

Supplementary Table S3: GO groups over-represented in *Dot1L*-downregulated genes

Biological Process Category	Genes in Category	% of Genes in Category	Genes in List in Category	% of Genes in List in Category	p-Value
GO:50803: regulation of synapse structure and function	3	0.0228	2	1.653	2.50E-04
GO:50804: regulation of synaptic transmission	3	0.0228	2	1.653	0.00025
GO:50805: negative regulation of synaptic transmission	3	0.0228	2	1.653	0.00025
GO:15694: mercury ion transport	5	0.038	2	1.653	0.00083
GO:46689: response to mercury ion	5	0.038	2	1.653	0.00083
GO:50787: detoxification of mercury ion	5	0.038	2	1.653	0.00083
GO:7264: small GTPase mediated signal transduction	528	4.015	13	10.74	0.00113
GO:6915: apoptosis	226	1.719	8	6.612	0.00114
GO:12501: programmed cell death	227	1.726	8	6.612	0.00118
GO:16265: death	244	1.855	8	6.612	0.00186
GO:8219: cell death	244	1.855	8	6.612	0.00186
GO:10035: response to inorganic substance	8	0.0608	2	1.653	0.00227
GO:10038: response to metal ion	8	0.0608	2	1.653	0.00227
GO:7165: signal transduction	2599	19.76	37	30.58	0.00293
GO:42981: regulation of apoptosis	157	1.194	6	4.959	0.00327
GO:43067: regulation of programmed cell death	158	1.201	6	4.959	0.00338
GO:7242: intracellular signaling cascade	990	7.528	18	14.88	0.00404
GO:6825: copper ion transport	12	0.0912	2	1.653	0.00522
GO:19827: stem cell maintenance	1	0.0076	1	0.826	0.0092
GO:35019: somatic stem cell maintenance	1	0.0076	1	0.826	0.0092
GO:51102: DNA ligation during DNA recombination	1	0.0076	1	0.826	0.0092
GO:6297: nucleotide-excision repair, DNA gap filling	1	0.0076	1	0.826	0.0092
GO:51402: programmed cell death, neurons	1	0.0076	1	0.826	0.0092
GO:48146: positive regulation of fibroblast proliferation	1	0.0076	1	0.826	0.0092
GO:46931: pore complex biogenesis	1	0.0076	1	0.826	0.0092
GO:45879: negative regulation of smoothened signaling pathway	1	0.0076	1	0.826	0.0092
GO:50850: positive regulation of calcium-mediated signaling	1	0.0076	1	0.826	0.0092
GO:10165: response to X-ray	1	0.0076	1	0.826	0.0092
GO:9314: response to radiation	19	0.144	2	1.653	0.013
GO:51056: regulation of small GTPase mediated signal transduction	286	2.175	7	5.785	0.0165
GO:45058: T cell selection	2	0.0152	1	0.826	0.0183
GO:45061: thymic T cell selection	2	0.0152	1	0.826	0.0183
GO:45060: negative thymic T cell selection	2	0.0152	1	0.826	0.0183
GO:19673: GDP-mannose metabolism	2	0.0152	1	0.826	0.0183
GO:6266: DNA ligation	2	0.0152	1	0.826	0.0183
GO:51103: DNA ligation during DNA repair	2	0.0152	1	0.826	0.0183
GO:12: single strand break repair	2	0.0152	1	0.826	0.0183
GO:50848: regulation of calcium-mediated signaling	2	0.0152	1	0.826	0.0183
GO:9966: regulation of signal transduction	367	2.791	8	6.612	0.02
GO:6888: ER to Golgi transport	27	0.205	2	1.653	0.0254
GO:6839: mitochondrial transport	27	0.205	2	1.653	0.0254
GO:50789: regulation of biological process	2486	18.9	32	26.45	0.0255
GO:43009: embryonic development (sensu Vertebrata)	28	0.213	2	1.653	0.0272
GO:46649: lymphocyte activation	28	0.213	2	1.653	0.0272
GO:45768: positive regulation of anti-apoptosis	3	0.0228	1	0.826	0.0274
GO:46641: positive regulation of alpha-beta T cell proliferation	3	0.0228	1	0.826	0.0274
GO:46635: positive regulation of alpha-beta T cell activation	3	0.0228	1	0.826	0.0274
GO:46640: regulation of alpha-beta T cell proliferation	3	0.0228	1	0.826	0.0274
GO:51302: regulation of cell division	3	0.0228	1	0.826	0.0274
GO:46633: alpha-beta T cell proliferation	3	0.0228	1	0.826	0.0274
GO:10212: response to ionizing radiation	3	0.0228	1	0.826	0.0274
GO:46634: regulation of alpha-beta T cell activation	4	0.0304	1	0.826	0.0363
GO:48145: regulation of fibroblast proliferation	4	0.0304	1	0.826	0.0363
GO:46631: alpha-beta T cell activation	4	0.0304	1	0.826	0.0363
GO:48144: fibroblast proliferation	4	0.0304	1	0.826	0.0363
GO:8589: regulation of smoothened signaling pathway	4	0.0304	1	0.826	0.0363
GO:50852: T cell receptor signaling pathway	4	0.0304	1	0.826	0.0363
GO:50794: regulation of cellular process	2365	17.98	30	24.79	0.0367
GO:48193: Golgi vesicle transport	33	0.251	2	1.653	0.0368
GO:7154: cell communication	3265	24.83	39	32.23	0.0396
GO:50731: positive regulation of peptidyl-tyrosine phosphorylation	5	0.038	1	0.826	0.0452
GO:50730: regulation of peptidyl-tyrosine phosphorylation	5	0.038	1	0.826	0.0452
GO:45937: positive regulation of phosphate metabolism	5	0.038	1	0.826	0.0452
GO:42327: positive regulation of phosphorylation	5	0.038	1	0.826	0.0452
GO:45767: regulation of anti-apoptosis	5	0.038	1	0.826	0.0452
GO:1775: cell activation	37	0.281	2	1.653	0.0454
GO:45321: immune cell activation	37	0.281	2	1.653	0.0454
GO:9792: embryonic development (sensu Metazoa)	38	0.289	2	1.653	0.0476
GO:8643: carbohydrate transport	38	0.289	2	1.653	0.0476
GO:8284: positive regulation of cell proliferation	39	0.297	2	1.653	0.0499
GO:41: transition metal ion transport	39	0.297	2	1.653	0.0499

