw intensity)	P value
294436	Rpf2	ribosome production factor 2 homolog	1.5	198.4	309.0	0.0016
691414	LOC691414	hypothetical protein LOC691414	1.5	250.0	389.2	0.0008
300050	Bop1	block of proliferation 1	1.5	233.1	362.7	0.0003
363472	Prrg1	proline rich and Gla domain 1	1.5	31.8	49.4	0.0295
687147	Ric3	RIC3 acetylcholine receptor chaperone	1.5	17.1	26.5	0.0082
362374	Vopp1	vesicular, overexpressed in cancer, prosurvival protein 1	-1.5	48.8	36.1	0.0169
56765	Plvap	plasmalemma vesicle associated protein	-1.5	1309.6	967.4	0.0020
59085	Asl	argininosuccinate lyase	-1.5	17819.0	13150.2	0.0217
60586	Cicn4	chloride voltage-gated channel 4	-1.5	219.0	161.6	0.0047
25642	Cyp3a23/3a1	cytochrome P450, family 3, subfamily a, polypeptide 23/polypeptide 1	-1.5	511.0	377.0	0.0240
288264	lfnar1	interferon alpha and beta receptor subunit 1	-1.5	41.3	30.5	0.0005
307726	Chd9	chromodomain helicase DNA binding protein 9	-1.5	321.8	237.3	0.0327
290529	Fam213a	family with sequence similarity 213, member A	-1.5	1028.8	758.1	0.0006
291359	Ly86	lymphocyte antigen 86	-1.5	411.5	303.2	0.0121
25164	Cdkn2b	cyclin-dependent kinase inhibitor 2B	-1.5	75.6	55.7	0.0120
301252	Hsp90ab1	heat shock protein 90 alpha family class B member 1	-1.5	8485.9	6249.7	0.0011
493909	Aox3	aldehyde oxidase 3	-1.5	1182.2	870.5	0.0100
25668	Cd38	CD38 molecule	-1.5	54.2	39.9	0.0287
313166	Nfx1	nuclear transcription factor, X-box binding 1	-1.5	1673.2	1231.3	0.0003
289175	Slc19a2	solute carrier family 19 member 2	-1.5	1188.5	874.5	0.0025
362479	Tcea1	transcription elongation factor A (SII) 1	-1.5	1921.2	1413.3	0.0000
311642	Sulf2	sulfatase 2	-1.5	1261.4	927.5	0.0065
303029	Ranbp17	RAN binding protein 17	-1.5	161.6	118.8	0.0066
367181	Gad1	glutamate decarboxylase-like 1	-1.5	218.2	160.4	0.0304
304971	Tomm40l	translocase of outer mitochondrial membrane 40 like	-1.5	77.1	56.6	0.0018
102549509	LOC102549509	MLV-related proviral Env polyprotein-like	-1.5	27.1	19.9	0.0001
362455	Fam234b	family with sequence similarity 234, member B	-1.5	39.0	28.6	0.0100
78969	Trib1	tribbles pseudokinase 1	-1.5	120.1	88.0	0.0351
89811	Vegfb	vascular endothelial growth factor B	-1.5	165.5	121.0	0.0003
315658	Zc3h12c	zinc finger CCCH type containing 12C	-1.5	237.8	173.8	0.0035
361313	Rel2	RELT-like 2	-1.5	64.0	46.7	0.0003
309891	Septin10	septin 10	-1.5	82.3	60.1	0.0001
304988	Mnda	myeloid cell nuclear differentiation antigen	-1.5	61.1	44.6	0.0023
679154	Garem1	GRB2 associated regulator of MAPK1 subtype 1	-1.5	59.1	43.1	0.0267
100362283	Tmem52	transmembrane protein 52	-1.5	1060.6	773.2	0.0115
29500	Slc10a2	solute carrier family 10 member 2	-1.5	32.9	23.9	0.0376
25211	Lyz2	lysozyme 2	-1.5	4557.8	3320.6	0.0034
361135	Marchf1	membrane associated ring-CH-type finger 1	-1.5	135.0	98.4	0.0042
305452	Fam193a	family with sequence similarity 193, member A	-1.5	61.8	45.0	0.0011
24811	Tap1	transporter 1, ATP binding cassette subfamily B member	-1.5	168.4	122.6	0.0038
362833	Mob3a	MOB kinase activator 3A	-1.5	27.9	20.3	0.0076
295647	Gca	grancalcin	-1.5	46.2	33.6	0.0051
499358	Scd4	stearoyl-coenzyme A desaturase 4	-1.5	12664.0	9199.0	0.0145
313838	Cdc42ep3	CDC42 effector protein 3	-1.5	105.6	76.7	0.0015
29197	Il18	interleukin 18	-1.5	729.5	529.1	0.0001
291705	Iws1	IWS1, SUPT6H interacting protein	-1.5	69.1	50.1	0.0033
24162	Acp2	acid phosphatase 2, lysosomal	-1.5	5406.1	3916.5	0.0001
367289	Kansl1l	KAT8 regulatory NSL complex subunit 1-like	-1.5	22.0	15.9	0.0058
299566	Cyp4f39	cytochrome P450, family 4, subfamily f, polypeptide 39	-1.5	240.9	174.4	0.0035
301549	Wdfy1	WD repeat and FYVE domain containing 1	-1.5	699.5	506.2	0.0001

