

Supplemental Material

Formaldehyde and Epigenetic Alterations: MicroRNA Changes in the Nasal Epithelium of Nonhuman Primates

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Supplemental Material

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Supplemental Material, Table S1: Transcriptional targets predicted to be regulated by miR-125b. P_{CT} refers to the probability of preferentially conserved targeting.

Target	Full Name	Context Score	P _{CT}
<i>GCNT1</i>	glucosaminyl (N-acetyl) transferase 1, core 2 (beta-1,6-N-acetylglucosaminyltransferase)	-0.67	> 0.99
<i>TMEM86A</i>	transmembrane protein 86A	-0.26	> 0.99
<i>PODXL</i>	podocalyxin-like	-0.47	> 0.99
<i>ARID3B</i>	AT rich interactive domain 3B (BRIGHT-like)	-0.51	> 0.99
<i>FLJ20309</i>	hypothetical protein FLJ20309	-0.37	0.99
<i>SH3TC2</i>	SH3 domain and tetratricopeptide repeats 2	-0.73	0.99
<i>PHF15</i>	PHD finger protein 15	-0.31	0.98
<i>GJC1</i>	gap junction protein, gamma 1, 45kDa	-0.37	0.98
<i>KLF13</i>	Kruppel-like factor 13	-0.51	0.97
<i>OLFML2A</i>	olfactomedin-like 2A	-0.49	0.97
<i>MFHAS1</i>	malignant fibrous histiocytoma amplified sequence 1	-0.52	0.97
<i>IRF4</i>	interferon regulatory factor 4	-0.58	0.97
<i>RAPGEF5</i>	Rap guanine nucleotide exchange factor (GEF) 5	-0.39	0.97
<i>LBH</i>	limb bud and heart development homolog (mouse)	-0.37	0.97
<i>ENPP1</i>	ectonucleotide pyrophosphatase/phosphodiesterase 1	-0.4	0.97
<i>UBN1</i>	ubiquitin 1	-0.33	0.97
<i>FAM176A</i>	family with sequence similarity 176, member A	-0.33	0.97
<i>MXD4</i>	MAX dimerization protein 4	-0.07	0.97
<i>SMURF1</i>	SMAD specific E3 ubiquitin protein ligase 1	-0.24	0.97
<i>TLE3</i>	transducin-like enhancer of split 3 (E(sp1) homolog, Drosophila)	-0.2	0.97
<i>TRPS1</i>	trichorhinophalangeal syndrome I	-0.19	0.97
<i>KIAA1522</i>	KIAA1522	-0.37	0.97
<i>ASAH3L</i>	N-acylsphingosine amidohydrolase 3-like	-0.34	0.97
<i>UBE2R2</i>	ubiquitin-conjugating enzyme E2R 2	-0.36	0.97
<i>SEMA4D</i>	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4D	-0.42	0.97
<i>LIN28</i>	lin-28 homolog (C. elegans)	-0.27	0.97
<i>CPSF6</i>	cleavage and polyadenylation specific factor 6, 68kDa	-0.34	0.97
<i>TGOLN2</i>	trans-golgi network protein 2	-0.39	0.97
<i>OSBPL9</i>	oxysterol binding protein-like 9	-0.45	0.97
<i>TBC1D1</i>	TBC1 (tre-2/USP6, BUB2, cdc16) domain family, member 1	-0.36	0.97
<i>SLC39A9</i>	solute carrier family 39 (zinc transporter), member 9	-0.47	0.96
<i>ENPEP</i>	glutamyl aminopeptidase (aminopeptidase A)	-0.52	0.96
<i>ST8SIA4</i>	ST8 alpha-N-acetyl-neuraminidase alpha-2,8-sialyltransferase 4	-0.26	0.96
<i>GRB10</i>	growth factor receptor-bound protein 10	-0.43	0.96
<i>MYT1</i>	myelin transcription factor 1	-0.39	0.96

