

BET inhibitors enhance embryonic and fetal *globin* expression in erythroleukemia cell lines

John Z. Cao,¹ Kristina Bigelow,² Amittha Wickrema^{1,2} and Lucy A. Godley^{1,2}

¹Committee on Cancer Biology, Biological Sciences Division, The University of Chicago and ²Section of Hematology/Oncology, Department of Medicine, The University of Chicago, Chicago IL, USA

Correspondence: LUCY A. GODLEY - lgodley@medicine.bsd.uchicago.edu

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Supplemental Table 1. Enriched GO terms in induced or suppressed genes.

EPO vs. DMSO, Induced (Supplemental Figure 2B, right panel)			
GO ID	Description	p.Val	FDR
GO:0070887	cellular response to chemical stimulus	7.48E-05	7.48E-05
GO:0015669	gas transport	1.45E-04	1.45E-04
GO:0055072	iron ion homeostasis	1.61E-04	1.61E-04
GO:0006779	porphyrin-containing compound biosynthetic process	2.71E-04	2.71E-04
GO:0006778	porphyrin-containing compound metabolic process	4.81E-04	4.81E-04
GO:0033014	tetrapyrrole biosynthetic process	6.34E-04	6.34E-04
GO:0046501	protoporphyrinogen IX metabolic process	7.28E-04	7.28E-04
GO:0006950	response to stress	1.96E-03	1.96E-03
GO:0042744	hydrogen peroxide catabolic process	2.20E-03	2.20E-03
GO:0055076	transition metal ion homeostasis	2.33E-03	2.33E-03
GO:0006879	cellular iron ion homeostasis	5.18E-03	5.18E-03
GO:0015671	oxygen transport	5.76E-03	5.76E-03
GO:0006782	protoporphyrinogen IX biosynthetic process	7.67E-03	7.67E-03
GO:0098754	detoxification	7.92E-03	7.92E-03
GO:0042168	heme metabolic process	9.89E-03	9.89E-03
GO:0006783	heme biosynthetic process	1.33E-02	1.33E-02
GO:0002376	immune system process	2.18E-02	2.18E-02
GO:0006826	iron ion transport	2.28E-02	2.28E-02
GO:0033013	tetrapyrrole metabolic process	2.41E-02	2.41E-02
GO:1990748	cellular detoxification	2.65E-02	2.65E-02
GO:0042743	hydrogen peroxide metabolic process	3.55E-02	3.55E-02
GO:0098869	cellular oxidant detoxification	3.75E-02	3.75E-02
GO:0098656	anion transmembrane transport	3.77E-02	3.77E-02
EPO vs. DMSO, Suppressed (Supplemental Figure 2B, left panel)			
GO ID	Description	p.Val	FDR
GO:0048856	anatomical structure development	3.94E-16	3.94E-16
GO:0048731	system development	7.89E-16	7.89E-16
GO:0007154	cell communication	1.05E-15	1.05E-15
GO:0032502	developmental process	2.13E-15	2.13E-15
GO:0048583	regulation of response to stimulus	2.46E-15	2.46E-15
GO:0009653	anatomical structure morphogenesis	2.97E-15	2.97E-15
GO:0007275	multicellular organism development	7.35E-15	7.35E-15
GO:0023052	signaling	8.35E-15	8.35E-15
GO:0035556	intracellular signal transduction	1.09E-14	1.09E-14
GO:0023051	regulation of signaling	4.42E-14	4.42E-14
GO:0010646	regulation of cell communication	2.12E-13	2.12E-13
GO:0050896	response to stimulus	7.60E-13	7.60E-13
GO:0007165	signal transduction	1.02E-12	1.02E-12
GO:0009966	regulation of signal transduction	1.41E-12	1.41E-12
GO:0040011	locomotion	7.72E-12	7.72E-12
GO:0007399	nervous system development	1.63E-11	1.63E-11
GO:0032501	multicellular organismal process	1.64E-11	1.64E-11
GO:0016477	cell migration	2.67E-11	2.67E-11
GO:0007166	cell surface receptor signaling pathway	2.71E-11	2.71E-11
GO:0050793	regulation of developmental process	8.42E-11	8.42E-11
GO:0022008	neurogenesis	9.06E-11	9.06E-11
GO:0051239	regulation of multicellular organismal process	1.09E-10	1.09E-10
GO:0051240	positive regulation of multicellular organismal process	5.98E-10	5.98E-10
GO:0048699	generation of neurons	1.34E-09	1.34E-09
GO:0051716	cellular response to stimulus	1.39E-09	1.39E-09
GO:0048468	cell development	1.44E-09	1.44E-09
GO:0048870	cell motility	1.52E-09	1.52E-09
GO:0051674	localization of cell	1.52E-09	1.52E-09
GO:0006928	movement of cell or subcellular component	3.65E-09	3.65E-09
GO:0030154	cell differentiation	7.27E-09	7.27E-09

Supplemental Table 1. Enriched GO terms in induced or suppressed genes, continued.