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Supplementary Table S8, continued

NCBI Entrez Gene ID ^{a)}	Gene Symbol	Gene Name	Fold Change	CT diet group (raw intensity) ^{b)}	LP diet group (raw intensity)	P value
678796	LOC678796	similar to acetyl-Coenzyme A acetyltransferase 2	-1.5	1628.4	1178.5	0.0031
681458	LOC681458	similar to stearyl-coenzyme A desaturase 3	-1.5	4026.8	2913.7	0.0186
116637	Ccl4	C-C motif chemokine ligand 4	-1.5	86.4	62.4	0.0278
286918	Mx2	MX dynamin like GTPase 2	-1.5	77.4	55.9	0.0071
58935	Gas6	growth arrest specific 6	-1.5	1661.1	1198.9	0.0116
25023	Prkcb	protein kinase C, beta	-1.5	62.9	45.4	0.0195
100910616	Hmgn5	high mobility group nucleosome binding domain 5	-1.5	413.1	297.7	0.0001
114247	Slnf4	schlafen 4	-1.5	357.2	257.1	0.0053
300807	Rora	RAR-related orphan receptor A	-1.5	106.3	76.5	0.0067
292710	Ethe1	ETHE1, persulfide dioxygenase	-1.5	3727.3	2679.5	0.0040
294273	RT1-DMb	RT1 class II, locus DMb	-1.5	602.7	433.2	0.0020
24230	Tspo	translocator protein	-1.5	908.3	652.8	0.0001
308350	Lilrb3	leukocyte immunoglobulin like receptor B3	-1.5	1749.4	1257.3	0.0017
54272	Mcpt9	mast cell protease 9	-1.5	369.1	265.3	0.0000
298296	Pcsk9	proprotein convertase subtilisin/kexin type 9	-1.5	10062.8	7222.6	0.0047
83502	Cdh1	cadherin 1	-1.5	2989.5	2144.6	0.0281
291770	Chst9	carbohydrate sulfotransferase 9	-1.5	35.1	25.2	0.0011
81670	Gpt	glutamic--pyruvic transaminase	-1.5	6475.7	4641.5	0.0021
25045	Dbi	diazepam binding inhibitor, acyl-CoA binding protein	-1.5	82323.4	58982.2	0.0000
246266	Aspg	asparaginase	-1.5	19013.7	13613.9	0.0002
500561	Themis2	thymocyte selection associated family member 2	-1.5	61.6	44.1	0.0042
192256	Pja2	praja ring finger ubiquitin ligase 2	-1.5	335.7	240.3	0.0001
24298	Cyp21a1	cytochrome P450, family 21, subfamily a, polypeptide 1	-1.5	159.0	113.7	0.0008
286888	Wfdc2	WAP four-disulfide core domain 2	-1.5	2905.9	2075.2	0.0000
288289	Chodl	chondrolectin	-1.5	218.5	155.9	0.0312
291840	Slc38a7	solute carrier family 38, member 7	-1.5	54.0	38.5	0.0018
501779	Cd200r1l	CD200 receptor 1-like	-1.5	224.2	159.8	0.0175
681820	Erich5	glutamate-rich 5	-1.5	91.9	65.5	0.0259
29618	Btg1	BTG anti-proliferation factor 1	-1.5	30110.7	21437.2	0.0016
689069	Parvg	parvin, gamma	-1.5	70.9	50.4	0.0140
302492	Mbnl3	muscleblind-like splicing regulator 3	-1.5	690.9	491.6	0.0028
171164	Gbp2	guanylate binding protein 2	-1.5	1201.0	854.4	0.0253
361663	Lhpp	phospholysine phosphohistidine inorganic pyrophosphate phosphatase	-1.5	34.9	24.8	0.0019
24629	Pdgfrb	platelet derived growth factor receptor beta	-1.5	290.2	206.4	0.0460
498407	Purb	purine rich element binding protein B	-1.5	267.2	190.0	0.0000
293645	Ppfa1	PTPRF interacting protein alpha 1	-1.5	197.9	140.5	0.0004
287532	Slc43a2	solute carrier family 43 member 2	-1.5	333.1	236.4	0.0028
314751	Tmcc3	transmembrane and coiled-coil domain family 3	-1.5	324.0	229.9	0.0107
25618	Acad5b	acyl-CoA dehydrogenase, short/branched chain	-1.5	107.7	76.4	0.0025
108348057	NEWGENE1591402	pleckstrin homology like domain family B member 2	-1.5	86.9	61.6	0.0317
287362	Nlrp3	NLR family, pyrin domain containing 3	-1.5	23.3	16.5	0.0160
294993	Hspa4l	heat shock protein family A (Hsp70) member 4 like	-1.5	175.9	124.4	0.0136
24575	Mx1	myxovirus (influenza virus) resistance 1	-1.5	1085.5	767.0	0.0009
500709	Itpk1	inositol-tetrakisphosphate 1-kinase	-1.5	29.8	21.0	0.0284
54308	Sik	STE20-like kinase	-1.5	243.1	171.5	0.0001
450235	Adgre4	adhesion G protein-coupled receptor E4	-1.5	300.7	212.2	0.0233
25107	Avpr1a	arginine vasopressin receptor 1A	-1.5	5005.1	3530.4	0.0467
58962	Hpgds	hematopoietic prostaglandin D synthase	-1.5	91.8	64.8	0.0022
688749	Tulp3	tubby-like protein 3	-1.5	680.1	479.4	0.0006
81805	Suox	sulfite oxidase	-1.5	4175.4	2942.4	0.0000

