

Table S1. GO analysis of *atg5*^{-/-} MEFs in DMEM with glucose

GO: <i>atg5</i> ^{-/-} MEF_Glucose UP								
GO_ID	Description	FisherPValue	FisherFDR	FisherBonf	nGenesIn Category	nAllGenesIn Category	logOR	direction
GO:0062023	collagen-containing_extracellular_matrix	1.0675E-07	3.49074E-05	3.49074E-05	19	97	1.670248667	UP
GO:0005576	extracellular_region	4.89106E-07	7.99689E-05	0.000159938	27	196	1.25503742	UP
GO:0005615	extracellular_space	1.31253E-06	0.000143066	0.000429199	29	231	1.148452728	UP
GO:0005886	plasma_membrane	6.42018E-05	0.005248495	0.020993979	73	999	0.581216686	UP
GO:0045171	intercellular_bridge	0.000419755	0.027451976	0.137259878	7	30	1.909726752	UP
GO:0031012	extracellular_matrix	0.000513372	0.027978754	0.167872526	9	50	1.577423538	UP
GO:0005783	endoplasmic_reticulum	0.003121578	0.145822271	1	43	592	0.524932548	UP
GO:0045177	apical_part_of_cell	0.007270943	0.297199802	1	7	48	1.346789315	UP
GO:0005797	Golgi_medial_cisterna	0.010130084	0.368059717	1	3	10	2.303320117	UP
GO:0031514	motile_cilium	0.0112593	0.368179109	1	4	19	1.835529145	UP
GO:0016021	integral_component_of_membrane	0.012632614	0.372234217	1	52	805	0.392619939	UP
GO:0048471	perinuclear_region_of_cytoplasm	0.013659971	0.372234217	1	24	312	0.576269283	UP
GO:0005801	cis-Golgi_network	0.022143914	0.557004616	1	4	23	1.611649487	UP
GO:0016324	apical_plasma_membrane	0.025720583	0.60075934	1	9	89	0.913409019	UP
GO:0043204	perikaryon	0.030105433	0.643168149	1	5	37	1.294496524	UP
GO:0005739	mitochondrion	0.033430624	0.643168149	1	57	946	0.310242888	UP
GO:0071944	cell_periphery	0.033436876	0.643168149	1	4	26	1.47133511	UP
GO:0043025	neuronal_cell_body	0.037207099	0.675928966	1	16	206	0.592188256	UP
GO:0014704	intercalated_disc	0.042524732	0.698242632	1	4	28	1.387585041	UP
GO:0098793	presynapse	0.044396675	0.698242632	1	5	41	1.179347757	UP
GO:0043195	terminal_bouton	0.04484127	0.698242632	1	3	17	1.673424811	UP
GO:0005911	cell-cell_junction	0.049537776	0.736311486	1	8	85	0.842594881	UP
GO: <i>atg5</i> ^{-/-} MEF_Glucose DOWN								
GO_ID	Description	FisherPValue	FisherFDR	FisherBonf	nGenesIn Category	nAllGenesIn Category	logOR	direction
GO:0005886	plasma_membrane	8.09217E-06	0.001419341	0.002646139	56	999	0.766489403	DOWN
GO:0005901	caveola	8.68099E-06	0.001419341	0.002838682	8	34	2.34046491	DOWN
GO:0031616	spindle_pole_centrosome	0.00080326	0.087555344	0.262666032	4	14	2.631169518	DOWN
GO:0005911	cell-cell_junction	0.001508456	0.101638477	0.493265114	9	85	1.394415077	DOWN
GO:0030054	cell_junction	0.001554105	0.101638477	0.508192386	17	238	0.942958979	DOWN
GO:0016324	apical_plasma_membrane	0.002085918	0.113682548	0.682095288	9	89	1.343039145	DOWN
GO:0030175	filopodium	0.002797828	0.13069855	0.914889853	5	31	1.918192684	DOWN
GO:0005736	RNA_polymerase_I_complex	0.003318769	0.135654677	1	3	10	2.721512293	DOWN
GO:0045177	apical_part_of_cell	0.004059195	0.145716841	1	6	48	1.609645764	DOWN
GO:0044853	plasma_membrane_raft	0.004456173	0.145716841	1	3	11	2.60354854	DOWN
GO:0043005	neuron_projection	0.005504257	0.158112384	1	13	182	0.944719973	DOWN
GO:0030659	cytoplasmic_vesicle_membrane	0.005802289	0.158112384	1	3	12	2.498007274	DOWN
GO:0001726	ruffle	0.014014163	0.344043192	1	5	45	1.497915725	DOWN
GO:0005912	adherens_junction	0.014729678	0.344043192	1	4	30	1.730330947	DOWN
GO:0030424	axon	0.01865429	0.406663518	1	10	146	0.908208103	DOWN
GO:0005903	brush_border	0.020417677	0.411267942	1	4	33	1.624426312	DOWN
GO:0005913	cell-cell_adherens_junction	0.021380902	0.411267942	1	5	50	1.381937056	DOWN
GO:0005882	intermediate_filament	0.02838371	0.515637396	1	3	21	1.854525165	DOWN
GO:0005615	extracellular_space	0.034290542	0.577958221	1	13	231	0.682283456	DOWN
GO:0009897	external_side_of_plasma_membrane	0.035349127	0.577958221	1	5	57	1.239012073	DOWN
GO:0005925	focal_adhesion	0.037590791	0.585342314	1	7	98	0.979240302	DOWN
GO:0042995	cell_projection	0.045439807	0.67017894	1	16	315	0.563990538	DOWN

Table of gene list enrichment results for Gene Ontology: Cellular Component (GO CC) categories.

