ARTICLES

Striatal microRNA controls cocaine intake through CREB signalling

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Cocaine addiction is characterized by a gradual loss of control over drug use, but the molecular mechanisms regulating vulnerability to this process remain unclear. Here we report that microRNA-212 (miR-212) is upregulated in the dorsal striatum of rats with a history of extended access to cocaine. Striatal miR-212 decreases responsiveness to the motivational properties of cocaine by markedly amplifying the stimulatory effects of the drug on cAMP response element binding protein (CREB) signalling. This action occurs through miR-212-enhanced Raf1 activity, resulting in adenylyl cyclase sensitization and increased expression of the essential CREB co-activator TORC (transducer of regulated CREB; also known as CRTC). Our findings indicate that striatal miR-212 signalling has a key role in determining vulnerability to cocaine addiction, reveal new molecular regulators that control the complex actions of cocaine in brain reward circuitries and provide an entirely new direction for the development of anti-addiction therapeutics based on the modulation of noncoding RNAs.

Cocaine triggers cellular and molecular alterations in brain reward systems, and cocaine addiction is commonly considered to be a disorder of neuroplasticity[1,2]. Such long-lasting structural and functional modifications are thought to increase sensitivity to the motivational effects of cocaine and associated environmental stimuli, culminating in a loss of control over intake[3]. However, recent findings support a more nuanced view in which cocaine also triggers adaptations in brain reward systems that decrease responsiveness to the drug[4,5]. This notion of 'yin-yang' neuroplastic responses to cocaine, which can increase or decrease sensitivity to its motivational effects, probably accounts for the fact that only a small fraction (~15%) of human cocaine users lose control over intake and develop compulsive drug-seeking behaviours[6]. Similar to human cocaine users, addiction-like drug seeking can be detected in rats that intravenously self-administer cocaine[7–9]. In particular, rats with a history of extended cocaine access demonstrate increasing motivation to obtain the drug, reflected in escalating consumption[7] and higher 'break points' under progressive ratio reinforcement schedules[10]. In a small percentage of rats (~15%) with extended cocaine access, motivation to obtain the drug increases to such a degree that their behaviour can be considered 'addiction-like' when assessed according to the same diagnostic criteria used for human drug users[9,11]. Understanding the factors that regulate the motivational properties of cocaine in rats under extended access conditions may therefore reveal important insights into the neurobiological basis of vulnerability to addiction.

Considering the complexity of cocaine-induced neuroadaptive responses in brain reward systems, it is likely that highly synchronized programs of gene regulation are involved. Particularly interesting in this regard are microRNAs (miRNAs), which are small (~21–23 nucleotides), noncoding RNA transcripts that regulate gene expression at the post-transcriptional level. miRNAs control gene expression by binding to complementary sequences (miRNA response elements (MREs)) in the 3′ untranslated region (3′ UTR) of target messenger RNA transcripts to facilitate their degradation and/or inhibit their translation[12]. Because of their ability to coordinate the expression of networks of related genes responsible for brain structure and function[13,14], it has been proposed that miRNAs may have important roles in complex psychiatric disorders[15,16]. Until now, little has been known about their potential involvement in addiction[17–19]. Here we identify a role for miRNAs in regulating compulsive-like cocaine intake.

Cocaine increases miR-212 expression

The dorsal striatum is a key brain region regulating the development of compulsive cocaine use[20–23]. Expression profiling showed that miR-212, and the closely related miR-132, was upregulated ~1.75-fold in the dorsal striatum of rats with extended (6 h) daily access to intravenous cocaine self-administration (0.5 mg kg^{-1} per injection; $n = 6$) compared with cocaine-naive control rats ($n = 6$) (Fig. 1a and Supplementary Figs 1 and 2), an effect verified by Taqman assay (Fig. 1b; see Supplementary Fig. 3 for other brain regions). Striatal miR-212 expression was also increased compared to rats with restricted (1 h) access ($n = 6$) and 'yoked' rats ($n = 6$), which received cocaine infusions at the same time points as extended access rats, but in a response-independent manner (Fig. 1b). miR-212 expression is highly responsive to CREB[14,24]. Accordingly, striatal phospho-S133-CREB (p-CREB) (Fig. 1c) and total CREB (t-CREB; Supplementary Fig. 4) were increased in extended access rats.

Effects of miR-212 on cocaine intake

Next, we used a lentivirus vector to overexpress miR-212 (Lenti-miR-212) in dorsal striatum (Fig. 2a), and verified this effect using fluorescent *in situ* hybridization (FISH; Fig. 2b) and Taqman assay (Supplementary Fig. 5). Lenti-miR-212 rats, and rats treated with an empty vector (Lenti-control rats), learned to respond for food reinforcement at similar rates (Supplementary Fig. 6), demonstrating that miR-212 overexpression did not alter operant performance. Cocaine intake did not differ between Lenti-miR-212 and Lenti-control rats with restricted access (Supplementary Fig. 7). In contrast, notably different patterns of intake were revealed under extended access conditions (Fig. 2c). Consistent with previous reports[7], cocaine

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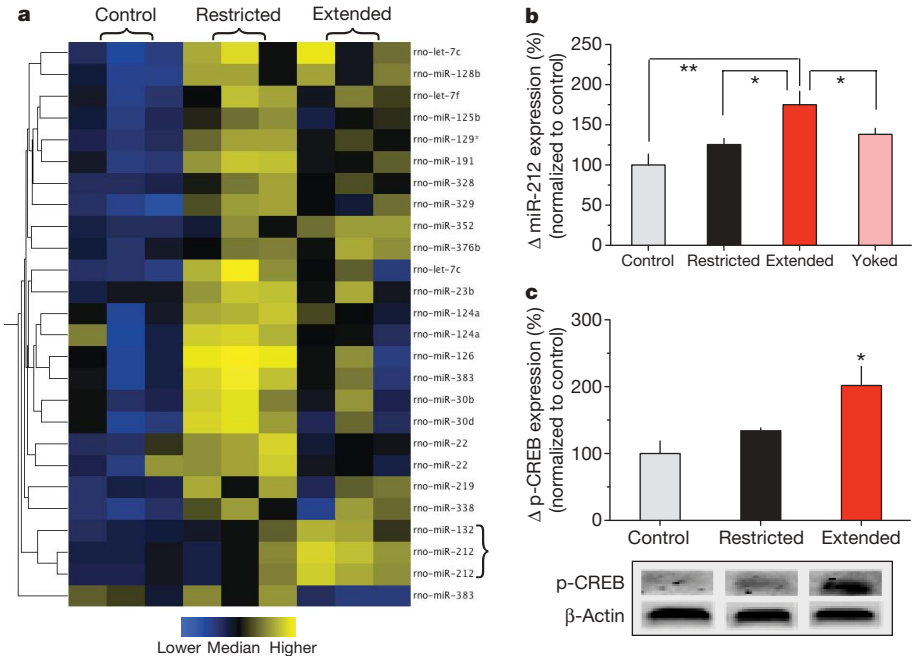