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Supplementary Table S8, continued

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316775	Ankrd12	ankyrin repeat domain 12	-1.5	77.3	54.4	0.0015
316009	Plxnb1	plexin B1	-1.5	149.8	105.4	0.0060
406008	Olr1694	olfactory receptor 1694	-1.5	26.9	18.9	0.0313
309375	Marveld1	MARVEL domain containing 1	-1.5	794.8	558.8	0.0099
246208	Ifi47	interferon gamma inducible protein 47	-1.5	142.6	100.3	0.0097
29269	Mcpt8	mast cell protease 8	-1.5	777.4	545.7	0.0000
296925	Aass	aminoadipate-semialdehyde synthase	-1.5	527.0	369.8	0.0081
691416	Aknad1	AKNA domain containing 1	-1.5	666.2	467.4	0.0001
294691	Naip5	NLR family, apoptosis inhibitory protein 5	-1.5	184.8	129.6	0.0018
288866	Olr1057	olfactory receptor 1057	-1.5	22.7	15.9	0.0230
307414	MGC108823	similar to interferon-inducible GTPase	-1.5	140.0	98.0	0.0016
24962	Cth	cystathionine gamma-lyase	-1.5	6930.5	4844.9	0.0060
361069	Dmtn	dematin actin binding protein	-1.5	113.3	79.1	0.0004
83801	Ptms	parathyrosin	-1.5	4174.4	2915.4	0.0001
304549	Oas2	2'-5' oligoadenylate synthetase-like 2	-1.5	197.4	137.8	0.0025
100361457	LOC100361457	actin, gamma 1 propeptide-like	-1.5	622.8	433.9	0.0026
246142	Bmf	Bcl2 modifying factor	-1.5	5309.2	3698.1	0.0005
361625	Nrip3	nuclear receptor interacting protein 3	-1.5	28.9	20.1	0.0034
641316	Aldh4a1	aldehyde dehydrogenase 4 family, member A1	-1.5	325.1	226.1	0.0003
100911537	LOC100911537	5'-3' exoribonuclease 1-like	-1.5	38.8	27.0	0.0078
293749	Ms4a6bl	membrane-spanning 4-domains, subfamily A, member 6B-like	-1.5	1548.4	1075.1	0.0005
161476	Hspb2	heat shock protein family B (small) member 2	-1.5	9970.5	6917.9	0.0009
362832	Izumo4	IZUMO family member 4	-1.5	180.9	125.4	0.0003
294274	RT1-DMa	RT1 class II, locus DMA	-1.5	245.6	170.1	0.0086
310917	Gbp4	guanylate binding protein 4	-1.6	17.5	12.1	0.0249
170841	Mutyh	mutY DNA glycosylase	-1.6	405.8	280.3	0.0003
25017	Myo5a	myosin VA	-1.6	23.6	16.3	0.0148
114490	Cited2	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2	-1.6	332.5	229.3	0.0003
100910577	LOC100910577	zinc finger protein 709-like	-1.6	88.5	61.0	0.0020
361422	Cotl1	coactosin-like F-actin binding protein 1	-1.6	18.9	13.0	0.0301
304061	Brwd1	bromodomain and WD repeat domain containing 1	-1.6	92.0	63.4	0.0037
171497	Sgk2	SGK2, serine/threonine kinase 2	-1.6	1060.6	730.6	0.0286
296653	Phf19	PHD finger protein 19	-1.6	836.3	573.1	0.0030
60371	Birc2	baculoviral IAP repeat-containing 2	-1.6	52.1	35.6	0.0082
497840	Cps1	carbamoyl-phosphate synthase 1	-1.6	4255.3	2907.6	0.0006
313033	Xkr8	XK related 8	-1.6	2050.3	1400.0	0.0000
83791	Fdps	farnesyl diphosphate synthase	-1.6	13595.1	9277.0	0.0022
306115	RGD1560797	similar to glyceraldehyde-3-phosphate dehydrogenase	-1.6	47.3	32.2	0.0010
316638	Sned1	sushi, nidogen and EGF-like domains 1	-1.6	99.2	67.5	0.0402
81718	Cdo1	cysteine dioxygenase type 1	-1.6	9016.4	6127.9	0.0015
102549391	LOC102549391	zinc finger protein 879-like	-1.6	37.2	25.2	0.0137
290032	Eddm3b	epididymal protein 3B	-1.6	74.7	50.7	0.0002
24950	Srd5a1	steroid 5 alpha-reductase 1	-1.6	6613.1	4488.2	0.0237
311569	Acss2	acyl-CoA synthetase short-chain family member 2	-1.6	1048.9	711.4	0.0047
362300	Agap3	ArfGAP with GTPase domain, ankyrin repeat and PH domain 3	-1.6	191.7	130.0	0.0001
59296	Dnase2b	deoxyribonuclease 2 beta	-1.6	1653.8	1120.4	0.0382
298033	Snx30	sorting nexin family member 30	-1.6	22.2	15.0	0.0046
309312	Gldc	glycine decarboxylase	-1.6	6090.9	4114.3	0.0002
116699	lnpp4b	inositol polyphosphate-4-phosphatase type II B	-1.6	100.2	67.6	0.0030
293624	Irf7	interferon regulatory factor 7	-1.6	1532.0	1033.9	0.0020