Table S2. GO analysis of *ulk1*^{-/-} MEFs in DMEM with glucose

GO: <i>ulk1</i> ^{-/-} MEF_Glucose UP								
GO_ID	Description	FisherPValue	FisherFDR	FisherBonf	nGenesIn Category	nAllGenesIn Category	logOR	direction
GO:0016021	integral_component_of_membrane	2.75633E-12	9.01319E-10	9.01319E-10	135	805	0.78877235	UP
GO:0005886	plasma_membrane	2.69847E-11	4.41199E-09	8.82398E-09	155	999	0.705418223	UP
GO:0005887	integral_component_of_plasma_membrane	7.55312E-06	0.00082329	0.00246987	27	115	1.118626781	UP
GO:0098993	anchored_component_of_synaptic_vesicle_membrane	7.37329E-05	0.006027668	0.024110672	7	13	2.38705004	UP
GO:0005783	endoplasmic_reticulum	0.000248778	0.016270112	0.081350561	82	592	0.482060174	UP
GO:0009986	cell_surface	0.001134589	0.061835076	0.371010458	28	160	0.745233811	UP
GO:0016529	sarcoplasmic_reticulum	0.002229876	0.104167082	0.729169573	8	26	1.505823783	UP
GO:0045335	phagocytic_vesicle	0.002807505	0.111713964	0.918053992	11	45	1.185040405	UP
GO:0048471	perinuclear_region_of_cytoplasm	0.003074696	0.111713964	1	45	312	0.511921521	UP
GO:0016324	apical_plasma_membrane	0.004121404	0.134769922	1	17	89	0.859170718	UP
GO:0045177	apical_part_of_cell	0.004798733	0.142165361	1	11	48	1.102218706	UP
GO:0005741	mitochondrial_outer_membrane	0.005217077	0.142165361	1	17	91	0.831750119	UP
GO:0005635	nuclear_envelope	0.008121633	0.20429031	1	17	95	0.779006066	UP
GO:0097038	perinuclear_endoplasmic_reticulum	0.010980559	0.256474481	1	4	10	1.911536755	UP
GO:0005901	caveola	0.01307405	0.263196667	1	8	34	1.152873704	UP
GO:0014704	intercalated_disc	0.014238632	0.263196667	1	7	28	1.239012165	UP
GO:0036064	ciliary_basal_body	0.015568068	0.263196667	1	8	35	1.116311866	UP
GO:0005923	bicellular_tight_junction	0.016087407	0.263196667	1	9	42	1.028197135	UP
GO:0005794	Golgi_apparatus	0.01681067	0.263196667	1	61	489	0.338793732	UP
GO:0031594	neuromuscular_junction	0.01726242	0.263196667	1	7	29	1.194366397	UP
GO:0009897	external_side_of_plasma_membrane	0.017825778	0.263196667	1	11	57	0.887904415	UP
GO:0030054	cell_junction	0.018354216	0.263196667	1	33	238	0.461817787	UP
GO:0001669	acrosomal_vesicle	0.018512304	0.263196667	1	6	23	1.305087186	UP
GO:0005789	endoplasmic_reticulum_membrane	0.022089364	0.289978443	1	20	130	0.59242206	UP
GO:0090543	Flemming_body	0.022169606	0.289978443	1	4	12	1.659835405	UP
GO:0005768	endosome	0.027373445	0.344273706	1	37	281	0.399551968	UP
GO:0031225	anchored_component_of_membrane	0.029787333	0.359757359	1	5	19	1.332002854	UP
GO:0005615	extracellular_space	0.032798058	0.359757359	1	31	231	0.422908746	UP
GO:0030141	secretory_granule	0.033866105	0.359757359	1	7	33	1.033247349	UP
GO:0005777	peroxisome	0.036004682	0.359757359	1	12	71	0.723069844	UP
GO:0043231	intracellular_membrane-bounded_organelle	0.037918406	0.359757359	1	44	352	0.337222998	UP
GO:0043235	receptor_complex	0.038087304	0.359757359	1	8	41	0.920989897	UP
GO:0031982	vesicle	0.038096219	0.359757359	1	10	56	0.79903947	UP
GO:0031410	cytoplasmic_vesicle	0.03830761	0.359757359	1	35	270	0.380843252	UP
GO:0005764	lysosome	0.039450605	0.359757359	1	23	164	0.479195029	UP
GO:0005770	late_endosome	0.039606315	0.359757359	1	12	72	0.706345096	UP
GO:0008021	synaptic_vesicle	0.042409079	0.374804561	1	10	57	0.77779111	UP
GO:0005604	basement_membrane	0.04517878	0.388775292	1	7	35	0.96139996	UP
GO: <i>ulk1</i> ^{-/-} MEF_Glucose DOWN								
GO_ID	Description	FisherPValue	FisherFDR	FisherBonf	nGenesIn Category	nAllGenesIn Category	logOR	direction
GO:0062023	collagen-containing_extracellular_matrix	4.65151E-25	1.52104E-22	1.52104E-22	41	97	2.52689158	DOWN
GO:0005576	extracellular_region	4.78186E-23	7.81833E-21	1.56367E-20	55	196	1.931438803	DOWN
GO:0005615	extracellular_space	2.12417E-22	2.31534E-20	6.94603E-20	59	231	1.810491516	DOWN
GO:0031012	extracellular_matrix	4.4506E-19	3.63837E-17	1.45535E-16	26	50	2.868425371	DOWN
GO:0001725	stress_fiber	5.50799E-11	3.60223E-09	1.80111E-08	20	57	2.177839449	DOWN
GO:0005581	collagen_trimer	2.03782E-09	1.11061E-07	6.66366E-07	11	19	3.03741687	DOWN
GO:0030018	Z_disc	7.62373E-08	3.56137E-06	2.49296E-05	16	54	1.928462507	DOWN
GO:0005911	cell-cell_junction	6.29401E-07	2.57268E-05	0.000205814	19	85	1.553502657	DOWN
GO:0015629	actin_cytoskeleton	1.91404E-06	6.95434E-05	0.00062589	22	117	1.337124089	DOWN
GO:0009986	cell_surface	3.99071E-06	0.000130496	0.001304962	26	160	1.161243504	DOWN