Figure 1 | Increased striatal miR-212 expression in extended access rats. **a**, Expression analysis showed that striatal miR-212 levels were increased in rats with extended access to cocaine self-administration. The bracket identifies miR-212 and miR-132, the expression of which was increased only in extended access rats. The asterisk beside rno-miR-129 refers to the rno-miR-129* miRNA encoded by the same pre-miRNA transcript that encodes rno-miR-129, but expressed on the opposite arm of the pre-miR-129 transcript. **b**, Taqman assay verified that striatal miR-212 levels were increased in extended access rats ($F_{3,23} = 6.6$, $P < 0.01$; $^*P < 0.05$, $^{**}P < 0.01$, statistically significant compared with the extended access group). **c**, Relative amounts of p-CREB in the dorsal striatum were quantified by densitometry ($F_{2,6} = 6.8$, $P < 0.05$; $^*P < 0.05$, compared with control). The lower panel is a representative immunoblot of the increased striatal p-CREB expression. Data are presented as mean ± s.e.m.

intake escalated in Lenti-control rats with extended access (Fig. 2c). Conversely, Lenti-miR-212 rats initially consumed the same high levels of cocaine, but their intake became progressively lower as exposure to the drug increased across sessions (Fig. 2c; see Supplementary Fig. 8 for non-reinforced, 'inactive' lever responses). Striatal overexpression of miR-1 did not alter cocaine intake (Supplementary Fig. 9), confirming that these effects were specific to miR-212. When the unit dose of cocaine available for self-administration was varied, we found that the cocaine dose–response curve was shifted upward in Lenti-control rats with extended access compared to those with restricted access (Supplementary Fig. 10). Remarkably, the opposite effect occurred in Lenti-miR-212 rats, with the cocaine dose–response curve shifting downward in those with extended access (Supplementary Fig. 11). Upward or downward shifts in the dose–response curve are interpreted as increased or decreased motivation to consume cocaine, respectively[7,25]. Therefore, in contrast with the progressively increasing motivation to consume cocaine typically seen in rats with extended drug access[7–9], Lenti-miR-212 rats were progressively less motivated to consume cocaine across sessions and cocaine may have become aversive, as reflected in low levels of intake across doses. The cocaine dose–response curve was similar in Lenti-miR-212 and Lenti-control rats with restricted access (Supplementary Fig. 12), demonstrating that striatal miR-212 regulates intake only under extended access conditions. Interestingly, non-reinforced responding during the 20-s timeout period after each cocaine infusion, which may reflect compulsive drug-seeking behaviour[9], increased over sessions in the extended access Lenti-control rats (Supplementary Fig. 13), and striatal miR-212 overexpression abolished this effect.

Inhibition of striatal miR-212 signalling using a locked nucleic acid (LNA)-modified antisense oligonucleotide[26,27] (LNA-anti-miR-212; Supplementary Figs 14 and 15) increased cocaine intake in rats with extended (Fig. 2d) but not restricted (Supplementary Fig. 16) access, as shown by sharply increased cocaine consumption 48 h after the last LNA-anti-miR-212 injection that persisted for >4 days (Fig. 2d). Non-reinforced responding during timeout periods also increased in the LNA-anti-miR-212-treated rats with extended but not restricted access (Supplementary Fig. 17). An antisense oligonucleotide against miR-1 (LNA-anti-miR-1) did not alter cocaine intake (Supplementary Fig. 18), confirming that these effects were specific to miR-212. Disruption of striatal miR-212 signalling therefore precipitates compulsive-like responding for cocaine[9]. Hence, cocaine-induced increases in striatal miR-212 may represent a previously unknown anti-addiction counter-adaptive response in brain reward circuitries, and deficits in miR-212 signalling may increase vulnerability to addiction.

miR-212 amplifies CREB signalling

It has been proposed that gene regulatory networks in the brain, similar to electronic circuits, are comprised of feedforward and feedback loops, and that miRNAs can amplify or curtail activity in these networks[28]. Cocaine-induced activation of CREB signalling is considered to be an important compensatory response that decreases the motivational properties of the drug[5,29,30], and miR-212 is highly CREB-responsive[14,24]. We proposed that excessive cocaine intake may engage a novel feedforward circuit in the dorsal striatum in which activation of CREB signalling increases miR-212 expression, which in turn loops back to amplify the actions of this transcription factor and thereby decrease the motivation to consume cocaine.

Consistent with this hypothesis, miR-212 markedly amplified CREB signalling evoked by a low concentration of forskolin (5 μM) compared with vector-transfected cells (Fig. 3a and Supplementary Fig. 19), measured using a luciferase-based CREB reporter construct (CRE-containing element from promoter of *EVX1*)[31]. CREB signalling was also amplified by the closely related miRNA, miR-132 (Supplementary Fig. 20), but not by unrelated miRNAs (miR-1 or miR-29b; Supplementary Fig. 21). Importantly, miR-212 potentiated increases in *Fos* mRNA (Fig. 3b), a known CREB-responsive gene, confirming that miR-212 acts on endogenous CREB-responsive genes and not just reporter constructs. Using a GAL4-luciferase reporter system in which the GAL4 DNA-binding domain is fused to the N terminus of the full-length CREB, we found that a phosphorylation-defective CREB mutant (ΔS133) no longer responded to miR-212 (Fig. 3c). miR-212

