

SUPPLEMENTARY INFORMATION

FMRP regulates miR196a-mediated repression of HOXB8 via interaction with AGO2 MID domain

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Supplementary Figures S1-2

Supplementary Table S1-2

Supplementary Figures

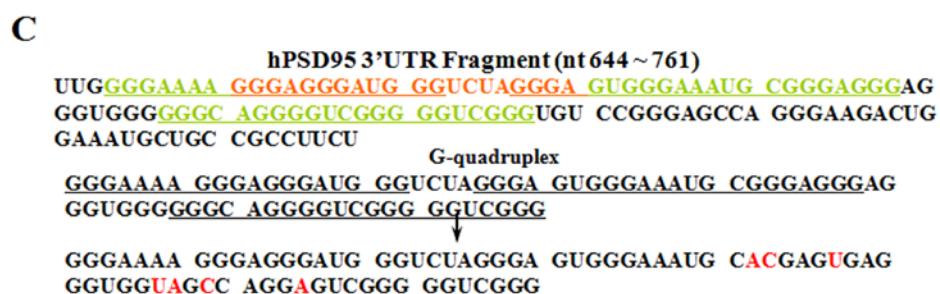
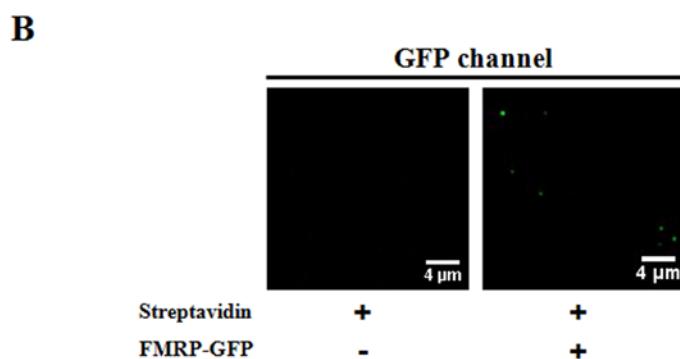
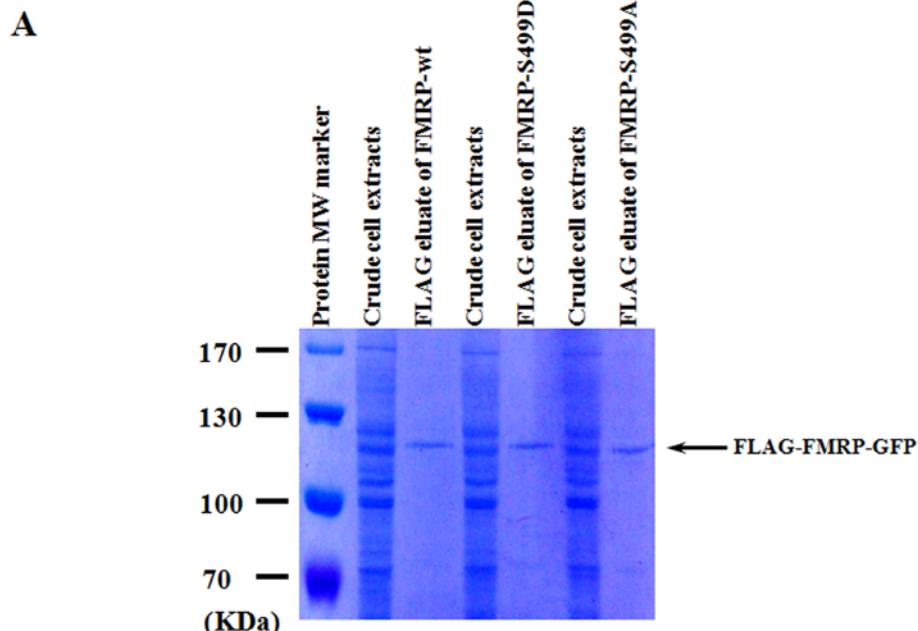


Fig. S1 (A) Commassie Blue Staining analysis of crude cell extracts and purified recombinant wild-type FMRP-GFP, phospho-FMRP mutant (S499D), and unphospho-FMRP mutant (S499A). Protein molecular-weight marker sizes are shown on the left. Purified protein is labeled with an arrow on the right. (B) Single-molecule images. The first one was from a clean surface with streptavidin conjugation. The second one was from a streptavidin-conjugated surface treated with FMRP-GFP expressed cell extracts. Few fluorescent debris molecules were visible. (C) Sequence of human PSD95 3'UTR fragment (nucleotide 644–761) and mutagenesis of the putative G-quadruplexes. The miRNA recognition sites are colored in orange. Red characters represent the introduced substitutions.

