Table S1. Statistics for High-Throughput Sequencing Datasets, Related to Experimental Procedures

Library	Total reads	≤4 alignments	0 alignments	>4 alignments
H3K4me3 IP 24 hpf	12,189,261	8,449,068	1,832,467	1,907,726
H3K4me3 IP 72 hpf	16,657,288	10,559,648	1,358,270	4,739,370
H3K4me3 IP Adult	9,146,789	5,487,668	1,114,291	2,544,830
H3K36me3 IP 24 hpf	12,939,306	6,834,681	1,008,475	5,096,150
H3K36me3 IP 72 hpf	19,956,175	11,589,103	1,813,807	6,553,265
H3K36me3 IP Adult	13,666,859	7,521,044	1,429,574	4,716,241
Input 24 hpf	9,961,209	4,877,619	1,762,600	3,320,990
(control for H3K4me3) Input 24 hpf (control for H3K36me3)	10,886,048	5,726,839	924,820	4,234,389
Input 72 hpf (control for H3K4me3)	17,892,954	9,105,274	1,891,952	6,895,728
Input 72 hpf (control for H3K36me3)	19,069,127	10,872,021	1,459,677	6,737,429
Input Adult	14,041,883	7,523,101	1,537,844	4,980,938
Strand-specific RNA-Seq 24 hpf	37,203,901	18,307,186	5,337,724	13,558,991
Strand-specific RNA-Seq 72 hpf	37,004,726	15,410,622	3,787,831	17,806,273
3P-Seq 24 hpf	22,448,667	13,179,736	8,524,042	744,889
3P-Seq 72 hpf	20,914,473	17,818,974	1,984,988	1,110,511
3P-Seq Adult	18,445,044	14,743,023	2,493,766	1,208,255

Table S4. Spatial Expression of lincRNAs Analyzed Using In Situ Hybridization, Related to Figure 2

lincRNA	Genomic location	Expression at 24 hpf	Expression at 72 hpf
malatl	chr14:48566202-48573730	ubiquitous, enriched in the brain, mucous cells	brain, mucous cells
linc-mipep1	chr10:40425061-40428902	enriched in the brain, spinal cord, blood vessels	enriched in the brain
linc-bin2a	chr23:33944861-33952782	lens	n/d
linc-cldn7a	chr7:23796995-23800090	pronephros, cranial ganglia	n/d
linc-gtf2f2b	chr9:19526783-19529739	cranial ganglia	n/d
linc-epb4.114	chr10:1734816-1745335	enriched in CNS	Brain
linc-srd5a2a	chr1:51582321-51592093	cranial ganglia, nose	n/d
linc-prr14	chr3:32992137-32996372	n/d	n/d
linc-agpat3	chr1:47327616-47330238	n/d	n/d
linc-mettl3	chr7:23027784-23042820	n/d	specific hindbrain neurons
linc-csnklal	chr14:40176987-40183099	n/d	cartilage of the jaw, nose epithelium
cyrano	chr13:33484735-33491213	brain, notochord,	brain, notochord, spinal cord
linc- loc100001135	chr7:4334540-4358502	n/d	n/d
linc-onecut1	chr18:37186817-37191791	n/d	n/d
linc-pou3f3b-2	chr6:14538090-14542184	n/d	n/d
linc-meis1	chr13:5245604-5250645	n/d	n/d
linc- <i>arid4a</i> linc- <i>setd1ba</i>	chr17:11281895-11282994 chr10:43348128-43351841	brain, eye, spinal cord specific neurons	n/d specific neurons
megamind	chr17:22517187-22519802	brain, eye	brain
linc-trpc7	chr14:1668370-1672051	brain, notochord	brain, notochord
linc-elovl1a linc-plcb2	chr2:19346942-19351962 chr17:2208928-2210522	specific face neurons n/d	n/d n/d
linc- <i>tbx2b</i> linc- <i>rogdi</i>	chr15:26704323-26717885 chr3:36765129-36766960	dorsal retina, ear n/d	n/d n/d

n/d, not detected.