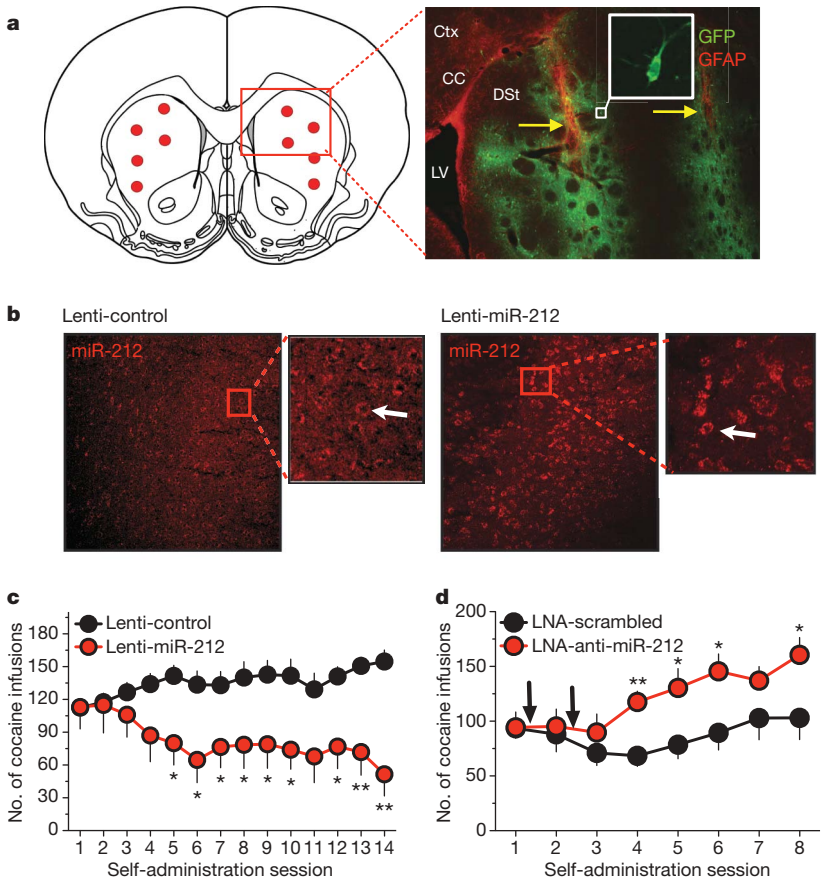

Figure 2 | Dissociable effects of striatal miR-212 on cocaine intake. a, Red circles in the left panel are locations at which viral infusions were targeted in the dorsal striatum. The right panel is representative immunochemistry staining (×10 magnification) from a Lenti-miR-212 rat. Green is GFP from virus; red is the astrocyte marker glial fibrillary acidic protein (GFAP). CC corpus callosum; Ctx, cortex; DSt, dorsal striatum; LV, lateral ventricle. Yellow arrows highlight the injector track used to deliver virus. Insert is a ×80 confocal image of a virus-infected neuron. **b**, FISH was used to visualize striatal miR-212 expression (shown in red) in Lenti-control and Lenti-miR-212 rats. **c**, Striatal miR-212 overexpression reverses the long-term trajectory of cocaine-taking behaviour in rats with extended access (virus × session: $F_{13,130} = 3.0$, $P < 0.001$; $^*P < 0.05$, $^{**}P < 0.01$, compared with intake on the same day in Lenti-control rats). **d**, LNA-anti-miR-212 delivered into dorsal striatum increases cocaine intake in extended access rats (LNA × session: $F_{4,36} = 5.3$, $P < 0.005$; $^*P < 0.05$, $^{**}P < 0.01$, compared with intake on the same day in the LNA-Scrambled rats). Data are presented as mean ± s.e.m.

also had no effects on GAL4–CREB with a mutation in the bZIP domain (ΔR314) that abolishes the recruitment of the essential CREB co-activator TORC (Fig. 3c). Similarly, a dominant-negative CREB polypeptide (A-CREB)[31] abolished the stimulatory effects of miR-212 on the *EVX1* reporter (Supplementary Fig. 22), and on *Fos* gene expression (Fig. 3d). Knockdown of TORC2, the most abundant family member in HEK cells[31], also abolished the effects of miR-212 on a CREB luciferase reporter (Supplementary Fig. 23) and on *Fos* expression (Fig. 3e). Finally, striatal CREB signalling was engaged in rats with extended but not restricted access to cocaine (Fig. 1c). Accordingly, striatal protein levels of the CREB-responsive genes *Fos* (Fig. 3f) and *Nurr1* (also known as *Nr4a2*) (Fig. 3g) were upregulated in Lenti-control rats with extended access, and this effect was amplified in Lenti-miR-212 rats (Fig. 2c). Thus, miR-212 amplifies cAMP-responsive gene expression through the canonical CREB–TORC signalling cascade.

Next, we found that miR-212 potentiated forskolin-induced accumulation of cAMP in HEK cells with 30 min but not 240 min treatment (Fig. 4a). Type IV phosphodiesterases (PDE4) are the major subtype of phosphodiesterase responsible for cAMP degradation in HEK cells and striatum[32,33]. The PDE4 inhibitor rolipram potentiated the effects of miR-212 on cAMP accumulation, and miR-212 did not alter expression of PDE4D, a major subtype of PDE4 (Supplementary Fig. 24). Thus, miR-212 probably increases cAMP levels by sensitizing its production rather than by inhibiting its breakdown. miR-212 also potentiated forskolin-stimulated increases of p-CREB (but not t-CREB; Fig. 4b), and increased expression of TORC2 (Fig. 4c, d and Supplementary Fig. 25). cAMP can trigger CBP/p300-mediated acetylation of TORC, which protects against its degradation[34]. miR-212 increased levels of total and acetylated TORC2 (Supplementary Fig. 26), indicating that miR-212 increases TORC expression indirectly through increased cAMP levels. Finally, miR-212 also increased TORC1 and TORC2 expression in dorsal striatum (Fig. 4e, f). Together, these data reveal miR-212 as a novel regulator of CREB signalling that acts by sensitizing cAMP production and increasing expression of the TORC family of CREB coactivators.

miR-212 amplifies CREB through Raf1

Raf1 phosphorylates various isoforms of adenylyl cyclases and sensitizes their activity[35,36]. Indeed, the characteristic increases in cAMP signalling associated with chronic opiate treatment[37] that are thought to contribute to the aversive opiate withdrawal syndrome occur through Raf1-mediated sensitization of adenylyl cyclase activity[38]. In many cases, phosphorylation of Raf1 at S338 is required for its activation[39], and we found that miR-212 increased p-S338-Raf1 levels in HEK cells (Fig. 5a) without altering total Raf1 levels (Supplementary Fig. 27). When we overexpressed exogenous GFP-tagged Raf1 (to elevate basal levels of Raf1), miR-212 also increased levels of the phosphorylated exogenous protein (Fig. 5a; for total Raf1 levels see Supplementary Fig. 27). Inhibition of Raf1 function using a dominant-negative truncated version (amino acids 51–220) of the protein (DN-Raf1), abolished the stimulatory effects of miR-212 on

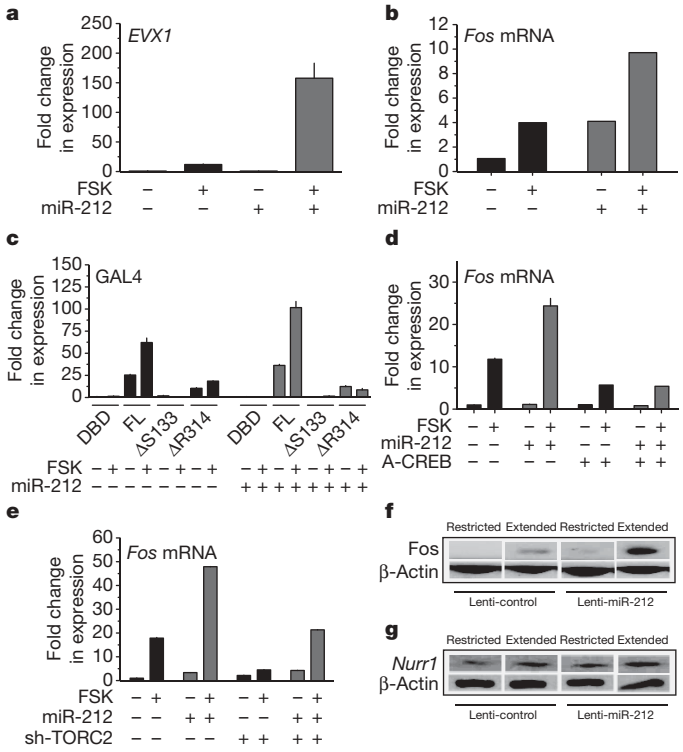

Figure 3 | miR-212 amplifies CREB signalling. **a**, miR-212 potentiated CREB signalling engaged by forskolin (FSK), measured using an *EVX1* luciferase reporter (miRNA × FSK: $F_{1,8} = 99.2$, $P < 0.001$). **b**, miR-212 potentiated forskolin-induced increases in *Fos* mRNA in HEK cells (miRNA × FSK: $F_{1,8} > 1{,}000$, $P < 0.001$). **c**, The effects of miR-212 on CREB signalling were abolished in GAL4-luciferase reporters containing phosphorylation-defective (ΔS133) or TORC-recruitment-defective (ΔR314) CREB mutants. FL, full-length CREB; DBD, DNA-binding domain. **d**, A-CREB polypeptide abolished the effects of miR-212 on *Fos* mRNA expression. **e**, RNAi-mediated knockdown of TORC2 also abolished the effects of miR-212 on *Fos* mRNA expression. **f**, Protein levels of Fos were enhanced in dorsal striatum from Lenti-miR-212 rats with extended cocaine access compared with other groups. **g**, Striatal levels of *Nurr1*, another CREB-responsive gene, were also enhanced in Lenti-miR-212 rats with extended access. Data are presented as mean ± s.e.m.