Cellular Component Category	Genes in Category	% of Genes in Category	Genes in List in Category	% of Genes in List in Category	p-Value
GO:30127: COPII vesicle coat	14	0.12	2	1.835	0.00734
GO:30138: COPII-coated vesicle	14	0.12	2	1.835	0.00734
GO:42101: T cell receptor complex	1	0.00859	1	0.917	0.00936
GO:42105: alpha-beta T cell receptor complex	1	0.00859	1	0.917	0.00936
GO:5834: heterotrimeric G-protein complex	21	0.18	2	1.835	0.0162
GO:19897: extrinsic to plasma membrane	23	0.198	2	1.835	1.93E-02
GO:16020: membrane	4909	42.16	56	51.38	0.032
GO:8091: spectrin	4	0.0344	1	0.917	0.0369
GO:30120: vesicle coat	34	0.292	2	1.835	0.0401

Molecular Function Category	Genes in Category	% of Genes in Category	Genes in List in Category	% of Genes in List in Category	p-Value
GO:8897: phosphopantetheinyltransferase activity	2	0.0115	2	1.37	7.01E-05
GO:5315: inorganic phosphate transporter activity	3	0.0173	2	1.37	0.00021
GO:4008: copper-exporting ATPase activity	5	0.0288	2	1.37	0.00069
GO:15097: mercury ion transporter activity	5	0.0288	2	1.37	0.00069
GO:30552: 3',5'-cAMP binding	7	0.0403	2	1.37	0.00143

