

Pathway analysis for Gene Ontology terms changed by diet (p<0.01) in gastrocnemius

Gene Ontology (GO) Term	GO ID	# of Genes	SM_pvalue	SS_pvalue	YS_pvalue	SM_zscore	SS_zscore	YS_zscore	Treatment
chromosome	GO:0005694	259	0.0007	0.0741	0.0020	-3.39	-1.79	-3.10	SM
intracellular transport	GO:0046907	422	0.0000	0.0454	0.0028	-4.63	-2.00	-2.98	SM
cellular localization	GO:0051641	562	0.0000	0.0198	0.0034	-4.43	-2.33	-2.93	SM
establishment of localization in cell	GO:0051649	532	0.0000	0.0258	0.0034	-4.24	-2.23	-2.92	SM
nuclear envelope	GO:0005635	107	0.0005	0.0059	0.0112	-3.50	-2.75	-2.54	SM
organelle organization and biogenesis	GO:0006996	812	0.0000	0.0383	0.0249	-4.56	-2.07	-2.24	SM
M phase of mitotic cell cycle	GO:0000087	148	0.0000	0.0041	0.0350	-4.72	-2.87	-2.11	SM
mitosis	GO:0007067	148	0.0000	0.0041	0.0350	-4.72	-2.87	-2.11	SM
mitotic cell cycle	GO:0000278	184	0.0000	0.0100	0.0451	-5.47	-2.58	-2.00	SM
M phase	GO:0000279	220	0.0000	0.0162	0.0505	-4.43	-2.40	-1.96	SM
vacuole	GO:0005773	179	0.0000	0.7099	0.0519	-4.08	-0.37	-1.94	SM
DNA polymerase activity	GO:0034061	29	0.0002	0.0656	0.0667	-3.68	-1.84	-1.83	SM
cell cycle phase	GO:0022403	251	0.0000	0.0303	0.0683	-4.90	-2.17	-1.82	SM
acute inflammatory response	GO:0002526	58	0.0002	0.4575	0.0709	3.79	0.74	-1.81	SM
DNA-directed DNA polymerase activity	GO:0003887	27	0.0002	0.1381	0.0764	-3.74	-1.48	-1.77	SM
cell cycle	GO:0007049	525	0.0000	0.8005	0.0974	-4.86	-0.25	-1.66	SM
lytic vacuole	GO:0000323	165	0.0007	0.9228	0.1213	-3.41	0.10	-1.55	SM
lysosome	GO:0005764	165	0.0007	0.9228	0.1213	-3.41	0.10	-1.55	SM
microtubule	GO:0005874	179	0.0009	0.5902	0.1754	-3.33	-0.54	-1.35	SM
microtubule cytoskeleton	GO:0015630	259	0.0000	0.2273	0.1768	-4.58	-1.21	-1.35	SM
microtubule-based process	GO:0007017	141	0.0001	0.1430	0.2705	-4.02	-1.46	-1.10	SM
cell cycle process	GO:0022402	301	0.0000	0.2680	0.3160	-4.42	-1.11	-1.00	SM
glutamine metabolic process	GO:0006541	15	0.0001	0.0105	0.5535	-3.94	-2.56	-0.59	SM
negative regulation of response to stimulus	GO:0048585	37	0.0007	0.2267	0.9681	3.41	1.21	-0.04	SM
negative regulation of defense response	GO:0031348	16	0.0000	0.0108	0.5032	4.56	2.55	0.67	SM
regulation of inflammatory response to antigenic stimulus	GO:0002861	11	0.0003	0.0019	0.4691	3.62	3.11	0.72	SM
substrate-specific transporter activity	GO:0022892	745	0.0008	0.3865	0.4425	3.37	0.87	0.77	SM
interspecies interaction between organisms	GO:0044419	15	0.0000	0.0624	0.2225	4.27	1.86	1.22	SM
response to gamma radiation	GO:0010332	15	0.0005	0.0501	0.2111	3.46	1.96	1.25	SM
hydrogen peroxide metabolic process	GO:0042743	16	0.0001	0.0295	0.1772	3.95	2.18	1.35	SM
negative regulation of inflammatory response	GO:0050728	13	0.0000	0.0026	0.1689	4.70	3.02	1.38	SM
regeneration	GO:0031099	13	0.0001	0.0177	0.1602	4.00	2.37	1.40	SM
tissue regeneration	GO:0042246	13	0.0001	0.0177	0.1602	4.00	2.37	1.40	SM
negative regulation of response to external stimulus	GO:0032102	23	0.0000	0.0108	0.1541	5.01	2.55	1.43	SM