GO:0005604	basement_membrane	4.5778E-06	0.000136086	0.001496941	11	35	2.012778316	DOWN
GO:0005913	cell-cell_adherens_junction	6.58917E-06	0.000179555	0.002154659	13	50	1.751632856	DOWN
GO:0005886	plasma_membrane	1.8277E-05	0.000454001	0.005976569	92	999	0.557035104	DOWN
GO:0030054	cell_junction	1.94374E-05	0.000454001	0.006356014	32	238	0.939091196	DOWN
GO:0005925	focal_adhesion	8.38497E-05	0.001827923	0.027418841	17	98	1.237332123	DOWN
GO:0005884	actin_filament	9.8323E-05	0.002009476	0.032151619	12	55	1.526867869	DOWN
GO:0043025	neuronal_cell_body	0.000137535	0.002645528	0.044973982	27	206	0.904354332	DOWN
GO:0016459	myosin_complex	0.000174789	0.003175327	0.057155889	7	21	2.108412611	DOWN
GO:0014704	intercalated_disc	0.000201532	0.003468466	0.065900863	8	28	1.891488966	DOWN
GO:0009897	external_side_of_plasma_membrane	0.000592951	0.009694756	0.193895127	11	57	1.377384367	DOWN
GO:0005903	brush_border	0.000686012	0.010682194	0.224326075	8	33	1.676980199	DOWN
GO:0045121	membrane_raft	0.000855772	0.012719886	0.279837484	16	108	1.049249332	DOWN
GO:0030426	growth_cone	0.002095711	0.029795545	0.685297528	11	66	1.200489025	DOWN
GO:0005901	caveola	0.004034662	0.054972266	1	7	34	1.481829075	DOWN
GO:0005856	cytoskeleton	0.005944481	0.077753806	1	49	557	0.448879636	DOWN
GO:0042383	sarcolemma	0.008304086	0.102111345	1	8	48	1.218695417	DOWN
GO:0005938	cell_cortex	0.008431212	0.102111345	1	9	58	1.126810004	DOWN
GO:0098685	Schaffer_collateral_-_CA1_synapse	0.008850461	0.103360743	1	7	39	1.316590132	DOWN
GO:0032991	protein-containing_complex	0.013198871	0.146242669	1	36	401	0.464825409	DOWN
GO:0008180	COP9_signalosome	0.013920945	0.146242669	1	5	24	1.526367704	DOWN
GO:0005788	endoplasmic_reticulum_lumen	0.014133126	0.146242669	1	6	33	1.345419983	DOWN
GO:0030863	cortical_cytoskeleton	0.014311209	0.146242669	1	4	16	1.773274655	DOWN
GO:0001726	ruffle	0.019037568	0.188644991	1	7	45	1.14841182	DOWN
GO:0016324	apical_plasma_membrane	0.02012601	0.19356486	1	11	89	0.852057733	DOWN
GO:0099092	postsynaptic_density,_intracellular_component	0.021829864	0.20334137	1	4	18	1.629800607	DOWN
GO:0030425	dendrite	0.022386206	0.20334137	1	17	163	0.641257687	DOWN
GO:0045177	apical_part_of_cell	0.026396871	0.222006927	1	7	48	1.07374126	DOWN
GO:0034663	endoplasmic_reticulum_chaperone_complex	0.02647789	0.222006927	1	3	11	1.915748805	DOWN
GO:0090734	site_of_DNA_damage	0.02647789	0.222006927	1	3	11	1.915748805	DOWN
GO:0070062	extracellular_exosome	0.027224986	0.222564257	1	6	38	1.18018104	DOWN
GO:0043005	neuron_projection	0.030775788	0.238580222	1	18	182	0.579333529	DOWN
GO:0005719	nuclear_euchromatin	0.031372934	0.238580222	1	4	20	1.504264121	DOWN
GO:0031941	filamentous_actin	0.031372934	0.238580222	1	4	20	1.504264121	DOWN
GO:0030175	filopodium	0.03916231	0.285682414	1	5	31	1.224954578	DOWN
GO:0045202	synapse	0.039314094	0.285682414	1	21	227	0.500035144	DOWN
GO:0032993	protein-DNA_complex	0.043014927	0.305780025	1	4	22	1.392665003	DOWN
GO:0005887	integral_component_of_plasma_membrane	0.049975523	0.347702042	1	12	115	0.655343591	DOWN

Table of gene list enrichment results for GO_CC categories.

