Supplementary Table 1. General demographic information of human postmortem brain samples. There were no significant differences between heroin addicts and control groups in pH and age. Student's *t*-tests, *p* = *n.s*.

GROUP	Cause of Death	SEX	pH	AGE	Blood - Morphine	Blood - ETOH
HEROIN	heroin	m	6.07	31	0.03	0
HEROIN	addict:heroin	f	6.48	32	0.30	0
HEROIN	heroin overdose	m	6.8	28	0.25	0
HEROIN	heroin overdose	m	6.66	27	0.24	0
HEROIN	heroin overdose	f	6.36	24	0.35	0
HEROIN	heroin overdose	m	6.52	20	0.74	0
HEROIN	heroin overdose	m	6.68	23	0.33	0
HEROIN	heroin overdose	m	6.47	27	0.96	0
HEROIN	heroin overdose	m	6.23	21	0.4	0
CONTROL	cardiac failure	m	6.33	30	0.00	0
CONTROL	cardiac failure	f	6.82	36	0.00	0
CONTROL	cardiac failure	f	6.98	31	0.00	0
CONTROL	sudden death	m	6.87	26	0.00	0
CONTROL	sudden natural	m	6.70	28	0.00	0

Supplementary Table 2. PCR Primers

Human qPCR primers

Target gene	Primer sequence (5' – 3')
hs-*Rn18s*	CGCCGCTAGAGGTGAAATTC
hs-*Rn18s*_rev	CATTCTTGGCAAATGCTTTCG
hs-*Bdnf* exon IX	TTTCTCGTGACAGCATGAGCAG
hs-*Bdnf* exon IX_rev	GTCCTCATCCAACAGCTCTTCTATC

Rat qPCR primers

Target gene	Primer sequence (5' – 3')
Gapdh	GTGGACCTCATGGCCTACAT
*Gapdh*_rev	TGTGAGGGAGATGCTCAGTG
Bdnf exon I	AGTTGCTTTGTCTTCTGTAATCGC
Bdnf exon I_rev	ATTCACGCTCTCCAGAGTCCCATG
Bdnf exon II	TTGGCTTCCTAGCGGTGTAG
Bdnf exon II_rev	CGTGGACGTTTGCTTCTTTC
Bdnf exon III	CCGGGCTGGATGCTTC
Bdnf exon III_rev	TCCAGAGGAAGTGAAAGTTTTGACT
Bdnf exon IV	CTGCCTTGATGTTTACTTTGACAAG
Bdnf exon IV_rev	ACCATAGTAAGGAAAAGGATGGTCAT
Bdnf exon V	CATAACCCCGCACACTCTGT
Bdnf exon V_rev	GACCCTCTCTGTCCATCCAG
Bdnf exon VI	CAGGAGCGTGACAACAATGTGA
Bdnf exon VI_rev	ACCATAGTAAGGAAAAGGATGGTCAT
Bdnf exon VII	CCTGAAAGGGTCTGCGGAACTCCA
Bdnf exon VII_rev	GAAGTGTACAAGTCCGCGTCCTTA
Bdnf exon VIII	GTGTGTGTCTCTGCGCCTCAGTGGA
Bdnf exon VIII_rev	GAAGTGTACAAGTCCGCGTCCTTA
Bdnf exon IX	GGGTGAAACAAAGTGGCTGT
Bdnf exon IX_rev	ATGTTGTCAAACGGCACAAA
Nurr1	GAAGATTCCTGGCTTTGCTG
*Nurr1*_rev	CTGGGTTGGACCTGTATGCT

Mouse qPCR primers

Target gene	Primer sequence (5' – 3')
m-*Gapdh*	AACTTTGGCATTGTGGAAGG
m-*Gapdh*_rev	ACACATTGGGGGTAGGAACA
m-*Bdnf* exon IX	CTCAGGCAGAATGAGCAATG
m-*Bdnf* exon IX_rev	AGCCGTCTGTGCTCTTCACT
m-*Ezh2*	ATCTGAGAAGGGACCGGTTT
m-*Ezh2*_rev	TGTGCACAGGCTGTATCCTC
m-*Creb1*	GTGTTACGTGGGGGAGAGAA
m-*Creb1*_rev	GGGCTAATGTGGCAATCTGT
m-*Nurr1*	GACCGGCTCTATGGAGATCA
m-*Nurr1*_rev	CTGGGTTGGACCTGTATGCT