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Supplementary Table S8, continued

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100302372	LOC100302372	hypothetical protein LOC100302372	-1.6	123.0	83.0	0.0333
100912573	Ms4a6e	membrane spanning 4-domains A6E	-1.6	24.1	16.3	0.0051
301363	Map4k4	mitogen-activated protein kinase kinase kinase 4	-1.6	303.6	204.4	0.0002
307526	Ammecr1l	AMMECR1 like	-1.6	997.0	670.3	0.0132
360733	Rtp4	receptor (chemosensory) transporter protein 4	-1.6	2268.9	1523.8	0.0242
679600	Xaf1	XIAP associated factor 1	-1.6	57.0	38.3	0.0002
688047	Lyc2	lysozyme C type 2	-1.6	949.6	636.9	0.0013
29412	Adra1a	adrenoceptor alpha 1A	-1.6	35.7	24.0	0.0264
29191	Tac3	tachykinin 3	-1.6	62.6	42.0	0.0309
361735	Ms4a6a	membrane spanning 4-domains A6A	-1.6	215.1	144.0	0.0005
366669	Syne2	spectrin repeat containing nuclear envelope protein 2	-1.6	681.9	456.3	0.0002
64322	Dap	death-associated protein	-1.6	4095.0	2740.0	0.0001
679692	Lpgat1	lysophosphatidylglycerol acyltransferase 1	-1.6	323.1	216.0	0.0001
680409	Prodh1	proline dehydrogenase 1	-1.6	1085.2	724.5	0.0300
140868	Fabp5	fatty acid binding protein 5, epidermal	-1.6	12215.0	8146.1	0.0160
89787	Lrp3	LDL receptor related protein 3	-1.6	1751.4	1167.2	0.0128
680656	Fndc10	fibronectin type III domain containing 10	-1.6	56.4	37.5	0.0010
29210	Epha3	Eph receptor A3	-1.6	118.1	78.7	0.0469
362454	Hebp1	heme binding protein 1	-1.6	10468.6	6956.0	0.0013
367391	Marco	macrophage receptor with collagenous structure	-1.6	361.2	240.0	0.0380
309962	Pde8b	phosphodiesterase 8B	-1.6	241.8	160.5	0.0015
64191	Dhcr7	7-dehydrocholesterol reductase	-1.6	3334.6	2206.1	0.0133
361604	Sytl2	synaptotagmin-like 2	-1.6	182.8	120.8	0.0468
305235	Art3	ADP-ribosyltransferase 3	-1.6	149.4	98.8	0.0339
24934	Klrk1	killer cell lectin like receptor K1	-1.6	19.8	13.0	0.0010
683415	Prss55	protease, serine, 55	-1.6	40.9	27.0	0.0030
54269	Mcpt10	mast cell protease 10	-1.6	284.5	187.3	0.0000
64552	Mpeg1	macrophage expressed 1	-1.6	83.6	55.1	0.0018
304645	Tbc1d9	TBC1 domain family member 9	-1.6	239.8	157.8	0.0002
312560	Xpc	XPC complex subunit, DNA damage recognition and repair factor	-1.6	526.6	346.6	0.0052
366352	Mob3b	MOB kinase activator 3B	-1.6	58.6	38.5	0.0016
367975	LOC367975	similar to B-cell translocation gene 1	-1.6	618.0	405.8	0.0019
291699	Stard4	StAR-related lipid transfer domain containing 4	-1.6	24.5	16.1	0.0022
338475	Nrep	neuronal regeneration related protein	-1.6	82.6	54.2	0.0134
295625	Pkp4	plakophilin 4	-1.6	1267.2	830.2	0.0000
24895	Cyp2a2	cytochrome P450, family 2, subfamily a, polypeptide 2	-1.6	11440.7	7488.7	0.0000
170641	Adgrl3	adhesion G protein-coupled receptor L3	-1.6	34.2	22.4	0.0066
289594	Nipal1	NIPA-like domain containing 1	-1.6	585.7	383.3	0.0042
303141	Rapgef6	Rap guanine nucleotide exchange factor 6	-1.6	58.7	38.3	0.0004
287472	Tlcd1	TLC domain containing 1	-1.6	337.4	220.3	0.0009
360942	Pcdh7	protocadherin 7	-1.6	36.4	23.7	0.0206
306600	Atp11a	ATPase phospholipid transporting 11A	-1.6	66.3	43.1	0.0014
84424	Tie3	transducin-like enhancer of split 3	-1.7	71.9	46.7	0.0037
81869	Gstm7	glutathione S-transferase, mu 7	-1.7	2244.1	1451.8	0.0025
688429	Arhgap10	Rho GTPase activating protein 10	-1.7	28.9	18.7	0.0175
500200	Atoh8	atonal bHLH transcription factor 8	-1.7	209.7	135.2	0.0018
317213	Brwd3	bromodomain and WD repeat domain containing 3	-1.7	89.3	57.6	0.0000
316626	Hes6	hes family bHLH transcription factor 6	-1.7	7287.5	4688.1	0.0012
368088	Dgkd	diacylglycerol kinase, delta	-1.7	363.6	233.8	0.0000
366518	Tnfrsf14	TNF receptor superfamily member 14	-1.7	74.1	47.6	0.0052