GO:0051094	positive regulation of developmental process	9.36E-09	9.36E-09
GO:0030182	neuron differentiation	1.03E-08	1.03E-08
GO:2000026	regulation of multicellular organismal development	1.04E-08	1.04E-08
GO:0048869	cellular developmental process	1.09E-08	1.09E-08
GO:0048585	negative regulation of response to stimulus	1.16E-08	1.16E-08
GO:0009968	negative regulation of signal transduction	1.23E-08	1.23E-08
GO:0001775	cell activation	3.99E-08	3.99E-08
GO:0030155	regulation of cell adhesion	4.67E-08	4.67E-08
GO:0065008	regulation of biological quality	5.18E-08	5.18E-08
GO:0023057	negative regulation of signaling	6.49E-08	6.49E-08
GO:0022610	biological adhesion	1.01E-07	1.01E-07
GO:0000902	cell morphogenesis	1.14E-07	1.14E-07
GO:0010648	negative regulation of cell communication	1.22E-07	1.22E-07
GO:0007155	cell adhesion	1.58E-07	1.58E-07
GO:1902531	regulation of intracellular signal transduction	1.98E-07	1.98E-07
GO:0120036	plasma membrane bounded cell projection organization	1.99E-07	1.99E-07
GO:0030030	cell projection organization	2.33E-07	2.33E-07
GO:0032879	regulation of localization	3.12E-07	3.12E-07
GO:0022603	regulation of anatomical structure morphogenesis	3.41E-07	3.41E-07
GO:0031175	neuron projection development	4.05E-07	4.05E-07
EPO+JQ1 vs. JQ1, Induced (Supplemental Figure 2C, right panel)			
GO ID	Description	p.Val	FDR
GO:0070887	cellular response to chemical stimulus	5.01E-10	5.01E-10
GO:0098754	detoxification	1.24E-08	1.24E-08
GO:0015669	gas transport	6.06E-07	6.06E-07
GO:1990748	cellular detoxification	3.76E-06	3.76E-06
GO:0009636	response to toxic substance	3.85E-06	3.85E-06
GO:0042221	response to chemical	5.44E-06	5.44E-06
GO:0097237	cellular response to toxic substance	9.22E-06	9.22E-06
GO:0042744	hydrogen peroxide catabolic process	1.50E-05	1.50E-05
GO:0010033	response to organic substance	3.34E-05	3.34E-05
GO:0015671	oxygen transport	3.60E-05	3.60E-05
GO:0098869	cellular oxidant detoxification	4.61E-05	4.61E-05
GO:0042168	heme metabolic process	8.86E-05	8.86E-05
GO:0071310	cellular response to organic substance	1.16E-04	1.16E-04
GO:0010035	response to inorganic substance	1.17E-04	1.17E-04
GO:0055076	transition metal ion homeostasis	4.52E-04	4.52E-04
GO:0055072	iron ion homeostasis	4.95E-04	4.95E-04
GO:0006778	porphyrin-containing compound metabolic process	5.76E-04	5.76E-04
GO:0051179	localization	6.06E-04	6.06E-04
GO:0006810	transport	8.35E-04	8.35E-04
GO:0140352	export from cell	1.27E-03	1.27E-03
GO:0051234	establishment of localization	1.78E-03	1.78E-03
GO:0046916	cellular transition metal ion homeostasis	2.08E-03	2.08E-03
GO:0006783	heme biosynthetic process	2.29E-03	2.29E-03
GO:0006879	cellular iron ion homeostasis	3.59E-03	3.59E-03
GO:0046903	secretion	3.65E-03	3.65E-03
GO:0032940	secretion by cell	4.03E-03	4.03E-03
GO:0042743	hydrogen peroxide metabolic process	4.22E-03	4.22E-03
GO:0006779	porphyrin-containing compound biosynthetic process	7.94E-03	7.94E-03
GO:0042127	regulation of cell population proliferation	1.08E-02	1.08E-02
GO:1901700	response to oxygen-containing compound	1.12E-02	1.12E-02
GO:0033014	tetrapyrrole biosynthetic process	1.50E-02	1.50E-02
GO:0033013	tetrapyrrole metabolic process	2.01E-02	2.01E-02
GO:0002486	antigen processing and presentation of endogenous peptide antigen via MHC class I via ER pathway, TAP-independent	2.05E-02	2.05E-02
GO:0002484	antigen processing and presentation of endogenous peptide antigen via MHC class I via ER pathway	2.05E-02	2.05E-02
GO:0010038	response to metal ion	2.72E-02	2.72E-02
GO:0042592	homeostatic process	2.92E-02	2.92E-02

Supplemental Table 1. Enriched GO terms in induced or suppressed genes, continued.

