Supplementary Tables

Table SI: Demographic data

	Control	Heroin
Number	N=30	N=39
Age (yrs)	33.23 ± 2.32	26.54 ± 0.89
Race	Caucasian	Caucasian
Gender	F=5, M=25	F=6, M=33
PMI	<24 hours	<24 hours
Brain pH	6.73 ± .04	6.57 ± .03
Ethanol toxicology	3	4
Morphine (ug/ul) urine	0	3.89 ± 1.61
6-MAM (ug/ml) urine	0	0.38 ± 0.11

Table S2: Probes used with Nanostring technologies.

Symbol	Full name	Accession #	Target region	Sequence
ACTB	Actin, beta	NM_001101.2	1010-1110	TGCAGAAGGAGATCACTGCCCTGGCACCCAGCACAATGAAGATCAAGATCATTGCTCCTCCTGAGCGCAAGTACTCCGTGTGGATCGGCGGCTCCATCCT
BAG1	BCL2-associated athanogene	NM_004323.3	1490-1590	CTCTTGTGATCGTGTAGTCCCATAGCTGTAAAACCAGAATCACCAGGAGGTTGCACCTAGTCAGGAATATTGGGAATGGCCTAGAACAAGGTGTTTGGCA
ELK1	ETS oncogene homolog	NM_005229.3	2350-2450	TTTTCAATAGGGGAGAGGGAGTCATCTCTTCCTATATTTGGTGGGGTGGGTGGGAAGGAAGGGATTTGGGGGGGAATCTTCCTGCCGCCTCCCCCACTCC
GAPDH	Glyceraldehyde-3-phosphate dehydrogenase	NM_002046.3	35-135	TCCTCCTGTTCGACAGTCAGCCGCATCTTCTTTTGCGTCGCCAGCCGAGCCACATCGCTCAGACACCATGGGGAAGGTGAAGGTCGGAGTCAACGGATTT
USE1	Unconventional SNARE in the ER 1 homolog	NM_018467.3	160-260	AGTACGTGGGAGCCCTAGAGGACATGTTGCAGGCCCTGAAGGTCCACGCGAGCAAACCGGCCTCTGAGGTGATCAATGAATATTCCTGGAAGGTGGATTT

Table S3- Primer pair sequences used in qPCR.

Symbol	Full name	Accession #	Distance from TSS	Sequence
Bag1	BCL2-associated athanogene	NM_004323.3	-.7kb	FWD 5'- AGCTCTTTCCGCTGCCCACTGT-3' REV 5'-GACGAAAGGGGGCGTAGTGACCT-3'
			-.1kb	FWD 5'-AGGATAGGGCGGTGCCTTGG-3' REV 5'-TACTCGCCACGCCCTCGGAA-3'
			+2kb	FWD 5'-GAGCCCGTGACCTTCCATGC-3' REV 5'-AATTCAGGGCCCCCAGGACA-3'
Use1	Unconventional SNARE in the ER 1 homolog	NM_018467.3	-3kb	FWD 5'- AACCTCCAGCAGGGCAGCCTA-3' REV 5'-CGAGGGCCTGTGCTCAAATCTC-3'
			.2kb	FWD 5'- ATGTCAGGGCTCCCGCCTCA-3' REV 5'-ACTGGACGGCAGGACCGGAA-3'
			+1kb	FWD 5'- ATTCGGCCCCTGGCGTGACA-3' REV 5'-TGGGAACCGCAGCCCCAGAA-3'

Table S4: Frequency of the rs2075572 *OPRM1* polymorphism in human subjects.

rs2075572	C/C	C/G	G/G
Control	0.455	0.364	0.182
Heroin	0.250	0.469	0.281

Table S5: ELK1 target genes identified in 49 subjects.

ETS1 (1589 genes)	**ELK1 (2282 genes)**
***p* value: 2.14E-03**	***p* value: 1.74E-02**
Overlapping genes (29)	**Overlapping genes (36)**
ACOT8	ACOT8
ARFGAP1	ADRM1
ARL6IP4	ARFGAP1
ASPSCR1	ARL6IP4
AURKAIP1	ASPSCR1
BCAP31	AURKAIP1
C11ORF2	BAG1
C12ORF44	C11ORF2
C17ORF62	C1QB
EIF3G	DNAJB2
ERCC1	ECSIT
FIBP	EIF3G
FIS1	EMG1
GPAA1	ERCC1
KLHDC4	FIBP
MFSD5	GPAA1
MYL6B	MRPL28
NME2	MYL6B
NOSIP	NDUFV1
NR1H3	NOSIP
NTHL1	NR1H3
PACS2	NTHL1
PAF1	PAF1
PIH1D1	PIGT
PUF60	PIH1D1
SCAND1	PRMT7
TSSC4	PTMA
UXT	PUF60
ZNF593	RFXANK
	SEC13
	SMARCD2
	TMEM204
	TSSC4
	USE1
	UXT
	ZNF593

Table S6: ELK1 target genes identified in 32 subjects.

