

GO Terms of Repressed Transcripts in Under-Replicated Regions

GO-ID	p-value	corr p-value	x (yellow if this >=10)	n	X	N	Description
7379	2.68E-07	7.99E-05	10	49	239	9591	segment specification
6357	6.12E-05	3.32E-03	15	186	239	9591	regulation of transcription from RNA polymerase II promoter
7498	9.20E-05	3.93E-03	10	92	239	9591	mesoderm development
45941	3.49E-04	1.12E-02	10	108	239	9591	positive regulation of transcription
7350	3.56E-04	1.12E-02	15	218	239	9591	blastoderm segmentation
10628	4.05E-04	1.24E-02	10	110	239	9591	positive regulation of gene expression
45935	4.67E-04	1.35E-02	10	112	239	9591	positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process
51173	4.67E-04	1.35E-02	10	112	239	9591	positive regulation of nitrogen compound metabolic process
48729	6.33E-04	1.55E-02	16	255	239	9591	tissue morphogenesis
48518	6.36E-04	1.55E-02	20	359	239	9591	positive regulation of biological process
9880	7.49E-04	1.71E-02	15	234	239	9591	embryonic pattern specification
7155	7.61E-04	1.71E-02	12	163	239	9591	cell adhesion
9888	9.14E-04	1.80E-02	23	453	239	9591	tissue development
35295	9.17E-04	1.80E-02	10	122	239	9591	tube development
10557	9.17E-04	1.80E-02	10	122	239	9591	positive regulation of macromolecule biosynthetic process
31328	1.04E-03	1.94E-02	11	146	239	9591	positive regulation of cellular biosynthetic process
9891	1.10E-03	1.96E-02	11	147	239	9591	positive regulation of biosynthetic process
22610	1.56E-03	2.62E-02	12	177	239	9591	biological adhesion
48522	1.72E-03	2.62E-02	17	307	239	9591	positive regulation of cellular process
45165	1.75E-03	2.62E-02	14	229	239	9591	cell fate commitment
6928	1.96E-03	2.78E-02	18	338	239	9591	cellular component movement
10604	1.98E-03	2.78E-02	10	135	239	9591	positive regulation of macromolecule metabolic process
31325	2.07E-03	2.87E-02	11	159	239	9591	positive regulation of cellular metabolic process
60541	2.39E-03	3.10E-02	11	162	239	9591	respiratory system development
7424	2.39E-03	3.10E-02	11	162	239	9591	open tracheal system development
9893	2.51E-03	3.22E-02	11	163	239	9591	positive regulation of metabolic process
35282	2.68E-03	3.22E-02	15	266	239	9591	segmentation
48870	2.70E-03	3.22E-02	12	189	239	9591	cell motility
10556	3.08E-03	3.50E-02	33	807	239	9591	regulation of macromolecule biosynthetic process
12501	3.34E-03	3.72E-02	10	145	239	9591	programmed cell death
51674	3.95E-03	4.24E-02	12	198	239	9591	localization of cell
8219	4.25E-03	4.53E-02	10	150	239	9591	cell death
16265	4.46E-03	4.70E-02	10	151	239	9591	death

1708	1.01E-05	1.34E-03	9	57	239	9591	cell fate specification
55123	9.56E-05	3.93E-03	9	75	239	9591	digestive system development
48565	9.56E-05	3.93E-03	9	75	239	9591	digestive tract development
7447	2.66E-03	3.22E-02	8	96	239	9591	imaginal disc pattern formation
35290	2.13E-07	7.99E-05	7	19	239	9591	trunk segmentation
7494	6.82E-06	1.34E-03	7	30	239	9591	midgut development
48634	7.00E-05	3.63E-03	7	42	239	9591	regulation of muscle organ development
8354	8.19E-05	3.76E-03	7	43	239	9591	germ cell migration
6915	1.01E-03	1.94E-02	7	64	239	9591	apoptosis
7507	2.57E-03	3.22E-02	7	75	239	9591	heart development
35292	6.04E-09	3.60E-06	6	8	239	9591	specification of segmental identity, trunk
7385	6.04E-09	3.60E-06	6	8	239	9591	specification of segmental identity, abdomen
7280	8.91E-06	1.34E-03	6	21	239	9591	pole cell migration
35287	1.20E-05	1.43E-03	6	22	239	9591	head segmentation
8406	1.18E-04	4.55E-03	6	32	239	9591	gonad development
48608	1.18E-04	4.55E-03	6	32	239	9591	reproductive structure development
43065	1.42E-04	5.28E-03	6	33	239	9591	positive regulation of apoptosis
45137	3.18E-04	1.08E-02	6	38	239	9591	development of primary sexual characteristics
10942	9.14E-04	1.80E-02	6	46	239	9591	positive regulation of cell death
43068	9.14E-04	1.80E-02	6	46	239	9591	positive regulation of programmed cell death
45944	1.03E-03	1.94E-02	6	47	239	9591	positive regulation of transcription from RNA polymerase II promoter
16337	3.08E-03	3.50E-02	6	58	239	9591	cell-cell adhesion
7548	3.66E-03	3.97E-02	6	60	239	9591	sex differentiation
7501	1.01E-05	1.34E-03	5	13	239	9591	mesodermal cell fate specification
7380	1.54E-05	1.53E-03	5	14	239	9591	specification of segmental identity, head
10623	2.26E-05	2.07E-03	5	15	239	9591	developmental programmed cell death
10552	4.46E-05	2.96E-03	5	17	239	9591	positive regulation of gene-specific transcription from RNA polymerase II promoter
48333	6.05E-05	3.32E-03	5	18	239	9591	mesodermal cell differentiation
1710	6.05E-05	3.32E-03	5	18	239	9591	mesodermal cell fate commitment
60795	8.05E-05	3.76E-03	5	19	239	9591	cell fate commitment involved in the formation of primary germ layers
43193	8.05E-05	3.76E-03	5	19	239	9591	positive regulation of gene-specific transcription
6917	2.66E-04	9.32E-03	5	24	239	9591	induction of apoptosis
10551	3.26E-04	1.08E-02	5	25	239	9591	regulation of gene-specific transcription from RNA polymerase II promoter
7156	4.75E-04	1.35E-02	5	27	239	9591	homophilic cell adhesion
51094	6.71E-04	1.57E-02	5	29	239	9591	positive regulation of developmental process