Table S5. Number of Embryos in $\it cyrano$ and $\it megamind$ Experiments, Related to Figures 5 and 6

Experiment	wild type	mutant
Control cyrano MO1	32	0
Control cyrano MO2	45	0
Conserved site cyrano MO	6	69
Splice cyrano MO	25	157
Splice cyrano MO + RFP RNA	7	53
Splice cyrano MO + zebrafish cyrano RNA	50	54
Splice cyrano MO + mouse cyrano RNA	21	11
Splice cyrano MO + human cyrano RNA	27	34
Splice cyrano MO + cyrano_mut_a RNA	19	45
Splice cyrano MO + cyrano_mut_b RNA	22	57
Splice cyrano MO + cyrano_mut_a+b RNA	13	80
Splice cyrano MO + cyrano conserved site RNA	5	26
Splice cyrano MO + hybrid 1 RNA	16	65
Control megamind MO1	46	0
Control megamind MO2	61	0
Conserved site megamind MO	10	83
Splice megamind MOs	19	174
Splice megamind MOs + RFP megamind RNA	5	39
Splice megamind MOs + zebrafish megamind RNA	53	60
Splice megamind MOs + mouse megamind RNA	32	15
Splice megamind MOs + human megamind RNA	35	43
Splice megamind MOs + megamind_stop RNA	38	38
Splice megamind MOs + megamind_frameshift RNA	25	29
Splice megamind MOs + megamind_mut_a RNA	20	35
Splice megamind MOs + megamind_mut_b RNA	27	32
Splice megamind MOs + megamind_mut_a+b RNA	8	72
Splice megamind MOs + megamind conserved site RNA	9	47
Splice megamind MOs + hybrid 2 RNA	16	107

Table S6. Morpholino Sequences and Concentrations, Related to Experimental Procedures

Morpholino	Sequence $(5' \rightarrow 3')$	Targeting description	
cyrano e1i1 MO (5.5 ng)	AACACTCATCCCGCACTTACCGTCA	cyrano intron 1 5' splice site	
cyrano e2i2 MO (5.5 ng)	TGCTGTTTTTGATGACCTACCTGGT	cyrano intron 2 5' splice site	
cyrano i2e3 MO (5.5 ng)	TCATCTGCACAGAATGGACATTTGA	cyrano intron 2 3' splice site	
cyrano conserved site MO (5 ng)	ATTGGTGATTTTGTTGTTTTTTGCGA	cyrano conserved site in exon 3	
cyrano control MO1 (4 ng)	ATTGGT <u>C</u> ATTTT <u>C</u> TT <u>C</u> TTT <u>A</u> T <u>C</u> CGA	Same as <i>cyrano</i> conserved site MO but with five mismatches (underlined)	
cyrano control MO2 (4 ng)	ACTAGGAATAATCTACCCACAGCTC	Non-conserved region in <i>cyrano</i> exon 3	
megamind e1i1 MO (1.6 ng)	GTAGAAAAACTGGCCCCCACCTTCT	megamind intron 1 5' splice site	
megamind i2e3 MO (1.6 ng)	ATGAAAATAGGGAGTCTTACCCTAC	megamind intron 2 3' splice site	
megamind conserved site MO (5 ng)	TGATCCCCAGAAGGGCCAATATGGA	megamind conserved site in exon 3	
megamind control MO1 (4 ng)	TG <u>T</u> T <u>G</u> CCCA <u>C</u> AAGG <u>C</u> CCAATAT <u>C</u> GA	Same as <i>megamind</i> conserved site MO but with five mismatches (highlighted)	
megamind control MO2 (4 ng)	GCATTTTCCTTTGCACAGAAACAAC	Non-conserved region in <i>megamind</i> exon 3	

 ${\bf Table~S7.~Oligonucleotide~Sequences,~Related~to~Experimental~Procedures}$

Amplicon	PCR primer pairs $(5' \rightarrow 3')$.
Insert for in situ probe template malat1	GACGTTTTCCGTTGGTTATACAAAGGTT AGTTGTAACACATTTACATTATAGCTGGC
linc- <i>mipep</i>	GCTCAACACAGTGTCGACTGTTTTTTCAGCGT TCAGAACGCTTTACAACTAAAGAGATC
linc-bin2a	GGTCATCGCCCTGATCCTGCTGACCCT ACAAGGAACATAATATTGTAACCCTGCACAAAACAC
linc-cldn7a	CTTCCGACTAGCGCCGAACAAACCGACACAGA AATGTCAAGGTAGACTCCAGTTACCAAG
linc-gtf2f2b	TCGAAGAATAGCTTGAAGAAACAGACGCAATCCCTG ACTGCAGCATTCATGGTTCGGGTGCTC
linc-epb4.114	GACTTTAATCTGCTCCTTGGTAAGGAAGCTCAG TGCTCCGACCGTCTTGGATTTCTGAGTTTCGC
line-srd5a2a	AGGACCCAAAATGGTGGCGGCGTGAGTGAAAAC TAATACGACTCACTATAGGAGCCGGCGCAGGCTGAGCGACGTACGACAC
linc-prr14	GACACTGTGAAACTGTTTATGACT AATGAATGCCTTAATACTCTCAGGATGGC
linc-agpat3	GAAGTCGTTACACAAACCGTCTGTCCAAGCAGA ATTACACAGTGATGCCATAATCAATTCAAC
linc-mettl3	GCTGAACGAGTCTCTCTACATCACCAGTGA ACACTGGCCAATGCCTACTTTGCACACTG
line-csnk1a1	CAACACCTGCTGAGTTTCCCACTCTAAACTCGCTCA TGGCATATTTATGGTTATTAGTTGTATTGACTGGACAGC
cyrano	GGTAATCACTATTAGTTGATGATAACGTCATAGCATGCT AGTCACAACACTGGTCCACTCATAGATTTAGTGTC
linc-loc100001135	CTCGAAGCCTGTCTTATTCATCTATCTCCTCACTTACGGT TCTCACAGTTGATATAAACAGAGTGCCATTGTGC
linc-onecut1	GCACGGATAACAGAATCTAGAGGCGAGAGACAAGCA ATTGTTGTGCTATTAAGAGTAACGAACCAAGCCATC
linc-pou3f3b-2	CAGGGAGAGGGCCTCCTTTCTACACTGGACCCA ATGACCGTACATGAAAGAAGAGGGTGGAGAACAGGTTC
linc-meis1	GCTGTGGTTCAGAAGTCAAACGGAGGTCATCCTTTAT TGAAATGCAAATTCCGTTACTTAAACTTTC
linc-arid4a	CCTATATGACTGCTTCAGCTCAGCATTCGACTAGGTTGCA TCCACAGAAACGACATAAAGACGCCATTACCGTTGC
linc-setd1ba	GCCTTTAAGTACAATTATTGTTTCCTCACTGTGT