EPO+JQ1 vs. JQ1, Suppressed (Supplemental Figure 2C, left panel)			
GO ID	Description	p.Val	FDR
GO:0002684	positive regulation of immune system process	1.85E-11	1.85E-11
GO:0002376	immune system process	7.28E-11	7.28E-11
GO:0023052	signaling	2.94E-10	2.94E-10
GO:0007154	cell communication	3.78E-10	3.78E-10
GO:0001775	cell activation	6.75E-10	6.75E-10
GO:0030097	hemopoiesis	1.04E-09	1.04E-09
GO:0002520	immune system development	1.36E-09	1.36E-09
GO:0007165	signal transduction	2.71E-09	2.71E-09
GO:0048534	hematopoietic or lymphoid organ development	3.89E-09	3.89E-09
GO:0045321	leukocyte activation	5.06E-09	5.06E-09
GO:0002696	positive regulation of leukocyte activation	6.35E-09	6.35E-09
GO:0050867	positive regulation of cell activation	1.24E-08	1.24E-08
GO:0035556	intracellular signal transduction	2.31E-08	2.31E-08
GO:0050865	regulation of cell activation	2.76E-08	2.76E-08
GO:0048583	regulation of response to stimulus	3.44E-08	3.44E-08
GO:0002521	leukocyte differentiation	3.72E-08	3.72E-08
GO:0002694	regulation of leukocyte activation	9.95E-08	9.95E-08
GO:0002682	regulation of immune system process	1.67E-07	1.67E-07
GO:0046649	lymphocyte activation	4.71E-07	4.71E-07
GO:0045785	positive regulation of cell adhesion	7.76E-07	7.76E-07
GO:0051239	regulation of multicellular organismal process	7.91E-07	7.91E-07
GO:0007166	cell surface receptor signaling pathway	1.64E-06	1.64E-06
GO:0051716	cellular response to stimulus	1.92E-06	1.92E-06
GO:0040011	locomotion	3.40E-06	3.40E-06
GO:1903039	positive regulation of leukocyte cell-cell adhesion	4.20E-06	4.20E-06
GO:2000026	regulation of multicellular organismal development	1.06E-05	1.06E-05
GO:0030155	regulation of cell adhesion	1.41E-05	1.41E-05
GO:1903131	mononuclear cell differentiation	1.49E-05	1.49E-05
GO:0008283	cell population proliferation	1.49E-05	1.49E-05
GO:0032944	regulation of mononuclear cell proliferation	1.61E-05	1.61E-05
GO:0032943	mononuclear cell proliferation	1.91E-05	1.91E-05
GO:0051251	positive regulation of lymphocyte activation	1.98E-05	1.98E-05
GO:0050896	response to stimulus	2.21E-05	2.21E-05
GO:0016477	cell migration	2.70E-05	2.70E-05
GO:0050776	regulation of immune response	2.72E-05	2.72E-05
GO:1903037	regulation of leukocyte cell-cell adhesion	2.85E-05	2.85E-05
GO:0042110	T cell activation	3.62E-05	3.62E-05
GO:0051240	positive regulation of multicellular organismal process	3.73E-05	3.73E-05
GO:0048584	positive regulation of response to stimulus	4.23E-05	4.23E-05
GO:0050870	positive regulation of T cell activation	4.73E-05	4.73E-05
GO:0048731	system development	4.95E-05	4.95E-05
GO:0032501	multicellular organismal process	5.00E-05	5.00E-05
GO:0070663	regulation of leukocyte proliferation	5.20E-05	5.20E-05
GO:0022409	positive regulation of cell-cell adhesion	5.53E-05	5.53E-05
GO:0006928	movement of cell or subcellular component	6.31E-05	6.31E-05
GO:0007155	cell adhesion	7.91E-05	7.91E-05
GO:0070661	leukocyte proliferation	8.14E-05	8.14E-05
GO:0022610	biological adhesion	9.08E-05	9.08E-05
GO:0046651	lymphocyte proliferation	9.39E-05	9.39E-05
GO:0050670	regulation of lymphocyte proliferation	9.41E-05	9.41E-05
JQ1 vs. DMSO, Induced (Supplemental Figure 2D, right panel)			
GO ID	Description	p.Val	FDR
GO:0071702	organic substance transport	2.55E-02	2.55E-02
GO:0006820	anion transport	4.50E-02	4.50E-02
JQ1 vs. DMSO, Suppressed (Supplemental Figure 2D, left panel)			

Supplemental Table 1. Enriched GO terms in induced or suppressed genes, continued.