Table S3. GO analysis of *ulk1/2*^{-/-} MEFs in DMEM with glucose

GO: <i>ulk1/2</i> ^{-/-} MEF_Glucose UP								
GO_ID	Description	FisherPValue	FisherFDR	FisherBonf	nGenesIn Category	nAllGenesIn Category	logOR	direction
GO:0016021	integral_component_of_membrane	2.48072E-37	8.11195E-35	8.11195E-35	145	805	1.570955426	UP
GO:0005886	plasma_membrane	1.98799E-27	3.25037E-25	6.50073E-25	147	999	1.297194111	UP
GO:0005783	endoplasmic_reticulum	1.04086E-17	1.13454E-15	3.40362E-15	92	592	1.211104007	UP
GO:0005615	extracellular_space	1.69588E-17	1.38638E-15	5.54553E-15	53	231	1.625409232	UP
GO:0009986	cell_surface	1.74932E-15	1.14406E-13	5.72029E-13	41	160	1.74707804	UP
GO:0005794	Golgi_apparatus	4.32537E-12	2.35732E-10	1.41439E-09	71	489	1.075450887	UP
GO:0005576	extracellular_region	5.01299E-11	2.34178E-09	1.63925E-08	39	196	1.409684059	UP
GO:0005887	integral_component_of_plasma_membrane	2.41293E-10	9.86285E-09	7.89028E-08	28	115	1.653119043	UP
GO:0062023	collagen-containing_extracellular_matrix	3.43675E-09	1.24869E-07	1.12382E-06	24	97	1.668679327	UP
GO:0031012	extracellular_matrix	2.95664E-08	9.66822E-07	9.66822E-06	16	50	2.015614982	UP
GO:0005604	basement_membrane	8.08787E-08	2.4043E-06	2.64473E-05	13	35	2.234903206	UP
GO:0005789	endoplasmic_reticulum_membrane	3.47849E-07	9.47888E-06	0.000113747	25	130	1.34543259	UP
GO:0009897	external_side_of_plasma_membrane	1.38196E-06	3.47617E-05	0.000451902	15	57	1.744742165	UP
GO:0000139	Golgi_membrane	5.66509E-06	0.00013232	0.001852483	16	71	1.541664351	UP
GO:0030176	integral_component_of_endoplasmic_reticulum_membrane	1.38066E-05	0.000300983	0.004514748	12	45	1.764998592	UP
GO:0099055	integral_component_of_postsynaptic_membrane	2.0944E-05	0.000428043	0.006848682	6	11	2.868752144	UP
GO:0031410	cytoplasmic_vesicle	2.67893E-05	0.000515301	0.008760112	35	270	0.87565069	UP
GO:0045121	membrane_raft	3.44966E-05	0.000626688	0.011280378	19	108	1.23203538	UP
GO:0016529	sarcoplasmic_reticulum	0.000129705	0.002232297	0.042413639	8	26	1.970608476	UP
GO:0005788	endoplasmic_reticulum_lumen	0.000139079	0.002273945	0.045478894	9	33	1.803246273	UP
GO:0071782	endoplasmic_reticulum_tubular_network	0.00018538	0.002886627	0.060619158	5	10	2.711788523	UP
GO:0005790	smooth_endoplasmic_reticulum	0.000274417	0.004078831	0.089734275	7	22	2.022407746	UP
GO:0005768	endosome	0.000314836	0.004476152	0.102951505	33	281	0.756217629	UP
GO:0005765	lysosomal_membrane	0.000374493	0.00490691	0.122459189	10	45	1.534696628	UP
GO:0016324	apical_plasma_membrane	0.000375146	0.00490691	0.122672753	15	89	1.182424377	UP
GO:0043005	neuron_projection	0.000395159	0.004969886	0.12921704	24	182	0.887647845	UP
GO:0030659	cytoplasmic_vesicle_membrane	0.000524361	0.006322529	0.17146617	5	12	2.423733247	UP
GO:0005764	lysosome	0.000541379	0.006322529	0.177030825	22	164	0.907476707	UP
GO:0098993	anchored_component_of_synaptic_vesicle_membrane	0.000808462	0.00911611	0.264367188	5	13	2.305763557	UP
GO:0030054	cell_junction	0.000873943	0.009525983	0.285779499	28	238	0.755017603	UP
GO:0014704	intercalated_disc	0.00137211	0.014473544	0.44867987	7	28	1.70283189	UP
GO:0045335	phagocytic_vesicle	0.001632729	0.016684446	0.53390227	9	45	1.408954887	UP
GO:0005911	cell-cell_junction	0.002285675	0.020521696	0.747415778	13	85	1.070535881	UP
GO:0043025	neuronal_cell_body	0.002306771	0.020521696	0.754313965	24	206	0.74244606	UP
GO:0042995	cell_projection	0.002316615	0.020521696	0.757533096	33	315	0.621556936	UP
GO:0005797	Golgi_medial_cisterna	0.002384784	0.020521696	0.779824449	4	10	2.372324651	UP
GO:0030140	trans-Golgi_network_transport_vesicle	0.002384784	0.020521696	0.779824449	4	10	2.372324651	UP
GO:0031527	filopodium_membrane	0.002384784	0.020521696	0.779824449	4	10	2.372324651	UP
GO:0008021	synaptic_vesicle	0.002580601	0.02115623	0.843856439	10	57	1.24476061	UP
GO:0030175	filopodium	0.002587918	0.02115623	0.846249183	7	31	1.574436984	UP
GO:0016323	basolateral_plasma_membrane	0.002767995	0.022076447	0.905134328	11	67	1.161081	UP
GO:0034663	endoplasmic_reticulum_chaperone_complex	0.003563284	0.027742712	1	4	11	2.238606639	UP
GO:0030424	axon	0.004354668	0.033115729	1	18	146	0.810400222	UP
GO:0005581	collagen_trimer	0.005338534	0.03879335	1	5	19	1.793817276	UP
GO:0031225	anchored_component_of_membrane	0.005338534	0.03879335	1	5	19	1.793817276	UP
GO:0031234	extrinsic_component_of_cytoplasmic_side_of_plasma_membrane	0.005678311	0.040365385	1	6	27	1.566479621	UP
GO:0031902	late_endosome_membrane	0.00685273	0.046597012	1	6	28	1.521840716	UP

GO:0048471	perinuclear_region_of_cytoplasm	0.006867886	0.046597012	1	31	312	0.55858981	UP
GO:0032588	trans-Golgi_network_membrane	0.006982427	0.046597012	1	4	13	2.015089744	UP
GO:0043231	intracellular_membrane-bounded_organelle	0.007289531	0.047004813	1	34	352	0.526746074	UP
GO:0005769	early_endosome	0.007331026	0.047004813	1	14	108	0.874823906	UP
GO:0005925	focal_adhesion	0.00793896	0.049203577	1	13	98	0.90418893	UP
GO:0045202	synapse	0.007974892	0.049203577	1	24	227	0.629752281	UP
GO:0031594	neuromuscular_junction	0.008193601	0.049616804	1	6	29	1.479093923	UP
GO:0098685	Schaffer_collateral_-_CA1_synapse	0.009816081	0.058361063	1	7	39	1.295306278	UP
GO:0001669	acrosomal_vesicle	0.012557148	0.070796332	1	5	23	1.556680694	UP
GO:0005801	cis-Golgi_network	0.012557148	0.070796332	1	5	23	1.556680694	UP
GO:0030315	T-tubule	0.012557148	0.070796332	1	5	23	1.556680694	UP
GO:0043235	receptor_complex	0.012883306	0.071404085	1	7	41	1.236090684	UP
GO:0030141	secretory_granule	0.015460543	0.084259961	1	6	33	1.324194179	UP
GO:0031965	nuclear_membrane	0.016083526	0.086218247	1	13	107	0.802953335	UP
GO:0030496	midbody	0.016735292	0.088265166	1	11	85	0.883247925	UP
GO:0005802	trans-Golgi_network	0.018148549	0.094199612	1	11	86	0.86981368	UP
GO:0030139	endocytic_vesicle	0.021035074	0.107427185	1	5	26	1.409516	UP
GO:0030426	growth_cone	0.021354028	0.107427185	1	9	66	0.955481302	UP
GO:0055037	recycling_endosome	0.023460413	0.116235683	1	7	46	1.101620941	UP
GO:0030285	integral_component_of_synaptic_vesicle_membrane	0.027878922	0.134064818	1	3	11	1.894696193	UP
GO:0042470	melanosome	0.027878922	0.134064818	1	3	11	1.894696193	UP
GO:0005770	late_endosome	0.03537361	0.163397055	1	9	72	0.855910221	UP
GO:0012506	vesicle_membrane	0.035477648	0.163397055	1	3	12	1.789148989	UP
GO:0042734	presynaptic_membrane	0.035477648	0.163397055	1	3	12	1.789148989	UP
GO:0005793	endoplasmic_reticulum-Golgi_intermediate_compartment	0.03710932	0.16853816	1	6	40	1.099738415	UP
GO:0005834	heterotrimeric_G-protein_complex	0.044026214	0.191954295	1	3	13	1.693652085	UP
GO:0009925	basal_plasma_membrane	0.044026214	0.191954295	1	3	13	1.693652085	UP
GO:0030016	myofibril	0.044026214	0.191954295	1	3	13	1.693652085	UP
GO:0055038	recycling_endosome_membrane	0.045725035	0.19673798	1	4	22	1.371554086	UP
GO: <i>ulk1/2</i> ^{-/-} MEF_Glucose DOWN								
GO_ID	Description	FisherPValue	FisherFDR	FisherBonf	nGenesInCategory	nAllGenesInCategory	logOR	direction
GO:0005747	mitochondrial_respiratory_chain_complex_I	5.11706E-05	0.016732787	0.016732787	9	30	1.956126584	DOWN
GO:0043025	neuronal_cell_body	0.000322312	0.040977905	0.105396083	26	206	0.862446508	DOWN
GO:0070469	respiratory_chain	0.000375944	0.040977905	0.122933716	9	38	1.644475769	DOWN
GO:0005856	cytoskeleton	0.008996298	0.683058482	1	48	557	0.426714219	DOWN
GO:0031012	extracellular_matrix	0.010444319	0.683058482	1	8	50	1.173774161	DOWN
GO:0009898	cytoplasmic_side_of_plasma_membrane	0.016358822	0.883073887	1	5	25	1.480446982	DOWN
GO:0005739	mitochondrion	0.018903722	0.883073887	1	73	946	0.30802779	DOWN
GO:0005938	cell_cortex	0.024382067	0.924158795	1	8	58	1.001646861	DOWN
GO:0005581	collagen_trimer	0.026099386	0.924158795	1	4	19	1.568123318	DOWN
GO:0042995	cell_projection	0.029549774	0.924158795	1	28	315	0.454757114	DOWN
GO:0097060	synaptic_membrane	0.031087911	0.924158795	1	4	20	1.507312042	DOWN
GO:0043679	axon_terminus	0.049199178	1	1	4	23	1.344232941	DOWN