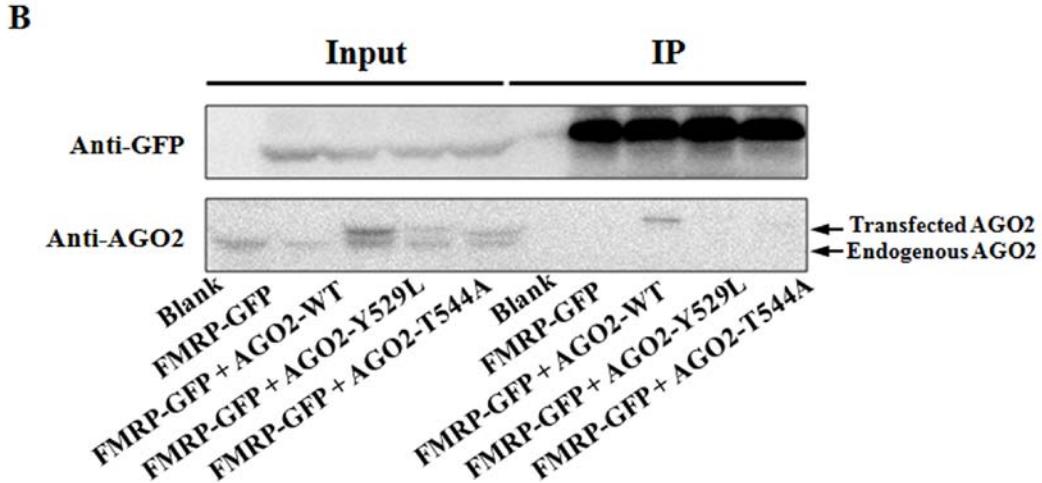
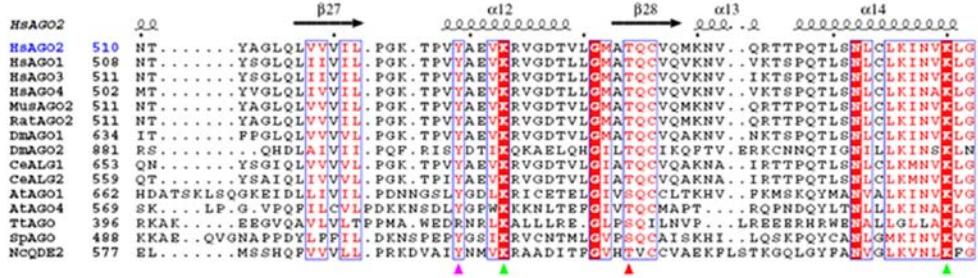
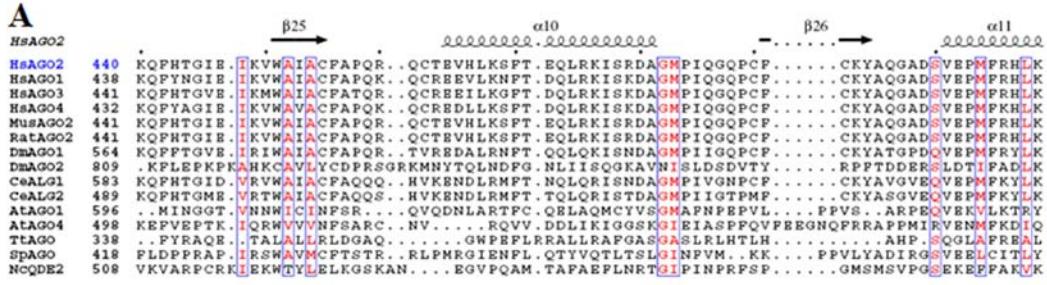