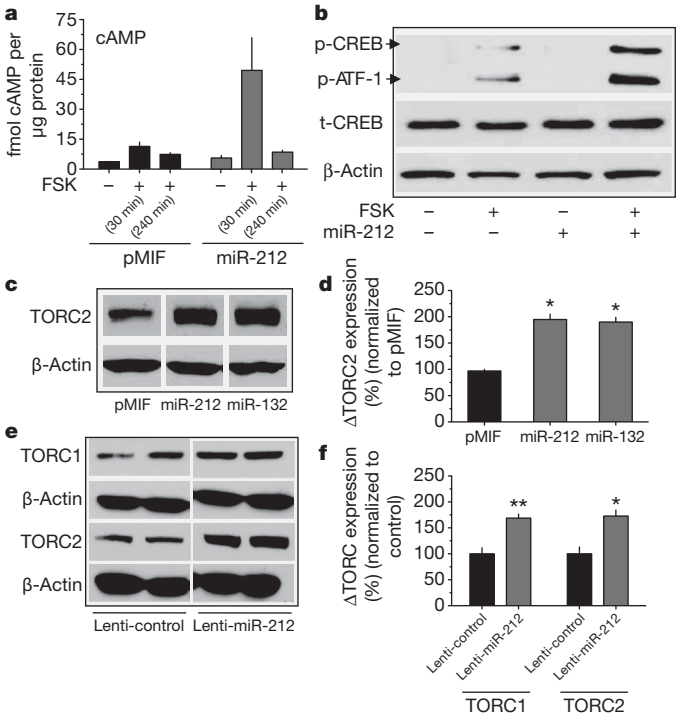

Figure 4 | miR-212 stimulates core CREB signalling components. **a**, miR-212 potentiated cAMP accumulation in HEK cells (miRNA × FSK: $F_{2,8} = 4.8$, $P < 0.05$). **b**, miR-212 also increased p-CREB and the related p-ATF-1, without altering t-CREB. **c**, Representative immunoblots of the increased TORC2 levels in HEK cells. **d**, Relative amounts of TORC2 in HEK cells expressing miR-212, miR-132 or vector (pMIF) were quantified by densitometry (*$P < 0.05$, compared with pMIF). **e**, Representative immunoblots showing that miR-212 increased striatal levels of TORC1 and TORC2. **f**, The relative amounts of striatal TORC1 and TORC2 were quantified by densitometry (*$P < 0.05$, **$P < 0.01$, compared with Lenti-control). Data are presented as mean ± s.e.m.

cAMP production (Fig. 5b), and lowered basal and forskolin-evoked increases in cAMP content in control cells (Fig. 5b). Disruption of Raf1 also abolished miR-212-induced amplification of p-CREB levels in response to forskolin (Fig. 5c) and decreased basal and forskolin-enhanced p-CREB levels in control cells (Fig. 5c), without altering total CREB expression levels (Supplementary Fig. 28). Finally, disruption of Raf1 signalling abolished miR-212-induced increases in TORC2 expression (Fig. 5d).

A useful feature of pharmacological inhibitors of Raf is their bimodal action on the activity of the kinase in intact cells[40]. Cells briefly exposed to a Raf inhibitor show a paradoxical increase in Raf activity when the inhibitor is washed away[40–42]. We verified that a brief pulse (30 min) of the Raf1 inhibitor GW5074 increased Raf1 activity in HEK cells (Supplementary Fig. 29). Using this approach to upregulate Raf activity, we found that activation of Raf1 signalling amplified forskolin-stimulated increases in cAMP content in cells (Fig. 5e), potentiated increases in p-CREB levels (Fig. 5f) and upregulated TORC2 levels (Fig. 5g), fully recapitulating the effects of miR-212.

miRNAs exert their actions by binding to the 3′ UTR of target mRNA transcripts to facilitate their degradation and/or inhibit their translation[12]. To identify gene targets for miR-212, which could shed light on its actions, we assessed gene expression profiles using microarrays in HEK cells transfected with miR-212 or vector[43,44]. All predicted targets for miR-212 whose expression was reduced by ≥30% by miR-212 were collated (http://www.targetscan.org/). This analysis identified ~100 predicted targets for miR-212 for which expression was knocked down (Supplementary Tables 1 and 2). Among these target transcripts there were at least seven previously shown to regulate Raf1 signalling: SMAD4, SPRED1, DACH1, ERBB2IP (Erbin), APC, RASA1 (p120GAP) and SLK (STE20-like kinase). Most notable was SPRED1 (sprouty-related, EVH1 domain containing 1), a recently identified core repressor of Raf1 function[45,46]. We tested the hypothesis that miR-212-mediated repression of SPRED1 may contribute to its stimulatory effects on Raf1 and CREB–TORC signalling. First, miR-212 knocked down protein levels of SPRED1 in HEK cells (Supplementary Fig. 30). SPRED1 was expressed in a punctuate fashion near the plasma membrane of dorsal striatal cells, and miR-212 knocked down striatal SPRED1 levels (Supplementary Fig. 31). Second, RNAi-mediated knockdown of SPRED1 increased levels of p-S338-Raf1 in HEK cells (Supplementary Fig. 32), similar to the actions of miR-212. Moreover, SPRED1 knockdown potentiated increases in p-CREB in response to forskolin (Fig. 5h) without altering t-CREB (Supplementary Fig. 32), and increased TORC2 expression levels (Fig. 5i), further recapitulating the effects of miR-212. Third, expression of a clone containing only the coding sequence of the SPRED1 gene, but not the 3′ UTR, attenuated but did not block the stimulatory effects of miR-212 on p-CREB levels (Supplementary Fig. 33). These data indicate that miR-212 activates Raf1 and thereby amplifies the CREB–TORC cascade in part through repression of SPRED1.