Table of gene list enrichment results for GO_CC categories.

Table S4. GO analysis of *atg5*^{-/-} MEFs in DMEM with galactose

GO: <i>atg5</i> ^{-/-} MEF_Galactose UP								
GO_ID	Description	FisherPValue	FisherFDR	FisherBonf	nGenesIn Category	nAllGenesIn Category	logOR	direction
GO:0005739	mitochondrion	2.65047E-05	0.008667032	0.008667032	71	946	0.622049831	UP
GO:0062023	collagen- containing_extracellular_matrix	0.000171063	0.027968855	0.05593771	14	97	1.308988528	UP
GO:0045171	intercellular_bridge	0.000401435	0.043756399	0.131269197	7	30	1.917585815	UP
GO:0005794	Golgi_apparatus	0.001480106	0.120998659	0.483994636	38	489	0.607887064	UP
GO:0005576	extracellular_region	0.005241877	0.324634363	1	18	196	0.786523587	UP
GO:0005615	extracellular_space	0.006440888	0.324634363	1	20	231	0.719005058	UP
GO:0070469	respiratory_chain	0.008333471	0.324634363	1	6	38	1.460189508	UP
GO:0031012	extracellular_matrix	0.008750638	0.324634363	1	7	50	1.307759971	UP
GO:0014704	intercalated_disc	0.009331352	0.324634363	1	5	28	1.622413071	UP
GO:0005797	Golgi_medial_cisterna	0.009927656	0.324634363	1	3	10	2.311067534	UP
GO:0031514	motile_cilium	0.010978985	0.326375295	1	4	19	1.843304436	UP
GO:0000139	Golgi_membrane	0.01857815	0.506254598	1	8	71	1.050912332	UP
GO:0001750	photoreceptor_outer_segment	0.021289226	0.517849596	1	3	13	1.992062788	UP
GO:0045177	apical_part_of_cell	0.02498142	0.517849596	1	6	48	1.193650573	UP
GO:0016021	integral_component_of_membrane	0.025068737	0.517849596	1	50	805	0.35150465	UP
GO:0005759	mitochondrial_matrix	0.026898548	0.517849596	1	8	76	0.974760836	UP
GO:0005886	plasma_membrane	0.026921844	0.517849596	1	60	999	0.318640781	UP
GO:0071944	cell_periphery	0.032666488	0.593441202	1	4	26	1.479110875	UP
GO:0005884	actin_filament	0.044908077	0.772891645	1	6	55	1.041533184	UP
GO: <i>atg5</i> ^{-/-} MEF_Galactose DOWN								
GO_ID	Description	FisherPValue	FisherFDR	FisherBonf	nGenesIn Category	nAllGenesIn Category	logOR	direction
GO:0005886	plasma_membrane	8.95003E-13	2.92666E-10	2.92666E-10	76	999	1.137589765	DOWN
GO:0043005	neuron_projection	1.3942E-05	0.002279514	0.004559028	19	182	1.290374239	DOWN
GO:0005901	caveola	0.000129488	0.012576803	0.04234266	7	34	2.102245031	DOWN
GO:0030054	cell_junction	0.000186227	0.012576803	0.060896147	20	238	1.045223675	DOWN
GO:0042995	cell_projection	0.000192306	0.012576803	0.062884014	24	315	0.940649176	DOWN
GO:0031234	extrinsic_component_of_cytoplasmic_ side_of_plasma_membrane	0.000255865	0.013944623	0.083667735	6	27	2.205771192	DOWN
GO:0030659	cytoplasmic_vesicle_membrane	0.000552666	0.025817391	0.180721739	4	12	2.75516574	DOWN
GO:0005911	cell-cell_junction	0.000636723	0.026026058	0.208208461	10	85	1.42915271	DOWN
GO:0031616	spindle_pole_centrosome	0.001058313	0.038452034	0.346068309	4	14	2.554132594	DOWN
GO:0005884	actin_filament	0.002642951	0.086424495	0.86424495	7	55	1.538803753	DOWN
GO:0009986	cell_surface	0.003426365	0.096639986	1	13	160	1.006542035	DOWN
GO:0031965	nuclear_membrane	0.003700096	0.096639986	1	10	107	1.170875192	DOWN
GO:0030175	filopodium	0.003841957	0.096639986	1	5	31	1.840749617	DOWN
GO:0044853	plasma_membrane_raft	0.005477074	0.127928808	1	3	11	2.526907088	DOWN
GO:0005887	integral_component_of_plasma_membrane	0.006183138	0.134792414	1	10	115	1.090929194	DOWN
GO:0015629	actin_cytoskeleton	0.00697097	0.136542638	1	10	117	1.071868125	DOWN
GO:0005913	cell-cell_adherens_junction	0.007098547	0.136542638	1	6	50	1.485965146	DOWN
GO:0016323	basolateral_plasma_membrane	0.007996061	0.145261776	1	7	67	1.317557604	DOWN
GO:0014069	postsynaptic_density	0.008837598	0.152099715	1	11	140	0.97471403	DOWN
GO:0030018	Z_disc	0.01029622	0.168343189	1	6	54	1.400077544	DOWN
GO:0016324	apical_plasma_membrane	0.011424282	0.177892395	1	8	89	1.140868575	DOWN
GO:0009897	external_side_of_plasma_membrane	0.013285821	0.197475618	1	6	57	1.340106428	DOWN
GO:0045335	phagocytic_vesicle	0.018718418	0.266127068	1	5	45	1.420466181	DOWN
GO:0005925	focal_adhesion	0.019583207	0.266821197	1	8	98	1.03507436	DOWN
GO:0045177	apical_part_of_cell	0.024150345	0.314125107	1	5	48	1.349301717	DOWN
GO:0030426	growth_cone	0.025795035	0.314125107	1	6	66	1.178831395	DOWN
GO:0005903	brush_border	0.025936935	0.314125107	1	4	33	1.547380641	DOWN
GO:0005615	extracellular_space	0.028495826	0.332790535	1	14	231	0.680546427	DOWN
GO:0032587	ruffle_membrane	0.034477099	0.388759018	1	4	36	1.451524659	DOWN
GO:0030027	lamellipodium	0.037350618	0.407121737	1	7	91	0.981380572	DOWN
GO:0070062	extracellular_exosome	0.04097606	0.429171927	1	4	38	1.392320126	DOWN