Target	Full Name	Context Score	P_{CT}
<i>STARD13</i>	StAR-related lipid transfer (START) domain containing 13	-0.99	0.96
<i>PTAR1</i>	protein prenyltransferase alpha subunit repeat containing 1	-0.26	0.96
<i>BMF</i>	Bcl2 modifying factor	-0.38	0.96
<i>ZNRF3</i>	zinc and ring finger 3	-0.24	0.96
<i>ZSCAN29</i>	zinc finger and SCAN domain containing 29	-0.58	0.96
<i>SPTB</i>	spectrin, beta, erythrocytic (includes spherocytosis, clinical type I)	-0.29	0.96
<i>NIN</i>	ninein (GSK3B interacting protein)	-0.38	0.96
<i>SMG1</i>	PI-3-kinase-related kinase SMG-1	-0.31	0.96
<i>NUP210</i>	nucleoporin 210kDa	-0.55	0.96
<i>GGA2</i>	golgi associated, gamma adaptin ear containing, ARF binding protein 2	-0.31	0.96
<i>DUS1L</i>	dihydrouridine synthase 1-like (<i>S. cerevisiae</i>)	-0.48	0.96
<i>MTF1</i>	metal-regulatory transcription factor 1	-0.33	0.96
<i>C14orf43</i>	chromosome 14 open reading frame 43	-0.13	0.96
<i>PPAT</i>	phosphoribosyl pyrophosphate amidotransferase	-0.43	0.96
<i>SMEK1</i>	SMEK homolog 1, suppressor of mek1 (<i>Dictyostelium</i>)	-0.61	0.96
<i>ORC2L</i>	origin recognition complex, subunit 2-like (yeast)	-0.33	0.96
<i>ACHE</i>	acetylcholinesterase (Yt blood group)	-0.57	0.96
<i>CGN</i>	cingulin	-0.43	0.95
<i>LRP4</i>	low density lipoprotein receptor-related protein 4	-0.28	0.95
<i>C6orf47</i>	chromosome 6 open reading frame 47	-0.3	0.95
<i>TMEM77</i>	transmembrane protein 77	-0.5	0.95
<i>KCNA1</i>	potassium voltage-gated channel, shaker-related subfamily, member 1 (episodic ataxia with myokymia)	-0.24	0.95
<i>KIAA0174</i>	KIAA0174	-0.29	0.95
<i>LFNG</i>	LFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase	-0.48	0.95
<i>HIC2</i>	hypermethylated in cancer 2	-0.02	0.95
<i>TNFAIP3</i>	tumor necrosis factor, alpha-induced protein 3	-0.29	0.95
<i>CASP2</i>	caspase 2, apoptosis-related cysteine peptidase (neural precursor cell expressed, developmentally down-regulated 2)	-0.25	0.95
<i>CRB2</i>	crumbs homolog 2 (<i>Drosophila</i>)	-0.44	0.95
<i>KIAA0317</i>	KIAA0317	-0.13	0.95
<i>SCARB1</i>	scavenger receptor class B, member 1	-0.34	0.95
<i>ANPEP</i>	alanyl (membrane) aminopeptidase (aminopeptidase N, aminopeptidase M, microsomal aminopeptidase, CD13, p150)	-0.3	0.95
<i>PSTPIP2</i>	proline-serine-threonine phosphatase interacting protein 2	-0.39	0.95
<i>CYP24A1</i>	cytochrome P450, family 24, subfamily A, polypeptide 1	-0.41	0.95
<i>ZSWIM5</i>	zinc finger, SWIM-type containing 5	-0.4	0.95