Fig. S2 (A) Structure-based sequence alignment of the hsAGO2 MID domain (Top) with eukaryotic MID domains as well as eubacterial homologues (Tt) involved in the miRNA pathway. The invariant positions are highlighted in red, and the highly conserved positions are colored in red. Two invariant Lys residues (K533 and K570 in hsAGO2) shared by the two sulphate-binding pockets are marked by green triangles. Conserved Tyr residues (Y529 in hsAGO2) involved in the coordination of first pocket for miRNA binding is marked by pink triangle. The invariant threonine or serine (T544 of hsAGO2) involved in the coordination of second pocket is marked by red triangle. AGO, Argonaute; At, *Arabidopsis thaliana*; Ce, *Caenorhabditis elegans*; Dm, *Drosophila melanogaster*; Hs, *Homo sapiens*; Mus, *Mus musculus*; Nc, *Neurospora crassa*; QDE-2, quelling-defective2; Rat, *Rattus norvegicus*; Sp, *Schizosaccharomyces pombe*; Tt, *Thermus thermophilus*. (B) Co-immunoprecipitation of FMRP with AGO2. Non-transfected HEK29T cells (Blank) and the indicated transfected cells were subjected to immunoprecipitation (IP) with anti-GFP followed by immunoblotting with antibodies as shown.

Table S1 oligonucleotides.**Synthetic RNA oligos:**

Biotin-miR196a: 5'P-UAGGUAGUUCAUGUUGUUGGG-3' Biotin

Random RNA: UUCAAGUAAGUAAUCCAGAUAGCUGUAUGACCAGAGUACCG

miRNA and 3'UTR cloning

Has-miR-196a	F: GAGCTCGAG CCAGATGCAGGGGAATAGCTC R: GAGGGTACC TTGGAATTGGCTGGACCCCTC
Full-length 3'UTR of PSD95	F: GAGGCGATCGC CCTACATCTGGGTTCCAGCC R: GCGACGCGT TCTGTCTCTCCTTCACCTCTC
Full-length 3'UTR of HOXB8	F: GAGGCGATCGC CGCTTCAGCTGGACTGC R: GCGACGCGT TCGGGTTCTCGCTTGTAAAC
G-quadruplex in PSD95	F: GAGGGTACC TTGGGGAAAAGGGAGGGATG R: GAGCTCGAG AGAAGGCGGCAGCATTTC
U-rich Fragment in HOXB8	F: GAGGGTACC CAATTGTCTTTTTCTTGAACG R: GAGCTCGAG GAGACAGAAAGAATTACGGCG

In vitro Transcription

G-quadruplex	F: CGCCAGGGTTTCCCAGTCACGAC R: TACCGTCGACCTCGAGAGAAGGCCAGCATTTTC
U-rich Fragment	F: CGCCAGGGTTTCCCAGTCACGAC R: TACCGTCGACCTCGAGGAGACAGAAAGAATTAC

Mutagenesis

ΔU I	F: AGCCTCTTGTGCAATTGTCGTGCGCTTGAAACGTGCTTCTTG R: CAAAGAACGACGTTCAAAGGCACGACACGACAATTGCACAAGGAGGCT
ΔU II	F: TTTCCTTGAACGTGCTTCGTAGTAATGACCAAGGTACCG R: CGGTACCTTGGTCATTACTACGAAGCACGTTCAAAGGAAA
ΔU III	F: GACCAAGGTACCGATACTGCTAAGCTCTCCAACAACATG R: CATGTTGTTGGGAGAGCTTAGCAGCTATCGTGTACCTTGGTC
ΔU IV (Luc report)	F: ACTGCCTATTACGCCGTAATGCTAGCTGTCTCCCTCTCTC R: GAGAGAGAAGGGAGACAGCTAGCATTACGGCGTGAATAGGCAGT
ΔU IV (In vitro transcription)	F: ACTGCCTATTACGCCGTAATGCTAGCTGTCTCCCTGAGGTGAC R: GTGACCTCGAGGAGACAGCTAGCATTACGGCGTGAATAGGCAGT
ΔG	F: GAGTGGAAATGCACGAGTGAGGGTGGTAGCCAGGAGTCGGGGTCGG R: CCGACCCCCGACTCCTGGCTACCACCCCTACTCGTGCATTCCCAC
AGO2-Y529L	F: CGGCAAGACGCCGTGTTGGCCGAGGTC R: GACCTCGGCCAACACGGCGCTTGCG
AGO2-T544A	F: CTGGGGATGGCCGCGCAGTGCCTG R: GCACGCACTGCGCGGCCATCCCCAG