GO:0030315	T-tubule	0.043394547	0.429171927	1	3	23	1.677432553	DOWN
GO:0005736	RNA_polymerase_I_complex	0.044623381	0.429171927	1	2	10	2.234135946	DOWN
GO:0101031	chaperone_complex	0.044623381	0.429171927	1	2	10	2.234135946	DOWN

Table of gene list enrichment results for GO_CC categories.

Table S5. GO analysis of *ulk1*^{-/-} MEFs in DMEM with galactose

GO: <i>ulk1</i> ^{-/-} MEF_Galactose UP								
GO_ID	Description	FisherPValue	FisherFDR	FisherBonf	nGenesIn Category	nAllGenesIn Category	logOR	direction
GO:0005615	extracellular_space	1.36629E-06	0.000446778	0.000446778	43	231	0.928288363	UP
GO:0000176	nuclear_exosome_(RNase_complex)	2.36432E-05	0.003865659	0.007731318	8	16	2.348118861	UP
GO:0005736	RNA_polymerase_I_complex	7.06688E-05	0.006465579	0.023108709	6	10	2.681350242	UP
GO:0005764	lysosome	7.90896E-05	0.006465579	0.025862314	30	164	0.897541518	UP
GO:0000178	exosome_(RNase_complex)	0.000137055	0.008963386	0.044816931	7	15	2.228329807	UP
GO:0005739	mitochondrion	0.0003308	0.018028613	0.108171677	112	946	0.409778114	UP
GO:0005576	extracellular_region	0.000414351	0.019356093	0.135492654	32	196	0.757685702	UP
GO:0000177	cytoplasmic_exosome_(RNase_complex)	0.002456928	0.100426948	0.803415587	5	12	2.054622611	UP
GO:0005758	mitochondrial_intermembrane_space	0.006884265	0.2501283	1	9	40	1.182555443	UP
GO:0005887	integral_component_of_plasma_membrane	0.011323135	0.349345101	1	18	115	0.710651579	UP
GO:0030315	T-tubule	0.012583525	0.349345101	1	6	23	1.397920954	UP
GO:0005730	nucleolus	0.012820004	0.349345101	1	52	435	0.385602136	UP
GO:0031225	anchored_component_of_membrane	0.021509455	0.499333146	1	5	19	1.424670253	UP
GO:0009925	basal_plasma_membrane	0.022474007	0.499333146	1	4	13	1.646779755	UP
GO:0016529	sarcoplasmic_reticulum	0.02290519	0.499333146	1	6	26	1.243193517	UP
GO:0005923	bicellular_tight_junction	0.02809678	0.574227932	1	8	42	0.984994405	UP
GO:0005759	mitochondrial_matrix	0.032898867	0.606104979	1	12	76	0.735942934	UP
GO:0005743	mitochondrial_inner_membrane	0.033363577	0.606104979	1	29	232	0.436148321	UP
GO:0005847	mRNA_cleavage_and_polyadenylation_specificity_factor_complex	0.037274188	0.614126661	1	4	15	1.464074321	UP
GO:0016021	integral_component_of_membrane	0.037561264	0.614126661	1	85	805	0.242908001	UP
GO: <i>ulk1</i> ^{-/-} MEF_Galactose DOWN								
GO_ID	Description	FisherPValue	FisherFDR	FisherBonf	nGenesIn Category	nAllGenesIn Category	logOR	direction
GO:0001725	stress_fiber	1.08628E-15	3.55215E-13	3.55215E-13	26	57	2.454883069	DOWN
GO:0005886	plasma_membrane	1.55296E-12	2.5391E-10	5.07819E-10	127	999	0.837722785	DOWN
GO:0015629	actin_cytoskeleton	1.16103E-11	1.26553E-09	3.79658E-09	32	117	1.672463971	DOWN
GO:0062023	collagen-containing_extracellular_matrix	1.71299E-09	1.40037E-07	5.60148E-07	26	97	1.636356918	DOWN
GO:0030018	Z_disc	1.3813E-08	9.03372E-07	4.51686E-06	18	54	1.936684259	DOWN
GO:0005615	extracellular_space	2.7228E-08	1.48393E-06	8.90356E-06	41	231	1.119589224	DOWN
GO:0005911	cell-cell_junction	6.33054E-08	2.95727E-06	2.07009E-05	22	85	1.58493141	DOWN
GO:0043025	neuronal_cell_body	9.8699E-08	4.03432E-06	3.22746E-05	37	206	1.129257437	DOWN
GO:0031012	extracellular_matrix	1.71534E-07	6.23242E-06	5.60918E-05	16	50	1.876305068	DOWN
GO:0005856	cytoskeleton	1.9563E-07	6.39709E-06	6.39709E-05	72	557	0.767183627	DOWN
GO:0005925	focal_adhesion	2.23102E-07	6.63221E-06	7.29543E-05	23	98	1.455941504	DOWN
GO:0005884	actin_filament	4.06503E-06	0.000110772	0.001329264	15	55	1.65377878	DOWN
GO:0005576	extracellular_region	6.43933E-06	0.000161974	0.00210566	32	196	1.005651248	DOWN
GO:0005581	collagen_trimer	2.33639E-05	0.000545714	0.007639991	8	19	2.294950035	DOWN
GO:0005903	brush_border	6.32517E-05	0.001378888	0.020683313	10	33	1.805209408	DOWN
GO:0014704	intercalated_disc	8.85889E-05	0.001810536	0.028968582	9	28	1.890472942	DOWN
GO:0043209	myelin_sheath	0.000268377	0.005162301	0.087759116	21	129	0.996832409	DOWN
GO:0030054	cell_junction	0.000315371	0.005729244	0.103126388	32	238	0.77069394	DOWN
GO:0005913	cell-cell_adherens_junction	0.000621556	0.010697314	0.203248973	11	50	1.380877707	DOWN
GO:0032991	protein-containing_complex	0.000695671	0.011374217	0.227484342	46	401	0.590378201	DOWN
GO:0015630	microtubule_cytoskeleton	0.001087101	0.016927708	0.355481877	15	87	1.070808893	DOWN
GO:0030175	filopodium	0.001139553	0.016937901	0.372633818	8	31	1.599538702	DOWN
GO:0042383	sarcolemma	0.001701048	0.023727966	0.556242596	10	48	1.316864175	DOWN
GO:0030027	lamellipodium	0.001741502	0.023727966	0.569471178	15	91	1.01669999	DOWN
GO:0043005	neuron_projection	0.00228976	0.029950061	0.748751532	24	182	0.74522633	DOWN
GO:0016459	myosin_complex	0.002730022	0.034335276	0.892717189	6	21	1.750224252	DOWN
GO:0030424	axon	0.00333277	0.040363542	1	20	146	0.791437643	DOWN