glycerol ether metabolic process	GO:0006662	29	0.0001	0.0067	0.0991	3.89	2.71	1.65	SM
cell redox homeostasis	GO:0045454	45	0.0000	0.0290	0.0915	4.45	2.18	1.69	SM
neutral lipid metabolic process	GO:0006638	27	0.0000	0.0011	0.0644	4.12	3.26	1.85	SM
acylglycerol metabolic process	GO:0006639	27	0.0000	0.0011	0.0644	4.12	3.26	1.85	SM
glycerolipid metabolic process	GO:0046486	28	0.0001	0.0018	0.0561	3.92	3.13	1.91	SM
circulatory system process	GO:0003013	76	0.0002	0.0030	0.0551	3.72	2.97	1.92	SM
blood circulation	GO:0008015	76	0.0002	0.0030	0.0551	3.72	2.97	1.92	SM
cytochrome-c oxidase activity	GO:0004129	16	0.0003	0.0390	0.0448	3.59	2.06	2.01	SM
heme-copper terminal oxidase activity	GO:0015002	16	0.0003	0.0390	0.0448	3.59	2.06	2.01	SM
oxidoreductase activity, acting on heme group of donors	GO:0016675	16	0.0003	0.0390	0.0448	3.59	2.06	2.01	SM
oxidoreductase activity, acting on heme group of donors, oxygen as acceptor	GO:0016676	16	0.0003	0.0390	0.0448	3.59	2.06	2.01	SM
vasodilation	GO:0042311	15	0.0000	0.0409	0.0320	4.08	2.04	2.14	SM
vascular process in circulatory system	GO:0003018	31	0.0007	0.0552	0.0241	3.41	1.92	2.26	SM
regulation of tube size	GO:0035150	31	0.0007	0.0552	0.0241	3.41	1.92	2.26	SM
regulation of blood vessel size	GO:0050880	31	0.0007	0.0552	0.0241	3.41	1.92	2.26	SM
temperature homeostasis	GO:0001659	13	0.0000	0.0062	0.0206	4.42	2.74	2.32	SM
regulation of neuron apoptosis	GO:0043523	47	0.0001	0.0190	0.0150	3.84	2.34	2.43	SM
ubiquitin-specific protease activity	GO:0004843	55	0.0765	0.0006	0.0012	-1.77	-3.44	-3.23	SS
ubiquitin thioesterase activity	GO:0004221	54	0.0560	0.0005	0.0014	-1.91	-3.48	-3.20	SS
RNA splicing	GO:0008380	168	0.0053	0.0000	0.0045	-2.79	-4.08	-2.84	SS
ATPase activity, coupled	GO:0042623	172	0.0096	0.0006	0.0045	-2.59	-3.44	-2.84	SS
nucleolus	GO:0005730	104	0.0345	0.0009	0.0046	-2.11	-3.33	-2.84	SS
small conjugating protein-specific protease activity	GO:0019783	56	0.1091	0.0010	0.0050	-1.60	-3.30	-2.81	SS
aminoacyl-tRNA ligase activity	GO:0004812	44	0.0017	0.0000	0.0073	-3.13	-4.29	-2.68	SS
ligase activity, forming carbon-oxygen bonds	GO:0016875	44	0.0017	0.0000	0.0073	-3.13	-4.29	-2.68	SS
ligase activity, forming aminoacyl-tRNA and related compounds	GO:0016876	44	0.0017	0.0000	0.0073	-3.13	-4.29	-2.68	SS
exosome (RNase complex)	GO:0001078	12	0.7919	0.0002	0.0140	-0.26	-3.72	-2.46	SS
tRNA aminoacylation for protein translation	GO:0006418	41	0.0029	0.0000	0.0140	-2.98	-4.15	-2.46	SS
amino acid activation	GO:0043038	41	0.0029	0.0000	0.0140	-2.98	-4.15	-2.46	SS
tRNA aminoacylation	GO:0043039	41	0.0029	0.0000	0.0140	-2.98	-4.15	-2.46	SS
cis-Golgi network	GO:0005801	10	0.1367	0.0006	0.0217	-1.49	-3.44	-2.30	SS
cholesterol biosynthetic process	GO:0006695	20	0.2444	0.0003	0.0344	-1.16	-3.63	-2.12	SS
ATP-dependent helicase activity	GO:0008026	65	0.0024	0.0002	0.0395	-3.03	-3.66	-2.06	SS
sterol biosynthetic process	GO:0016126	26	0.1059	0.0001	0.0475	-1.62	-3.89	-1.98	SS