1707	6.71E-04	1.57E-02	5	29	239	9591	mesoderm formation
48332	7.89E-04	1.71E-02	5	30	239	9591	mesoderm morphogenesis
1704	9.22E-04	1.80E-02	5	31	239	9591	formation of primary germ layer
46620	1.07E-03	1.96E-02	5	32	239	9591	regulation of organ growth
12502	1.42E-03	2.42E-02	5	34	239	9591	induction of programmed cell death
7478	1.62E-03	2.62E-02	5	35	239	9591	leg disc morphogenesis
17148	1.62E-03	2.62E-02	5	35	239	9591	negative regulation of translation
48645	2.66E-03	3.22E-02	5	39	239	9591	organ formation
32583	2.98E-03	3.45E-02	5	40	239	9591	regulation of gene-specific transcription
35110	4.53E-03	4.74E-02	5	44	239	9591	leg morphogenesis
35054	1.84E-06	4.40E-04	4	5	239	9591	embryonic heart tube anterior/posterior pattern formation
48636	2.43E-05	2.07E-03	4	8	239	9591	positive regulation of muscle organ development
35221	4.29E-05	2.96E-03	4	9	239	9591	genital disc pattern formation
35224	4.29E-05	2.96E-03	4	9	239	9591	genital disc anterior/posterior pattern formation
7506	4.29E-05	2.96E-03	4	9	239	9591	gonadal mesoderm development
60911	1.59E-04	5.75E-03	4	12	239	9591	cardiac cell fate commitment
45570	5.40E-04	1.43E-02	4	16	239	9591	regulation of imaginal disc growth
35050	1.09E-03	1.96E-02	4	19	239	9591	embryonic heart tube development
7448	1.33E-03	2.30E-02	4	20	239	9591	anterior/posterior pattern formation, imaginal disc
35051	2.70E-03	3.22E-02	4	24	239	9591	cardiac cell differentiation
9954	2.70E-03	3.22E-02	4	24	239	9591	proximal/distal pattern formation
9190	3.15E-03	3.55E-02	4	25	239	9591	cyclic nucleotide biosynthetic process
9187	4.81E-03	4.99E-02	4	28	239	9591	cyclic nucleotide metabolic process
7384	1.53E-05	1.53E-03	3	3	239	9591	specification of segmental identity, thorax
10092	6.00E-05	3.32E-03	3	4	239	9591	specification of organ identity
46667	4.97E-04	1.35E-02	3	7	239	9591	compound eye retinal cell programmed cell death
7415	4.97E-04	1.35E-02	3	7	239	9591	defasciculation of motor neuron axon
7366	7.80E-04	1.71E-02	3	8	239	9591	periodic partitioning by pair rule gene
46666	1.15E-03	2.02E-02	3	9	239	9591	retinal cell programmed cell death
35225	2.17E-03	2.88E-02	3	11	239	9591	determination of genital disc primordium
7482	2.17E-03	2.88E-02	3	11	239	9591	haltere development
7445	2.17E-03	2.88E-02	3	11	239	9591	determination of imaginal disc primordium
7414	2.17E-03	2.88E-02	3	11	239	9591	axonal defasciculation
35216	2.85E-03	3.33E-02	3	12	239	9591	haltere disc development
48806	2.85E-03	3.33E-02	3	12	239	9591	genitalia development

35052	6.18E-04	1.55E-02	2	2	239	9591	dorsal vessel aortic cell fate commitment
8627	6.18E-04	1.55E-02	2	2	239	9591	induction of apoptosis by ionic changes
10921	1.82E-03	2.62E-02	2	3	239	9591	regulation of phosphatase activity
35096	1.82E-03	2.62E-02	2	3	239	9591	larval midgut cell programmed cell death
43666	1.82E-03	2.62E-02	2	3	239	9591	regulation of phosphoprotein phosphatase activity
35053	1.82E-03	2.62E-02	2	3	239	9591	dorsal vessel heart proper cell fate commitment
8624	1.82E-03	2.62E-02	2	3	239	9591	induction of apoptosis by extracellular signals
7514	1.82E-03	2.62E-02	2	3	239	9591	garland cell differentiation
48730	1.82E-03	2.62E-02	2	3	239	9591	epidermis morphogenesis
7383	1.82E-03	2.62E-02	2	3	239	9591	specification of segmental identity, antennal segment
35069	3.59E-03	3.93E-02	2	4	239	9591	larval midgut histolysis
48846	3.59E-03	3.93E-02	2	4	239	9591	axon extension involved in axon guidance