GO:0045177	apical_part_of_cell	0.006019059	0.070294014	1	9	48	1.193543609	DOWN
GO:0030426	growth_cone	0.006375407	0.071888205	1	11	66	1.041369415	DOWN
GO:0045121	membrane_raft	0.009148909	0.099723109	1	15	108	0.813961702	DOWN
GO:0005604	basement_membrane	0.010423613	0.109952304	1	7	35	1.289078094	DOWN
GO:0017101	aminoacyl- tRNA_synthetase_multienzyme_compl ex	0.010842651	0.110798336	1	4	13	1.879936148	DOWN
GO:0031941	filamentous_actin	0.011377062	0.112736337	1	5	20	1.593595256	DOWN
GO:0001726	ruffle	0.01296032	0.124057002	1	8	45	1.137358367	DOWN
GO:0048471	perinuclear_region_of_cytoplasm	0.013278272	0.124057002	1	33	312	0.486746235	DOWN
GO:0070062	extracellular_exosome	0.016276466	0.147844562	1	7	38	1.190070645	DOWN
GO:0005868	cytoplasmic_dynein_complex	0.018478856	0.163313137	1	4	15	1.69723773	DOWN
GO:0043679	axon_terminus	0.020704918	0.178171266	1	5	23	1.421179015	DOWN
GO:0030425	dendrite	0.022138947	0.185626559	1	19	163	0.604059862	DOWN
GO:0005901	caveola	0.030892672	0.252547596	1	6	34	1.153062228	DOWN
GO:0043034	costamere	0.038580478	0.295816008	1	3	11	1.759875397	DOWN
GO:0042995	cell_projection	0.039397065	0.295816008	1	31	315	0.402124034	DOWN
GO:0032587	ruffle_membrane	0.039719327	0.295816008	1	6	36	1.085992639	DOWN
GO:0014069	postsynaptic_density	0.039803989	0.295816008	1	16	140	0.586156839	DOWN
GO:0002102	podosome	0.041898543	0.304462744	1	4	19	1.40880151	DOWN
GO:0032839	dendrite_cytoplasm	0.048791775	0.346845876	1	3	12	1.654326504	DOWN

Table of gene list enrichment results for GO_CC categories.