ETS1 (1589 genes)			**ELK1 (2282 genes)**		
***p* value: 5.7E-09**			***p* value: 2.26E-07**		
Overlapping genes (91)			**Overlapping genes (115)**		
ACOT8	MYL6B	WDR74	ACOT8	MPG	SEC13
ACP2	NECAP2	XAB2	ACP2	MRPL28	SEC24C
ARFGAP1	NISCH	YKT6	ADRM1	MRPL52	SF3A3
ARL6IP4	NME2	ZBTB48	ARFGAP1	MRPS18B	SF3B2
ASB1	NOSIP	ZNF408	ARL6IP4	MVP	SLC27A5
ASPSCR1	NR1H3	ZNF593	ASB1	MYL5	SLC9A8
ATG9A	NTHL1	ZNF768	ASPSCR1	MYL6B	SMARCD2
ATP5I	PACS2		ATG9A	NDUFV1	SNF8
AURKAIP1	PAF1		ATP5I	NECAP2	STK19
B3GAT3	PEX16		AURKAIP1	NISCH	STOML1
BCAP31	PIH1D1		B3GAT3	NOSIP	STX4
C11ORF2	PNKP		BAG1	NR1H3	SUPT5H
C11ORF51	POLL		BAP1	NSUN5	TARS2
C12ORF44	POLR2G		C11ORF10	NTHL1	TIMM10
C16ORF7	POP4		C11ORF2	NUDC	TMED3
C17ORF62	PPIE		C11ORF51	PAF1	TMEM204
C20ORF43	PPP4C		C16ORF7	PIGT	TOLLIP
CARS	PRPF19		C1QB	PIH1D1	TSSC4
CCDC130	PRPF6		C20ORF43	PMPCA	TUBGCP2
CD2BP2	PSMC1		CARS	PNKP	UBTF
CHMP1A	PSME2		CHMP1A	POLL	UQCRQ
COG4	PUF60		COG4	POLR1E	USE1
CORO7	RAD23A		CORO7	POLR2G	UXT
DDX49	SART1		CPSF3L	POP4	VPS37B
DHX8	SCAND1		CTNNBL1	PPIE	WDR25
EDC4	SEC24C		DDX49	PPP4C	WDR46
EIF3D	SF3A3		DHX8	PRMT7	XAB2
EIF3G	SF3B2		DNAJB2	PRPF19	YKT6
ERCC1	SLC9A8		ECSIT	PRPF6	ZBTB48
FDXR	SNF8		EIF3G	PSMB1	ZNF593
FIBP	STOML1		EMG1	PSMC1	ZNF768
FIS1	SUPT5H		ERCC1	PSMC4	
GNL1	TIMM10		FCGRT	PSMD13	
GPAA1	TMEM186		FDPS	PSME2	
IDH3B	TSSC4		FEN1	PTMA	
ITPA	UBTF		FIBP	PUF60	
KLHDC4	UQCRQ		GIMAP6	RAD23A	
MCRS1	UXT		GNL1	RBP1	
MFSD5	VPS33B		GPAA1	RFXANK	
MRPL52	VPS37B		IMMT	RNF25	
MRPS18A	WDR25		ITPA	SART1	
MYL5	WDR46		MCRS1	SCAMP3	

Supplementary Figures

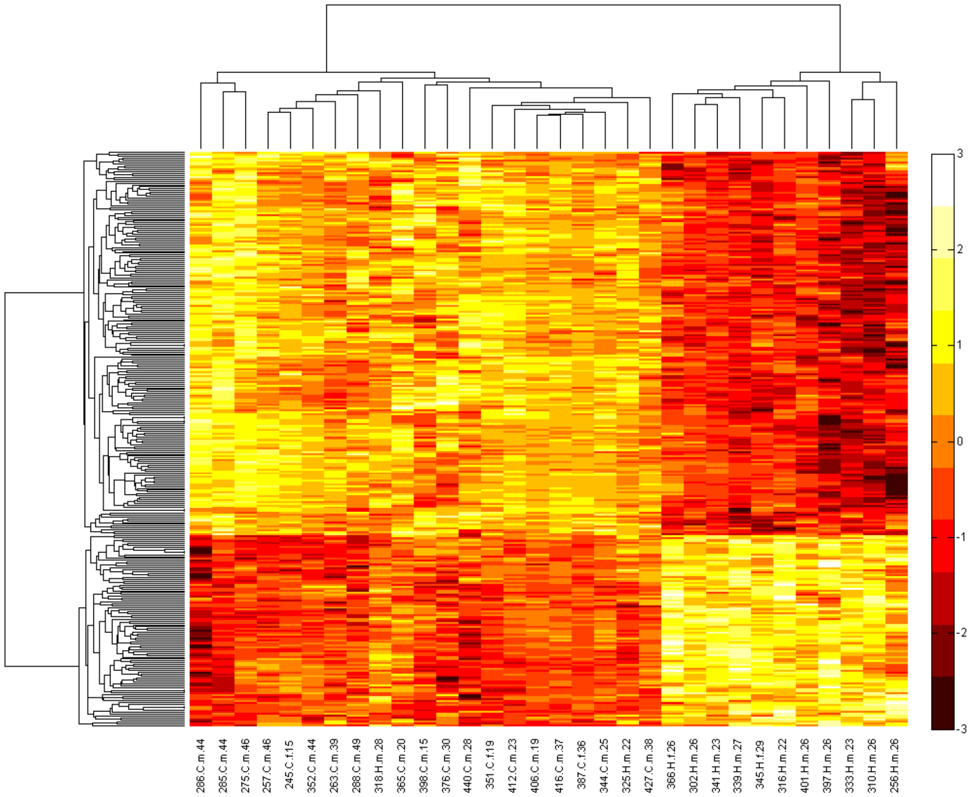

Figure S1: Heatmap of gene expression changes in the NAc of human heroin abusers. The hierarchical clustering of differentially expressed genes detected between the control (N=19) and heroin (N=13) groups in the NAc using mRNA microarrays. Dark colors represent normalized low expression and light colors high expression. The x-axis lists subjects represented by a three digit ID number; C-control, H-heroin user; m-male, f-female; age.