

This view shows Gene Ontology information about the selected cluster. The following links provide with three different CSV files where the rows are linked to a probeset and the columns are the gene ontologies each probeset belongs. A 1 means that the probeset belongs to that particular ontology. Each file will provide information about Biological Process, Molecular Function or Cellular Component.

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This part shows a list of Gene Ontology terms sorted by their p-value. This p-value shows the probability, measured from 0 to 1, that the given Gene Ontology term has appeared in the cluster by chance. This can be used as a measure of how reliable this cluster is, thus lower values are better.

The following table shows the most probable GO terms sorted by their probability of random appearance. The columns are the following:

- *GO term*: Gene ontology term accession name.
- *Name*: GO name.
- *Ratio cluster/total*: Number of times this GO term appears in the cluster compared with the times that appears in the microarray.
- *p-value*: Probability of random appearance.

Cluster size: 43 probesets

Cluster attributes: MaleIP5, Clone1Dox, Clone3Dox

Number of probesets in microarray: 610

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GO term	Description	Ontology	Ratio cluster/total	p-value	probeset
GO_0051124	synaptic growth at neuromuscular junction	BP	11/14	0.0000	1742211_x_at
GO_0031594	neuromuscular junction	CC	11/106	0.0000	1742211_x_at
GO_0051402	neuron apoptosis	BP	11/90	0.0000	1742211_x_at
GO_0016199	axon midline choice point recognition	BP	11/24	0.0000	1742211_x_at
GO_003130	acetylcholine receptor binding	MF	11/24	0.0000	1742211_x_at
GO_0030414	peptidase inhibitor activity	MF	13/262	0.0000	1742211_x_at
GO_003198	dendrite shaft	CC	11/89	0.0000	1742211_x_at
GO_0045931	positive regulation of mitotic cell cycle	BP	11/87	0.0000	1742211_x_at
GO_0007626	locomotory behavior	BP	11/198	0.0000	1742211_x_at
GO_0031175	neuron projection development	BP	11/197	0.0000	1742211_x_at
GO_0040014	regulation of multicellular organism growth	BP	11/89	0.0000	1742211_x_at
GO_0016504	peptidase activator activity	MF	11/34	0.0000	1742211_x_at
GO_0051563	smooth endoplasmic reticulum calcium ion homeostasis	BP	11/17	0.0000	1742211_x_at
GO_0035235	ionotropic glutamate receptor signaling pathway	BP	11/41	0.0000	1742211_x_at
GO_0007219	Notch signaling pathway	BP	11/196	0.0000	1742211_x_at
GO_0007617	miting behavior	BP	11/25	0.0000	1742211_x_at
GO_0059885	neuroinflammatory process controlling balance	BP	11/104	0.0000	1742211_x_at
GO_0016322	neuron remodeling	BP	11/28	0.0000	1742211_x_at
GO_0007174	regulation of epidermal growth factor receptor activity	BP	11/30	0.0000	1742211_x_at
GO_0008542	visual learning	BP	11/98	0.0000	1742211_x_at
GO_0045177	apical part of cell	CC	11/192	0.0000	1742211_x_at
GO_0059803	regulation of synapse structure and activity	BP	11/24	0.0000	1742211_x_at
GO_001967	suckling behavior	BP	11/24	0.0000	1742211_x_at
GO_0005085	G2 phase of mitotic cell cycle	BP	11/25	0.0000	1742211_x_at
GO_0051233	spindle midzone	CC	11/28	0.0000	1742211_x_at
GO_0008088	axon cargo transport	BP	11/25	0.0000	1742211_x_at
GO_0005905	coated pit	CC	11/188	1.1102e-16	1742211_x_at
GO_0016358	dendrite development	BP	11/99	1.1102e-16	1742211_x_at
GO_0008434	adult locomotory behavior	BP	13/133	1.1102e-16	1742211_x_at
GO_0035253	ciliogenesis	CC	11/46	1.1102e-16	1742211_x_at
GO_0006378	mRNA polyadenylation	BP	11/48	1.1102e-16	1742211_x_at
GO_0048669	collateral sprouting in absence of injury	BP	11/13	1.1102e-16	1742211_x_at
GO_0009690	forebrain development	BP	11/209	1.1102e-16	1742211_x_at
GO_0019717	synaptosomes	CC	14/368	1.1102e-16	1742211_x_at
GO_004867	serine-type endopeptidase inhibitor activity	MF	11/207	1.1102e-16	1742211_x_at
GO_0043197	dendrite spine	CC	11/227	2.2204e-16	1742211_x_at
GO_0006897	endocytosis	BP	14/452	2.2204e-16	1742211_x_at
GO_0006878	cellular copper ion homeostasis	BP	11/31	2.2204e-16	1742211_x_at
GO_0030198	extracellular matrix organization	BP	11/255	3.3307e-16	1742211_x_at
GO_0006417	regulation of translation	BP	11/284	8.8818e-16	1742211_x_at
GO_0007409	exogenous	BP	11/297	1.4433e-15	1742211_x_at
GO_0043005	neuron projection	CC	11/315	2.6645e-15	1742211_x_at
GO_0008201	heparin binding	MF	11/333	5.1070e-15	1742211_x_at
GO_0045202	synapse	CC	14/916	2.4869e-14	1742211_x_at
GO_0008219	cell death	BP	11/46	2.0628e-13	1742211_x_at
GO_0003042	axon	CC	11/504	4.8239e-13	1742211_x_at
GO_0006917	induction of apoptosis	BP	11/628	5.1440e-12	1742211_x_at
GO_0005102	receptor binding	MF	11/671	1.0447e-11	1742211_x_at
GO_0009986	cell surface	CC	11/883	1.9226e-10	1742211_x_at
GO_0006915	apoptosis	BP	14/1815	2.2554e-10	1742211_x_at
GO_0031410	cytoplasmic vesicle	CC	11/925	3.1342e-10	1742211_x_at
GO_0048471	perinuclear region of cytoplasm	CC	11/1134	2.6264e-9	1742211_x_at
GO_0042802	identical protein binding	MF	11/1172	3.6943e-9	1742211_x_at
GO_0045944	positive regulation of transcription from RNA polymerase II promoter	BP	11/1203	4.8377e-9	1742211_x_at
GO_0008233	peptidase activity	MF	11/1366	1.7832e-8	1742211_x_at
GO_0007155	cell adhesion	BP	12/1744	2.0168e-8	1742211_x_at
GO_0045202	synapse	BP	12/1780	2.5245e-8	1742211_x_at
GO_0008129	axon	CC	11/504	4.8239e-13	1742211_x_at
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