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Supplementary Table S8, continued

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287734	Atxn7I3	ataxin 7-like 3	-1.7	55.4	35.6	0.0003
171105	Lnpep	leucyl and cystinyl aminopeptidase	-1.7	31.7	20.3	0.0000
312275	Ephb6	Eph receptor B6	-1.7	1256.5	801.3	0.0009
306038	Enox1	ecto-NOX disulfide-thiol exchanger 1	-1.7	32.6	20.8	0.0322
24778	Slc2a1	solute carrier family 2 member 1	-1.7	420.4	267.8	0.0250
288665	Cux2	cut-like homeobox 2	-1.7	25.5	16.2	0.0113
24912	Sult2a1	sulfotransferase family 2A member 1	-1.7	864.1	549.2	0.0357
308797	Cemip	cell migration-inducing hyaluronan binding protein	-1.7	88.9	56.4	0.0081
360509	Dock2	dedicator of cytokinesis 2	-1.7	525.6	333.1	0.0002
687064	Col25a1	collagen type XXV alpha 1 chain	-1.7	27.8	17.6	0.0150
192268	Gls2	glutaminase 2	-1.7	28655.7	18142.3	0.0001
102556096	LOC102556096	pyrin domain-containing protein 3-like	-1.7	44.6	28.2	0.0001
304507	Oas1i	2'-5' oligoadenylate synthetase 1I	-1.7	471.5	296.4	0.0006
293587	Fuom	fructose mutarotase	-1.7	279.7	175.4	0.0003
29536	Rmrp	RNA component of mitochondrial RNA processing endoribonuclease	-1.7	918.6	575.9	0.0036
308100	Acat2	acetyl-CoA acetyltransferase 2	-1.7	2234.8	1400.4	0.0023
362282	Pck1	phosphoenolpyruvate carboxykinase 1	-1.7	13784.0	8630.6	0.0260
309622	RT1-Bb	RT1 class II, locus Bb	-1.7	505.0	315.3	0.0136
494198	Oas1k	2'-5' oligoadenylate synthetase 1K	-1.7	516.7	321.1	0.0004
312607	Pdzrn3	PDZ domain containing RING finger 3	-1.7	188.5	117.1	0.0316
25427	Cyp51	cytochrome P450, family 51	-1.7	10134.1	6271.0	0.0004
294945	RGD1562890	RGD1562890	-1.7	92.4	57.1	0.0000
246771	Slc25a25	solute carrier family 25 member 25	-1.7	23072.5	14258.9	0.0157
114554	Pi4k2a	phosphatidylinositol 4-kinase type 2 alpha	-1.7	163.0	100.5	0.0007
294251	Ncr3	natural cytotoxicity triggering receptor 3	-1.7	195.5	120.3	0.0000
192281	Oas1a	2'-5' oligoadenylate synthetase 1A	-1.7	565.7	347.2	0.0001
108352751	LOC108352751	S-antigen protein-like	-1.7	2403.6	1474.3	0.0143
315644	Bco2	beta-carotene oxygenase 2	-1.7	421.9	258.8	0.0009
170573	Slc38a4	solute carrier family 38, member 4	-1.7	8866.3	5432.8	0.0004
25081	Apoa1	apolipoprotein A1	-1.8	58117.5	35596.9	0.0002
684984	Cd300lg	Cd300 molecule-like family member G	-1.8	81.0	49.5	0.0152
312907	Slco5a1	solute carrier organic anion transporter family, member 5A1	-1.8	38.4	23.5	0.0001
81681	Lss	lanosterol synthase	-1.8	1292.9	788.2	0.0001
100360180	Pgd	phosphogluconate dehydrogenase	-1.8	813.7	494.8	0.0044
171400	Elov15	ELOVL fatty acid elongase 5	-1.8	203.9	123.5	0.0000
501145	Satb2	SATB homeobox 2	-1.8	57.4	34.8	0.0378
280670	Lzts3	leucine zipper tumor suppressor family member 3	-1.8	471.6	285.1	0.0000
500011	RGD1563091	similar to OEF2	-1.8	44.0	26.5	0.0006
24932	Cd4	Cd4 molecule	-1.8	1819.7	1097.4	0.0000
304077	Dopey2	dopey family member 2	-1.8	169.5	102.1	0.0000
365352	Mical2	microtubule associated monoxygenase, calponin and LIM domain containing 2	-1.8	42.6	25.6	0.0151
316729	Fam114a11	family with sequence similarity 114, member A1-like 1	-1.8	86.7	52.1	0.0003
29157	Ccng2	cyclin G2	-1.8	373.7	224.2	0.0007
301444	LOC301444	pseudogene for diazepam binding inhibitor 1	-1.8	1493.3	893.9	0.0000
288280	Ncam2	neural cell adhesion molecule 2	-1.8	68.3	40.8	0.0025
84575	Fads1	fatty acid desaturase 1	-1.8	4985.4	2979.8	0.0000
25599	Cd74	CD74 molecule	-1.8	2962.9	1770.4	0.0115
498728	Elov12	ELOVL fatty acid elongase 2	-1.8	2321.8	1381.0	0.0039
298579	Pla2g2d	phospholipase A2, group IID	-1.8	208.7	124.0	0.0020
84012	Slc1a6	solute carrier family 1 member 6	-1.8	85.1	50.5	0.0041