GO:17124: SH3 domain binding	7	0.0403	2	1.37	0.00143
GO:16712: oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen	32	0.184	3	2.055	0.00241
GO:30551: cyclic nucleotide binding	9	0.0518	2	1.37	0.00243
GO:15114: phosphate transporter activity	11	0.0633	2	1.37	0.00367
GO:5375: copper ion transporter activity	12	0.0691	2	1.37	0.00438
GO:16780: phosphotransferase activity, for other substituted phosphate groups	16	0.0921	2	1.37	0.00779
GO:3868: 4-hydroxyphenylpyruvate dioxygenase activity	1	0.00576	1	0.685	0.0084
GO:8432: JUN kinase binding	1	0.00576	1	0.685	0.0084
GO:16705: oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen	96	0.553	4	2.74	0.00875
GO:46915: transition metal ion transporter activity	17	0.0978	2	1.37	0.00878
GO:16208: AMP binding	18	0.104	2	1.37	0.00982
GO:30234: enzyme regulator activity	843	4.852	14	9.589	0.0116
GO:4497: monooxygenase activity	115	0.662	4	2.74	0.0161
GO:8446: GDP-mannose 4,6-dehydratase activity	2	0.0115	1	0.685	0.0167
GO:8138: protein tyrosine/serine/threonine phosphatase activity	66	0.38	3	2.055	0.0181
GO:5386: carrier activity	751	4.323	12	8.219	0.0246
GO:5351: sugar porter activity	32	0.184	2	1.37	0.0295
GO:43167: ion binding	4245	24.43	46	31.51	0.0311
GO:3950: NAD+ ADP-ribosyltransferase activity	33	0.19	2	1.37	0.0312
GO:4185: serine carboxypeptidase activity	4	0.023	1	0.685	0.0332
GO:15928: fucosidase activity	4	0.023	1	0.685	0.0332
GO:4560: alpha-L-fucosidase activity	4	0.023	1	0.685	0.0332
GO:51059: NF-kappaB binding	4	0.023	1	0.685	0.0332
GO:19904: protein domain specific binding	35	0.201	2	1.37	0.0348
GO:5085: guanyl-nucleotide exchange factor activity	289	1.663	6	4.11	0.0354
GO:15082: di-, tri-valent inorganic cation transporter activity	36	0.207	2	1.37	0.0367
GO:46872: metal ion binding	4185	24.09	45	30.82	0.0374
GO:5083: small GTPase regulator activity	460	2.648	8	5.479	0.0406
GO:30695: GTPase regulator activity	545	3.137	9	6.164	0.0407
GO:8191: metalloendopeptidase inhibitor activity	5	0.0288	1	0.685	0.0413
GO:19887: protein kinase regulator activity	40	0.23	2	1.37	0.0444
GO:9055: electron carrier activity	313	1.802	6	4.11	0.0489
GO:16715: oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen	6	0.0345	1	0.685	0.0494
GO:4500: dopamine beta-monoxygenase activity	6	0.0345	1	0.685	0.0494
GO:8839: dihydrodipicolinate reductase activity	6	0.0345	1	0.685	0.0494
GO:4810: tRNA adenyllyltransferase activity	6	0.0345	1	0.685	0.0494
GO:16437: tRNA cytidyltransferase activity	6	0.0345	1	0.685	0.0494
GO:8929: methylglyoxal synthase activity	6	0.0345	1	0.685	0.0494
GO:5338: nucleotide-sugar transporter activity	6	0.0345	1	0.685	0.0494
GO:19900: kinase binding	6	0.0345	1	0.685	0.0494
GO:19901: protein kinase binding	6	0.0345	1	0.685	0.0494
GO:19210: kinase inhibitor activity	6	0.0345	1	0.685	0.0494
GO:4860: protein kinase inhibitor activity	6	0.0345	1	0.685	0.0494
GO:16538: cyclin-dependent protein kinase regulator activity	6	0.0345	1	0.685	0.0494