Target	Full Name	Context Score	P_{CT}
<i>NCAN</i>	neurocan	-0.23	0.95
<i>TNFSF4</i>	tumor necrosis factor (ligand) superfamily, member 4 (tax-transcriptionally activated glycoprotein 1, 34kDa)	-0.49	0.95
<i>NECAB3</i>	N-terminal EF-hand calcium binding protein 3	-0.39	0.95
<i>SLC6A17</i>	solute carrier family 6, member 17	-0.22	0.95
<i>LRFN2</i>	leucine rich repeat and fibronectin type III domain containing 2	-0.25	0.95
<i>FAM134A</i>	family with sequence similarity 134, member A	-0.25	0.95
<i>C11orf57</i>	chromosome 11 open reading frame 57	-0.28	0.94
<i>CACNB1</i>	calcium channel, voltage-dependent, beta 1 subunit	-0.08	0.94
<i>NIPA1</i>	non imprinted in Prader-Willi/Angelman syndrome 1	-0.18	0.94
<i>GTPBP2</i>	GTP binding protein 2	-0.39	0.94
<i>EBF4</i>	early B-cell factor 4	-0.24	0.94
<i>CDR2L</i>	cerebellar degeneration-related protein 2-like	-0.2	0.94
<i>ETV6</i>	ets variant gene 6 (TEL oncogene)	-0.31	0.94
<i>RAPGEFL1</i>	Rap guanine nucleotide exchange factor (GEF)-like 1	-0.22	0.94
<i>CGREF1</i>	cell growth regulator with EF-hand domain 1	-0.35	0.94
<i>CCNJ</i>	cyclin J	-0.46	0.94
<i>KCNIP3</i>	Kv channel interacting protein 3, calsenilin	-0.25	0.94
<i>PSCD1</i>	pleckstrin homology, Sec7 and coiled-coil domains 1(cytohesin 1)	-0.3	0.93
<i>CTF8</i>	chromosome transmission fidelity factor 8 homolog (S. cerevisiae)	-0.38	0.93
<i>MSH1</i>	musashi homolog 1 (Drosophila)	-0.21	0.93
<i>TAF9B</i>	TAF9B RNA polymerase II, TATA box binding protein (TBP)-associated factor, 31kDa	-0.39	0.93
<i>SGPL1</i>	sphingosine-1-phosphate lyase 1	-0.25	0.93
<i>TMPRSS13</i>	transmembrane protease, serine 13	-0.31	0.93
<i>SEMA4C</i>	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4C	-0.28	0.93
<i>CDH5</i>	cadherin 5, type 2, VE-cadherin (vascular epithelium)	-0.43	0.93
<i>ABHD6</i>	abhydrolase domain containing 6	-0.31	0.93
<i>ENTPD4</i>	ectonucleoside triphosphate diphosphohydrolase 4	-0.22	0.92
<i>ZFYVE1</i>	zinc finger, FYVE domain containing 1	-0.37	0.92
<i>MTUS1</i>	mitochondrial tumor suppressor 1	-0.23	0.92
<i>ATXN1</i>	ataxin 1	-0.19	0.92
<i>LNPEP</i>	leucyl/cystinyl aminopeptidase	-0.25	0.92
<i>DIRAS1</i>	DIRAS family, GTP-binding RAS-like 1	-0.3	0.92
<i>ESRRA</i>	estrogen-related receptor alpha	-0.37	0.92
<i>SH3BP4</i>	SH3-domain binding protein 4	-0.28	0.92
<i>ICHTHYIN</i>	ichthyin protein	-0.51	0.92
<i>SUV39H1</i>	suppressor of variegation 3-9 homolog 1 (Drosophila)	-0.3	0.92
<i>MTMR3</i>	myotubularin related protein 3	-0.2	0.92
<i>FAM118A</i>	family with sequence similarity 118, member A	-0.27	0.92