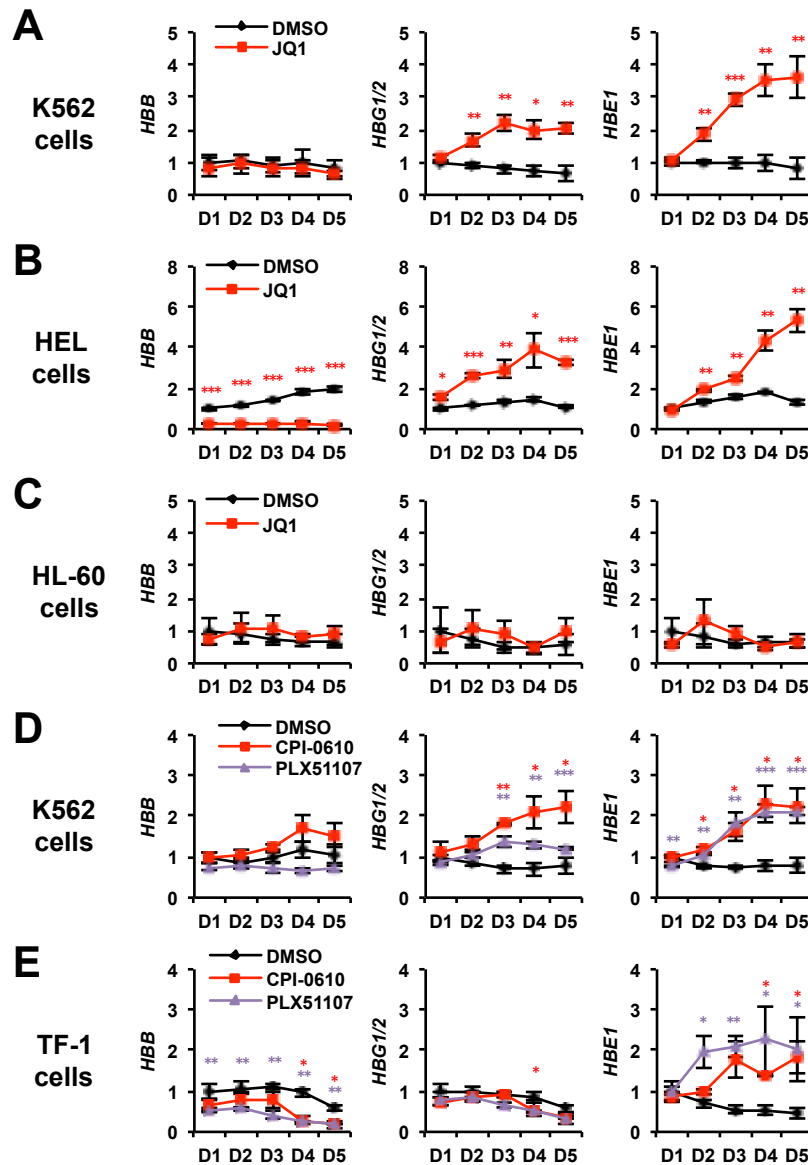
GO ID	Description	p.Val	FDR
GO:0001775	cell activation	6.50E-21	6.50E-21
GO:0002376	immune system process	2.77E-19	2.77E-19
GO:0006955	immune response	1.99E-17	1.99E-17
GO:0045321	leukocyte activation	4.30E-17	4.30E-17
GO:0002682	regulation of immune system process	2.30E-15	2.30E-15
GO:0009605	response to external stimulus	3.90E-15	3.90E-15
GO:0048583	regulation of response to stimulus	1.14E-14	1.14E-14
GO:0050776	regulation of immune response	2.95E-14	2.95E-14
GO:0050896	response to stimulus	1.19E-13	1.19E-13
GO:0034097	response to cytokine	2.59E-13	2.59E-13
GO:0010033	response to organic substance	7.36E-13	7.36E-13
GO:0051239	regulation of multicellular organismal process	2.46E-12	2.46E-12
GO:0046649	lymphocyte activation	3.41E-12	3.41E-12
GO:0016477	cell migration	3.59E-12	3.59E-12
GO:0002684	positive regulation of immune system process	3.62E-12	3.62E-12
GO:0002252	immune effector process	4.23E-12	4.23E-12
GO:0048584	positive regulation of response to stimulus	6.73E-12	6.73E-12
GO:0030155	regulation of cell adhesion	1.74E-11	1.74E-11
GO:0007166	cell surface receptor signaling pathway	2.78E-11	2.78E-11
GO:0007154	cell communication	7.54E-11	7.54E-11
GO:0045785	positive regulation of cell adhesion	1.34E-10	1.34E-10
GO:0051240	positive regulation of multicellular organismal process	1.53E-10	1.53E-10
GO:1903039	positive regulation of leukocyte cell-cell adhesion	2.01E-10	2.01E-10
GO:0070661	leukocyte proliferation	2.27E-10	2.27E-10
GO:0070663	regulation of leukocyte proliferation	2.80E-10	2.80E-10
GO:0001816	cytokine production	3.24E-10	3.24E-10
GO:0002263	cell activation involved in immune response	3.86E-10	3.86E-10
GO:0007159	leukocyte cell-cell adhesion	5.11E-10	5.11E-10
