

## Enriched GOBP categories by differentially more abundant

Gene Ontology ID	Odds ratio	Adjusted p-value
GO:0044237	3.19	0.0002
GO:0008152	2.93	0.0020
GO:0044238	2.64	0.0023
GO:0009987	4.30	0.0029
GO:0044281	2.31	0.0029
GO:0019752	2.80	0.0060
GO:0043436	2.80	0.0060
GO:0006082	2.77	0.0062
GO:0042180	2.77	0.0062
GO:0008150	4.67	0.0086
GO:0016054	4.95	0.0089
GO:0046395	4.95	0.0089
GO:0010467	2.02	0.0106
GO:0034641	1.96	0.0148
GO:0000377	2.96	0.0155
GO:0000398	2.96	0.0155
GO:0043487	9.06	0.0155
GO:0043488	9.06	0.0155
GO:0006807	1.94	0.0172
GO:0000375	2.89	0.0174
GO:0007091	8.41	0.0180
GO:0055114	2.65	0.0187
GO:0008380	2.70	0.0219
GO:0033539	23.16	0.0233
GO:0006397	2.47	0.0265
GO:0090304	1.88	0.0276
GO:0050769	6.92	0.0276
GO:0030049	9.34	0.0291
GO:0033275	9.34	0.0291
GO:0043489	9.34	0.0291
GO:0048255	9.34	0.0291
GO:0070252	9.34	0.0291
GO:0006635	6.53	0.0291
GO:0009062	6.53	0.0291
GO:0072329	6.53	0.0291
GO:0016584	17.37	0.0291
GO:0070934	17.37	0.0291
GO:0016070	1.87	0.0294
GO:0006099	6.19	0.0328
GO:0009109	6.19	0.0328
GO:0010948	6.19	0.0328
GO:0046356	6.19	0.0328
GO:0044085	2.02	0.0330
GO:0010720	5.88	0.0360
GO:0044260	1.79	0.0360
GO:0043170	1.80	0.0360
GO:0051187	5.59	0.0385
GO:0032787	3.22	0.0394
GO:0022607	2.02	0.0497
GO:0006139	1.73	0.0497
GO:0019395	5.10	0.0500
GO:0034440	5.10	0.0500

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GO:0016053	3.61	0.0540
GO:0046394	3.61	0.0540
GO:0009060	4.89	0.0562
GO:0055006	9.93	0.0582
GO:0055013	9.93	0.0582
GO:0030048	6.22	0.0582
GO:0051289	6.22	0.0582
GO:0009063	4.51	0.0674
GO:0030258	4.51	0.0674
GO:0006396	1.97	0.0690
GO:0030239	8.69	0.0693
GO:0008104	0.36	0.0700
GO:0015980	2.61	0.0702
GO:0006084	4.34	0.0702
GO:0009310	4.34	0.0702
GO:0006631	3.25	0.0702
GO:0007088	5.48	0.0713
GO:0051783	5.48	0.0713
GO:0051090	3.62	0.0720
GO:0070727	0.27	0.0744
GO:0031324	2.10	0.0786
GO:0031032	7.72	0.0786
GO:0044242	4.04	0.0819
GO:0016071	1.85	0.0831
GO:0045333	3.01	0.0890
GO:0015031	0.35	0.0890
GO:0045184	0.35	0.0890
GO:0006936	3.90	0.0890
GO:0055007	6.95	0.0916
GO:0034613	0.27	0.0935

nt proteins in differentiating NSCs in comparison to proliferating NSCs

**Gene Ontology name**

cellular metabolic process  
metabolic process  
primary metabolic process  
cellular process  
small molecule metabolic process  
carboxylic acid metabolic process  
oxoacid metabolic process  
organic acid metabolic process  
cellular ketone metabolic process  
biological\_process  
organic acid catabolic process  
carboxylic acid catabolic process  
gene expression  
cellular nitrogen compound metabolic process  
RNA splicing, via transesterification reactions with bulged adenosine as nucleophile  
nuclear mRNA splicing, via spliceosome  
regulation of RNA stability  
regulation of mRNA stability  
nitrogen compound metabolic process  
RNA splicing, via transesterification reactions  
mitotic metaphase/anaphase transition  
oxidation-reduction process  
RNA splicing  
fatty acid beta-oxidation using acyl-CoA dehydrogenase  
mRNA processing  
nucleic acid metabolic process  
positive regulation of neurogenesis  
muscle filament sliding  
actin-myosin filament sliding  
RNA stabilization  
mRNA stabilization  
actin-mediated cell contraction  
fatty acid beta-oxidation  
fatty acid catabolic process  
monocarboxylic acid catabolic process  
nucleosome positioning  
CRD-mediated mRNA stabilization  
RNA metabolic process  
tricarboxylic acid cycle  
coenzyme catabolic process  
negative regulation of cell cycle process  
acetyl-CoA catabolic process  
cellular component biogenesis  
positive regulation of cell development  
cellular macromolecule metabolic process  
macromolecule metabolic process  
cofactor catabolic process  
monocarboxylic acid metabolic process  
cellular component assembly  
nucleobase-containing compound metabolic process  
fatty acid oxidation  
lipid oxidation

## Sheet1

organic acid biosynthetic process  
carboxylic acid biosynthetic process  
aerobic respiration  
cardiac cell development  
cardiac muscle cell development  
actin filament-based movement  
protein homotetramerization  
cellular amino acid catabolic process  
lipid modification  
RNA processing  
myofibril assembly  
protein localization  
energy derivation by oxidation of organic compounds  
acetyl-CoA metabolic process  
amine catabolic process  
fatty acid metabolic process  
regulation of mitosis  
regulation of nuclear division  
regulation of sequence-specific DNA binding transcription factor activity  
cellular macromolecule localization  
negative regulation of cellular metabolic process  
actomyosin structure organization  
cellular lipid catabolic process  
mRNA metabolic process  
cellular respiration  
protein transport  
establishment of protein localization  
muscle contraction  
cardiac muscle cell differentiation  
cellular protein localization



Sheet1

