Supplemental Table 3. *Gene Set Enrichment Analysis (GSEA) by diet.*

Metabolic Pathways	FF/L	FF/C	C/L
CHOLESTEROL_BIOSYNTHESIS	0.00791/-2.365	0.0281/-2.337	0.0465/-2.039
HSA00100_BIOSYNTHESIS_OF_STEROIDS	0.0181/-2.230	0.118/-1.992	0.0354/-2.195
CERAMIDEPATHWAY	0.0219/-2.165	0.0777/-2.078	0.0579/-1.989
HSA00071_FATTY_ACID_METABOLISM	0.873/-0.706	0.0012/-2.835	0.514/1.764
HSA04920_ADIPOCYTOKINE_SIGNALING_PATHWAY	0.00426/-2.526	0.544/-1.229	0.313/-1.340
HSA01040_POLYUNSATURATED_FATTY_ACID_BIOSYNTHESIS	0.0466/-1.963	0.038/-2.242	0.512/-1.088
HSA00190_OXIDATIVE_PHOSPHORYLATION	0.36/1.747	0.142/-1.931	0.033/2.395
AMINOACYL_TRNA_BIOSYNTHESIS	0.019/-2.197	0.627/-1.074	0.384/-1.221
KERATAN_SULFATE_BIOSYNTHESIS	0.00467/-2.492	0.571/-1.151	0.0337/-2.195
HSA00510_N_GLYCAN_BIOSYNTHESIS	0.0879/-1.769	0.855/1.007	0.0446/-2.055
N_GLYCAN_BIOSYNTHESIS	0.0251/-2.134	0.962/0.652	0.04/-2.106
HSA01030_GLYCAN_STRUCTURES_BIOSYNTHESIS_1	0.175/-1.554	0.921/0.858	0.0311/-2.164
HSA00230_PURINE_METABOLISM	0.139/-1.643	0.883/0.941	0.043/-2.090
HSA00310_LYSINE_DEGRADATION	0.283/-1.330	0.0474/-2.191	1/0.602
HSA00280_VALINE_LEUCINE_AND_ISOLEUCINE_DEGRAD	0.85/-0.742	0.0287/-2.316	0.655/1.773
HSA00650_BUTANOATE_METABOLISM	0.691/-0.890	0.0374/-2.351	0.95/1.304

Regulation of Metabolism			
PPARAPATHWAY	0.0108/-2.314	0.0122/-2.578	0.509/-1.085
ST_JNK_MAPK_PATHWAY	0.00169/-2.711	0.358/-1.573	0.218/-1.514
SIG_INSULIN_RECEPTOR_PATHWAY_IN_CARDIAC_MYOCYTES	0.00433/-2.578	0.491/-1.287	0.0828/-1.883
GHPATHWAY	0.00163/-3.087	0.257/-1.692	0.26/-1.438
PHOSPHATIDYLINOSITOL_SIGNALING_SYSTEM	0.00423/-2.541	0.363/-1.442	0.15/-1.657
PDGFPATHWAY	0.00662/-2.424	0.822/-0.844	0.0862/-1.855
CXCR4PATHWAY	0.00664/-2.416	0.433/-1.368	0.207/-1.531
TPOPATHWAY	0.0181/-2.221	0.435/-1.364	0.081/-1.898
SPPAPATHWAY	0.0772/-1.812	0.865/1.257	0.0117/-2.411
EDG1PATHWAY	0.00786/-2.360	0.425/-1.381	0.3/-1.364
HSA04910_INSULIN_SIGNALING_PATHWAY	0.0225/-2.165	0.543/-1.212	0.0865/-1.848
BIOPEPTIDESPATHWAY	0.00803/-2.384	0.746/-0.935	0.35/-1.269
SIG_PIP3_SIGNALING_IN_CARDIAC_MYOCTES	0.0306/-2.079	0.791/-0.893	0.0868/-1.860
MTA3PATHWAY	0.0362/-2.037	0.46/-1.331	0.186/-1.573
INSULINPATHWAY	0.0414/-2.003	0.994/0.544	0.0818/-1.892
PROSTAGLANDIN_SYNTHESIS_REGULATION	0.176/-1.551	0.697/-0.997	0.0342/-2.140
G_PROTEIN_SIGNALING	0.274/-1.351	0.88/-0.790	0.0257/-2.264
HSA03320_PPAR_SIGNALING_PATHWAY	0.628/-0.961	0.0387/-2.253	0.322/1.967
SIG_CD40PATHWAYMAP	0.039/-2.017	0.571/-1.149	0.471/-1.133
SA_PTEN_PATHWAY	0.277/-1.347	0.964/0.739	0.0435/-2.072
NUCLEAR_RECEPTORS	0.465/-1.113	0.0312/-2.344	0.982/1.229
AKTPATHWAY	0.0417/-2.004	0.622/-1.091	0.745/-0.871