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Supplementary Table S8, continued

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84426	Wnt4	Wnt family member 4	-1.8	38.3	22.7	0.0380
266729	Dab1	DAB1, reelin adaptor protein	-1.8	163.0	96.5	0.0455
298077	RGD1305807	hypothetical LOC298077	-1.8	1579.4	934.7	0.0000
361049	RGD1563302	RGD1563302	-1.8	23.3	13.8	0.0337
294269	RT1-Da	RT1 class II, locus Da	-1.8	1508.2	891.0	0.0088
445271	Jph4	junctionophilin 4	-1.8	56.8	33.6	0.0257
115768	Zfp37	zinc finger protein 37	-1.8	73.4	43.4	0.0429
363143	Gnat1	G protein subunit alpha transducin 1	-1.8	180.1	106.4	0.0011
24482	Igf1	insulin-like growth factor 1	-1.8	2330.6	1375.7	0.0000
293166	Insc	INSC, spindle orientation adaptor protein	-1.8	438.2	258.0	0.0040
362319	Tmbim7	transmembrane BAX inhibitor motif containing 7	-1.8	38.3	22.6	0.0016
360406	Ptprf	protein tyrosine phosphatase, receptor type, F	-1.8	20956.3	12290.0	0.0037
25060	Hk3	hexokinase 3	-1.8	105.0	61.5	0.0032
304445	Glt1d1	glycosyltransferase 1 domain containing 1	-1.8	136.6	79.9	0.0015
361834	RGD1306739	similar to RIKEN cDNA 1700040L02	-1.8	37.7	22.0	0.0035
83512	Fads2	fatty acid desaturase 2	-1.8	2488.3	1444.6	0.0013
286954	Ugt2b1	UDP glucuronosyltransferase 2 family, polypeptide B1	-1.8	3105.0	1800.5	0.0304
294270	RT1-Db1	RT1 class II, locus Db1	-1.9	1283.4	741.0	0.0061
58975	Klrg1	killer cell lectin like receptor G1	-1.9	30.4	17.5	0.0055
114024	Acsl3	acyl-CoA synthetase long-chain family member 3	-1.9	372.2	214.4	0.0001
64554	Slc7a2	solute carrier family 7 member 2	-1.9	607.6	349.0	0.0143
24981	RT1-Db2	RT1 class II, locus Db2	-1.9	464.8	266.3	0.0076
78968	Srebf1	sterol regulatory element binding transcription factor 1	-1.9	1128.5	646.0	0.0159
25317	Fgf1	fibroblast growth factor 1	-1.9	112.6	64.4	0.0038
81677	Itpka	inositol-trisphosphate 3-kinase A	-1.9	397.8	227.2	0.0002
314349	Ston2	stonin 2	-1.9	44.6	25.4	0.0021
25698	Ass1	argininosuccinate synthase 1	-1.9	40916.8	23228.6	0.0005
24237	C6	complement C6	-1.9	3798.0	2148.4	0.0000
502776	Scrn1	secernin 1	-1.9	85.0	47.8	0.0372
60391	Nrxn1	neurexin 1	-1.9	51.0	28.7	0.0055
299131	Dhrs7l1	dehydrogenase/reductase (SDR family) member 7-like 1	-1.9	1955.2	1092.0	0.0265
309866	Crybg1	crystallin beta-gamma domain containing 1	-1.9	1748.8	970.7	0.0281
300158	Kif21a	kinesin family member 21A	-1.9	29.6	16.4	0.0000
114856	Dusp1	dual specificity phosphatase 1	-1.9	302.5	167.7	0.0247
289392	Plxna2	plexin A2	-1.9	2412.0	1335.2	0.0004
295649	Fign	fidgetin, microtubule severing factor	-1.9	371.0	205.3	0.0002
60582	Il1rn	interleukin 1 receptor antagonist	-1.9	1823.2	1008.1	0.0020
103694826	LOC103694826	P2Y purinoceptor 2-like	-1.9	172.9	95.5	0.0000
685940	Samd3	sterile alpha motif domain containing 3	-1.9	65.6	36.1	0.0003
29619	Btg2	BTG anti-proliferation factor 2	-1.9	475.1	261.5	0.0013
29597	P2ry2	purinergic receptor P2Y2	-2.0	1180.4	644.6	0.0000
306534	Unc5d	unc-5 netrin receptor D	-2.0	29.6	16.1	0.0009
25117	Hsd11b2	hydroxysteroid 11-beta dehydrogenase 2	-2.0	298.8	162.1	0.0006
25453	Gdnf	glial cell derived neurotrophic factor	-2.0	96.0	51.6	0.0000
316940	Spetex-2F	Spetex-2F protein	-2.0	47.1	25.3	0.0000
102556734	LOC102556734	igE-binding protein-like	-2.0	25.2	13.5	0.0068
312381	Ppm1k	protein phosphatase, Mg ²⁺ /Mn ²⁺ dependent, 1K	-2.0	138.4	74.0	0.0054
498834	Myo7b	myosin VIIb	-2.0	131.6	70.0	0.0009
300691	Nnmt	nicotinamide N-methyltransferase (NNMT)	-2.0	530.6	281.9	0.0135
498545	Tsc22d1	TSC22 domain family, member 1	-2.0	4514.2	2390.4	0.0015

