

**Supplementary Table 2.** Enrichment for Gene Ontology (GO) terms in genes up- and down-regulated after 3 days of ETC-159 treatment. For each GO category (biological process, cellular component and molecular function) we report the significant GO terms (adjusted P-value <5%). Enrichments were calculated by Webgestalt (WEB-based GENE SeT AnaLysis Toolkit, (Zhang, B., Kirov, S.A., Snoddy, J.R. (2005). WebGestalt: an integrated system for exploring gene sets in various biological contexts. *Nucleic Acids Res*, 33(Web Server issue), W741-748)) and using the set of tumor expressed genes as the background (see Methods). For each significant GO term we report: the number of reference genes in the category (C), the number of genes in the gene set and also in the category (O), the expected number in the category (E), the ratio of enrichment (R), and P-value of significance of the enrichment adjusted by the multiple tests

Enrichment for GO terms in genes up-regulated after 3 days of ETC-159 treatment							
GO category	Genes in the category (C)	Genes in the gene set (O)	Expected number (E)	Ratio of enrichment (R)	Adjusted P-value	GO term name	GO term
biological process	919	30	11.43	2.62	7.00E-04	response to wounding	GO:0009611
biological process	4499	85	55.98	1.52	7.00E-04	single-multicellular organism process	GO:0044707
biological process	4518	85	56.22	1.51	7.00E-04	multicellular organismal process	GO:0032501
biological process	1109	32	13.8	2.32	1.80E-03	response to external stimulus	GO:0009605
biological process	13	4	0.16	24.73	4.20E-03	heat generation	GO:0031649
biological process	1469	37	18.28	2.02	4.20E-03	regulation of multicellular organismal process	GO:0051239
biological process	156	10	1.94	5.15	4.40E-03	regulation of inflammatory response	GO:0050727
biological process	387	16	4.82	3.32	4.40E-03	inflammatory response	GO:0006954
biological process	306	14	3.81	3.68	4.40E-03	regulation of response to external stimulus	GO:0032101
biological process	170	10	2.12	4.73	7.40E-03	positive regulation of cytokine production	GO:0001819
biological process	174	10	2.17	4.62	8.00E-03	regulation of immune effector process	GO:0002697
biological process	86	7	1.07	6.54	8.00E-03	acute inflammatory response	GO:0002526
biological process	223	11	2.77	3.96	8.00E-03	negative regulation of phosphate metabolic process	GO:0045936
biological process	223	11	2.77	3.96	8.00E-03	negative regulation of phosphorus metabolic process	GO:0010563
biological process	269	12	3.35	3.59	8.00E-03	anion transport	GO:0006820
biological process	355	14	4.42	3.17	8.00E-03	cytokine production	GO:0001816
biological process	39	5	0.49	10.3	8.00E-03	regulation of acute inflammatory response	GO:0002673
biological process	401	15	4.99	3.01	8.00E-03	positive regulation of multicellular organismal process	GO:0051240
biological process	10	3	0.12	24.11	1.03E-02	positive regulation of steroid biosynthetic process	GO:0010893
biological process	195	10	2.43	4.12	1.03E-02	negative regulation of phosphorylation	GO:0042326
biological process	2	2	0.02	80.37	1.03E-02	positive regulation of calcidiol 1-monooxygenase activity	GO:0060559
biological process	237	11	2.95	3.73	1.03E-02	gland development	GO:0048732
biological process	24	4	0.3	13.39	1.03E-02	regulation of humoral immune response	GO:0002920
biological process	244	11	3.04	3.62	1.03E-02	steroid metabolic process	GO:0008202
biological process	2916	56	36.28	1.54	1.03E-02	system development	GO:0048731
biological process	317	13	3.94	3.3	1.03E-02	regulation of cytokine production	GO:0001817
biological process	832	23	10.35	2.22	1.03E-02	defense response	GO:0006952
biological process	9	3	0.11	26.79	1.03E-02	fever generation	GO:0001660