GO:0040011	locomotion	6.14E-10	6.14E-10
GO:0023052	signaling	6.32E-10	6.32E-10
GO:0002366	leukocyte activation involved in immune response	6.71E-10	6.71E-10
GO:0042110	T cell activation	7.09E-10	7.09E-10
GO:0002274	myeloid leukocyte activation	7.43E-10	7.43E-10
GO:0022409	positive regulation of cell-cell adhesion	1.02E-09	1.02E-09
GO:1903037	regulation of leukocyte cell-cell adhesion	1.38E-09	1.38E-09
GO:0042221	response to chemical	1.65E-09	1.65E-09
GO:0050670	regulation of lymphocyte proliferation	1.88E-09	1.88E-09
GO:0032944	regulation of mononuclear cell proliferation	2.63E-09	2.63E-09
GO:0050900	leukocyte migration	2.64E-09	2.64E-09
GO:0048870	cell motility	3.01E-09	3.01E-09
GO:0051674	localization of cell	3.01E-09	3.01E-09
GO:0098609	cell-cell adhesion	3.03E-09	3.03E-09
GO:0070887	cellular response to chemical stimulus	3.25E-09	3.25E-09
GO:0002443	leukocyte mediated immunity	4.29E-09	4.29E-09
GO:0071345	cellular response to cytokine stimulus	4.61E-09	4.61E-09
GO:0032943	mononuclear cell proliferation	6.72E-09	6.72E-09
GO:0035556	intracellular signal transduction	6.73E-09	6.73E-09
GO:0022610	biological adhesion	7.88E-09	7.88E-09
GO:0022407	regulation of cell-cell adhesion	8.49E-09	8.49E-09
GO:0050865	regulation of cell activation	9.78E-09	9.78E-09
EPO+JQ1 vs. EPO, Induced (Supplemental Figure 2E, right panel)			
GO ID	Description	p.Val	FDR
GO:0006468	protein phosphorylation	2.65E-05	2.65E-05
GO:0120036	plasma membrane bounded cell projection organization	4.75E-05	4.75E-05
GO:0007275	multicellular organism development	9.71E-05	9.71E-05
GO:0030030	cell projection organization	1.14E-04	1.14E-04
GO:0048731	system development	1.41E-04	1.41E-04
GO:0009653	anatomical structure morphogenesis	1.67E-04	1.67E-04