Table S6. GO analysis of *ulk1/2*^{-/-} MEFs in DMEM with galactose

GO: <i>ulk1/2</i> ^{-/-} MEF_Galactose UP								
GO_ID	Description	FisherPValue	FisherFDR	FisherBonf	nGenesIn Category	nAllGenesIn Category	logOR	direction
GO:0005886	plasma_membrane	3.56985E-14	1.16734E-11	1.16734E-11	123	999	0.924806704	UP
GO:0005615	extracellular_space	1.53004E-10	2.50162E-08	5.00325E-08	43	231	1.289790995	UP
GO:0062023	collagen- containing_extracellular_matrix	6.99125E-09	7.62046E-07	2.28614E-06	24	97	1.628369542	UP
GO:0031012	extracellular_matrix	4.88745E-08	3.99549E-06	1.5982E-05	16	50	1.976184868	UP
GO:0005576	extracellular_region	9.09282E-08	5.9467E-06	2.97335E-05	34	196	1.187141219	UP
GO:0009986	cell_surface	3.22292E-07	1.75649E-05	0.000105389	29	160	1.235295275	UP
GO:0005925	focal_adhesion	8.57393E-07	4.00525E-05	0.000280367	21	98	1.438599528	UP
GO:0005604	basement_membrane	7.80746E-06	0.00031913	0.00255304	11	35	1.952359203	UP
GO:0005581	collagen_trimer	1.2065E-05	0.000438361	0.003945249	8	19	2.392852774	UP
GO:0016021	integral_component_of_membrane	3.86413E-05	0.001263569	0.012635693	80	805	0.562983361	UP
GO:0001725	stress_fiber	5.46334E-05	0.001624102	0.017865122	13	57	1.520487277	UP
GO:0005834	heterotrimeric_G-protein_complex	8.52535E-05	0.002323158	0.027877897	6	13	2.542302493	UP
GO:0030054	cell_junction	0.000139341	0.003504953	0.045564394	31	238	0.836248024	UP
GO:0005856	cytoskeleton	0.000289349	0.006758366	0.094617129	57	557	0.572081406	UP
GO:0031594	neuromuscular_junction	0.000384294	0.008377609	0.125664141	8	29	1.784842907	UP
GO:0016529	sarcoplasmic_reticulum	0.00105006	0.021460596	0.343369541	7	26	1.760016631	UP
GO:0005923	bicellular_tight_junction	0.0012505	0.024053734	0.408913473	9	42	1.45536781	UP
GO:0005783	endoplasmic_reticulum	0.001339063	0.024326317	0.43787371	57	592	0.497313682	UP
GO:0016324	apical_plasma_membrane	0.001667082	0.028185919	0.545135895	14	89	1.062325863	UP
GO:0016459	myosin_complex	0.001723909	0.028185919	0.563718384	6	21	1.847657465	UP
GO:0005790	smooth_endoplasmic_reticulum	0.002242246	0.034914974	0.733214457	6	22	1.786845454	UP
GO:0098685	Schaffer_collateral_-_CA1_synapse	0.003103997	0.044985808	1	8	39	1.408271876	UP
GO:0030175	filopodium	0.003164139	0.044985808	1	7	31	1.535935081	UP
GO:0009897	external_side_of_plasma_membrane	0.003342931	0.045547431	1	10	57	1.205945445	UP
GO:0045121	membrane_raft	0.004042241	0.052872506	1	15	108	0.913667725	UP
GO:0005789	endoplasmic_reticulum_membrane	0.004308934	0.054193132	1	17	130	0.840323447	UP
GO:0043025	neuronal_cell_body	0.007406409	0.089699842	1	23	206	0.652766374	UP
GO:0005884	actin_filament	0.008429376	0.096301538	1	9	55	1.129133672	UP
GO:0015629	actin_cytoskeleton	0.008540503	0.096301538	1	15	117	0.820520701	UP
GO:0048471	perinuclear_region_of_cytoplasm	0.01126914	0.122833631	1	31	312	0.5173917	UP
GO:0001669	acrosomal_vesicle	0.014493801	0.146919545	1	5	23	1.518380551	UP
GO:0005913	cell-cell_adherens_junction	0.014499942	0.146919545	1	8	50	1.110738242	UP
GO:0098978	glutamatergic_synapse	0.015072628	0.146919545	1	20	183	0.629655376	UP
GO:0043235	receptor_complex	0.015444734	0.146919545	1	7	41	1.197584204	UP
GO:0005794	Golgi_apparatus	0.015725334	0.146919545	1	44	489	0.405668919	UP
GO:0005887	integral_component_of_plasma_membrane	0.016691915	0.151618229	1	14	115	0.76314717	UP
GO:0005911	cell-cell_junction	0.021240085	0.187716424	1	11	85	0.844318219	UP
GO:0005797	Golgi_medial_cisterna	0.023352106	0.200951015	1	3	10	1.97456758	UP
GO:0030139	endocytic_vesicle	0.024144351	0.202441098	1	5	26	1.371214489	UP
GO:0032587	ruffle_membrane	0.027110364	0.221627226	1	6	36	1.183444458	UP
GO:0034663	endoplasmic_reticulum_chaperone_complex	0.030588528	0.238153538	1	3	11	1.856597436	UP
GO:0099055	integral_component_of_postsynaptic_membrane	0.030588528	0.238153538	1	3	11	1.856597436	UP
GO:0014704	intercalated_disc	0.032440869	0.246701489	1	5	28	1.283827877	UP
GO:0045177	apical_part_of_cell	0.034308331	0.254973281	1	7	48	1.013945496	UP
GO:0030425	dendrite	0.035615308	0.25880457	1	17	163	0.579770475	UP
GO:0014069	postsynaptic_density	0.038076696	0.270675647	1	15	140	0.614577206	UP
GO:0005635	nuclear_envelope	0.043702088	0.304054954	1	11	95	0.717258622	UP
GO:0030496	midbody	0.048389267	0.329651884	1	10	85	0.741121098	UP

GO: <i>ulk1/2</i> ^{-/-} MEF_Galactose DOWN								
GO_ID	Description	FisherPValue	FisherFDR	FisherBonf	nGenesIn Category	nAllGenesIn Category	logOR	direction
GO:0005747	mitochondrial_respiratory_chain_complex_I	6.28863E-11	2.05638E-08	2.05638E-08	16	30	2.640509438	DOWN
GO:0005739	mitochondrion	1.17013E-09	1.91316E-07	3.82632E-07	121	946	0.718664953	DOWN
GO:0070469	respiratory_chain	5.38475E-09	5.86937E-07	1.76081E-06	16	38	2.211546243	DOWN
GO:0005743	mitochondrial_inner_membrane	1.31575E-05	0.001075623	0.004302494	37	232	0.89042106	DOWN
GO:0031966	mitochondrial_membrane	0.001258214	0.082287179	0.411435895	10	43	1.369282974	DOWN
GO:0005576	extracellular_region	0.002030435	0.110658684	0.663952107	27	196	0.708060231	DOWN
GO:0071944	cell_periphery	0.002783078	0.130009503	0.910066524	7	26	1.577199662	DOWN
GO:0030122	AP-2_adaptor_complex	0.005017425	0.205087259	1	4	10	2.15261137	DOWN
GO:0043195	terminal_bouton	0.007545797	0.274163969	1	5	17	1.717041993	DOWN
GO:0043209	myelin_sheath	0.009511631	0.311030349	1	18	129	0.727414723	DOWN
GO:0005759	mitochondrial_matrix	0.01260347	0.374666801	1	12	76	0.88702956	DOWN
GO:0017101	aminoacyl-tRNA_synthetase_multienzyme_complex	0.014190417	0.386473392	1	4	13	1.795367867	DOWN
GO:0010008	endosome_membrane	0.015364386	0.386473392	1	8	43	1.106453966	DOWN
GO:0005615	extracellular_space	0.0182501	0.426270188	1	27	231	0.513982551	DOWN
GO:0062023	collagen-containing_extracellular_matrix	0.034076885	0.684518284	1	13	97	0.691363059	DOWN
GO:0098793	presynapse	0.035055611	0.684518284	1	7	41	1.014730805	DOWN
GO:0031012	extracellular_matrix	0.035586577	0.684518284	1	8	50	0.927438311	DOWN
GO:0043025	neuronal_cell_body	0.044191822	0.77012901	1	23	206	0.462439031	DOWN
GO:0099092	postsynaptic_density_intracellular_component	0.044747557	0.77012901	1	4	18	1.388954442	DOWN

Table of gene list enrichment results for GO_CC categories.