biological process	101	7	1.26	5.57	1.27E-02	protein processing	GO:0016485
biological process	11	3	0.14	21.92	1.27E-02	hemidesmosome assembly	GO:0031581
biological process	26	4	0.32	12.36	1.27E-02	positive regulation of reactive oxygen species metabolic process	GO:2000379
biological process	26	4	0.32	12.36	1.27E-02	temperature homeostasis	GO:0001659
biological process	481	16	5.98	2.67	1.27E-02	response to biotic stimulus	GO:0009607
biological process	6247	99	77.73	1.27	1.27E-02	single-organism process	GO:0044699
biological process	1040	26	12.94	2.01	1.52E-02	locomotion	GO:0040011
biological process	258	11	3.21	3.43	1.52E-02	epithelial cell differentiation	GO:0030855
biological process	3770	67	46.91	1.43	1.52E-02	developmental process	GO:0032502
biological process	51	5	0.63	7.88	1.52E-02	regulation of reactive oxygen species metabolic process	GO:2000377
biological process	113	7	1.41	4.98	1.60E-02	protein maturation	GO:0051604
biological process	13	3	0.16	18.55	1.60E-02	regulation of hair cycle	GO:0042634
cellular component	1456	53	18.6	2.85	9.99E-11	extracellular region	GO:0005576
cellular component	3180	73	40.63	1.8	2.75E-06	cell periphery	GO:0071944
cellular component	3102	69	39.63	1.74	1.82E-05	plasma membrane	GO:0005886
cellular component	816	29	10.42	2.78	1.82E-05	extracellular region part	GO:0044421
cellular component	101	10	1.29	7.75	1.94E-05	anchored to membrane	GO:0031225
cellular component	3920	78	50.08	1.56	0.0001	intrinsic to membrane	GO:0031224
cellular component	633	23	8.09	2.84	0.0001	extracellular space	GO:0005615
cellular component	198	12	2.53	4.74	0.0002	apical plasma membrane	GO:0016324
cellular component	3837	74	49.02	1.51	0.0005	integral to membrane	GO:0016021
cellular component	4577	84	58.47	1.44	0.0006	membrane part	GO:0044425
cellular component	6063	103	77.46	1.33	0.0009	membrane	GO:0016020
cellular component	260	12	3.32	3.61	0.0013	apical part of cell	GO:0045177
cellular component	1492	35	19.06	1.84	0.0036	plasma membrane part	GO:0044459
cellular component	921	24	11.77	2.04	0.0077	intrinsic to plasma membrane	GO:0031226
cellular component	887	23	11.33	2.03	0.0092	integral to plasma membrane	GO:0005887
cellular component	18	3	0.23	13.05	0.0144	basal lamina	GO:0005605
cellular component	612	17	7.82	2.17	0.0199	cell junction	GO:0030054
cellular component	268	10	3.42	2.92	0.0205	proteinaceous extracellular matrix	GO:0005578
cellular component	376	12	4.8	2.5	0.0254	cell surface	GO:0009986
cellular component	7	2	0.09	22.36	0.0254	hemidesmosome	GO:0030056
cellular component	10	2	0.13	15.65	0.0499	laminin complex	GO:0043256
molecular function	139	9	1.71	5.28	0.0119	cytokine activity	GO:0005125
molecular function	3	2	0.04	54.32	0.0301	cyclase activator activity	GO:0010853

molecular function	3	2	0.04	54.32	0.0301	guanylate cyclase activator activity	GO:0030250
molecular function	952	24	11.68	2.05	0.0339	receptor binding	GO:0005102
molecular function	4	2	0.05	40.74	0.0339	cyclase regulator activity	GO:0010851
molecular function	4	2	0.05	40.74	0.0339	guanylate cyclase regulator activity	GO:0030249
molecular function	40	4	0.49	8.15	0.0424	receptor regulator activity	GO:0030545
molecular function	5	2	0.06	32.59	0.0424	protein-glutamine gamma-glutamyltransferase activity	GO:0003810