Striatal CREB–TORC limits cocaine intake

A major consequence of striatal miR-212 overexpression was increased TORC expression. Knockdown of TORC1, the predominant family member in brain[47], abolishes CREB-regulated gene

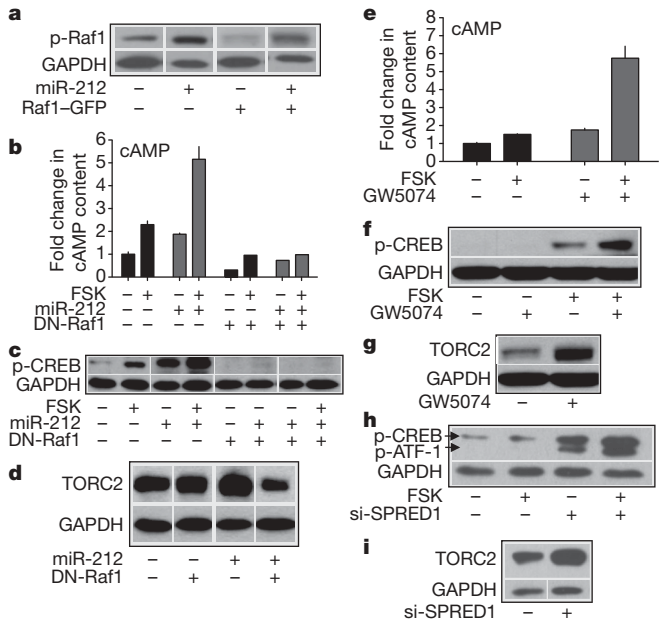

Figure 5 | miR-212 amplifies CREB signalling through Raf1. **a**, miR-212 activates Raf1 signalling, as shown by increased levels of phosphorylated endogenous and exogenous (Raf1–GFP) Raf1 protein. **b**, DN-Raf1 abolished the stimulatory effects of miR-212 on cAMP accumulation. **c**, DN-Raf1 abolished miR-212-induced increases in p-CREB. **d**, DN-Raf1 also abolished miR-212-induced increases in TORC2. **e**, Enhancing Raf1 signalling by pulsing cells with the Raf1 inhibitor GW5074 potentiated cAMP accumulation. **f**, Potentiation of Raf1 signalling increased p-CREB levels. **g**, Potentiation of Raf1 signalling increased TORC2 levels. **h**, Knockdown of the Raf1 repressor SPRED1, a target for miR-212, increased p-CREB levels. **i**, SPRED1 knockdown also increased TORC2 levels. Data are presented as mean ± s.e.m.

expression, dendritic growth and synaptic plasticity in neurons[48–50]. Conversely, TORC1 overexpression enhances CREB-responsive gene expression[31]. To investigate directly the functional relevance of miR-212-induced amplification of striatal CREB–TORC signalling, we next tested the effects of striatal TORC1 overexpression on cocaine intake.

Using a lentivirus vector to overexpress TORC1 (Lenti-TORC1) in dorsal striatum (Fig. 6a–c and Supplementary Fig. 34), we found that Lenti-TORC1 and Lenti-control rats acquired operant responding for food reinforcement at the same rate (Supplementary Fig. 35), and that their mean daily cocaine intake (Supplementary Fig. 36) and cocaine dose–response curves (Supplementary Fig. 37) did not differ under restricted access conditions. Cocaine intake progressively escalated in the Lenti-control rats under extended access conditions (Fig. 6d). In contrast, cocaine intake was significantly lower in the Lenti-TORC1 rats and did not escalate (Fig. 6d). Similarly, the cocaine dose–response curve was shifted downward in the Lenti-TORC1 rats compared with the Lenti-controls (Supplementary Fig. 38). These data support a conceptual framework in which miR-212 amplification of striatal CREB–TORC signalling counters the motivational properties of the drug (Supplementary Fig. 39).

Conclusions

Repeated cocaine overconsumption is considered to be an important risk factor for drug-seeking behaviours to switch from controlled to uncontrolled[7–9]. Here we show that miR-212 is a cocaine-responsive noncoding RNA whose expression is increased in the dorsal striatum of rats with extended but not restricted cocaine access, and that striatal miR-212 signalling decreases responsiveness to the motivational properties of cocaine. miR-212 controls cocaine intake by markedly amplifying the activity of CREB, a known negative regulator of cocaine reward. This action occurs through Raf1-mediated sensitization of adenylyl cyclase activity and increased TORC expression (see Supplementary Fig. 39). Striatal miR-212 therefore protects against development of compulsive drug taking, and factors that regulate miR-212 signalling may have key roles in determining vulnerability to cocaine addiction. Hence, miRNAs are important molecular regulators that control the complex actions of cocaine in brain reward circuitries and the neuroadaptations associated with addiction.

METHODS SUMMARY

Male Wistar rats (Charles River Laboratories) weighing 300–320 g were surgically prepared with silastic catheters in the jugular vein and trained to respond on an 'active' lever for food pellets (45 mg; 60 min sessions) under a fixed ratio 5 timeout 20 s (FR5TO20) schedule of reinforcement. Rats then responded for cocaine on

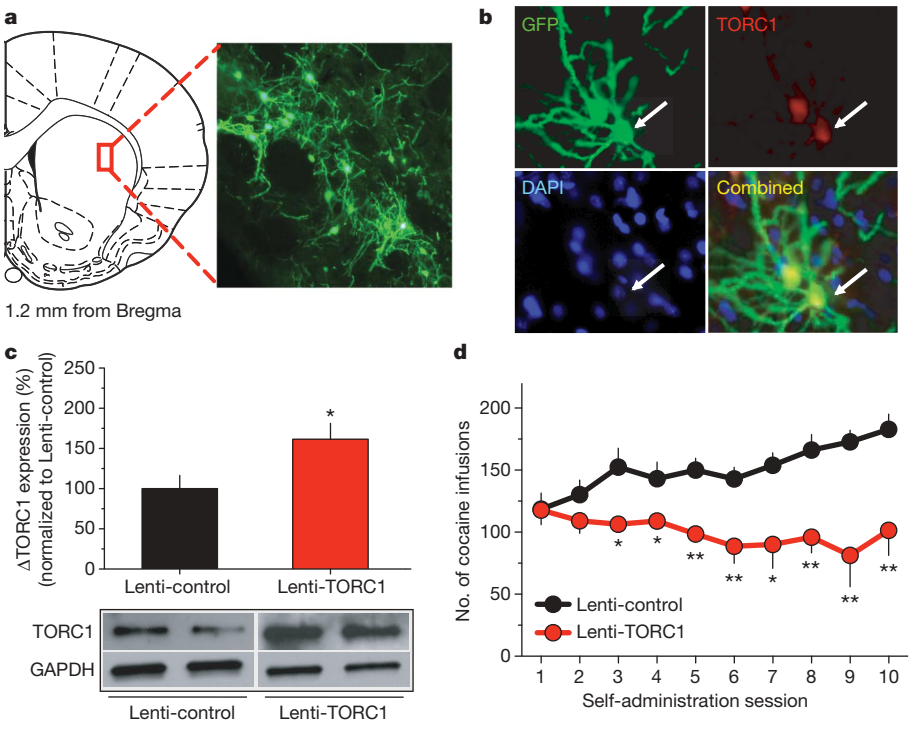

Figure 6 | Striatal CREB–TORC signalling controls cocaine intake. **a**, Representative image of Lenti-TORC1-infected neurons (green) in the dorsal striatum (×20 magnification). **b**, Representative high-magnification (×80 confocal) images of Lenti-TORC1 infected cells (green), demonstrating the viral-driven upregulation of TORC1 expression (red). Cell nuclei are shown in blue using DAPI staining. **c**, Relative amounts of TORC1 in dorsal striatum were quantified by densitometry ($^*P < 0.05$). The lower panel is a representative immunoblot. **d**, Cocaine intake under extended access conditions is far lower in Lenti-TORC1 rats compared with Lenti-controls (virus × session: $F_{9,90} = 2.9$, $P < 0.001$; $^*P < 0.05$, $^{**}P < 0.001$, compared with intake on the same day in Lenti-control rats). Data are presented as mean ± s.e.m.