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Supplementary Table S8, continued

NCBI Entrez Gene ID ^{a)}	Gene Symbol	Gene Name	Fold Change	CT diet group (raw intensity) ^{b)}	LP diet group (raw intensity)	P value
362790	Inf2	inverted formin, FH2 and WH2 domain containing	-2.0	694.8	367.6	0.0001
311676	Pmepa1	prostate transmembrane protein, androgen induced 1	-2.0	195.7	103.3	0.0002
24267	Comt	catechol-O-methyltransferase	-2.0	5385.9	2838.0	0.0002
300679	Mpzl2	myelin protein zero-like 2	-2.1	130.8	67.8	0.0457
498950	Marveld3	MARVEL domain containing 3	-2.1	158.2	81.9	0.0001
296787	Sema3c	semaphorin 3C	-2.1	74.8	38.6	0.0054
24401	Got1	glutamic-oxaloacetic transaminase 1	-2.1	5452.7	2803.3	0.0085
29298	Cyp2c7	cytochrome P450, family 2, subfamily c, polypeptide 7	-2.1	7306.0	3721.2	0.0001
362720	Rrm2	ribonucleotide reductase regulatory subunit M2	-2.1	191.4	97.4	0.0037
691517	Megf11	multiple EGF-like-domains 11	-2.1	92.1	46.8	0.0197
25598	Fabp2	fatty acid binding protein 2	-2.1	659.9	334.2	0.0064
309810	RGD1304770	similar to Na ⁺ dependent glucose transporter 1	-2.1	39.7	20.1	0.0000
24706	Rarb	retinoic acid receptor, beta	-2.1	38.1	19.2	0.0005
314640	Tjp3	tight junction protein 3	-2.1	4881.6	2456.0	0.0000
366275	Plk6	protein tyrosine kinase 6	-2.2	43.9	21.5	0.0139
310645	Pmvk	phosphomevalonate kinase	-2.2	2329.1	1137.4	0.0001
363974	Nckap5	NCK-associated protein 5	-2.2	97.8	47.3	0.0009
171352	Cyp3a9	cytochrome P450, family 3, subfamily a, polypeptide 9	-2.2	1907.6	912.3	0.0016
24249	S100g	S100 calcium binding protein G	-2.3	112.9	52.9	0.0009
192213	Rasgrf1	RAS protein-specific guanine nucleotide-releasing factor 1	-2.3	2464.0	1151.5	0.0002
360228	Wfdc21	WAP four-disulfide core domain 21	-2.3	26589.1	12407.0	0.0013
308739	Rgma	repulsive guidance molecule family member A	-2.3	214.6	99.9	0.0177
304537	Bicd1	BICD family like cargo adaptor 1	-2.3	75.4	34.8	0.0001
171385	Acmsd	aminocarboxymuconate semialdehyde decarboxylase	-2.3	337.4	155.6	0.0003
65984	Aacs	acetoacetyl-CoA synthetase	-2.3	92.4	42.6	0.0261
298079	Aldh1b1	aldehyde dehydrogenase 1 family, member B1	-2.3	4537.7	2079.2	0.0011
303336	Wsb1	WD repeat and SOCS box-containing 1	-2.4	2466.6	1118.6	0.0007
316052	Eomes	eomesodermin	-2.4	33.6	15.2	0.0002
362378	Fam13a	family with sequence similarity 13, member A	-2.4	653.0	295.7	0.0032
361749	Il33	interleukin 33	-2.4	1863.8	836.6	0.0000
311396	Atp8b4	ATPase phospholipid transporting 8B4 (putative)	-2.4	96.0	42.5	0.0001
29517	Sgk1	serum/glucocorticoid regulated kinase 1	-2.4	983.3	435.1	0.0051
293688	Tm7sf2	transmembrane 7 superfamily member 2	-2.4	2661.4	1165.4	0.0001