Supplemental Table 1. Enriched GO terms in induced or suppressed genes, continued.

GO:0048856	anatomical structure development	1.83E-04	1.83E-04
GO:0032502	developmental process	2.25E-04	2.25E-04
GO:0048522	positive regulation of cellular process	2.79E-04	2.79E-04
GO:0048518	positive regulation of biological process	9.18E-04	9.18E-04
GO:0007169	transmembrane receptor protein tyrosine kinase signaling pathway	1.51E-03	1.51E-03
GO:0007154	cell communication	1.91E-03	1.91E-03
GO:0030182	neuron differentiation	2.18E-03	2.18E-03
GO:0007399	nervous system development	2.42E-03	2.42E-03
GO:0051716	cellular response to stimulus	2.50E-03	2.50E-03
GO:0023052	signaling	2.81E-03	2.81E-03
GO:0016310	phosphorylation	3.04E-03	3.04E-03
GO:0022008	neurogenesis	5.34E-03	5.34E-03
GO:0048699	generation of neurons	7.12E-03	7.12E-03
GO:0048468	cell development	7.24E-03	7.24E-03
GO:0007167	enzyme linked receptor protein signaling pathway	8.80E-03	8.80E-03
GO:0048666	neuron development	9.76E-03	9.76E-03
GO:0032989	cellular component morphogenesis	1.01E-02	1.01E-02
GO:0050794	regulation of cellular process	1.12E-02	1.12E-02
GO:0051128	regulation of cellular component organization	1.15E-02	1.15E-02
GO:0000902	cell morphogenesis	1.24E-02	1.24E-02
GO:0050789	regulation of biological process	1.38E-02	1.38E-02
GO:0032990	cell part morphogenesis	1.82E-02	1.82E-02
GO:0048812	neuron projection morphogenesis	1.95E-02	1.95E-02
GO:0031399	regulation of protein modification process	2.34E-02	2.34E-02
GO:0097061	dendritic spine organization	2.59E-02	2.59E-02
GO:0001932	regulation of protein phosphorylation	2.65E-02	2.65E-02
GO:0007165	signal transduction	2.72E-02	2.72E-02
GO:0120039	plasma membrane bounded cell projection morphogenesis	2.87E-02	2.87E-02
GO:0030154	cell differentiation	2.88E-02	2.88E-02
GO:0051338	regulation of transferase activity	2.91E-02	2.91E-02
GO:0065009	regulation of molecular function	3.06E-02	3.06E-02
GO:0048858	cell projection morphogenesis	3.19E-02	3.19E-02
GO:0043549	regulation of kinase activity	3.50E-02	3.50E-02
GO:0031175	neuron projection development	4.29E-02	4.29E-02
EPO+JQ1 vs. EPO, Suppressed (Supplemental Figure 2E left panel)			
GO ID	Description	p.Val	FDR
GO:0002376	immune system process	1.41E-30	1.41E-30
GO:0001775	cell activation	6.71E-27	6.71E-27
GO:0006955	immune response	3.84E-26	3.84E-26
GO:0045321	leukocyte activation	2.12E-25	2.12E-25
GO:0002252	immune effector process	8.48E-19	8.48E-19
GO:0002443	leukocyte mediated immunity	3.95E-18	3.95E-18
GO:0002274	myeloid leukocyte activation	6.14E-18	6.14E-18
GO:0002682	regulation of immune system process	1.25E-17	1.25E-17
GO:0002366	leukocyte activation involved in immune response	6.27E-17	6.27E-17
GO:0002263	cell activation involved in immune response	9.13E-17	9.13E-17
GO:0009605	response to external stimulus	1.04E-16	1.04E-16
GO:0043299	leukocyte degranulation	7.83E-16	7.83E-16
GO:0002444	myeloid leukocyte mediated immunity	1.13E-15	1.13E-15
GO:0050776	regulation of immune response	1.78E-15	1.78E-15
GO:0046649	lymphocyte activation	2.37E-15	2.37E-15
GO:0002275	myeloid cell activation involved in immune response	2.82E-15	2.82E-15
GO:0002684	positive regulation of immune system process	3.57E-15	3.57E-15
GO:0050865	regulation of cell activation	1.44E-14	1.44E-14
GO:0070661	leukocyte proliferation	2.06E-14	2.06E-14
GO:0050896	response to stimulus	2.68E-14	2.68E-14
GO:0051707	response to other organism	3.58E-14	3.58E-14
GO:0043207	response to external biotic stimulus	3.99E-14	3.99E-14