RNA processing	GO:0006396	333	0.0019	0.0001	0.0743	-3.10	-3.92	-1.78	SS
RNA metabolic process	GO:0016070	483	0.0017	0.0001	0.0808	-3.14	-3.88	-1.75	SS
structural constituent of ribosome	GO:0003735	92	0.0013	0.0000	0.1192	-3.21	-4.40	-1.56	SS
amino acid metabolic process	GO:0006520	161	0.0633	0.0000	0.1212	-1.86	-4.51	-1.55	SS
ncRNA metabolic process	GO:0034680	147	0.0089	0.0000	0.1234	-2.62	-4.16	-1.54	SS
ligase activity	GO:0016874	307	0.0512	0.0005	0.1498	-1.95	-3.46	-1.44	SS
amino acid and derivative metabolic process	GO:0006519	216	0.1218	0.0002	0.1607	-1.55	-3.78	-1.40	SS
amine metabolic process	GO:0009308	237	0.0620	0.0009	0.1638	-1.87	-3.32	-1.39	SS
organic acid metabolic process	GO:0006082	378	0.3211	0.0000	0.1716	-0.99	-4.49	-1.37	SS
carboxylic acid metabolic process	GO:0019752	378	0.3211	0.0000	0.1716	-0.99	-4.49	-1.37	SS
nitrogen compound metabolic process	GO:0006807	253	0.0735	0.0006	0.1780	-1.79	-3.43	-1.35	SS
ribosome biogenesis	GO:0042254	84	0.0184	0.0007	0.2788	-2.36	-3.38	-1.08	SS
cellular biosynthetic process	GO:0044249	801	0.0064	0.0000	0.5413	-2.73	-4.26	-0.61	SS
protein tyrosine kinase activity	GO:0004713	143	0.2685	0.0008	0.7191	-1.11	3.35	-0.36	SS
cell migration	GO:0016477	248	0.0631	0.0007	0.0168	1.86	3.37	2.39	SS
mitochondrion	GO:0005739	836	0.6990	0.0000	0.0047	0.39	-4.23	2.83	SS
anatomical structure morphogenesis	GO:0009653	952	0.3989	0.0001	0.0027	0.84	3.96	3.00	SS
sphingolipid catabolic process	GO:0030149	11	0.0068	0.0056	0.0000	-2.71	-2.77	-4.98	YS
membrane lipid catabolic process	GO:0046466	16	0.0742	0.0486	0.0001	-1.79	-1.97	-3.85	YS
clathrin coat	GO:0030118	30	0.1455	0.0215	0.0003	-1.46	-2.30	-3.58	YS
immune response	GO:0006955	300	0.6668	0.5829	0.0004	0.43	-0.55	-3.54	YS
oxidoreductase activity, acting on the CH-NH group of donors, NAD or NADP as acceptor	GO:0016646	15	0.1977	0.0019	0.0005	-1.29	-3.11	-3.49	YS
I-kappaB kinase/NF-kappaB cascade	GO:0007249	23	0.0213	0.2171	0.0006	-2.30	-1.23	-3.42	YS
protein targeting to membrane	GO:0006612	14	0.2693	0.0275	0.0008	-1.10	-2.21	-3.36	YS
protein polyubiquitination	GO:0000209	10	0.0149	0.0091	0.0008	-2.43	-2.61	-3.35	YS
coated pit	GO:0005905	29	0.0532	0.0399	0.0008	-1.93	-2.05	-3.34	YS
oxidoreductase activity, acting on NADH or NADPH	GO:0016651	37	0.0342	0.2429	0.0008	2.12	1.17	3.36	YS
steroid dehydrogenase activity	GO:0016229	24	0.3661	0.3645	0.0001	0.90	0.91	3.80	YS
mitochondrial part	GO:0044429	290	0.0022	0.9322	0.0000	3.06	0.09	4.72	YS
nucleoside-triphosphatase activity	GO:0017111	371	0.0000	0.0000	0.0012	-4.07	-4.37	-3.24	SM & SS
pyrophosphatase activity	GO:0016462	391	0.0000	0.0000	0.0021	-4.15	-4.51	-3.08	SM & SS
hydrolase activity, acting on acid anhydrides	GO:0016817	395	0.0000	0.0000	0.0028	-4.13	-4.51	-2.99	SM & SS
hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides	GO:0016818	394	0.0000	0.0000	0.0033	-4.11	-4.49	-2.94	SM & SS