116719	Acacb	acetyl-CoA carboxylase beta	-2.5	72.8	31.7	0.0000
361206	Slc25a48	solute carrier family 25, member 48	-2.5	35.2	15.3	0.0002
315179	Efcab6	EF-hand calcium binding domain 6	-2.5	114.0	48.7	0.0000
681319	Ido2	indoleamine 2,3-dioxygenase 2	-2.5	995.9	420.9	0.0000
114097	Ltc4s	leukotriene C4 synthase	-2.6	217.4	90.2	0.0022
24913	Pla2g16	phospholipase A2, group XVI	-2.7	7969.8	3173.9	0.0000
171516	Akr1c3	aldo-keto reductase family 1, member C3	-2.8	1399.4	545.4	0.0000
100359918	Lnp1	leukemia NUP98 fusion partner 1	-2.8	40.8	15.5	0.0000
361008	Spetex-2H	Spetex-2H protein	-2.8	140.9	53.5	0.0000
306490	Mtmr7	myotubularin related protein 7	-2.8	366.0	137.8	0.0008
266998	Slc13a5	solute carrier family 13 member 5	-3.0	875.1	315.9	0.0001
29168	Ubd	ubiquitin D	-3.0	10397.5	3745.7	0.0050
362662	Rbp7	retinol binding protein 7	-3.0	243.9	87.8	0.0000
25650	Atp1b1	ATPase Na ⁺ /K ⁺ transporting subunit beta 1	-3.1	4422.6	1546.0	0.0003
305816	Ddhd1	DDHD domain containing 1	-3.2	78.1	26.1	0.0001
25304	Comp	cartilage oligomeric matrix protein	-3.4	94.9	30.3	0.0034
25011	Cyp2c12	cytochrome P450, family 2, subfamily c, polypeptide 12	-3.4	2837.2	892.0	0.0022

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Supplementary Table S8, continued

NCBI Entrez Gene ID ^{a)}	Gene Symbol	Gene Name	Fold Change	CT diet group (raw intensity) ^{b)}	LP diet group (raw intensity)	P value
24377	G6pd	glucose-6-phosphate dehydrogenase	-3.5	3157.9	963.0	0.0000
306748	Cxcl14	C-X-C motif chemokine ligand 14	-3.6	283.2	85.1	0.0002
108350694	LOC108350694	insulin-induced gene 1 protein pseudogene	-3.6	1333.2	392.1	0.0005
170566	Slc16a10	solute carrier family 16 member 10	-3.9	1443.7	401.0	0.0000
24813	Tat	tyrosine aminotransferase	-4.0	1745.4	473.3	0.0001
64194	Insig1	insulin induced gene 1	-4.1	13598.1	3518.4	0.0027
64313	Oat	ornithine aminotransferase	-4.4	21073.4	5079.9	0.0000
315962	Ky	kyphoscoliosis peptidase	-4.5	97.4	23.4	0.0014
84021	Irs3	insulin receptor substrate 3	-4.9	99.4	21.8	0.0000
680110	Rprm	reprimin, TP53 dependent G2 arrest mediator homolog	-4.9	430.5	94.1	0.0007
298062	Plppr1	phospholipid phosphatase related 1	-5.2	124.2	25.4	0.0079
300108	Pnpla5	patatin-like phospholipase domain containing 5	-5.7	6676.0	1262.6	0.0000
102557436	LOC102557436	cell surface A33 antigen-like	-7.3	442.8	64.7	0.0000
29464	Slc6a6	solute carrier family 6 member 6	-10.9	361.8	35.5	0.0000
362972	Pnpla3	patatin-like phospholipase domain containing 3	-15.8	929.4	62.9	0.0002
368066	Inmt	indolethylamine N-methyltransferase	-16.0	998.7	66.8	0.0000
25044	Sds	serine dehydratase	-35.7	2284.8	68.6	0.0000

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