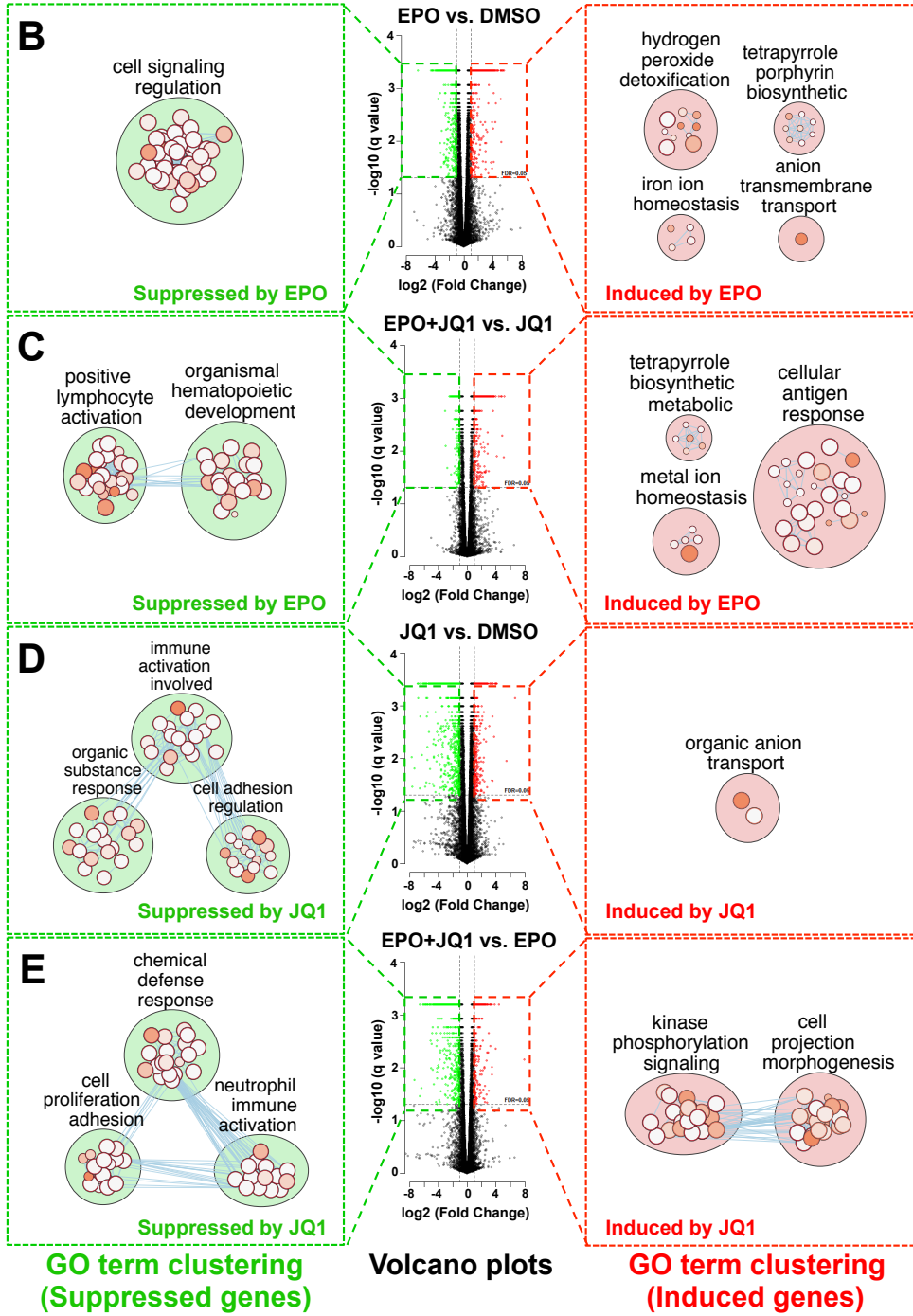
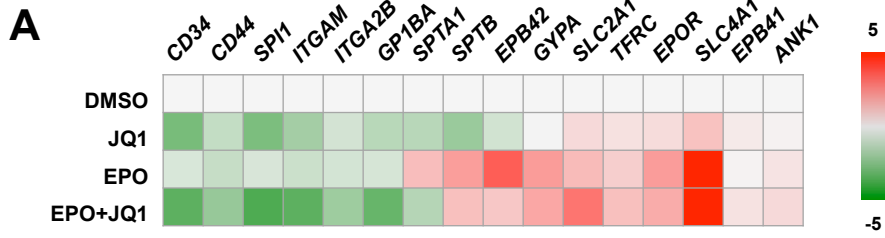
Supplemental Table 1. Enriched GO terms in induced or suppressed genes, continued.

