























DAVID functional enrichment analysis with the top 100 down- and up-regulated genes

Down-regulated genes:

Sublist	Category	Term	RT	Genes	Count	%	P-Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">defense response to bacterium</a>	<a href="#">RT</a>		8	1.2	1.6E-6	1.3E-3
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">response to bacterium</a>	<a href="#">RT</a>		8	1.2	5.5E-5	2.2E-2
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">immune response</a>	<a href="#">RT</a>		13	1.9	1.7E-4	4.6E-2
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Hematopoietic cell lineage</a>	<a href="#">RT</a>		5	0.7	7.4E-4	4.8E-2
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">defense response to fungus</a>	<a href="#">RT</a>		3	0.4	1.9E-3	3.3E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">killing of cells of another organism</a>	<a href="#">RT</a>		3	0.4	2.2E-3	3.1E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">defense response</a>	<a href="#">RT</a>		10	1.5	3.9E-3	4.1E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">cell killing</a>	<a href="#">RT</a>		3	0.4	6.6E-3	5.4E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">response to fungus</a>	<a href="#">RT</a>		3	0.4	6.6E-3	5.4E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of locomotion</a>	<a href="#">RT</a>		4	0.6	1.4E-2	7.6E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of locomotion</a>	<a href="#">RT</a>		5	0.7	1.7E-2	7.8E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">response to virus</a>	<a href="#">RT</a>		4	0.6	1.8E-2	7.8E-1
<input type="checkbox"/>	GOTERM_MF_FAT	<a href="#">antigen binding</a>	<a href="#">RT</a>		3	0.4	2.1E-2	9.9E-1
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Intestinal immune network for IgA production</a>	<a href="#">RT</a>		3	0.4	2.4E-2	5.5E-1
<input type="checkbox"/>	GOTERM_MF_FAT	<a href="#">copper ion binding</a>	<a href="#">RT</a>		3	0.4	3.1E-2	9.6E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">membrane organization</a>	<a href="#">RT</a>		6	0.9	4.5E-2	9.7E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">defense response to Gram-negative bacterium</a>	<a href="#">RT</a>		2	0.3	5.0E-2	9.7E-1
<input type="checkbox"/>	GOTERM_MF_FAT	<a href="#">carbohydrate binding</a>	<a href="#">RT</a>		5	0.7	5.3E-2	9.8E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of cell migration</a>	<a href="#">RT</a>		4	0.6	5.5E-2	9.7E-1
<input type="checkbox"/>	GOTERM_MF_FAT	<a href="#">oxidoreductase activity, acting on the CH-NH2 group of donors</a>	<a href="#">RT</a>		2	0.3	7.0E-2	9.8E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of cell migration</a>	<a href="#">RT</a>		3	0.4	7.6E-2	9.9E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of cell motion</a>	<a href="#">RT</a>		4	0.6	7.6E-2	9.9E-1









<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">amino acid transport</a>	RT		3	0.4	7.7E-2	9.8E-1
<input type="checkbox"/>	GOTERM_MF_FAT	<a href="#">neurotransmitter:sodium symporter activity</a>	RT		2	0.3	7.7E-2	9.7E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of cell motion</a>	RT		3	0.4	8.9E-2	9.9E-1
<input type="checkbox"/>	GOTERM_MF_FAT	<a href="#">neurotransmitter transporter activity</a>	RT		2	0.3	9.2E-2	9.7E-1

### Up-regulated genes:

Sublist	Category	Term	RT	Genes	Count	%	P-Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">anti-apoptosis</a>	RT		8	1.0	7.6E-5	9.1E-2
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">inflammatory response</a>	RT		9	1.1	2.1E-4	1.3E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of cell communication</a>	RT		9	1.1	2.3E-4	9.3E-2
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">response to wounding</a>	RT		11	1.3	2.9E-4	8.9E-2
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of apoptosis</a>	RT		13	1.6	6.0E-4	1.4E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of programmed cell death</a>	RT		13	1.6	6.5E-4	1.3E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of cell death</a>	RT		13	1.6	6.7E-4	1.1E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">defense response</a>	RT		11	1.3	9.4E-4	1.4E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of response to stimulus</a>	RT		7	0.9	1.2E-3	1.5E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of response to external stimulus</a>	RT		6	0.7	1.2E-3	1.4E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of immune system process</a>	RT		7	0.9	1.2E-3	1.3E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">response to oxidative stress</a>	RT		6	0.7	1.4E-3	1.4E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of MAP kinase activity</a>	RT		5	0.6	1.7E-3	1.5E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">negative regulation of apoptosis</a>	RT		8	1.0	2.0E-3	1.6E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">response to protein stimulus</a>	RT		5	0.6	2.0E-3	1.6E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of cellular biosynthetic process</a>	RT		11	1.3	2.1E-3	1.5E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">negative regulation of programmed cell death</a>	RT		8	1.0	2.1E-3	1.4E-1

