

Table S4 FunCat analysis for identified *N. crassa* transcripts with at least one spliced 3'UTR intron.

The FunCat database (Ruepp *et al.* 2004) was used to calculate functional enrichments for the products specified by the 31 identified mRNAs with spliced 3'UTR introns as described in Materials and Methods.

FUNCTIONAL CATEGORY	abs SET	rel SET	genes SET	abs GENOME	rel GENOME	rel SET/rel GENOME	P-VALUE
01.03 nucleotide/nucleoside/nucleobase metabolism	8	28.5	NCU00261 NCU02423 NCU01234 NCU11426 NCU01888 NCU07408 NCU08026 NCU03226	745	7.4	3.851	0.001
01.03.04 pyrimidine nucleotide/nucleoside/nucleobase metabolism	3	10.7	NCU00261 NCU11426 NCU01888	159	1.57	6.815	0.009
01.03.04.01 pyrimidine nucleotide/nucleoside/nucleobase catabolism	2	7.14	NCU11426 NCU01888	29	0.28	25.500	0.003
01.03.16 polynucleotide degradation	5	17.8	NCU01234 NCU11426 NCU07408 NCU08026 NCU03226	220	2.18	8.165	0.000
01.03.16.01 RNA degradation	4	14.2	NCU01234 NCU07408 NCU08026 NCU03226	153	1.51	9.404	0.001
01.06.02 membrane lipid metabolism	3	10.7	NCU00261 NCU04699 NCU11426	262	2.6	4.115	0.035
01.06.02.01 phospholipid metabolism	3	10.7	NCU00261 NCU04699 NCU11426	189	1.87	5.722	0.015
10 CELL CYCLE AND DNA PROCESSING	9	32.1	NCU02249 NCU01312 NCU01234 NCU04650 NCU11426 NCU06322 NCU07587 NCU02885 NCU03226	1715	17	1.888	0.038
10.01 DNA processing	8	28.5	NCU02249 NCU01312 NCU01234 NCU11426 NCU06322 NCU07587 NCU02885 NCU03226	1117	11	2.591	0.009
10.01.03 DNA synthesis and replication	4	14.2	NCU02249 NCU01234 NCU06322 NCU07587	365	3.62	3.923	0.017
10.01.05 DNA recombination and DNA repair	5	17.8	NCU02249 NCU01234 NCU11426 NCU07587 NCU02885	558	5.54	3.213	0.017
10.01.05.01 DNA repair	4	14.2	NCU02249 NCU01234 NCU11426 NCU02885	477	4.73	3.002	0.041
10.03.01.01.03 G1/S transition of mitotic cell cycle	3	10.7	NCU01312 NCU07587 NCU02885	159	1.57	6.815	0.009
10.03.04 nuclear and chromosomal cycle	3	10.7	NCU04650 NCU11426 NCU02885	289	2.87	3.728	0.045
11 TRANSCRIPTION	15	53.5	NCU02249 NCU02423 NCU01312 NCU01234 NCU04986 NCU11426 NCU01888 NCU06869 NCU07408 NCU07587 NCU08026 NCU02948 NCU02885 NCU09615 NCU03226	1759	17.4	3.075	0.000
11.02 RNA synthesis	10	35.7	NCU02249 NCU01312 NCU01234 NCU04986 NCU11426 NCU06869 NCU07587 NCU02948 NCU09615 NCU03226	1489	14.7	2.429	0.005
11.02.03 mRNA synthesis	10	35.7	NCU02249 NCU01312 NCU01234 NCU04986 NCU11426 NCU06869 NCU07587 NCU02948 NCU09615 NCU03226	1426	14.1	2.532	0.004
11.02.03.04 transcriptional control	9	32.1	NCU02249 NCU01312 NCU01234 NCU11426 NCU06869 NCU07587 NCU02948 NCU09615 NCU03226	1279	12.7	2.528	0.006