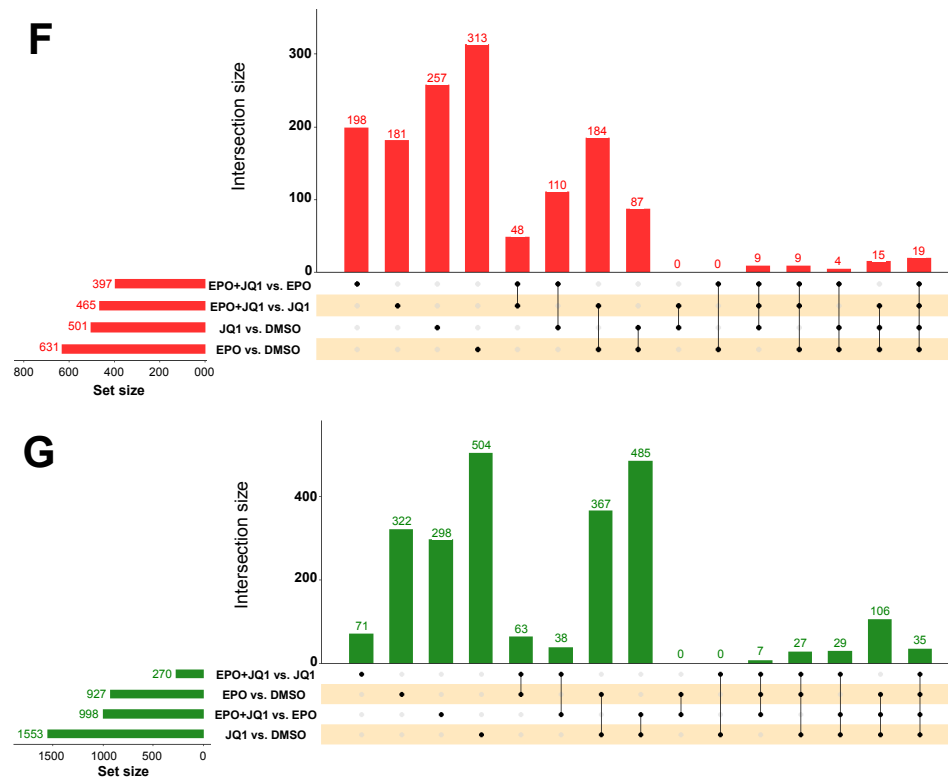
GO:0009607	response to biotic stimulus	9.15E-14	9.15E-14
GO:0006887	exocytosis	1.03E-13	1.03E-13
GO:0002694	regulation of leukocyte activation	1.09E-13	1.09E-13
GO:0034097	response to cytokine	1.23E-13	1.23E-13
GO:0045055	regulated exocytosis	2.41E-13	2.41E-13
GO:0042110	T cell activation	2.65E-13	2.65E-13
GO:0022610	biological adhesion	3.00E-13	3.00E-13
GO:0098609	cell-cell adhesion	4.25E-13	4.25E-13
GO:0007155	cell adhesion	5.03E-13	5.03E-13
GO:0046651	lymphocyte proliferation	6.33E-13	6.33E-13
GO:0001816	cytokine production	8.02E-13	8.02E-13
GO:0032943	mononuclear cell proliferation	9.65E-13	9.65E-13
GO:0030155	regulation of cell adhesion	1.16E-12	1.16E-12
GO:0051239	regulation of multicellular organismal process	2.82E-12	2.82E-12
GO:0070663	regulation of leukocyte proliferation	3.30E-12	3.30E-12
GO:0001817	regulation of cytokine production	3.62E-12	3.62E-12
GO:0071345	cellular response to cytokine stimulus	5.89E-12	5.89E-12
GO:0048583	regulation of response to stimulus	7.00E-12	7.00E-12
GO:0006952	defense response	8.12E-12	8.12E-12
GO:0002703	regulation of leukocyte mediated immunity	8.56E-12	8.56E-12
GO:0042119	neutrophil activation	8.70E-12	8.70E-12
GO:0036230	granulocyte activation	1.55E-11	1.55E-11
GO:0050670	regulation of lymphocyte proliferation	1.73E-11	1.73E-11
GO:0098542	defense response to other organism	2.19E-11	2.19E-11
GO:0032944	regulation of mononuclear cell proliferation	2.36E-11	2.36E-11
GO:0140352	export from cell	2.70E-11	2.70E-11
GO:0070887	cellular response to chemical stimulus	3.61E-11	3.61E-11
GO:0042098	T cell proliferation	4.67E-11	4.67E-11



Supplemental Figure 1. BET inhibitors induces embryonic and fetal ϵ/γ -globin genes in erythroid, but not myeloid, cell lines.

Expression of *HBB* (left), *HBG1/2* (middle), *HBE1* (right) in cell lines treated with BET inhibitors (red) versus DMSO control (black). **(A)** K562 cells treated with JQ1 versus DMSO. **(B)** HEL cells treated with JQ1 versus DMSO. **(C)** HL-60 cells treated with JQ1 versus DMSO. **(D)** K562 cells treated with CPI-0610 or PLX51107 versus DMSO. **(E)** TF-1 cells treated with CPI-0610 or PLX51107 versus DMSO. JQ1 (200nM) and PLX51107 (200nM) were applied to the cells at day 0 without additional treatments. CPI-0610 (200nM) was applied to the cells at day 0 and re-applied every subsequent day until day 5. 0.002% DMSO was used in controls. N=3. D, days of treatment. *: $p < 0.05$, **: $p < 0.01$, ***: $p < 0.001$ (Student's t-test).





Supplemental Figure 2. Effects of EPO or JQ1 on TF-1 cell transcriptome.

(A) Heatmap representing log₂ (fold-change) of representative erythroid/myeloid lineage genes. (B-E) Volcano plots of transcription changes (middle column) and GO term clustering of induced (red, right column) or suppressed (green, left column) genes. Black dots represent genes with log₂ (fold-change) less than 1 in either direction, or genes with FDR (q values) greater than 0.05. Genes with FPKM<1 were excluded from the volcano plots. GO analysis and GO term clustering were performed using g:Profiler and Cytoscape on genes with significant expression changes. Each node represent a GO term, and edges denote >60% similarity. Size of each node correspond to the number of genes related to the GO term, and lighter fill denotes lower FDR. (B) Genes induced (red) or suppressed (green) by EPO (comparing EPO versus DMSO). (C) Genes induced (red) or suppressed (green) by EPO (comparing EPO+JQ1 versus JQ1). (D) Genes induced (red) or suppressed (green) by JQ1 (comparing JQ1 versus DMSO). (E) Genes induced (red) or suppressed (green) by JQ1 (comparing EPO+JQ1 versus EPO). (F-G) Intersections between (F) induced or (G) suppressed genes as shown in (B-E). Total number of genes in each set is represented by the horizontal bars next to the set

labels. Connected dots in the matrix represent common genes in the corresponding sets, with the exact numbers plotted above.