### Enrichment for GO terms in genes down-regulated after 3 days of ETC-159 treatment

GO category	Genes in the category (C)	Genes in the gene set (O)	Expected number (E)	Ratio of enrichment (R)	Adjusted P-value	GO term name	GO term
biological process	995	183	49.28	3.71	1.73E-57	cell cycle process	GO:0022402
biological process	746	153	36.95	4.14	2.46E-53	mitotic cell cycle	GO:0000278
biological process	1301	198	64.43	3.07	2.81E-49	cell cycle	GO:0007049
biological process	499	119	24.71	4.82	1.13E-47	M phase	GO:0000279
biological process	365	96	18.08	5.31	9.94E-42	M phase of mitotic cell cycle	GO:0000087
biological process	356	94	17.63	5.33	4.52E-41	nuclear division	GO:0000280
biological process	356	94	17.63	5.33	4.52E-41	mitosis	GO:0007067
biological process	379	96	18.77	5.11	2.34E-40	organelle fission	GO:0048285
biological process	786	129	38.93	3.31	1.56E-33	DNA metabolic process	GO:0006259
biological process	408	83	20.21	4.11	3.50E-27	regulation of cell cycle process	GO:0010564
biological process	437	85	21.64	3.93	1.86E-26	cell division	GO:0051301
biological process	140	48	6.93	6.92	8.30E-26	chromosome segregation	GO:0007059
biological process	253	63	12.53	5.03	2.08E-25	DNA replication	GO:0006260
biological process	259	60	12.83	4.68	2.30E-22	regulation of cell cycle arrest	GO:0071156
biological process	237	56	11.74	4.77	2.92E-21	cell cycle checkpoint	GO:0000075
biological process	687	100	34.02	2.94	2.95E-21	regulation of cell cycle	GO:0051726
biological process	392	72	19.41	3.71	1.02E-20	interphase	GO:0051325
biological process	386	71	19.12	3.71	1.80E-20	interphase of mitotic cell cycle	GO:0051329
biological process	366	68	18.13	3.75	8.10E-20	cell cycle arrest	GO:0007050
biological process	84	32	4.16	7.69	1.20E-18	mitotic prometaphase	GO:0000236
biological process	427	71	21.15	3.36	6.32E-18	negative regulation of cell cycle	GO:0045786
biological process	35	21	1.73	12.12	3.44E-17	DNA strand elongation	GO:0022616
biological process	32	20	1.58	12.62	7.34E-17	DNA strand elongation involved in DNA replication	GO:0006271
biological process	627	86	31.05	2.77	1.82E-16	chromosome organization	GO:0051276
biological process	92	31	4.56	6.8	2.55E-16	DNA-dependent DNA replication	GO:0006261
biological process	393	65	19.46	3.34	2.89E-16	microtubule-based process	GO:0007017
biological process	385	63	19.07	3.3	1.66E-15	DNA repair	GO:0006281
biological process	1949	176	96.52	1.82	3.86E-15	organelle organization	GO:0006996
biological process	53	23	2.62	8.76	7.66E-15	sister chromatid segregation	GO:0000819
biological process	50	22	2.48	8.88	2.42E-14	mitotic sister chromatid segregation	GO:0000070
biological process	265	48	13.12	3.66	2.12E-13	microtubule cytoskeleton organization	GO:0000226
biological process	82	26	4.06	6.4	5.93E-13	spindle organization	GO:0007051
biological process	154	35	7.63	4.59	1.15E-12	DNA conformation change	GO:0071103