qPCR

Firefly Luc	F: GACCGGCTGAAGAGCCTGATC R: TTGCAGCAGGATGCTCTCCAG
β-Actin	F: AGAGCTATGAGCTGCCTGAC R: TACGGATGTCAACGTCACAC

Table S2 Putative FMRP recognition sites in the downstream neighborhood of MRE in the reported neural targets of FMRP-associated miRNA.

miRNAs	Target in neurons	Function	Cell or Tissue	Potential FMRP binding sites in 3'UTR of target mRNA	Sp.	Ref.
miR-9	Foxp1	Modify motor neuron columnar organization in the spinal cord	Spinal cord from chick embryos; Neuro2A	AAUUUAUAUUCUUUGUACCUUUUUUCUAA AAUUACCAAAGAUAAUACACAAAGGUAAU UAUGUUCUCUGUUUUUAUGCUUUAUCUGA AUUUAGAAGACCAGUAGGUAAUGGAACCA AAGUUGUUACUUUUUCUAGUAGUUUU UUCCUUUUUCUUUUUGUGUA	gga	¹
miR-9	Foxp2	Relate to Neurite outgrowth and their radial migration in embryonic mouse neocortex	Mouse embryonic neocortex	AGCCAUGGUAUUAAAUCAGUCAAACCA AAGUACAUAAUAAUUCGCCUCUGCUUUA CGGGAUUAGAACACACACUCCCUCA AAGACUUGUGCAG	mmu	²
miR-9	Her6	Control timing of commitment and cell-cycle exit within progenitor populations during neurogenesis	Zebrafish embryos	GGUAUCUUUUCCACGUUGUGAUGCCAAAGA UAUGUUGAAUGCGCUUCAAGUUUCUUCUU UUUGGAAGACAAAUAUAGACAUUUGAAA UGAAAAAA	dre	³
miR-9	Zic5	Control timing of commitment and cell-cycle exit within progenitor populations during neurogenesis	Zebrafish embryos	UUAUUAUUGUUGGUUCUGGAAGUACAGAUA CACCAAAGAAUAAUAAUAAUUUGGUGAAA AGAAUGUAUUGCUUUAUCGUGUUCUGUA AAAAAGGUCUUACUUG	dre	³
miR-9	Hes1	Regulate the proliferation and differentiation of neural stem cells in the developing brain	Mouse Embryos; HEK293T	UUUUUACACGAGAUUUCUUUUUUUAUGU GAUGCCAAAGAUGUUGAAAAUGCUCUUA AAAUAUCUUCUUCGGGAAGUUUAUUG AGAAUUAUAAA	rno	⁴
miR-124	BACE1	Alleviate cell death in the process of AD by targeting BACE1	PC12; Hippocampal neurons	UGGAUCACCCAAGGUCACCAAACAACUU GGUUGUGAACCAACUGCCUUAACCUUCUUG GGAGGGAUUAUGGGAAAGGUGAG AGAAUGAAUUGGGAAAGGUGAG	hsa	⁵
miR-124	Zif-268 (EGR1)	Regulate spatial learning and social interaction	Mouse hippocampus and cortex; HEK293	AAUUUUUGCCGUCCUUUGGUUUCAAA AGUUUCACGCUUUGGUUGCCUUUGUUGAC ACGCCUUGCCGAUGGGCUGAUGCAUGCGCAGA UGUGAGGGACAC	mmu	⁶
miR-124	Sox9	Regulate the timing of neuronal differentiation along the SVZ stem cell lineage	Mouse SVZ; HeLa	CUUGGAUUCAAGAGUAGCUGCCUAAAAG AAAGAAAGAAAAAAGAAAGAAAGGAAGGA AGGAAGGAAGGAAGGAAGAGAGAGAGA AAGCCUUCUUUUGC	mmu	⁷
miR-124	Dlx2	Involve in interneuron formation	Mouse SVZ; HeLa	UUUUUUUUUUUUUUUUUUUUUUUUUU UGCCUUUGCGGAUGACCUCAUUCUGAU AAAAAAAAACUGAUUUUUUUAAAUGUGG ACGCUGCAAAAAA	mmu	⁷
miR-124	CREB1	Constrain serotonin-induced synaptic facilitation	Aplysia pleural ganglia; HEK293	AAUGGUGGGGAACUUUCAGGGCAUGUUU GCGUGUCUUAUCCCCUCCUGCACUACAU GCCACUCUGGGUUGUGGGACACCGUGUUC UGAUGUGUGUG AUGAUUUCAAGGUUGUGCUGAGCUCCUUG AUUGCUCUAGGGACAGAAUUACCCCAGCCU CUUGAGCUGAAGUAUUGUGUGGGCCGCAUG CAUAAAGUAAGU	apc hsa	⁸