Target	Full Name	Context Score	P_{CT}
<i>RBM38</i>	RNA binding motif protein 38	-0.2	0.92
<i>EIF5A2</i>	eukaryotic translation initiation factor 5A2	-0.15	0.92
<i>FAM116A</i>	family with sequence similarity 116, member A	-0.33	0.92
<i>CDC42SE1</i>	CDC42 small effector 1	-0.29	0.92
<i>HCN3</i>	hyperpolarization activated cyclic nucleotide-gated potassium channel 3	-0.34	0.92
<i>USP37</i>	ubiquitin specific peptidase 37	-0.19	0.91
<i>KIAA0644</i>	KIAA0644 gene product	-0.33	0.91
<i>FUT4</i>	fucosyltransferase 4 (alpha (1,3) fucosyltransferase, myeloid-specific)	-0.65	0.91
<i>RND2</i>	Rho family GTPase 2	-0.31	0.91
<i>SOX11</i>	SRY (sex determining region Y)-box 11	-0.41	0.91
<i>FBXO45</i>	F-box protein 45	-0.29	0.91
<i>PCSK7</i>	proprotein convertase subtilisin/kexin type 7	-0.28	0.91
<i>TP53INP1</i>	tumor protein p53 inducible nuclear protein 1	-0.29	0.91
<i>MCL1</i>	myeloid cell leukemia sequence 1 (BCL2-related)	-0.42	0.91
<i>EAF1</i>	ELL associated factor 1	-0.12	0.91
<i>NFIB</i>	nuclear factor I/B	-0.09	0.91
<i>LIFR</i>	leukemia inhibitory factor receptor alpha	-0.28	0.91
<i>MAN1B1</i>	mannosidase, alpha, class 1B, member 1	-0.3	0.91
<i>NEU1</i>	sialidase 1 (lysosomal sialidase)	-0.4	0.91
<i>BAK1</i>	BCL2-antagonist/killer 1	-0.56	0.9
<i>SLC35A4</i>	solute carrier family 35, member A4	-0.34	0.9
<i>KIAA1244</i>	KIAA1244	-0.18	0.9
<i>MAP2K7</i>	mitogen-activated protein kinase kinase 7	-0.26	0.9
<i>VDR</i>	vitamin D (1,25- dihydroxyvitamin D3) receptor	-0.26	0.9
<i>SLC39A13</i>	solute carrier family 39 (zinc transporter), member 13	-0.24	0.9

Supplemental Material, Table S2: Transcriptional targets predicted to be regulated by miR-142-3p. P_{CT} refers to the probability of preferentially conserved targeting.

Target	Full Name	Context Score	P_{CT}
<i>ASH1L</i>	ash1 (absent, small, or homeotic)-like (Drosophila)	-0.59	> 0.99
<i>RICTOR</i>	rapamycin-insensitive companion of mTOR	-0.57	> 0.99
<i>ITGB8</i>	integrin, beta 8	-0.62	0.98
<i>C20orf194</i>	chromosome 20 open reading frame 194	-0.72	0.97
<i>SNF1LK</i>	SNF1-like kinase	-0.39	0.97
<i>FAM44B</i>	family with sequence similarity 44, member B	-0.65	0.95
<i>C10orf18</i>	chromosome 10 open reading frame 18	-0.87	0.95
<i>ZCCHC14</i>	zinc finger, CCHC domain containing 14	-0.5	0.94
<i>AFF1</i>	AF4/FMR2 family, member 1	-0.25	0.94
<i>EML4</i>	echinoderm microtubule associated protein like 4	-0.42	0.93
<i>LCOR</i>	ligand dependent nuclear receptor corepressor	-0.33	0.93
<i>CCDC6</i>	coiled-coil domain containing 6	-0.33	0.92
<i>BNC2</i>	basonuclin 2	-0.32	0.9

Supplemental Material, Table S3: Pathways significantly associated with the predicted targets of miR-142-3p.

Canonical Pathways	p-value	miR-142-3p Predicted Targets
ILK Signaling	0.008	<i>ITGB8, RICTOR</i>
Role of IL-17F in Allergic Inflammatory Airway Diseases	0.031	<i>SIK1</i>
Macropinocytosis Signaling	0.048	<i>ITGB8</i>

Supplemental Material, Figure S1: Predicted mRNA targets of formaldehyde-altered miR-125b are involved in apoptosis signaling. The apoptosis signaling pathway is illustrated, where molecules predicted to be targeted by miR-125b are shaded in dark grey.