biological process	194	39	9.61	4.06	2.55E-12	DNA recombination	GO:0006310
biological process	143	33	7.08	4.66	3.89E-12	S phase	GO:0051320
biological process	583	73	28.87	2.53	7.61E-12	response to DNA damage stimulus	GO:0006974
biological process	294	48	14.56	3.3	1.09E-11	regulation of mitotic cell cycle	GO:0007346
biological process	119	28	5.89	4.75	1.79E-10	DNA packaging	GO:0006323
biological process	33	15	1.63	9.18	5.93E-10	centromere complex assembly	GO:0034508
cellular component	577	103	27.04	3.81	6.38E-31	chromosome	GO:0005694
cellular component	487	90	22.82	3.94	3.85E-28	chromosomal part	GO:0044427
cellular component	162	50	7.59	6.59	8.60E-26	condensed chromosome	GO:0000793
cellular component	145	44	6.8	6.47	2.30E-22	chromosome, centromeric region	GO:0000775
cellular component	85	34	3.98	8.53	1.10E-21	condensed chromosome, centromeric region	GO:0000779
cellular component	80	33	3.75	8.8	1.27E-21	condensed chromosome kinetochore	GO:0000777
cellular component	101	36	4.73	7.61	4.18E-21	kinetochore	GO:0000776
cellular component	226	49	10.59	4.63	2.78E-18	spindle	GO:0005819
cellular component	814	93	38.15	2.44	1.55E-14	microtubule cytoskeleton	GO:0015630
cellular component	3414	250	160.01	1.56	1.90E-14	non-membrane-bounded organelle	GO:0043228
cellular component	3414	250	160.01	1.56	1.90E-14	intracellular non-membrane-bounded organelle	GO:0043232
cellular component	2858	214	133.95	1.6	8.47E-13	nuclear part	GO:0044428
cellular component	2553	194	119.65	1.62	5.95E-12	nuclear lumen	GO:0031981
cellular component	5263	333	246.67	1.35	2.20E-11	nucleus	GO:0005634
cellular component	3054	219	143.14	1.53	2.98E-11	intracellular organelle lumen	GO:0070013
cellular component	3092	220	144.92	1.52	5.45E-11	organelle lumen	GO:0043233
cellular component	3135	222	146.93	1.51	6.25E-11	membrane-enclosed lumen	GO:0031974
cellular component	93	24	4.36	5.51	7.29E-11	spindle pole	GO:0000922
cellular component	1093	101	51.23	1.97	2.77E-10	cytoskeletal part	GO:0044430
cellular component	1383	119	64.82	1.84	3.39E-10	nucleoplasm	GO:0005654
cellular component	265	39	12.42	3.14	2.65E-09	nuclear chromosome	GO:0000228
cellular component	463	53	21.7	2.44	1.97E-08	microtubule organizing center	GO:0005815
cellular component	6063	357	284.16	1.26	3.03E-08	intracellular organelle part	GO:0044446
cellular component	11	8	0.52	15.52	4.13E-08	MCM complex	GO:0042555
cellular component	42	14	1.97	7.11	4.13E-08	spindle microtubule	GO:0005876
cellular component	6135	359	287.54	1.25	5.30E-08	organelle part	GO:0044422
cellular component	360	44	16.87	2.61	5.82E-08	centrosome	GO:0005813
cellular component	12	8	0.56	14.22	1.03E-07	condensed chromosome outer kinetochore	GO:0000940
cellular component	46	14	2.16	6.49	1.36E-07	replication fork	GO:0005657
cellular component	223	32	10.45	3.06	1.54E-07	nuclear chromosome part	GO:0044454

