

**Table 2.** Functional Classification of Rapidly and Slowly Evolving Nematode Genes

GO description (hierarchical biological function)	Fraction	P-value	GO term
Rapidly evolving genes (upper 10%)			
Regulation of transcription, DNA-dependent	45/753	4.27E-005	GO:0006355
Regulation of transcription	45/753	5.72E-005	GO:0045449
Transcription, DNA-dependent	45/753	7.63E-005	GO:0006351
Nucleobase, nucleoside, nucleotide and nucleic acid metabolism	53/753	0.036752	GO:0006139
Slowly evolving genes (lower 10%)			
Embryogenesis and morphogenesis	107/753	9.30E-018	GO:0007345
Physiological processes	268/753	4.04E-012	GO:0007582
Protein biosynthesis	48/753	1.82E-011	GO:0006412
Cellular process	132/753	4.89E-011	GO:0009987
Biosynthesis	63/753	5.25E-011	GO:0009058
Small GTPase-mediated signal transduction	23/753	7.89E-011	GO:0007264
Cell growth and/or maintenance	94/753	3.33E-008	GO:0008151
Intracellular protein transport	15/753	9.92E-006	GO:0006886
Development	89/753	1.31E-005	GO:0007275
Metabolism	189/753	2.17E-005	GO:0008152
Protein metabolism	92/753	3.01E-005	GO:0019538
Cell organization and biogenesis	20/753	8.09E-005	GO:0016043
Transport	68/753	0.000318	GO:0006810
Reproduction	43/753	0.000377	GO:0000003
Nucleosome assembly	8/753	0.001020	GO:0006334
Intracellular signaling cascade	30/753	0.001910	GO:0007242
Signal transduction	38/753	0.002579	GO:0007165
Two-component signal transduction system (phosphorelay)	7/753	0.002746	GO:0000160
Main pathways of carbohydrate metabolism	11/753	0.003427	GO:0006092
Energy derivation by oxidation of organic compounds	12/753	0.004455	GO:0015980
Energy pathways	12/753	0.004455	GO:0006091
DNA packaging	8/753	0.010077	GO:0006323
Establishment and/or maintenance of chromatin architecture	8/753	0.010077	GO:0006325
Chromatin assembly/disassembly	8/753	0.010077	GO:0006333
Cell communication	40/753	0.012676	GO:0007154
mRNA splicing	5/753	0.016747	GO:0006371

Upper and lower 10% is scaled according to *dN*. Note the entire hierarchy of Gene Ontology terms for each gene was used when assessing functional overrepresentation; therefore, categories often contain the same sets of genes. All *P*-values are Bonferroni-corrected.