the FR5TO20 reinforcement schedule during 1-h daily testing sessions for at least seven consecutive days. Cocaine hydrochloride was dissolved in sterile saline solution (0.9% w/v). Each cocaine infusion earned resulted in the delivery of 0.5 mg kg^{-1} per infusion cocaine (0.1 ml injection volume delivered over 4 s), and initiated a 20-s timeout period signalled by a light cue located above the active lever during which responding on the lever was without consequence. In all cases, a control group of rats were surgically prepared with jugular catheters and trained to respond for food reinforcement as described above, but remained cocaine-naive for the duration of the experiment. To determine the cocaine dose–response curve, the unit dose of cocaine available for self-administration was adjusted upward or downward during 3-h testing sessions every other day between regular 6-h self-administration sessions; for detailed description see ref. 7. Doses of cocaine were tested once, and in the following order: 0.5, 0.0625, 0.25, 0.125 and 0 mg kg^{-1} per infusion.

Full Methods and any associated references are available in the online version of the paper at www.nature.com/nature.

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Supplementary Information is linked to the online version of the paper at www.nature.com/nature.

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Author Information Microarray data are deposited at the Gene Expression Omnibus (http://www.ncbi.nlm.nih.gov/geo) under accession number GSE21901. Reprints and permissions information is available at www.nature.com/reprints. The authors declare no competing financial interests. Readers are welcome to comment on the online version of this article at www.nature.com/nature. Correspondence and requests for materials should be addressed to P.J.K. (pjkenny@scripps.edu).

METHODS

Animals. Male Wistar rats (Charles River Laboratories) weighing 300–320 g were housed in groups of 1–2 per cage in a temperature-controlled vivarium on a 12-h reverse light/dark cycle (lights off at 7:00). Food and water were available ad libitum except when animals were trained to perform the operant response to receive food rewards, when animals were restricted to 20 g chow per day. All procedures were conducted in strict adherence with the National Institutes of Health Guide for the Care and Use of Laboratory Animals and were approved by the Institutional Animal Care and Use Committee of The Scripps Research Institute.

Cocaine self-administration. Rats were anaesthetized by inhalation of 1–3% isoflurane in oxygen, and surgically prepared with silastic catheters in the jugular vein[51]. The catheter was passed subcutaneously to a polyethylene assembly mounted on the rat's back. Rats were permitted at least 7 days recovery before behavioural training commenced. Animals were food restricted (20 g per day; 3–4 days) then trained to respond on an 'active' lever for food pellets (45 mg; 60 min sessions) under a fixed ratio 5 timeout 20 s (FR5TO20) reinforcement schedule[52]. Rats were also presented with an 'inactive' lever during training and testing sessions, responses on which were recorded but were without scheduled consequences. Rats responded for food until criteria was reached (>80 pellets per 1 h session). Rats then responded for cocaine on the FR5TO20 reinforcement schedule during 1-h daily testing sessions for at least seven consecutive days. Cocaine hydrochloride was dissolved in sterile saline solution (0.9% w/v). Each cocaine infusion earned resulted in the delivery of 0.5 mg kg^{-1} per infusion cocaine (0.1 ml injection volume delivered over 4 s), and initiated a 20-s timeout period signalled by a light cue located above the active lever during which responding on the lever was recorded but was without consequence. After training in the cocaine self-administration procedure as described earlier, two balanced groups of rats were formed so that they consumed similar amounts of cocaine. One group of rats continued to respond for cocaine infusions during 1-h daily testing session or responded for cocaine during 6-h daily sessions. Additionally, a separate control group of rats were matched to individual animals in the extended access group to receive the same number and frequency of food and cocaine rewards in a response-independent manner (yoked rats). To determine the cocaine dose–response curve, the unit dose of cocaine available for self-administration was adjusted upward or downward during 3-h testing sessions every other day between regular 6-h self-administration sessions. When comparing the dose–response curves between restricted and extended access groups, only intake during the first 60 min of the 3 h session was included in statistical analyses[53]. Doses of cocaine were tested once, and in the following order: 0.5, 0.0625, 0.25, 0.125 and 0 mg kg^{-1} per infusion.

Intracerebral injection procedures. For intra-striatal administration of lentivirus vectors, rats were first anaesthetized by inhalation of 1–3% isoflurane in oxygen and positioned in a stereotaxic frame (Kopf Instruments). A total of five viral supernatant injections (1 μl per injection; viral supernatant concentrations ranged from 3.6×10^7 to 4.5×10^9 infectious units (IFU) per ml) were delivered into each side of the striatum, for a total of ten striatal injections per rat. The viruses were directed towards medial and lateral portions of the dorsal striatum. Medial injection sites were according to the following stereotaxic coordinates[54]: anterioposterior (AP), 1.20 mm from Bregma; mediolateral (ML), ± 2.00 mm from midline; dorsoventral (DV), −5.0 and −3.8 mm below dura. Lateral injection sites were according to the following stereotaxic coordinates[54]: AP, 1.20 mm from Bregma; ML, ±3.25 mm from midline; DV, −6.5, −5.5 and −4.5 mm below dura. To deliver the virus, a small hole was drilled through the skull at the ML coordinate, and a stainless steel injector (32 gauge, 14 mm in length) was lowered to the most ventral injection site. The viral supernatant injection was delivered over 60 s. After the infusion, the injector was left in place for a further 60 s. The injector was then raised to the next more dorsal injection site, and the injection procedure repeated. After the final virus supernatant injection, the drill holes in the skull were filled with dental acrylic, the scalp sutured and the incision site treated with antibiotic ointment.

For intrastriatal administration of LNA oligonucleotides, chronic indwelling intracerebral cannula were first implanted above the dorsal striatum. Briefly, rats were anaesthetized by inhalation of 1–3% isoflurane in oxygen and positioned in a stereotaxic frame (Kopf Instruments). Bilateral stainless steel guide cannulae (23 gauge, 12 mm in length) were implanted 2.0 mm above the most dorsal injection site in the dorsal striatum according to the following stereotaxic coordinates[54]: AP, 1.20 mm from bregma; ML, ±3.25 mm from midline; DV, −2.40 mm from dura. Four stainless steel skull screws and dental acrylic held the cannulae in place. Cannulae were kept patent using 12 mm long stainless steel stylets. The oligonucleotides were delivered on two consecutive days. On each day, animals were anaesthetized after their daily cocaine self-administration session, and received a total of three oligonucleotide injections (1 μl per injection; 25 μM concentration) into each side of the dorsal striatum (a total of six striatal injections per rat per day). A stainless steel injector (32 gauge, 16 mm in length) was lowered into the most ventral injection site. The molecule was delivered over 60 s. After the infusion, the injector was left in place for a further 60 s. The injector was then raised 1 mm to the next more dorsal injection site, and the injection procedure repeated. After the final LNA injection, the 12 mm long stylet was re-inserted into the cannula.

