Pathway	Gene ranks	NES	pval	padj
GO:0005576 extracellular region	MI (MINISTER MILES AND MIL	1.73	1.1e-04	2.2e-03
GO:0002376 immune system process		2.15	1.1e-04	2.2e-03
GO:0005198 structural molecule activity	MI 11	2.07	1.1e-04	2.2e-03
GO:0005615 extracellular space	Minimum remains a construction of the accordance of the contract of the contra	1.67	1.1e-04	2.2e-03
GO:0005840 ribosome	## ###################################	2.31	1.2e-04	2.2e-03
GO:0003735 structural constituent of ribosome	II seemstaan taa taa marka aa a	2.39	1.2e-04	2.2e-03
GO:0042254 ribosome biogenesis	MIRON (MILITIAL AND ADMINISTRATION OF THE PROPERTY OF THE PROP	1.51	7.6e-04	8.3e-03
GO:0019843 rRNA binding	CHILD CONTRACTOR CONTR	1.72	3.6e-03	1.8e-02
GO:0006412 translation		1.35	8.3e-03	3.8e-02
GO:0050877 nervous system process	MINISTER (1980) 10 10 10 10 10 10 10 10 10 10 10 10 10	1.45	8.3e-03	3.8e-02
GO:0031012 extracellular matrix	MINITED TO 100 100 100 100 100 100 100 100 100 10	1.55	9.2e-03	3.9e-02
GO:0034655 nucleobase-containing compound catabolic process		-1.34	1.2e-02	4.7e-02
GO:0009790 embryo development		-1.32	9.6e-03	3.9e-02
GO:0003677 DNA binding		-1.39	9.4e-03	3.9e-02
GO:0005635 nuclear envelope	The first of the second of the	-1.56	3.6e-03	1.8e-02
GO:0007059 chromosome segregation	11 1 1	-1.52	3.1e-03	1.7e-02
GO:0051276 chromosome organization	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	-2.16	2.7e-03	1.6e-02
GO:0005694 chromosome		-2.00	2.2e-03	1.3e-02
GO:0000278 mitotic cell cycle		-1.71	2.1e-03	1.3e-02
GO:0016779 nucleotidyltransferase activity	The state of the s	-1.80	1.8e-03	1.2e-02
GO:0006259 DNA metabolic process	1 111 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	-1.78	1.7e-03	1.2e-02
GO:0005654 nucleoplasm		-1.85	1.6e-03	1.2e-02
GO:0051301 cell division	H 1 11 1111 (0111000000011100000011100000000	-1.70	1.4e-03	1.2e-02
GO:0006397 mRNA processing	The state of the s	-2.22	9.6e-04	8.7e-03
GO:0000228 nuclear chromosome	The state of the s	-1.67	9.3e-04	8.7e-03
GO:0140014 mitotic nuclear division	T 1.1 WE TO SECURE OF THE SECU	-1.98	6.8e-04	8.3e-03
GO:0000988 transcription factor activity, protein binding	The final control of the second control of the second of t	-1.73	6.0e-04	8.2e-03
GO:0042393 histone binding	The second secon	-2.12	3.9e-04	6.1e-03
	0 2500 5000 7500 10000			