cellular macromolecule biosynthetic process	GO:0034645	351	0.0008	0.0000	0.0038	-3.36	-4.75	-2.89	SM & SS
nuclear part	GO:0044428	743	0.0000	0.0000	0.0057	-5.26	-4.24	-2.77	SM & SS
translation	GO:0006412	216	0.0000	0.0000	0.0114	-4.19	-5.33	-2.53	SM & SS

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Gene Ontology (GO) Term	GO ID	# of Genes	SM_pvalue	SS_pvalue	YS_pvalue	SM_zscore	SS_zscore	YS_zscore	Treatment
DNA replication	GO:0006260	123	0.0000	0.0002	0.0118	-4.54	-3.79	-2.52	SM & SS
nucleotidyltransferase activity	GO:0016779	98	0.0009	0.0009	0.0259	-3.31	-3.31	-2.23	SM & SS
xenobiotic metabolic process	GO:0006805	10	0.0000	0.0001	0.0322	-4.76	-3.81	-2.14	SM & SS
ribosome	GO:0005840	140	0.0008	0.0000	0.0983	-3.34	-4.68	-1.65	SM & SS
heart process	GO:0003015	11	0.0000	0.0000	0.0403	5.29	5.47	2.05	SM & SS
heart contraction	GO:0060047	11	0.0000	0.0000	0.0403	5.29	5.47	2.05	SM & SS
hydrogen peroxide catabolic process	GO:0042744	10	0.0000	0.0009	0.0234	4.66	3.33	2.27	SM & SS
triacylglycerol metabolic process	GO:0006641	23	0.0000	0.0005	0.0158	4.68	3.50	2.41	SM & SS
mitochondrial membrane part	GO:0044455	59	0.0000	0.3725	0.0002	4.44	0.89	3.79	SM & YS
mitochondrial respiratory chain	GO:0005746	49	0.0000	0.2817	0.0001	4.29	1.08	4.03	SM & YS
organelle inner membrane	GO:0019866	223	0.0002	0.7396	0.0000	3.72	0.33	4.27	SM & YS
mitochondrial envelope	GO:0005740	252	0.0002	0.5584	0.0000	3.77	0.59	4.73	SM & YS
mitochondrial inner membrane	GO:0005743	212	0.0000	0.5130	0.0000	4.24	0.65	4.95	SM & YS
mitochondrial membrane	GO:0031966	233	0.0001	0.5809	0.0000	3.87	0.55	4.95	SM & YS
proteasome core complex	GO:0005839	19	0.0095	0.0000	0.0000	-2.59	-4.91	-4.24	SS & YS
threonine-type endopeptidase activity	GO:0004298	20	0.0310	0.0000	0.0001	-2.16	-4.65	-3.89	SS & YS
threonine-type peptidase activity	GO:0070003	20	0.0310	0.0000	0.0001	-2.16	-4.65	-3.89	SS & YS
translational elongation	GO:0006414	13	0.0845	0.0008	0.0001	-1.73	-3.34	-3.85	SS & YS
RNA binding	GO:0003723	491	0.0144	0.0000	0.0003	-2.45	-4.62	-3.58	SS & YS
ATPase activity	GO:0016887	207	0.0025	0.0002	0.0010	-3.02	-3.71	-3.29	SS & YS
sulfuric ester hydrolase activity	GO:0008484	11	0.1350	0.0001	0.0003	-1.49	3.81	3.59	SS & YS
skeletal muscle development	GO:0007519	86	0.0029	0.0002	0.0003	2.98	3.70	3.64	SS & YS
glutathione transferase activity	GO:0004364	22	0.0000	0.0000	0.0000	-8.21	-7.72	-6.17	ALL
transferase activity, transferring alkyl or aryl (other than methyl) groups	GO:0016765	45	0.0000	0.0000	0.0001	-6.14	-5.64	-3.88	ALL
cytosol	GO:0005829	293	0.0008	0.0000	0.0002	-3.35	-4.52	-3.69	ALL
proteasome complex	GO:0005052	30	0.0001	0.0000	0.0003	-3.80	-4.08	-3.64	ALL
ribonucleoprotein complex	GO:0030529	339	0.0000	0.0000	0.0006	-4.73	-5.74	-3.44	ALL
DNA metabolic process	GO:0006259	310	0.0000	0.0000	0.0010	-4.81	-4.27	-3.29	ALL
myotube differentiation	GO:0014902	10	0.0001	0.0001	0.0000	4.02	4.05	4.75	ALL
selenium binding	GO:0008430	29	0.0000	0.0000	0.0000	15.13	8.71	9.09	ALL