Statistical analyses. Cocaine intake data were analysed by one- or two-way repeated-measures analysis of variance (ANOVA). Significant main or interaction effects were followed by Bonferroni or Newman–Keuls post-hoc tests as appropriate. All statistical analyses were performed using Graphpad Prism software. The level of significance was set at 0.05.

RNA isolation from cells. Total RNA was extracted from HEK 293 cells using the RNASTAT60 (Tel-Test Company) kit according to the manufacturer's instructions. The preparation of complementary DNA was by reverse transcription of 500 ng total RNA using Superscript II enzyme and oligo dT primer. The resulting cDNAs were amplified using Taqman kits (System Biosciences) and an ABIPRISM 7700 sequence detector (Perkin Elmer). All mRNA expression data were normalized to GAPDH expression in the corresponding sample.

RNA isolation from tissues. Rats were killed and their brains were rapidly removed and frozen in chilled isopentane previously stored at −80 °C and kept on dry ice. Brains were sliced on a cryostat (HM 505 E, Microm) and kept at −20 °C until each region of interest came into the cutting plane. Bilateral 1 mm^2 punches of the prefrontal cortex, dorsal striatum, nucleus accumbens, hippocampus, ventral tegmental area and cerebellum were collected in Eppendorf tubes on dry ice for RNA isolation. Total RNA for miRNA and mRNA expression analyses was isolated from tissue samples using phenol and chloroform extractions. Approximately 30 mg of tissue was homogenized in 1 ml of RNASTAT60 (Tel-Test Company) using 26 or 27 gauge needles, followed by addition of 250 μl of chloroform and vortexed for 1 min. After centrifugation of the samples for 15 min at 12,000*g* (at 4 °C), the upper aqueous RNA-containing layer was removed for an additional RNASTAT60/chloroform extraction. The RNA was precipitated with two volumes of isopropanol overnight at −200 °C and centrifuged for 30 min at 12,000*g*. The RNA pellets were washed twice with 70% ethanol (made using RNAase-free water) and subsequently re-suspended in RNAsecure (Ambion). Approximately 10 μg of RNA from each sample was treated with Turbo DNase (Ambion) for 60 min at 37 °C to degrade genomic DNA.

miRNA expression profiling and data analysis. Samples of small RNA (≤200 nucleotides) from the isolated RNA samples generated from rat dorsal striatum tissues were obtained by size fractionation on YM-100 ultrafiltration columns (Millipore). The small RNAs were 3′-end labelled with Oyster-550 fluorescent dye using the Flash-Tag kit (Genisphere). The labelled RNA was hybridized overnight to epoxide glass slides double-spotted with the NCode version 2.0 microRNA oligonucleotide probe set (Invitrogen). There was a total of $n = 6$ rats for each access group (extended, restricted and naive). Three microarrays were analysed for each access condition, with each microarray containing pooled RNA from two animals per group. Hence, a total of nine microarrays were analysed, three per cocaine access level. Microarrays were scanned on an Axon Genepix 4000B scanner, and data was extracted from images using GenePix V4.1 software. After scanning and feature extraction, background-subtracted data were log base 2 transformed, then normalized and scaled on the basis of the median rat miRNA probe intensity for each probe. The normalized data (transformed from log to linear) was imported into Agilent GeneSpring GX 7.3. Experiment interoperation mode was set to log of ratio. Only probes with a signal higher than the array median (721) in at least one array were selected for further analysis (141 probes out of 474). Each probe signal was normalized to the median signal value of that probe across all nine arrays. Differentially expressed probes (twofold up- or downregulated, $P < 0.05$) were identified using GX Volcano Plot feature (26 probes). To visualize the results, a heatmap was generated using GX Gene Tree (hierarchical clustering) feature (shown in Fig. 1a). Pearson correlation was used as the similarity measure between probes and the clustering algorithm was set to average linkage.

Gene expression profiling and data analysis. Total RNA was isolated from HEK cells as described earlier. Samples were quantified using the NanoDrop ND-1000 spectrophotometer. Double-stranded cDNA was prepared from 1 μg of total RNA using the Affymetrix cDNA synthesis kit and was then transcribed *in vitro* using an IVT labelling kit (Affymetrix), with the antisense RNA (cRNA) product purified using a GeneChip Sample Cleanup Module (Affymetrix). Biotin-labelled cRNA (20 μg) was fragmented and hybridized to an Affymetrix Rat Genome 230 2.0 microarray overnight in the Affymetrix 640 hybridization oven with a speed of 60 r.p.m. for 16 h. Microarrays were washed and stained using an Affymetrix Fluidics Station FS400. GeneChip arrays were scanned using a GeneChip Scanner 3000 (Affymetrix). The probe set intensities were quantified

using the GeneChip Operating Software and analysed with GeneChip Robust Multichip Average (GC-RMA) normalization using Array Assist Software (Stratagene). All hybridized chips met standard quality control criteria, and mean fluorescence values of each array were scaled to a mean intensity of 500. Only probe sets with intensities greater than 100 were considered reliably detected.

Taqman real-time PCR. Taqman analyses of miRNA expression levels were performed using miRNA assays and other stock primers commercially available from Applied Biosystems (ABI). For all reactions, 1–2 μg of total RNA were reverse transcribed using miRNA-specific primers (ABI), and primers to small nucleolar RNA (snoRNA) as endogenous controls for miRNA (ABI), or GAPDH for *Fos*. The protocol followed the manufacturer's specifications with the exception of using 1.5 μl for each primer in a 15 μl total reaction volume. The cDNA was amplified by real-time PCR using Universal Taqman Mix (with no Amperase Ung) and miRNA-specific primers (ABI) according to the manufacturer's protocol. Comparison between groups was made using the method of $2^{-\Delta\Delta Ct}$.

***In situ* hybridization.** To detect miR212 in frozen rat brain tissue, a 3′ digitonin (DIG)-labelled LNA probe was purchased from Exiqon. Rat brain sections (12–18 μm) were made in the coronal plane that incorporated the dorsal striatum on a cryostat (HM 505 E, Microm) kept at −80 °C. miR-212 expression was detected as previously described[55].

Immunochemistry. Rats were anaesthetized and perfused transcardially with cold 4% paraformaldehyde (PFA) in PBS, pH 7.4. Brains were post-fixed in 4% PFA overnight and stored in 30% sucrose in PBS. Brains were sectioned (30 μm) in the coronal plane that incorporated the dorsal striatum on a cryostat (HM 505 E, Microm) kept at −20 °C. Immunohistochemistry was performed on free-floating sections using the following primary antibodies: anti-copGFP (Axxora); anti-GFAP (Covance); and/or TORC1 (Santa Cruz). Primary antibodies were incubated overnight at 4 °C in 1% bovine serum albumin (BSA) in PBS at 1:1,000 (copGFP), 1:1,000 (GFAP) and 1:50 (DARPP-32) dilutions. This was followed by incubation for 1 h with the following fluorescent-tagged secondary antibodies: Alexa Fluor 488 goat anti-rabbit (Invitrogen) or Alexa Fluor 660 donkey anti-goat IgG (Invitrogen), both at a 1:100 dilution. Sections were mounted on Superfrost Plus slides (Fischer Scientific), dehydrated and coverslipped. Sections were visualized by using a BX61 (Olympus) fluorescence microscope at ×20 and ×40.