miR-124	SCP1 (CTDSP1)	Induce neurogenesis	P19; HEK293	UUCAUUUUUAGGUGCCUCUAAACCCCAGAU GUCACGUGC CUUCA GAGAU AUC AAC AGGG GUGGA ACCUUCUUGUGGG UUA GGG A GUC UCCAAACC UUA AC	mmu	⁹
miR-124	wit	Retrograde BMP signaling pathway, whose activation in neurons increases synaptic release at the NMJ	S2-R+	UAUCUAGUAUACCCCCUU UGGAUGAAUUU UCGGUGAAUGCCUUU UAGUCGUUCUCUUUA GUACUUAGACAAAACACCCACAGCC <u>UUUC</u> AAUCACAUAAA AU	dme	¹⁰
miR-124	Med	Retrograde BMP signaling pathway, whose activation in neurons increases synaptic release at the NMJ	S2-R+	GGAUUUUGUGUUUUUCAUUUGCAAU <u>CUG</u> AUUA C G A U U A U G U U U G C C U U U G A U U A U U GAUAAA <u>AUU</u> UUUA AAAA AAUUGA AACA ACUUAGAAGUCUUAAG	dme	¹⁰
miR-124	Mad	Retrograde BMP signaling pathway, whose activation in neurons increases synaptic release at the NMJ	S2-R+	AUCUUUUGUUAUCUUAAGUAAAACUAAUA UUGUU UAGACCACGAGAAA UGCUU UU AUAAAUAUACAU <u>GUUAUA</u> ACUU <u>UACU</u> UA GUUAUCGUAGCUU AUGA UUUCUCUGAUU UUGUU UUGA AUUA	dme	¹⁰
miR-125b	NR2A (GRIN2A)	Affect dendritic spine morphology	Rat Hippocampal neurons	AUGUACGUAGUUUGCAUU UCCUCCCUUCU GGUGAUGACUCAGGGU UGUUAAGUAUCUG UUACCCUUCCCUCCAGAGUAACCAUAAC UCGUUCGUUUC	rno	¹¹
miR-125b	Nestin (NES)	Orchestrates cell proliferation, differentiation and migration in neural stem/progenitor cells	Neural progenitors	GAAAAGACCAUCUG CCC GG CAC UGGGGACU UAGGGGUGCGGGAGGGAAAGGA CGCCUC CAAGCCCGCUCCCUGCUC AGGA GCAGCACU CUUA <u>ACU</u> ACGA	hsa	¹²
miR-125b	SMO	Withdraw Hedgehog activity during cerebellar neuronal progenitor differentiation	Daoy cells	CACCCCAGG GACAGGGCCCUGGAGCUCAGG GUCCUUGUUUCUGCCCUGCCAGCUGCAGCC UGGUUGGCAGCAUCUGCUCCAUCG	hsa	¹³
miR-128	PDGFRA	Repress gliNSC self-renewal and enhance differentiation	giNSCs; HEK293	CCUUUGUUUAU UUUUUUUUUACUGUGAU AUUCCCCACAGGCACGUUA <u>ACUGUUGCACU</u> <u>UUUGA</u> AUGUCCAA <u>AAUU</u> UUAU <u>UUU</u> AGAA	mmu	¹⁴
miR-128	Reelin (RELN)	Modulating neuroblastoma progression and aggressiveness	SH-SY5Y; HEK293	AACAGA GUGA UUUGUAAAACAGU GGUUGU UUUUUCAUUGUGU UUUCUUCGGUGGA <u>UUGU</u> UUUUUCUGCGGGUCA <u>AAUUCAUACCUCUG</u> AUGAAGUUGUACAA AGCCCUUCUCAAGACCGAGGUGUACACCACU UCCCCACACUGUGAACU AAUGACAAGUGAC UUAUUUGCUCAUAAGUA <u>AAUG</u> UCUCAUGU UGA UGUGUCCGU	has	¹⁵
		Regulate neural plasticity	Mouse cortical neurons; HEK293T	AGAAAGCCUUCGAGA <u>ACU</u> UUGUG UACCCC CCU UCCACACUGUGAGCU <u>AAUG</u> AUGUGUG GU UUCUCUGCACAUAGUA <u>AAUG</u> UCUUCAC GUCAGUGCGUCC	mmu	¹⁶
miR-128	DCX	Modulating Neuroblastoma progression and aggressiveness	SH-SY5Y; HEK293	UGCCUUGUUACAG CCAACACUGAAAACAC UGUGAGAAU UGUUUUCAGGUUCUGACACCU UUCAGUCU UUUUUA <u>UAGCAAGAAUCAAU</u> AUCCUUUUUAUAA	hsa	¹⁵
miR-128	NTRK3	Regulate cytoskeleton organization	SH-SY5Y; HeLa	AUCCACC ACUG GCAGGGUUGCCCU UCCU CCAAUCAUCACUGUGC UCCUUUUUCCGG CCUACGAGGCAGCUCCUGGCCACAU <u>U</u> CUUA GAGCCA <u>AA</u> AAAG	hsa	¹⁷
miR-128	Sp1	Regulate neural plasticity	Mouse cortical neurons;	AGCCCAGAA <u>ACAAAAAGA</u> AAUCUUGUCUAC CACUGUGGAUUAUAGGA GAACUGGGAGA AAUUA <u>CCUGCUU</u> UCUCAUGGCCUGAUUC	mmu	¹⁶

