

# Mice deficient of Myc super-enhancer region reveal differences between normal and pathological growth

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Mice deficient of Myc super-enhancer region reveal differential control mechanism between normal and pathological growth. <i>ELife</i> , 2017, 6, .	2.8	52
2	Transcriptional Dysregulation of MYC Reveals Common Enhancer-Docking Mechanism. <i>Cell Reports</i> , 2018, 23, 349-360.	2.9	144
3	Super enhancers – new analyses and perspectives on the low hanging fruit. <i>Transcription</i> , 2018, 9, 123-130.	1.7	11
4	Deletion of the murine ortholog of the 8q24 gene desert has anti-cancer effects in transgenic mammary cancer models. <i>BMC Cancer</i> , 2018, 18, 1233.	1.1	7
5	The MYC Enhancer-ome: Long-Range Transcriptional Regulation of MYC in Cancer. <i>Trends in Cancer</i> , 2018, 4, 810-822.	3.8	99
6	Single-Cell Transcriptomics of Traced Epidermal and Hair Follicle Stem Cells Reveals Rapid Adaptations during Wound Healing. <i>Cell Reports</i> , 2018, 25, 585-597.e7.	2.9	137
7	Targeting Super-Enhancers as a Therapeutic Strategy for Cancer Treatment. <i>Frontiers in Pharmacology</i> , 2019, 10, 361.	1.6	47
8	Super-enhancers in cancer. , 2019, 199, 129-138.		114
9	Using Gene Expression Profiling to Move Beyond MYC/BCL2 Rearrangements in High-Grade Lymphoma. <i>Journal of Clinical Oncology</i> , 2019, 37, 175-177.	0.8	7
10	Lineage-specific RUNX2 super-enhancer activates MYC and promotes the development of blastic plasmacytoid dendritic cell neoplasm. <i>Nature Communications</i> , 2019, 10, 1653.	5.8	34
11	Super-enhancers in transcriptional regulation and genome organization. <i>Nucleic Acids Research</i> , 2019, 47, 11481-11496.	6.5	85
12	Chromatin Interactions and Regulatory Elements in Cancer: From Bench to Bedside. <i>Trends in Genetics</i> , 2019, 35, 145-158.	2.9	22
13	Cell Specificity of Human Regulatory Annotations and Their Genetic Effects on Gene Expression. <i>Genetics</i> , 2019, 211, 549-562.	1.2	16
14	Dissecting Tissue-Specific Super-Enhancers by Integrating Genome-Wide Analyses and CRISPR/Cas9 Genome Editing. <i>Journal of Mammary Gland Biology and Neoplasia</i> , 2019, 24, 47-59.	1.0	11
15	FUBP1 and FUBP2 enforce distinct epigenetic setpoints for MYC expression in primary single murine cells. <i>Communications Biology</i> , 2020, 3, 545.	2.0	8
16	The Oncogenic Potential of the Centromeric Border Protein FAM84B of the 8q24.21 Gene Desert. <i>Genes</i> , 2020, 11, 312.	1.0	12
17	Molecular Complexity of Diffuse Large B-Cell Lymphoma: Can It Be a Roadmap for Precision Medicine?. <i>Cancers</i> , 2020, 12, 185.	1.7	22
18	Genetic Dissection of a Super Enhancer Controlling the Nppa-Nppb Cluster in the Heart. <i>Circulation Research</i> , 2021, 128, 115-129.	2.0	32

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19	Super-enhancer-mediated core regulatory circuitry in human cancer. Computational and Structural Biotechnology Journal, 2021, 19, 2790-2795.	1.9	11
20	Transcriptionally active enhancers in human cancer cells. Molecular Systems Biology, 2021, 17, e9873.	3.2	28
23	EphA2 super-enhancer promotes tumor progression by recruiting FOSL2 and TCF7L2 to activate the target gene EphA2. Cell Death and Disease, 2021, 12, 264.	2.7	18
24	Enhancer rewiring in tumors: an opportunity for therapeutic intervention. Oncogene, 2021, 40, 3475-3491.	2.6	10
26	Identification of Four Enhancer-Associated Genes as Risk Signature for Diffuse Glioma Patients. Journal of Molecular Neuroscience, 2021, , 1.	1.1	3
28	Mutational inactivation of Apc in the intestinal epithelia compromises cellular organisation. Journal of Cell Science, 2021, 134, .	1.2	2
29	Targeting complexes of super-enhancers is a promising strategy for cancer therapy (Review). Oncology Letters, 2020, 20, 2557-2566.	0.8	12
30	Controlling gene activation by enhancers through a drug-inducible topological insulator. ELife, 2020, 9, .	2.8	8
31	LncRNA SNHG17 interacts with LRPPRC to stabilize c-Myc protein and promote G1/S transition and cell proliferation. Cell Death and Disease, 2021, 12, 970.	2.7	27
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34	Targeting of non-coding RNAs encoded by novel MYC enhancers inhibits the proliferation of human hepatic carcinoma cells in vitro. Scientific Reports, 2022, 12, 855.	1.6	6
35	Genetic and Histopathological Heterogeneity of Neuroblastoma and Precision Therapeutic Approaches for Extremely Unfavorable Histology Subgroups. Biomolecules, 2022, 12, 79.	1.8	12
36	Sequence determinants of human gene regulatory elements. Nature Genetics, 2022, 54, 283-294.	9.4	87
38	KLF6 Super-enhancer Regulates Cell Proliferation by Recruiting GATA2 and SOX10 in Human Hepatoma Cells. Molecular Biology, 0, , 1.	0.4	0
40	Upregulation of ribosome biogenesis via canonical E-boxes is required for Myc-driven proliferation. Developmental Cell, 2022, 57, 1024-1036.e5.	3.1	10
41	Programmable RNA-Guided Large DNA Transgenesis by CRISPR/Cas9 and Site-Specific Integrase Bxb1. Frontiers in Bioengineering and Biotechnology, 0, 10, .	2.0	6
42	<scp>BRD4</scp> and <scp>MYC</scp>: power couple in transcription and disease. FEBS Journal, 2023, 290, 4820-4842.	2.2	19
43	Reversible Myc hypomorphism identifies a key Myc-dependency in early cancer evolution. Nature Communications, 2022, 13, .	5.8	7

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45	SOX9 and TCF transcription factors associate to mediate Wnt/ $\beta$ 2-catenin target gene activation in colorectal cancer. <i>Journal of Biological Chemistry</i> , 2023, 299, 102735.	1.6	8
46	ATM suppresses c-Myc overexpression in the mammary epithelium in response to estrogen. <i>Cell Reports</i> , 2023, 42, 111909.	2.9	2
47	Survey of activation-induced genome architecture reveals a novel enhancer of <i>Myc</i> . <i>Immunology and Cell Biology</i> , 2023, 101, 345-357.	1.0	0