Supplementary Table 3. Rat qChIP PCR Primers

Target gene	**Primer sequence (5’ – 3’)**
Bdnf–p1	TTCGATTCACGCAGTTGTTC
Bdnf–p1_rev	GCAGCCTCTCTGAGCCAGT
Bdnf–p2	CGTGGAACAAACTTGGGACT
Bdnf–p2_rev	CCCTTGCGGATGTCAATTAT
Bdnf–p4	GCGCGGAATTCTGATTCTGGTAAT
Bdnf–p4_rev	GAGAGGGCTCCACGCTGCCTTGACG
Bdnf–p6	TGCAGGGGAATTAGGGATAC
Bdnf–p6_rev	TCTTCGGTTGAGCTTCGATT
Bdnf–eI	CAGTGACAGGCGTTGAGAAA
Bdnf–eI_rev	AACGCCCTCATTCTGAGAGA
Bdnf–eII	AAAGCGTCTTTTCCGAGGTT
Bdnf–eII_rev	CAGCCTACACCGCTAGGAAG
Bdnf–eIV	ACTGAAGGCGTGCGAGTATT
Bdnf–eIV_rev	AGTCTTTGGTGGCCGATATG
Bdnf–eVI	CTGGCAGGCTTTGATGAGAC
Bdnf–eVI_rev	CACATTGTTGTCACGCTCCT
Th–p	CTAATGGGACGGAGGCCTTT
Th–p_rev	GTCCCGAGTTCTGTCTCCAC
Gria1–p	CTGGGAGAGAAGCAGAGGAA
Gria1–p_rev	CTGCCAGCTCTCTATGCTGA
Nurr1–p	ATCGTCGAGCAAGGGTAGTG
Nurr1–p_rev	CCGCCCTTGAAAATATGTCT

Supplementary Table 4. Rat qChIP PCR Primers for validation

Target gene	Location (from TSS)	Primer sequence (5' – 3')	Related epigenetic modification
Actb-1	-250	TCGCCAAACTCTTCATCCTC	Pol II[49-51], H3K36me3[51]
*Actb-1*_rev	-52	GCCATAAAAGGCAACTTTCG	
Actb-2	1639	CGATCGCCTTTCTGACTAGG	Pol II[49-51], H3K36me3[51] (Within intron3)
*Actb-2*_rev	1808	GCTGGGAGTATCAGGACAGG	
Actb-3	2770	GATCATTGCTCCTCCTGAGC	Pol II[49-51], H3K36me3[51] (Within exon6)
*Actb-3*_rev	2922	AGTCCGCCTAGAAGCATTTG	
Gapdh	-156	TGAGAGAGGCCCAGCTACTC	Pol II[52] , acH3[52], acH4[52], H3K4me3[53], H3K36me3[53]
*Gapdh*_rev	-4	AGGGCTGCAGTCCGTATTTA	
Rpl30	498	GGAAAGTACGTGCTGGGGTA	acH3[54], H3K4me3[55] (Within exon3)
*Rpl30*_rev	650	TTCTTCCCAATGCTGGAATC	
Myod1	-115	CAAGCTCCGCCCTACTACAC	H3K27me3[52], EZH2[56], SUZ12[57]
*Myod1*_rev	49	TGTGGTGAAGAAAGCAGTCG	
Afm	444	TGTACACACTCACACACAAACACA	H3K9me2[52], H3K27me3[52], G9a[58] (Within intron1)
*Afm*_rev	632	GCTTTGCTCTTGGCGTAGTC	
Myt1-1	-184	GATGGGAAAGTGGATCTGGA	H3K9me3[59], H3K27me3[59]
*Myt1-1*_rev	-26	GGGCCAGGAAGGATAGTCTC	
Myt1-2	-1903	TCCCCTTTAGAGGAGGCACT	H3K9me3[59], H3K27me3[59]
*Myt1-2*_rev	-1732	CCGGGAAAGGGAATAACATT	
Hoxa2	-165	CCCCATACGGCTGTAATCAG	H3K27me3[60], RING1A[61], RING1B[62], BMI1[63]
*Hoxa2*_rev	10	CGTAATTCATGGCCTTCTCC	
Esr1	-203	GGGGGCTGGAGTTTCTTCTA	mSIN3a[64]
*Esr1*_rev	10	TATGTGGAGTGGCAGGGACT	
Nr4a3	-674	GGGCCAGAGAGACGTAAACA	CREB[65] Containing CREB binding motif
*Nr4a3*_rev	-524	CTTCCGAAAGGGAAGGCTAC	
Bdnf	1219	CGCACGTGACAAAACGTAAG	NURR1[32] *Containing NBRE (NGFI-B response element)–like sequence[30] -Within exon2
*Bdnf*_rev	1294	CTACCACCTCGGACAAATCC	
Pitx3	-1293	GGTGGGAAGTCCTGAAGGT	NURR1[30] *Containing NBRE (NGFI-B response element)–like sequence[30]
*Pitx3*_rev	-1095	ATTTGCAAGGGACAGGACAG	
Th	-1055	AGGAAATGACTCCAGGGACA	NURR1[66] *Containing NBRE (NGFI-B response element)–like sequence[30]
*Th*_rev	-865	CATGGTACCCCGAGGTCTAA	

* Putative Nurr1 binding motif, 5'-AAAGGTCA-3' or one base deviation