			HEK293T	CAGAAGAGACUGAU		
miR-128	Ppp1cc	Regulate neural plasticity	Mouse cortical neurons; HEK293T	<u>AAU</u> GUCAUAAAUGCAUUC <u>GUUGAUACAA</u> <u>ACCACUGUGA</u> ACAA <u>UU</u> UUUU <u>CCAGUUUG</u> <u>UUUGAAAGGG</u> A <u>CUGC</u> UU <u>CCC</u> CUAU <u>UGUC</u> <u>UGUCAU</u> GUACAAA	mmu	¹⁶
miR-132	p250GAP	Regulate neuronal morphogenesis and dendritic growth	PC12; Rat cortical neurons; Rat hippocampal neurons	GCCCUGCGAGCAAUAGAG <u>UUGA</u> AGCAG <u>CU</u> <u>CUGC</u> UGGACAGUGGAC <u>GUU</u> CUAUUUUU CAAUAACCAAAAAGAUUAACAAAAAAU	hsa	^{18, 19}
miR-219	PLK2	Relate to synaptic dysfunction implicated in ASD	Human lymphoblastoid cell lines	AGGCUAAGGCAUACA <u>GUUC</u> UUGACUUUGGA <u>CAAU</u> CCAAGA <u>GUGA</u> ACCAG <u>AAUG</u> CAGUUUU <u>CCUUGA</u> GAUACC <u>GUUU</u> AAAAGGUUUUC AGAC <u>AAU</u> UUGC	hsa	²⁰

The experimentally validated miRNA recognition sites (MREs) are highlighted in yellow, and the predicted but unvalidated MREs are highlighted in grey. Three putative modes for FMRP to recognize the MRE are displayed distinctively. The first oligo(U) elements are underlined. The potential G-quartet is shown in box. The frequent RNA-recognition elements of FMRP discovered in recent reports are colored in cyan. apc: Aplysia californica; dme: Drosophila melanogaster; dre: Danio rerio; gga: Gallus gallus; hsa: Homo sapiens; mmu: Mus musculus; rno: Rattus norvegicus; xla: Xenopus laevis.

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