Inflammation/Infection

HSA04670_LEUKOCYTE_TRANSENDOTHELIAL_MIGRAT	0.0308/-2.081	0.827/1.073	0/-2.886
IL6PATHWAY	0.0441/-1.981	0.867/0.971	0/-2.853
HSA05131_PATHOGENIC_ESCHERICHIA_COLI_INFECTION_EPEC	0.000655/-2.781	0.749/-0.936	0.00431/-2.558
HSA05130_PATHOGENIC_ESCHERICHIA_COLI_INFECTION_EHEC	0.00109/-2.822	0.736/-0.956	0.00421/-2.604
MAPKPATHWAY	0.000819/-2.799	0.14/-1.924	0.12/-1.735
INTRINSICPATHWAY	0.00451/-2.503	0.871/1.532	0.00773/-2.497
STAT3PATHWAY	0.00468/-2.526	0.353/-1.473	0.0395/-2.113
HSA05211_RENAL_CELL_CARCINOMA	0.00798/-2.381	0.696/-0.999	0.0124/-2.380
ST_T_CELL_SIGNAL_TRANSDUCTION	0.0274/-2.110	0.962/0.676	0.179/-1.584
IL2RBPATHWAY	0.0175/-2.218	0.797/-0.885	0.0126/-2.385
ST_TYPE_I_INTERFERON_PATHWAY	0.00884/-2.344	0.367/-1.528	0.0664/-1.952
HSA05212_PANCREATIC_CANCER	0.00733/-2.398	0.364/-1.485	0.0856/-1.847
HSA04115_P53_SIGNALING_PATHWAY	0.0658/-1.876	0.0122/-2.509	0.338/-1.300
HSA04610_COMPLEMENT_AND_COAGULATION_CASCADES	0.282/-1.329	0.247/2.018	0.00398/-2.566
IL4PATHWAY	0.00794/-2.372	0.538/-1.225	0.0824/-1.887
HSA05220_CHRONIC_MYELOID_LEUKEMIA	0.00659/-2.431	0.363/-1.565	0.178/-1.599
IL22BPPATHWAY	0.018/-2.219	0.556/-1.198	0.0857/-1.859
ST_INTERLEUKIN_4_PATHWAY	0.0486/-1.955	0.961/0.753	0.0422/-2.066
IL3PATHWAY	0.029/-2.094	0.905/-0.749	0.0856/-1.865
ST_B_CELL_ANTIGEN_RECEPTOR	0.0706/-1.841	0.979/0.762	0.0336/-2.176
BLOOD_CLOTTING_CASCADE	0.0657/-1.865	0.859/1.133	0.0427/-2.086
CLASSICPATHWAY	0.926/1.444	0.0796/2.220	0.0349/-2.179
RELAPATHWAY	0.0188/-2.195	0.376/-1.431	0.417/-1.186
ST_P38_MAPK_PATHWAY	0.0374/-2.028	0.46/-1.336	0.306/-1.355
SIG_IL4RECEPTOR_IN_B_LYPHOCYTES	0.135/-1.650	0.865/-0.804	0.0472/-2.042
BREAST_CANCER_ESTROGEN_SIGNALING	0.194/-1.510	0.963/0.719	0.0323/-2.155
IL2PATHWAY	0.261/-1.380	0.845/1.232	0.0428/-2.070
IL10PATHWAY	0.678/-0.900	0.706/1.430	0.0298/-2.232
ST_T_CELL_SIGNAL_TRANSDUCTION	0.0274/-2.110	0.962/0.676	0.179/-1.584

Cell Cycle/Cell Division

DNA_REPLICATION_REACTOME	0.0331/-2.059	0.933/0.896	0.0312/-2.174
HSA04110_CELL_CYCLE	0.00547/-2.454	0.263/-1.677	0.0726/-1.934
CELL_CYCLE_KEGG	0.013/-2.284	0.541/-1.228	0.125/-1.723
HSA03030_DNA_POLYMERASE	0.0652/-1.876	0.746/-0.941	0.0423/-2.082
APOPTOSIS	0.0284/-2.094	0.553/-1.186	0.142/-1.689

Cell Structure/Adhesion

RIBOSOMAL_PROTEINS	0/3.008	0/3.341	0.00432/-2.578
HSA03010_RIBOSOME	0/3.211	0/3.742	0.00435/-2.625
MRNA_PROCESSING_REACTOME	0.0183/-2.207	0.815/1.199	0/-2.936

HSA04510_FOCAL_ADHESION	0.000813/-2.919	0.695/-1.005	0.0323/-2.175
HSA04530_TIGHT_JUNCTION	0.00471/-2.590	0.732/-0.956	0.00544/-2.629
HSA04514_CELL_ADHESION_MOLECULES	0.0246/-2.140	0.691/1.502	0.0124/-2.417
KERATINOCYTEPATHWAY	0.0184/-2.223	0.361/-1.524	0.0575/-1.985
ST_GA13_PATHWAY	0.0213/-2.165	0.925/0.844	0.0312/-2.219
SMOOTH_MUSCLE_CONTRACTION	0.192/-1.517	0.604/1.772	0.00765/-2.486
ECMPATHWAY	0.034/-2.051	0.607/-1.106	0.0527/-2.014
INTEGRIN_MEDIATED_CELL_ADHESION_KEGG	0.0176/-2.240	0.355/-1.468	0.185/-1.573
ST_INTEGRIN_SIGNALING_PATHWAY	0.0253/-2.129	0.595/-1.118	0.144/-1.676
HSA04512_ECM_RECEPTOR_INTERACTION	0.0315/-2.070	0.964/0.742	0.313/-1.338

Statistically significantly enriched pathways and other gene sets in dietary comparisons as identified by Gene set enrichment analysis. Comparisons include Fish fungal versus Lard, Fish fungal versus Canola, and Canola versus Lard. The numbers indicate FDR *q*-value for the pathway (gene set)/normalized enrichment score (NES).