11.04 RNA processing	9	32.1	NCU02423 NCU01312 NCU01234 NCU11426 NCU06869 NCU07408 NCU08026 NCU02885 NCU03226	732	7.27	4.415	0.000
11.04.01 rRNA processing	4	14.2	NCU01234 NCU07408 NCU08026 NCU03226	363	3.6	3.944	0.017
11.04.03 mRNA processing (splicing, 5 [^] -, 3 [^] -end processing)	9	32.1	NCU02423 NCU01312 NCU01234 NCU11426 NCU06869 NCU07408 NCU08026 NCU02885 NCU03226	538	5.34	6.011	0.000
11.04.03.01 splicing	5	17.8	NCU02423 NCU01312 NCU01234 NCU06869 NCU03226	437	4.34	4.101	0.006
11.04.03.05 3 [^] -end processing	2	7.14	NCU06869 NCU03226	84	0.83	8.602	0.023
11.04.03.11 control of mRNA stability	3	10.7	NCU01234 NCU02885 NCU03226	95	0.94	11.383	0.002
12 PROTEIN SYNTHESIS	6	21.4	NCU00410 NCU01234 NCU07408 NCU08026 NCU02885 NCU03226	753	7.47	2.865	0.016
12.04 translation	4	14.2	NCU00410 NCU01234 NCU07408 NCU03226	460	4.56	3.114	0.037
16 PROTEIN WITH BINDING FUNCTION OR COFACTOR REQUIREMENT (structural or catalytic)	17	60.7	NCU00410 NCU02249 NCU02423 NCU01312 NCU01234 NCU00778 NCU04650 NCU11426 NCU06322 NCU01888 NCU01907 NCU06869 NCU07408 NCU07587 NCU08026 NCU02885 NCU03226	3639	36.1	1.681	0.007
16.01 protein binding	13	46.4	NCU00410 NCU02249 NCU01312 NCU01234 NCU00778 NCU04650 NCU11426 NCU01907 NCU06869 NCU07408 NCU07587 NCU02885 NCU03226	2333	23.1	2.009	0.006
16.03 nucleic acid binding	10	35.7	NCU02249 NCU01312 NCU01234 NCU04650 NCU11426 NCU06322 NCU06869 NCU07587 NCU08026 NCU03226	1290	12.8	2.789	0.002
16.03.01 DNA binding	7	25	NCU02249 NCU01312 NCU01234 NCU11426 NCU06322 NCU07587 NCU03226	854	8.48	2.948	0.007
16.03.03 RNA binding	6	21.4	NCU01234 NCU04650 NCU11426 NCU06869 NCU08026 NCU03226	552	5.48	3.905	0.004
16.07 structural protein binding	2	7.14	NCU04650 NCU07408	94	0.93	7.677	0.028
18.02.01.01 enzyme activator	4	14.2	NCU00410 NCU11426 NCU06869 NCU02885	376	3.73	3.807	0.019
18.02.01.02.05 kinase inhibitor	2	7.14	NCU11426 NCU02885	103	1.02	7.000	0.033
20 CELLULAR TRANSPORT, TRANSPORT FACILITIES AND TRANSPORT ROUTES	11	39.2	NCU02423 NCU01312 NCU01234 NCU00778 NCU04650 NCU11426 NCU01907 NCU07587 NCU08026 NCU02948 NCU02885	2165	21.5	1.823	0.025
20.01.13 lipid/fatty acid transport	3	10.7	NCU02423 NCU11426 NCU07587	206	2.04	5.245	0.019
20.09 transport routes	8	28.5	NCU02423 NCU01234 NCU00778 NCU04650 NCU11426 NCU01907 NCU07587 NCU02885	1454	14.4	1.979	0.040
20.09.07 vesicular transport (Golgi network, etc.)	6	21.4	NCU00778 NCU04650 NCU11426 NCU01907 NCU07587 NCU02885	521	5.17	4.139	0.003
20.09.07.05 intra Golgi transport	2	7.14	NCU00778 NCU01907	74	0.73	9.781	0.018
30.01.09.03 Ca ²⁺ mediated signal transduction	2	7.14	NCU11426 NCU02885	125	1.24	5.758	0.047
32.01.06 cold shock response	2	7.14	NCU01234 NCU11426	65	0.64	11.156	0.014

34.11.09 temperature perception and response	2	7.1 4	NCU02423 NCU11426	110	1.09	6.550	0.037
42.04.03 actin cytoskeleton	3	10. 7	NCU11426 NCU07587 NCU02885	275	2.73	3.919	0.040

^aThe comparison is done to p3_p13841_Neu_crass_MIPS containing 10067 annotated genes.

28 out of 31 genes are found:

NCU00261 NCU00410 NCU00778 NCU00854 NCU01234 NCU01312 NCU01888 NCU01907 NCU02174 NCU02249 NCU02423 NCU02885 NCU02948
 NCU03226 NCU03682 NCU04650 NCU04699 NCU04986 NCU05243 NCU05964 NCU06322 NCU06869 NCU07408 NCU07587 NCU08026 NCU08727
 NCU09615 NCU11426