ACTACACAAAATAGATTAGAATCCACATTTATTATAG

megamind GCACATCTGTAGGGCTTCTACACCCACAGAAAAAGCGGA

AGATGGGTTTCAGAGTCTAACATTCTTCTCTGTTAATTC

GTGAGGATACTGCGAGCCGTCATGCGCGCTCGCTGATCTTC linc-trpc7

TCAGTATATACAGACAAATCAGCGAGTTTCAGTCCACGCTGGTC

GGTTGGGAAGCGCAACATAAACTGCATGCTAACAAACAAT linc-elovl1a

TCAGAAAATGTAAAGACTACAGTGAAAACAGGTGTGGAC

linc-plcb2 GATATTTGACCTCAGAAACATCTCAGTCTTCA

AGCCCATGCAAGCTTTGTATTTTCTTAAAAAGCTCGCGTC

GCGGGACCATTCTGACTGAAGTCATGGACAAAAGCA linc-rogdi

TCATACAAATAATGTCATCCATTCAAAACATTCCAAC

linc-tbx2b GATACACAGACAACCAAGACTTAAGATTATTGACGTGTA

TAAACGCACACATGATGTTTCGCAGTGCAGTTTGTGGAAC

Insert for expression constructs

Zebrafish megamind

full-length

GCAATGCACGGCGCTCTCAGGCTCCGAGACGGGACCTATA GTATGTAATCATGTATCAATACAAAAGCATTTTCCTTTGCA

Zebrafish cyrano full-

length

GACCGAAATGGCGTAACGCGCAGTCGAGCACCGCAGCAGCGCA

TACAAAACCATGCGGGACGCTTCTGTAGTGCATAGATCA

cyrano conserved site for

the hybrid 1 construct

GGAAGATCTGTATATTGTACAAACAAGTGACAAGTTGTTCGCA GGAAGATCTACCCTAAAGCAAGCACATGAAACTATACATC

megamind conserved site

for the hybrid 2 construct

ACTAGTAGGCCTGTAAAGAGGAGCGAGAGGAGTCCATA

ACTAGTAGGCCTTTGTGTAGATGTAAACAAACACAATGACGAAGAG

T7 in vitro transcription templates

cyrano conserved site

TAATACGACTCACTATAGGGGTATATTGTACAAACAAGTGACAAGTTGTTC

ACCCTAAAGCAAGCACATGAAACTATACATC

megamind conserved site TAATACGACTCACTATAGGGGTAAAGAGGAGCGAGAGGAGTCCATA

TTGTGTAGATGTAAACAAACACAATGACGAAGAG

cyrano RNA-blot probe CCTCAATGACTGGAATGCAA

TTCTAATACGACTCACTATAGGAAGAGCAAAAGCCCTGCATA

qRT-PCR

Zebrafish cyrano

ACAAACCAAGACAGGCAGTGGCA TGCAACTCAATAGCACCCCGCT

Zebrafish megamind GCAATGCACGGCGCTCTCAGGCTCCGAGACGGGACCTATA

GCATTTTCCTTTGCACAGAAACAACGTGTCTGACACTGCACT

CTCTTCCAGCCTTCCTT β-actin1

CTTCTGCATACGGTCAGCAA