cellular component	313	39	14.67	2.66	2.27E-07	microtubule	GO:0005874
cellular component	1542	117	72.27	1.62	5.93E-07	cytoskeleton	GO:0005856
cellular component	60	15	2.81	5.33	6.84E-07	condensed nuclear chromosome	GO:0000794
cellular component	12	7	0.56	12.45	2.81E-06	condensed nuclear chromosome, centromeric region	GO:0000780
cellular component	6	5	0.28	17.78	1.14E-05	condensin complex	GO:0000796
cellular component	264	31	12.37	2.51	1.98E-05	chromatin	GO:0000785
cellular component	4	4	0.19	21.34	3.98E-05	condensed nuclear chromosome kinetochore	GO:0000778
cellular component	56	12	2.62	4.57	6.88E-05	centriole	GO:0005814
cellular component	9335	485	437.51	1.11	0.0001	organelle	GO:0043226
cellular component	9326	484	437.09	1.11	0.0001	intracellular organelle	GO:0043229
molecular function	69	17	3.28	5.19	4.29E-06	DNA-dependent ATPase activity	GO:0008094
molecular function	70	17	3.32	5.11	4.29E-06	microtubule motor activity	GO:0003777
molecular function	1358	107	64.49	1.66	9.33E-06	ATP binding	GO:0005524
molecular function	1386	107	65.82	1.63	1.84E-05	adenyl ribonucleotide binding	GO:0032559
molecular function	1390	107	66.01	1.62	1.84E-05	adenyl nucleotide binding	GO:0030554
molecular function	165	23	7.84	2.94	0.0002	structure-specific DNA binding	GO:0043566
molecular function	118	18	5.6	3.21	0.0007	motor activity	GO:0003774
molecular function	5	4	0.24	16.85	0.0012	ribonuclease H activity	GO:0004523
molecular function	5	4	0.24	16.85	0.0012	single-stranded DNA-dependent ATPase activity	GO:0043142
molecular function	1930	128	91.65	1.4	0.0014	DNA binding	GO:0003677
molecular function	293	30	13.91	2.16	0.0024	chromatin binding	GO:0003682
molecular function	699	56	33.19	1.69	0.0024	nucleoside-triphosphatase activity	GO:0017111
molecular function	12	5	0.57	8.77	0.0024	histone kinase activity	GO:0035173
molecular function	142	18	6.74	2.67	0.0024	helicase activity	GO:0004386
molecular function	1680	111	79.78	1.39	0.0024	ribonucleoside binding	GO:0032549
molecular function	1690	112	80.26	1.4	0.0024	nucleoside binding	GO:0001882
molecular function	61	11	2.9	3.8	0.0024	single-stranded DNA binding	GO:0003697
molecular function	730	57	34.67	1.64	0.0024	pyrophosphatase activity	GO:0016462
molecular function	733	57	34.81	1.64	0.0024	hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhy	GO:0016818
molecular function	158	19	7.5	2.53	0.0038	nuclease activity	GO:0004518
molecular function	1667	110	79.16	1.39	0.0038	purine ribonucleoside triphosphate binding	GO:0035639
molecular function	1676	110	79.59	1.38	0.0038	purine ribonucleoside binding	GO:0032550
molecular function	1679	110	79.73	1.38	0.0038	purine nucleoside binding	GO:0001883
molecular function	738	57	35.05	1.63	0.0038	hydrolase activity, acting on acid anhydrides	GO:0016817
molecular function	1698	110	80.64	1.36	0.0052	purine ribonucleotide binding	GO:0032555
molecular function	1705	111	80.97	1.37	0.0052	purine nucleotide binding	GO:0017076

molecular function	1709	110	81.16	1.36	0.0065	ribonucleotide binding	GO:0032553
molecular function	48	9	2.28	3.95	0.0065	damaged DNA binding	GO:0003684
molecular function	43	8	2.04	3.92	0.0125	DNA helicase activity	GO:0003678
molecular function	329	29	15.62	1.86	0.0151	ATPase activity	GO:0016887
molecular function	12	4	0.57	7.02	0.0262	DNA N-glycosylase activity	GO:0019104
molecular function	2	2	0.09	21.06	0.0276	double-stranded DNA specific exodeoxyribonuclease activity	GO:0008309
molecular function	2	2	0.09	21.06	0.0276	H3 histone acetyltransferase activity	GO:0010484
molecular function	2	2	0.09	21.06	0.0276	site-specific endodeoxyribonuclease activity, specific for altered base	GO:0016890
molecular function	2	2	0.09	21.06	0.0276	CD8 receptor binding	GO:0042610
molecular function	2138	128	101.53	1.26	0.0276	anion binding	GO:0043168
molecular function	30	6	1.42	4.21	0.0276	ATP-dependent DNA helicase activity	GO:0004003
molecular function	40	7	1.9	3.69	0.0276	deoxyribonuclease activity	GO:0004536
molecular function	62	9	2.94	3.06	0.0276	exonuclease activity	GO:0004527
molecular function	62	9	2.94	3.06	0.0276	ribonuclease activity	GO:0004540