Immunoblotting. For protein analyses, brain sections were collected on a frozen cryostat as described earlier and sonicated in RIPA buffer. Protein content was determined using the Bio-Rad DC Protein Assay kit, and the concentration of each sample was adjusted to 2 mg ml^{-1} protein or 4–6 mg ml^{-1} for less abundant proteins. Protein samples were separated by gel electrophoresis and proteins transferred to Nitrocellulose (NC membrane, Invitrogen iBlot system). HiMark high molecular weight pre-stained standards (BIO-RAD) were also run on each gel. Nonspecific binding sites on the membranes were blocked by 5% nonfat dry milk in TBS and 0.1% Tween 20 (TBS-T). Blots were incubated in primary antibody in PBS-T, washed and then incubated in secondary antibody. Blots were washed and immunological detection was carried out using SuperSignal Chemiluminescent Substrate (Thermo Scientific). Antibodies were stripped from the blots, and the blots probed for anti-β-actin or GAPDH (Sigma or Cell Signaling). Primary antibodies used were: anti-CREB (Millipore); S133-p-CREB (Santa Cruz or Millipore); Fos (Santa Cruz); Nurr1 (NR4A) (Santa Cruz); TORC1 (Cell Signaling); p-TORC1 (Cell Signaling); acetylated lysine (Cell Signaling); p-Raf1 (Cell Signaling); Raf1 (Santa Cruz); SPRED1 (Santa Cruz); ERK (Cell Signaling); and p-ERK (Santa Cruz). Antiserum against TORC2 was generated using peptide [H]-CAETDKTLSKQSWDSKKAG-[NH_2] at Covance as previously described[56]. Secondary antibodies used were: Amersham ECL anti-rabbit IgG and horseradish-peroxidise-linked species-specific whole antibody from donkey (GE Healthcare).

Clones, miRNA precursors and lentiviral constructs. The Raf1–GFP and dominant-negative Raf151-220–GFP constructs were obtained from T. Balla[57]. The SPRED1 vector expressing only the coding sequence was purchased from OriGene Technologies (Rockville; catalogue number SC101247). The pMIF–copGFP and expression vectors for immature miRNAs (rat in each case) were purchased from System Biosciences, and are feline immunodeficiency virus lentiviral vectors that contain the miRNA precursor and a copGFP reporter under the control of a cytomegalovirus (CMV) promoter. TORC1 was cloned into the pCDF1 lentiviral expression vector from System Biosciences. The pCDF1 vector is a feline immunodeficiency virus that contains the cloned TORC1 gene under the control of a CMV promoter and a copGFP reporter under the control of an EF1 promoter. Correct insertion of the TORC1 gene was verified in functional assays (potentiation of CREB signalling) and by western blotting.

Generation of lentivirus. To generate lentivirus supernatant, HEK-293FT packaging cells (3.75×10^6 293TN cells per 10 cm plate) were transfected with the vectors (pMIF or pCDF1, respectively), along with the pPACKF1TM Lentiviral Packaging Kit using lipofectamine reagent and plus reagent (Invitrogen) according to the manufacturer's instructions. Medium containing virus particles (~10 ml) was harvested 48–60 h post-transfection by centrifugation at 76,755*g* at room temperature for 5 min to pellet cell debris and filtered through 0.45 mm PVDF filters (Millex-HV). To concentrate the viral supernatant for intrastriatal administration, supernatants were centrifuged at 32,000*g* for 90 min at 4 °C, and the precipitate re-suspended in 100 μl cold PBS. Supernatants were aliquoted into 10 ml volumes and stored at −80 °C until use.

Estimation of lentivirus titer. Viral supernatant titres were determined using the Lentivector Rapid Titer Kit from System Biosciences, according to the manufacturer's instructions. The number of infectious units per ml of supernatant (IFU ml^{-1}) was calculated as follows: Multiplicity of infection (MOI) of the sample × the number of cells in the well upon infection × 1,000 / μl of viral supernatant used.

Oligonucleotides and short hairpin RNAs. The SPRED1 short interfering RNA (siRNA) was purchased from Invitrogen. The LNA-anti-miR molecules were purchased from Exiqon. The short hairpin RNA (shRNA) targeting TORC2 (GGTCTCTGCCCAATGTTAACCA) was created by subcloning annealed oligonucleotides into the pBS/U65 expression vectors[58] as previously described[59].

3′ UTR Analyses. Bioinformatic identification of 3′ UTR MREs was carried out using TargetScan 5.1. The HMGA2 3′ UTR renilla luciferase reporter construct (Addgene) has been previously described[60]. To assess the effects of miRNA overexpression on HMGA2 3′ UTR luciferase expression, HEK-293 cells, (3×10^5 cells per well) were co-transfected with the immature miRNA constructs or the empty control vector (pMIF) (500 ng), the HMGA2 3′ UTR renilla luciferase reporter construct (100 ng), the Rous sarcoma virus β-galactosidase (RSV-β-galactosidase) control vector (50 ng), and where indicated with LNA-anti-miR-212 or LNA-Scrambled (40 nM) in lipofectamine according to the manufacturer's instructions, as described[60,61]. Renilla luciferase assays were performed (Renilla Luciferase Assay System, Promega) and normalized to β-galactosidase activity.

CREB reporter assays. CRE-containing luciferase reporter plasmids were used as described previously[59]. To assess the effects of miRNA overexpression on CREB signalling, HEK-293 cells (3×10^5 cells per well in 96-well plates) were reverse transfected with the EVX1 CRE-containing luciferase reporter plasmid (80 ng), the pre-miR-212, pre-miR-1, pre-miR-132 or pre-miR-29b expression vector (40 ng), and RSV-β-galactosidase expression plasmid such that the total amount of transfected DNA was held constant at 150 ng per well. Twenty-four to forty-eight hours post-transfection, cells were treated for 30 min or 4 h with 5, 10 or 15 μM forskolin or vehicle (0.75% dimethylsuphoxide (DMSO)) as indicated. The cells were then lysed and assayed for luciferase activity using the Bright Glo luciferase assay system (Promega) as described previously[59], normalizing to activity from co-transfected RSV-β-galactosidase expression plasmid.

cAMP assay. cAMP accumulation was measured using a competitive immunoassay (BioVision). Briefly, HEK-293 cells were transiently transfected with the miR-212 or control pMIF expression vectors (2.5 μg). Forty-eight hours after transfection cells were treated with 10 μM forskolin or vehicle (0.1% DMSO) for 30 or 240 min, and the cell lysed in 0.1 N HCl. Levels of cAMP were then assayed according to the manufacturer's instructions.

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