Sublist	Category	Term	RT	Genes	Count	%	P-Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">negative regulation of cell death</a>	RT		8	1.0	2.1E-3	1.4E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of biosynthetic process</a>	RT		11	1.3	2.3E-3	1.4E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">response to abiotic stimulus</a>	RT		8	1.0	2.4E-3	1.4E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">protein kinase cascade</a>	RT		8	1.0	2.5E-3	1.4E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">response to organic substance</a>	RT		11	1.3	3.1E-3	1.6E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">response to radiation</a>	RT		6	0.7	3.3E-3	1.7E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of macromolecule metabolic process</a>	RT		12	1.5	3.4E-3	1.6E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of signal transduction</a>	RT		7	0.9	3.6E-3	1.7E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">response to inorganic substance</a>	RT		6	0.7	3.7E-3	1.6E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of response to external stimulus</a>	RT		4	0.5	4.1E-3	1.7E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of catalytic activity</a>	RT		9	1.1	4.4E-3	1.8E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">cytokine-mediated signaling pathway</a>	RT		4	0.5	5.2E-3	2.0E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of MAP kinase activity</a>	RT		5	0.6	5.5E-3	2.1E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">response to gamma radiation</a>	RT		3	0.4	5.9E-3	2.1E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">response to reactive oxygen species</a>	RT		4	0.5	6.3E-3	2.2E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">response to cytokine stimulus</a>	RT		4	0.5	7.3E-3	2.4E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of multicellular organismal process</a>	RT		6	0.7	7.6E-3	2.5E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">activation of MAPK activity</a>	RT		4	0.5	8.1E-3	2.5E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of protein kinase cascade</a>	RT		6	0.7	8.2E-3	2.5E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of molecular function</a>	RT		9	1.1	8.9E-3	2.6E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">response to molecule of bacterial origin</a>	RT		4	0.5	9.2E-3	2.6E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of chemotaxis</a>	RT		3	0.4	9.3E-3	2.6E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of cellular protein metabolic process</a>	RT		8	1.0	9.5E-3	2.6E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of leukocyte activation</a>	RT		5	0.6	9.7E-3	2.6E-1

Sublist	Category	Term	RT	Genes	Count	%	P-Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of protein kinase cascade</a>	RT		5	0.6	9.9E-3	2.6E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of anti-apoptosis</a>	RT		3	0.4	9.9E-3	2.5E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of chemotaxis</a>	RT		3	0.4	1.1E-2	2.6E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">negative regulation of macromolecule metabolic process</a>	RT		10	1.2	1.1E-2	2.6E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">cellular ion homeostasis</a>	RT		7	0.9	1.1E-2	2.6E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">mitochondrial membrane organization</a>	RT		3	0.4	1.1E-2	2.6E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of cell activation</a>	RT		5	0.6	1.2E-2	2.6E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">cellular chemical homeostasis</a>	RT		7	0.9	1.2E-2	2.7E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">locomotory behavior</a>	RT		6	0.7	1.2E-2	2.6E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of behavior</a>	RT		3	0.4	1.3E-2	2.7E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">negative regulation of cellular protein metabolic process</a>	RT		5	0.6	1.3E-2	2.7E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of developmental process</a>	RT		6	0.7	1.3E-2	2.6E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of cytokine production</a>	RT		5	0.6	1.3E-2	2.6E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">negative regulation of protein metabolic process</a>	RT		5	0.6	1.4E-2	2.8E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">cell activation</a>	RT		6	0.7	1.5E-2	2.8E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of nitrogen compound metabolic process</a>	RT		9	1.1	1.5E-2	2.8E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of anti-apoptosis</a>	RT		3	0.4	1.6E-2	2.9E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of locomotion</a>	RT		5	0.6	1.6E-2	2.9E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of leukocyte activation</a>	RT		4	0.5	1.6E-2	2.9E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of protein modification process</a>	RT		6	0.7	1.6E-2	2.9E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of macromolecule biosynthetic process</a>	RT		9	1.1	1.6E-2	2.9E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of cell proliferation</a>	RT		10	1.2	1.7E-2	2.8E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">ion homeostasis</a>	RT		7	0.9	1.7E-2	2.8E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of MAPKKK cascade</a>	RT		4	0.5	1.7E-2	2.9E-1

Sublist	Category	Term	RT	Genes	Count	%	P-Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">positive regulation of cell activation</a>	<b>RT</b>		4	0.5	1.8E-2	3.0E-1
<input type="checkbox"/>	GOTERM_MF_FAT	<a href="#">structural molecule activity</a>	<b>RT</b>		9	1.1	1.9E-2	9.9E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">response to cAMP</a>	<b>RT</b>		3	0.4	1.9E-2	3.0E-1
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Jak-STAT signaling pathway</a>	<b>RT</b>		5	0.6	1.9E-2	6.4E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">cellular response to oxidative stress</a>	<b>RT</b>		3	0.4	2.0E-2	3.1E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">myeloid leukocyte activation</a>	<b>RT</b>		3	0.4	2.2E-2	3.4E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of behavior</a>	<b>RT</b>		3	0.4	2.2E-2	3.4E-1
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">cellular response to stress</a>	<b>RT</b>		8	1.0	2.3E-2	3.4E-1